

(19) World Intellectual Property
Organization
International Bureau



(43) International Publication Date
15 April 2004 (15.04.2004)

PCT

(10) International Publication Number
WO 2004/030615 A2

(51) International Patent Classification⁷: **A61K**

(21) International Application Number:
PCT/US2003/028547

(22) International Filing Date:
29 September 2003 (29.09.2003)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/414,971 2 October 2002 (02.10.2002) US

(71) Applicant (*for all designated States except US*): **GENENTECH, INC.** [US/US]; 1 DNA Way, South San Francisco, CA 94080-4990 (US).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): **WU, Thomas, D.** [US/US]; 41 Nevada Street, San Francisco, CA 94110 (US). **ZHANG, Zemin** [US/US]; 876 Taurus Drive, Foster City, CA 94404 (US). **ZHOU, Yan** [CN/US]; #111, 525 N Curtis Avenue, Alhambra, CA 91801 (US).

(74) Agents: **KRESNAK, Mark T.** et al.; c/o Genentech, Inc., MS49, 1 DNA Way, South San Francisco, CA 94080-4990 (US).

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF TUMOR

(57) Abstract: The present invention is directed to compositions of matter useful for the diagnosis and treatment of tumor in mammals and to methods of using those compositions of matter for the same.



WO 2004/030615 A2

COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF TUMOR

FIELD OF THE INVENTION

The present invention is directed to compositions of matter useful for the diagnosis and treatment of tumor in mammals and to methods of using those compositions of matter for the same.

BACKGROUND OF THE INVENTION

Malignant tumors (cancers) are the second leading cause of death in the United States, after heart disease (Boring et al., *CA Cancer J. Clin.* 43:7 (1993)). Cancer is characterized by the increase in the number of abnormal, or neoplastic, cells derived from a normal tissue which proliferate to form a tumor mass, the invasion of adjacent tissues by these neoplastic tumor cells, and the generation of malignant cells which eventually spread via the blood or lymphatic system to regional lymph nodes and to distant sites via a process called metastasis. In a cancerous state, a cell proliferates under conditions in which normal cells would not grow. Cancer manifests itself in a wide variety of forms, characterized by different degrees of invasiveness and aggressiveness.

In attempts to discover effective cellular targets for cancer diagnosis and therapy, researchers have sought to identify transmembrane or otherwise membrane-associated polypeptides that are specifically expressed on the surface of one or more particular type(s) of cancer cell as compared to on one or more normal non-cancerous cell(s). Often, such membrane-associated polypeptides are more abundantly expressed on the surface of the cancer cells as compared to on the surface of the non-cancerous cells. The identification of such tumor-associated cell surface antigen polypeptides has given rise to the ability to specifically target cancer cells for destruction via antibody-based therapies. In this regard, it is noted that antibody-based therapy has proved very effective in the treatment of certain cancers. For example, HERCEPTIN® and RITUXAN® (both from Genentech Inc., South San Francisco, California) are antibodies that have been used successfully to treat breast cancer and non-Hodgkin's lymphoma, respectively. More specifically, HERCEPTIN® is a recombinant DNA-derived humanized monoclonal antibody that selectively binds to the extracellular domain of the human epidermal growth factor receptor 2 (HER2) proto-oncogene. HER2 protein overexpression is observed in 25-30% of primary breast cancers. RITUXAN® is a genetically engineered chimeric murine/human monoclonal antibody directed against the CD20 antigen found on the surface of normal and malignant B lymphocytes. Both these antibodies are recombinantly produced in CHO cells.

In other attempts to discover effective cellular targets for cancer diagnosis and therapy, researchers have sought to identify (1) non-membrane-associated polypeptides that are specifically produced by one or more particular type(s) of cancer cell(s) as compared to by one or more particular type(s) of non-cancerous normal cell(s), (2) polypeptides that are produced by cancer cells at an expression level that is significantly higher than that of one or more normal non-cancerous cell(s), or (3) polypeptides whose expression is specifically limited

to only a single (or very limited number of different) tissue type(s) in both the cancerous and non-cancerous state (e.g., normal prostate and prostate tumor tissue). Such polypeptides may remain intracellularly located or may be secreted by the cancer cell. Moreover, such polypeptides may be expressed not by the cancer cell itself, but rather by cells which produce and/or secrete polypeptides having a potentiating or growth-enhancing effect on cancer cells. Such secreted polypeptides are often proteins that provide cancer cells with a growth advantage over normal cells and include such things as, for example, angiogenic factors, cellular adhesion factors, growth factors, and the like. Identification of antagonists of such non-membrane associated polypeptides would be expected to serve as effective therapeutic agents for the treatment of such cancers. Furthermore, identification of the expression pattern of such polypeptides would be useful for the diagnosis of particular cancers in mammals.

Despite the above identified advances in mammalian cancer therapy, there is a great need for additional diagnostic and therapeutic agents capable of detecting the presence of tumor in a mammal and for effectively inhibiting neoplastic cell growth, respectively. Accordingly, it is an objective of the present invention to identify: (1) cell membrane-associated polypeptides that are more abundantly expressed on one or more type(s) of cancer cell(s) as compared to on normal cells or on other different cancer cells, (2) non-membrane-associated polypeptides that are specifically produced by one or more particular type(s) of cancer cell(s) (or by other cells that produce polypeptides having a potentiating effect on the growth of cancer cells) as compared to by one or more particular type(s) of non-cancerous normal cell(s), (3) non-membrane-associated polypeptides that are produced by cancer cells at an expression level that is significantly higher than that of one or more normal non-cancerous cell(s), or (4) polypeptides whose expression is specifically limited to only a single (or very limited number of different) tissue type(s) in both a cancerous and non-cancerous state (e.g., normal prostate and prostate tumor tissue), and to use those polypeptides, and their encoding nucleic acids, to produce compositions of matter useful in the therapeutic treatment and diagnostic detection of cancer in mammals. It is also an objective of the present invention to identify cell membrane-associated, secreted or intracellular polypeptides whose expression is limited to a single or very limited number of tissues, and to use those polypeptides, and their encoding nucleic acids, to produce compositions of matter useful in the therapeutic treatment and diagnostic detection of cancer in mammals.

SUMMARY OF THE INVENTION

A. Embodiments

In the present specification, Applicants describe for the first time the identification of various cellular polypeptides (and their encoding nucleic acids or fragments thereof) which are expressed to a greater degree on the surface of or by one or more types of cancer cell(s) as compared to on the surface of or by one or more types of normal non-cancer cells. Alternatively, such polypeptides are expressed by cells which produce and/or secrete polypeptides having a potentiating or growth-enhancing effect on cancer cells. Again alternatively, such polypeptides may not be overexpressed by tumor cells as compared to normal cells of the same tissue type, but rather may be specifically expressed by both tumor cells and normal cells of only a single or very limited

number of tissue types (preferably tissues which are not essential for life, e.g., prostate, etc.). All of the above polypeptides are herein referred to as Tumor-associated Antigenic Target polypeptides ("TAT" polypeptides) and are expected to serve as effective targets for cancer therapy and diagnosis in mammals.

Accordingly, in one embodiment of the present invention, the invention provides an isolated nucleic acid molecule having a nucleotide sequence that encodes a tumor-associated antigenic target polypeptide or fragment thereof (a "TAT" polypeptide).

In certain aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% nucleic acid sequence identity, to (a) a DNA molecule encoding a full-length TAT polypeptide having an amino acid sequence as disclosed herein, a TAT polypeptide amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane TAT polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length TAT polypeptide amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In other aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% nucleic acid sequence identity, to (a) a DNA molecule comprising the coding sequence of a full-length TAT polypeptide cDNA as disclosed herein, the coding sequence of a TAT polypeptide lacking the signal peptide as disclosed herein, the coding sequence of an extracellular domain of a transmembrane TAT polypeptide, with or without the signal peptide, as disclosed herein or the coding sequence of any other specifically defined fragment of the full-length TAT polypeptide amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In further aspects, the invention concerns an isolated nucleic acid molecule comprising a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% nucleic acid sequence identity, to (a) a DNA molecule that encodes the same mature polypeptide encoded by the full-length coding region of any of the human protein cDNAs deposited with the ATCC as disclosed herein, or (b) the complement of the DNA molecule of (a).

Another aspect of the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding a TAT polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated, or is complementary to such encoding nucleotide sequence, wherein the transmembrane domain(s) of such polypeptide(s) are disclosed herein. Therefore, soluble extracellular domains of the herein described TAT polypeptides are contemplated.

In other aspects, the present invention is directed to isolated nucleic acid molecules which hybridize to (a) a nucleotide sequence encoding a TAT polypeptide having a full-length amino acid sequence as disclosed herein, a TAT polypeptide amino acid sequence lacking the signal peptide as disclosed herein, an extracellular

domain of a transmembrane TAT polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length TAT polypeptide amino acid sequence as disclosed herein, or (b) the complement of the nucleotide sequence of (a). In this regard, an embodiment of the present invention is directed to fragments of a full-length TAT polypeptide coding sequence, or the complement thereof, as disclosed herein, that may find use as, for example, hybridization probes useful as, for example, diagnostic probes, antisense oligonucleotide probes, or for encoding fragments of a full-length TAT polypeptide that may optionally encode a polypeptide comprising a binding site for an anti-TAT polypeptide antibody, a TAT binding oligopeptide or other small organic molecule that binds to a TAT polypeptide. Such nucleic acid fragments are usually at least about 5 nucleotides in length, alternatively at least about 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800, 810, 820, 830, 840, 850, 860, 870, 880, 890, 900, 910, 920, 930, 940, 950, 960, 970, 980, 990, or 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length. It is noted that novel fragments of a TAT polypeptide-encoding nucleotide sequence may be determined in a routine manner by aligning the TAT polypeptide-encoding nucleotide sequence with other known nucleotide sequences using any of a number of well known sequence alignment programs and determining which TAT polypeptide-encoding nucleotide sequence fragment(s) are novel. All of such novel fragments of TAT polypeptide-encoding nucleotide sequences are contemplated herein. Also contemplated are the TAT polypeptide fragments encoded by these nucleotide molecule fragments, preferably those TAT polypeptide fragments that comprise a binding site for an anti-TAT antibody, a TAT binding oligopeptide or other small organic molecule that binds to a TAT polypeptide.

In another embodiment, the invention provides isolated TAT polypeptides encoded by any of the isolated nucleic acid sequences hereinabove identified.

In a certain aspect, the invention concerns an isolated TAT polypeptide, comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity, to a TAT polypeptide having a full-length amino acid sequence as disclosed herein, a TAT polypeptide amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane TAT polypeptide protein, with or without the signal peptide, as disclosed herein, an amino acid sequence encoded by any of the nucleic acid sequences disclosed herein or any other specifically defined fragment of a full-length TAT polypeptide amino acid sequence as disclosed herein.

In a further aspect, the invention concerns an isolated TAT polypeptide comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% amino acid

sequence identity, to an amino acid sequence encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein.

In a specific aspect, the invention provides an isolated TAT polypeptide without the N-terminal signal sequence and/or without the initiating methionine and is encoded by a nucleotide sequence that encodes such an amino acid sequence as hereinbefore described. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the TAT polypeptide and recovering the TAT polypeptide from the cell culture.

Another aspect of the invention provides an isolated TAT polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the TAT polypeptide and recovering the TAT polypeptide from the cell culture.

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described polypeptides. Host cells comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli* cells, or yeast cells. A process for producing any of the herein described polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired polypeptide and recovering the desired polypeptide from the cell culture.

In other embodiments, the invention provides isolated chimeric polypeptides comprising any of the herein described TAT polypeptides fused to a heterologous (non-TAT) polypeptide. Example of such chimeric molecules comprise any of the herein described TAT polypeptides fused to a heterologous polypeptide such as, for example, an epitope tag sequence or a Fc region of an immunoglobulin.

In another embodiment, the invention provides an antibody which binds, preferably specifically, to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, antibody fragment, chimeric antibody, humanized antibody, single-chain antibody or antibody that competitively inhibits the binding of an anti-TAT polypeptide antibody to its respective antigenic epitope. Antibodies of the present invention may optionally be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The antibodies of the present invention may optionally be produced in CHO cells or bacterial cells and preferably induce death of a cell to which they bind. For diagnostic purposes, the antibodies of the present invention may be detectably labeled, attached to a solid support, or the like.

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described antibodies. Host cell comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli* cells, or yeast cells. A process for producing any of the herein described antibodies is further provided and comprises culturing host cells under conditions suitable for expression of the desired antibody and recovering the desired antibody from the cell culture.

In another embodiment, the invention provides oligopeptides ("TAT binding oligopeptides") which

bind, preferably specifically, to any of the above or below described TAT polypeptides. Optionally, the TAT binding oligopeptides of the present invention may be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The TAT binding oligopeptides of the present invention may optionally be produced in CHO cells or bacterial cells and preferably induce death of a cell to which they bind. For diagnostic purposes, the TAT binding oligopeptides of the present invention may be detectably labeled, attached to a solid support, or the like.

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described TAT binding oligopeptides. Host cell comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli* cells, or yeast cells. A process for producing any of the herein described TAT binding oligopeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired oligopeptide and recovering the desired oligopeptide from the cell culture.

In another embodiment, the invention provides small organic molecules ("TAT binding organic molecules") which bind, preferably specifically, to any of the above or below described TAT polypeptides. Optionally, the TAT binding organic molecules of the present invention may be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The TAT binding organic molecules of the present invention preferably induce death of a cell to which they bind. For diagnostic purposes, the TAT binding organic molecules of the present invention may be detectably labeled, attached to a solid support, or the like.

In a still further embodiment, the invention concerns a composition of matter comprising a TAT polypeptide as described herein, a chimeric TAT polypeptide as described herein, an anti-TAT antibody as described herein, a TAT binding oligopeptide as described herein, or a TAT binding organic molecule as described herein, in combination with a carrier. Optionally, the carrier is a pharmaceutically acceptable carrier.

In yet another embodiment, the invention concerns an article of manufacture comprising a container and a composition of matter contained within the container, wherein the composition of matter may comprise a TAT polypeptide as described herein, a chimeric TAT polypeptide as described herein, an anti-TAT antibody as described herein, a TAT binding oligopeptide as described herein, or a TAT binding organic molecule as described herein. The article may further optionally comprise a label affixed to the container, or a package insert included with the container, that refers to the use of the composition of matter for the therapeutic treatment or diagnostic detection of a tumor.

Another embodiment of the present invention is directed to the use of a TAT polypeptide as described herein, a chimeric TAT polypeptide as described herein, an anti-TAT polypeptide antibody as described herein, a TAT binding oligopeptide as described herein, or a TAT binding organic molecule as described herein, for the preparation of a medicament useful in the treatment of a condition which is responsive to the TAT polypeptide, chimeric TAT polypeptide, anti-TAT polypeptide antibody, TAT binding oligopeptide, or TAT

binding organic molecule.

B. Additional Embodiments

Another embodiment of the present invention is directed to a method for inhibiting the growth of a cell that expresses a TAT polypeptide, wherein the method comprises contacting the cell with an antibody, an oligopeptide or a small organic molecule that binds to the TAT polypeptide, and wherein the binding of the antibody, oligopeptide or organic molecule to the TAT polypeptide causes inhibition of the growth of the cell expressing the TAT polypeptide. In preferred embodiments, the cell is a cancer cell and binding of the antibody, oligopeptide or organic molecule to the TAT polypeptide causes death of the cell expressing the TAT polypeptide. Optionally, the antibody is a monoclonal antibody, antibody fragment, chimeric antibody, humanized antibody, or single-chain antibody. Antibodies, TAT binding oligopeptides and TAT binding organic molecules employed in the methods of the present invention may optionally be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The antibodies and TAT binding oligopeptides employed in the methods of the present invention may optionally be produced in CHO cells or bacterial cells.

Yet another embodiment of the present invention is directed to a method of therapeutically treating a mammal having a cancerous tumor comprising cells that express a TAT polypeptide, wherein the method comprises administering to the mammal a therapeutically effective amount of an antibody, an oligopeptide or a small organic molecule that binds to the TAT polypeptide, thereby resulting in the effective therapeutic treatment of the tumor. Optionally, the antibody is a monoclonal antibody, antibody fragment, chimeric antibody, humanized antibody, or single-chain antibody. Antibodies, TAT binding oligopeptides and TAT binding organic molecules employed in the methods of the present invention may optionally be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The antibodies and oligopeptides employed in the methods of the present invention may optionally be produced in CHO cells or bacterial cells.

Yet another embodiment of the present invention is directed to a method of determining the presence of a TAT polypeptide in a sample suspected of containing the TAT polypeptide, wherein the method comprises exposing the sample to an antibody, oligopeptide or small organic molecule that binds to the TAT polypeptide and determining binding of the antibody, oligopeptide or organic molecule to the TAT polypeptide in the sample, wherein the presence of such binding is indicative of the presence of the TAT polypeptide in the sample. Optionally, the sample may contain cells (which may be cancer cells) suspected of expressing the TAT polypeptide. The antibody, TAT binding oligopeptide or TAT binding organic molecule employed in the method may optionally be detectably labeled, attached to a solid support, or the like.

A further embodiment of the present invention is directed to a method of diagnosing the presence of a tumor in a mammal, wherein the method comprises detecting the level of expression of a gene encoding a TAT polypeptide (a) in a test sample of tissue cells obtained from said mammal, and (b) in a control sample of known normal non-cancerous cells of the same tissue origin or type, wherein a higher level of expression of the

TAT polypeptide in the test sample, as compared to the control sample, is indicative of the presence of tumor in the mammal from which the test sample was obtained.

Another embodiment of the present invention is directed to a method of diagnosing the presence of a tumor in a mammal, wherein the method comprises (a) contacting a test sample comprising tissue cells obtained from the mammal with an antibody, oligopeptide or small organic molecule that binds to a TAT polypeptide and
5 (b) detecting the formation of a complex between the antibody, oligopeptide or small organic molecule and the TAT polypeptide in the test sample, wherein the formation of a complex is indicative of the presence of a tumor in the mammal. Optionally, the antibody, TAT binding oligopeptide or TAT binding organic molecule employed is detectably labeled, attached to a solid support, or the like, and/or the test sample of tissue cells is obtained from an individual suspected of having a cancerous tumor.

10 Yet another embodiment of the present invention is directed to a method for treating or preventing a cell proliferative disorder associated with altered, preferably increased, expression or activity of a TAT polypeptide, the method comprising administering to a subject in need of such treatment an effective amount of an antagonist of a TAT polypeptide. Preferably, the cell proliferative disorder is cancer and the antagonist of the TAT polypeptide is an anti-TAT polypeptide antibody, TAT binding oligopeptide, TAT binding organic
15 molecule or antisense oligonucleotide. Effective treatment or prevention of the cell proliferative disorder may be a result of direct killing or growth inhibition of cells that express a TAT polypeptide or by antagonizing the cell growth potentiating activity of a TAT polypeptide.

Yet another embodiment of the present invention is directed to a method of binding an antibody, oligopeptide or small organic molecule to a cell that expresses a TAT polypeptide, wherein the method
20 comprises contacting a cell that expresses a TAT polypeptide with said antibody, oligopeptide or small organic molecule under conditions which are suitable for binding of the antibody, oligopeptide or small organic molecule to said TAT polypeptide and allowing binding therebetween.

Other embodiments of the present invention are directed to the use of (a) a TAT polypeptide, (b) a nucleic acid encoding a TAT polypeptide or a vector or host cell comprising that nucleic acid, (c) an anti-TAT polypeptide antibody, (d) a TAT-binding oligopeptide, or (e) a TAT-binding small organic molecule in the
25 preparation of a medicament useful for (i) the therapeutic treatment or diagnostic detection of a cancer or tumor, or (ii) the therapeutic treatment or prevention of a cell proliferative disorder.

Another embodiment of the present invention is directed to a method for inhibiting the growth of a cancer cell, wherein the growth of said cancer cell is at least in part dependent upon the growth potentiating effect(s) of a TAT polypeptide (wherein the TAT polypeptide may be expressed either by the cancer cell itself or a cell that produces polypeptide(s) that have a growth potentiating effect on cancer cells), wherein the method
30 comprises contacting the TAT polypeptide with an antibody, an oligopeptide or a small organic molecule that binds to the TAT polypeptide, thereby antagonizing the growth-potentiating activity of the TAT polypeptide and, in turn, inhibiting the growth of the cancer cell. Preferably the growth of the cancer cell is completely inhibited.
35 Even more preferably, binding of the antibody, oligopeptide or small organic molecule to the TAT polypeptide induces the death of the cancer cell. Optionally, the antibody is a monoclonal antibody, antibody fragment,

chimeric antibody, humanized antibody, or single-chain antibody. Antibodies, TAT binding oligopeptides and TAT binding organic molecules employed in the methods of the present invention may optionally be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The antibodies and TAT binding oligopeptides employed in the methods of the present invention may optionally be produced in CHO cells or bacterial cells.

Yet another embodiment of the present invention is directed to a method of therapeutically treating a tumor in a mammal, wherein the growth of said tumor is at least in part dependent upon the growth potentiating effect(s) of a TAT polypeptide, wherein the method comprises administering to the mammal a therapeutically effective amount of an antibody, an oligopeptide or a small organic molecule that binds to the TAT polypeptide, thereby antagonizing the growth potentiating activity of said TAT polypeptide and resulting in the effective therapeutic treatment of the tumor. Optionally, the antibody is a monoclonal antibody, antibody fragment, chimeric antibody, humanized antibody, or single-chain antibody. Antibodies, TAT binding oligopeptides and TAT binding organic molecules employed in the methods of the present invention may optionally be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The antibodies and oligopeptides employed in the methods of the present invention may optionally be produced in CHO cells or bacterial cells.

Yet further embodiments of the present invention will be evident to the skilled artisan upon a reading of the present specification.

BRIEF DESCRIPTION OF THE DRAWINGS

In the list of figures for the present application, specific cDNA sequences which are upregulated in certain tumor tissues as compared to their normal tissue counterparts are individually identified with a designation beginning with the letters "DNA" followed by a specific numerical designation. A full or partial length protein sequence that is encoded by a cDNA sequence identified and shown herein is individually identified with a designation beginning with the letters "PRO" followed by a specific numerical designation. Figures showing encoded amino acid sequences immediately follow the figure showing the cDNA sequence encoding that specific amino acid sequence. If start and/or stop codons have been identified in a cDNA sequence shown in the attached figures, they are shown in bold and underlined font.

List of Figures

- Figure 1: DNA323717, XM_059201, gen.XM_059201
 Figure 2: DNA323718, XM_117159, gen.XM_117159
 Figure 3: DNA323719, XM_114062, gen.XM_114062
 Figure 4: DNA323720, XM_086178, gen.XM_086178
 Figure 5: PRO80480
 Figure 6: DNA323721, XM_051556, gen.XM_051556
 Figure 7: PRO80481
 Figure 8: DNA323722, NM_017891, gen.NM_017891
 Figure 9: PRO80482
 Figure 10: DNA323723, NM_018188, gen.NM_018188
 Figure 11: PRO80483
 Figure 12: DNA323724, NM_002617, gen.NM_002617
 Figure 13: PRO23746
 Figure 14: DNA323725, XM_049742, gen.XM_049742
 Figure 15: DNA323726, NM_033534, gen.NM_033534
 Figure 16: PRO80484
 Figure 17: DNA323727, NM_014188, gen.NM_014188
 Figure 18: PRO80485
 Figure 19: DNA323728, XM_086180, gen.XM_086180
 Figure 20: DNA323729, XM_166599, gen.XM_166599
 Figure 21: PRO80487
 Figure 22: DNA323730, NM_017900, gen.NM_017900
 Figure 23: PRO80488
 Figure 24: DNA323731, XM_001589, gen.XM_001589
 Figure 25: PRO80489
 Figure 26: DNA323732, NM_016176, gen.NM_016176
 Figure 27: PRO80490
 Figure 28: DNA323733, XM_117692, gen.XM_117692
 Figure 29: DNA323734, XM_086360, gen.XM_086360
 Figure 30: PRO80492
 Figure 31: DNA287173, NM_001428, gen.NM_001428
 Figure 32: PRO69463
 Figure 33: DNA323735, XM_001299, gen.XM_001299
 Figure 34: DNA323736, NM_000983, gen.NM_000983
 Figure 35: PRO80493
 Figure 36A-B: DNA227821, NM_014851, gen.NM_014851
 Figure 37: PRO38284
 Figure 38A-B: DNA323737, XM_086204, gen.XM_086204
 Figure 39: PRO80494
 Figure 40: DNA323738, XM_030920, gen.XM_030920
 Figure 41: DNA323739, NM_018948, gen.NM_018948
 Figure 42: DNA273712, NM_007262, gen.NM_007262
 Figure 43: PRO61679
 Figure 44: DNA151148, NM_004781, gen.NM_004781
 Figure 45: PRO12618
 Figure 46: DNA323740, XM_086151, gen.XM_086151
 Figure 47: PRO80497
 Figure 48: DNA171408, NM_004401, gen.NM_004401
 Figure 49: PRO20136
 Figure 50: DNA323741, NM_003132, gen.NM_003132
 Figure 51: PRO80498
 Figure 52: DNA323742, XM_086586, gen.XM_086586
 Figure 53: PRO80499
 Figure 54: DNA323743, XM_086587, gen.XM_086587
 Figure 55: DNA323744, XM_059230, gen.XM_059230
 Figure 56: PRO80501
 Figure 57A-B: DNA323745, XM_048780, gen.XM_048780
 Figure 58: DNA323746, XM_053183, gen.XM_053183
 Figure 59: DNA323747, XM_165442, gen.XM_165442
 Figure 60: DNA323748, NM_033440, gen.NM_033440
 Figure 61: PRO2269
 Figure 62: DNA323749, NM_024329, gen.NM_024329
 Figure 63: PRO80505
 Figure 64: DNA323750, XM_018205, gen.XM_018205
 Figure 65: PRO80506
 Figure 66: DNA323751, XM_011650, gen.XM_011650
 Figure 67: DNA323752, XM_017315, gen.XM_017315
 Figure 68A-B: DNA323753, XM_030470, gen.XM_030470
 Figure 69: DNA323754, NM_004930, gen.NM_004930
 Figure 70: PRO80510
 Figure 71: DNA323755, NM_003689, gen.NM_003689
 Figure 72: PRO80511
 Figure 73: DNA323756, NM_016183, gen.NM_016183
 Figure 74: PRO80512
 Figure 75: DNA323757, XM_015234, gen.XM_015234
 Figure 76A-B: DNA323758, XM_027916, gen.XM_027916
 Figure 77: DNA323759, XM_033683, gen.XM_033683
 Figure 78: DNA323760, XM_001826, gen.XM_001826
 Figure 79: DNA323761, XM_033654, gen.XM_033654
 Figure 80: PRO80517
 Figure 81: DNA323762, NM_001791, gen.NM_001791
 Figure 82: PRO26194
 Figure 83: DNA323763, NM_005826, gen.NM_005826
 Figure 84: PRO60815
 Figure 85: DNA323764, XM_086357, gen.XM_086357
 Figure 86: PRO80518
 Figure 87: DNA323765, NM_000975, gen.NM_000975
 Figure 88: PRO80519
 Figure 89: DNA323766, NM_007260, gen.NM_007260
 Figure 90: PRO61250
 Figure 91: DNA323767, NM_017761, gen.NM_017761
 Figure 92: PRO80520
 Figure 93: DNA323768, NM_006625, gen.NM_006625
 Figure 94: PRO22196
 Figure 95: DNA323769, NM_054016, gen.NM_054016
 Figure 96: PRO80521
 Figure 97: DNA323770, XM_086375, gen.XM_086375
 Figure 98: DNA323771, XM_006290, gen.XM_006290
 Figure 99: DNA323772, NM_015484, gen.NM_015484
 Figure 100: PRO80524
 Figure 101A-B: DNA323773, XM_001616, gen.XM_001616
 Figure 102: DNA323774, XM_058240,

gen.XM_058240
Figure 103: DNA323775, XM_059117,
gen.XM_059117
Figure 104: PRO80527
Figure 105: DNA226262, NM_005563,
gen.NM_005563
Figure 106: PRO36725
Figure 107: DNA323776, NM_022778,
gen.NM_022778
Figure 108: PRO80528
Figure 109: DNA323777, XM_017846,
gen.XM_017846
Figure 110: DNA323778, NM_005517,
gen.NM_005517
Figure 111: PRO80530
Figure 112A-C: DNA323779, XM_046918,
gen.XM_046918
Figure 113: DNA323780, XM_002114,
gen.XM_002114
Figure 114: DNA323781, XM_059066,
gen.XM_059066
Figure 115: PRO80533
Figure 116: DNA323782, NM_018066,
gen.NM_018066
Figure 117: PRO80534
Figure 118: DNA323783, NM_006600,
gen.NM_006600
Figure 119: PRO80535
Figure 120: DNA323784, XM_059067,
gen.XM_059067
Figure 121: PRO80536
Figure 122: DNA323785, NM_032872,
gen.NM_032872
Figure 123: PRO80537
Figure 124: DNA196349, NM_006990,
gen.NM_006990
Figure 125: PRO24856
Figure 126: DNA323788, XM_001640,
gen.XM_001640
Figure 127: DNA323789, NM_002946,
gen.NM_002946
Figure 128: PRO59099
Figure 129: DNA323790, XM_114044,
gen.XM_114044
Figure 130: DNA323791, XM_059088,
gen.XM_059088
Figure 131: DNA323792, NM_031459,
gen.NM_031459
Figure 132: PRO80542
Figure 133: DNA323793, XM_010664,
gen.XM_010664
Figure 134: DNA323794, XM_001812,
gen.XM_001812
Figure 135: DNA323795, XM_001807,
gen.XM_001807
Figure 136: DNA323796, XM_086444,

gen.XM_086444
Figure 137: DNA323797, NM_024640,
gen.NM_024640
Figure 138: PRO80547
Figure 139A-B: DNA323798, XM_049310,
gen.XM_049310
Figure 140: DNA323799, XM_113374,
gen.XM_113374
Figure 141: DNA323800, XM_002105,
gen.XM_002105
Figure 142: DNA323801, NM_014571,
gen.NM_014571
Figure 143: PRO80550
Figure 144: DNA323802, XM_165438,
gen.XM_165438
Figure 145: DNA323803, XM_029844,
gen.XM_029844
Figure 146: DNA188748, NM_006559,
gen.NM_006559
Figure 147: PRO22304
Figure 148: DNA323804, NM_003757,
gen.NM_003757
Figure 149: PRO80553
Figure 150: DNA323805, NM_004964,
gen.NM_004964
Figure 151: PRO80554
Figure 152: DNA323806, NM_023009,
gen.NM_023009
Figure 153: PRO80555
Figure 154: DNA323807, XM_030423,
gen.XM_030423
Figure 155A-B: DNA323808, XM_036299,
gen.XM_036299
Figure 156: PRO80557
Figure 157: DNA227213, NM_003680,
gen.NM_003680
Figure 158: PRO37676
Figure 159: DNA323809, NM_006112,
gen.NM_006112
Figure 160: PRO80558
Figure 161: DNA323810, XM_018136,
gen.XM_018136
Figure 162: PRO80559
Figure 163: DNA323811, XM_117184,
gen.XM_117184
Figure 164: PRO80560
Figure 165: DNA323812, NM_017825,
gen.NM_017825
Figure 166: PRO80561
Figure 167: DNA189315, NM_014408,
gen.NM_014408
Figure 168: PRO22262
Figure 169A-B: DNA323813, XM_029031,
gen.XM_029031
Figure 170: PRO80562
Figure 171: DNA323814, XM_059171,

gen.XM_059171
Figure 172: PRO80563
Figure 173: DNA83085, NM_000760, gen.NM_000760
Figure 174: PRO2583
Figure 175: DNA323815, XM_165984, gen.XM_165984
Figure 176: DNA323816, XM_029842, gen.XM_029842
Figure 177: PRO2851
Figure 178: DNA323817, XM_086384, gen.XM_086384
Figure 179: PRO80565
Figure 180A-C: DNA274487, NM_014747, gen.NM_014747
Figure 181: PRO62389
Figure 182: DNA323818, XM_010712, gen.XM_010712
Figure 183: DNA323819, NM_024664, gen.NM_024664
Figure 184: PRO80567
Figure 185: DNA323820, XM_059214, gen.XM_059214
Figure 186: PRO80568
Figure 187: DNA323821, XM_046349, gen.XM_046349
Figure 188: DNA103253, NM_006516, gen.NM_006516
Figure 189: PRO4583
Figure 190: DNA323822, XM_086543, gen.XM_086543
Figure 191: PRO80570
Figure 192: DNA274745, NM_006824, gen.NM_006824
Figure 193: PRO62518
Figure 194: DNA273060, NM_001255, gen.NM_001255
Figure 195: PRO61125
Figure 196: DNA323823, NM_030587, gen.NM_030587
Figure 197: PRO80571
Figure 198: DNA323824, XM_097649, gen.XM_097649
Figure 199: DNA256503, NM_003780, gen.NM_003780
Figure 200: PRO51539
Figure 201: DNA323825, XM_046450, gen.XM_046450
Figure 202A-B: DNA272024, NM_014663, gen.NM_014663
Figure 203: PRO60298
Figure 204: DNA323826, XM_046565, gen.XM_046565
Figure 205: PRO80574
Figure 206: DNA323827, NM_024602, gen.NM_024602
Figure 207: PRO80575

Figure 208: DNA323828, XM_046557, gen.XM_046557
Figure 209: PRO80576
Figure 210: DNA323829, NM_001012, gen.NM_001012
Figure 211: PRO10760
Figure 212: DNA323830, XM_046551, gen.XM_046551
Figure 213A-B: DNA323831, XM_027983, gen.XM_027983
Figure 214: DNA323832, XM_086324, gen.XM_086324
Figure 215: PRO80579
Figure 216: DNA323833, XM_032391, gen.XM_032391
Figure 217: PRO80580
Figure 218: DNA103214, NM_006066, gen.NM_006066
Figure 219: PRO4544
Figure 220: DNA304686, NM_002574, gen.NM_002574
Figure 221: PRO71112
Figure 222: DNA323834, NM_032756, gen.NM_032756
Figure 223: PRO80581
Figure 224: DNA323835, XM_059133, gen.XM_059133
Figure 225: PRO80582
Figure 226: DNA323836, XM_027313, gen.XM_027313
Figure 227: PRO80583
Figure 228: DNA323837, XM_054868, gen.XM_054868
Figure 229: DNA323838, NM_001262, gen.NM_001262
Figure 230: PRO59546
Figure 231: DNA323839, XM_086391, gen.XM_086391
Figure 232: PRO80584
Figure 233: DNA323840, XM_114798, gen.XM_114798
Figure 234: PRO80585
Figure 235: DNA272748, NM_002979, gen.NM_002979
Figure 236: PRO60860
Figure 237: DNA323841, XM_038911, gen.XM_038911
Figure 238: PRO80586
Figure 239: DNA323842, NM_018070, gen.NM_018070
Figure 240: PRO80587
Figure 241: DNA323843, NM_024603, gen.NM_024603
Figure 242: PRO80588
Figure 243: DNA323844, XM_086389, gen.XM_086389

Figure 244: DNA323845, XM_038852,
gen.XM_038852
Figure 245: DNA323846, NM_032864,
gen.NM_032864
Figure 246: PRO80591
Figure 247: DNA323847, NM_024586,
gen.NM_024586
Figure 248: PRO80592
Figure 249A-B: DNA323848, XM_097565,
gen.XM_097565
Figure 250: DNA323849, XM_001472,
gen.XM_001472
Figure 251A-C: DNA323850, XM_055481,
gen.XM_055481
Figure 252: PRO80593
Figure 253: DNA323851, XM_010615,
gen.XM_010615
Figure 254A-B: DNA323852, XM_089138,
gen.XM_089138
Figure 255: PRO80595
Figure 256A-B: DNA323853, XM_059180,
gen.XM_059180
Figure 257: DNA323854, XM_015717,
gen.XM_015717
Figure 258: PRO80597
Figure 259: DNA323855, XM_114125,
gen.XM_114125
Figure 260: DNA323856, NM_015640,
gen.NM_015640
Figure 261: PRO80599
Figure 262: DNA323857, NM_017768,
gen.NM_017768
Figure 263: PRO80600
Figure 264: DNA323858, XM_165977,
gen.XM_165977
Figure 265: DNA323859, XM_086343,
gen.XM_086343
Figure 266: PRO80602
Figure 267: DNA269708, NM_007034,
gen.NM_007034
Figure 268: PRO58118
Figure 269: DNA323860, NM_001554,
gen.NM_001554
Figure 270: PRO80603
Figure 271: DNA226260, NM_006769,
gen.NM_006769
Figure 272: PRO36723
Figure 273: DNA323861, NM_004261,
gen.NM_004261
Figure 274: PRO80604
Figure 275: DNA323862, XM_165983,
gen.XM_165983
Figure 276: DNA323863, XM_016164,
gen.XM_016164
Figure 277: DNA323864, XM_086164,
gen.XM_086164

Figure 278: PRO80607
Figure 279: DNA323865, XM_086165,
gen.XM_086165
Figure 280: DNA323866, XM_086167,
gen.XM_086167
Figure 281: DNA323867, XM_086166,
gen.XM_086166
Figure 282: DNA323868, XM_086138,
gen.XM_086138
Figure 283: PRO80611
Figure 284: DNA323869, NM_000969,
gen.NM_000969
Figure 285: PRO80612
Figure 286: DNA323870, XM_088863,
gen.XM_088863
Figure 287: PRO80613
Figure 288: DNA271003, NM_003729,
gen.NM_003729
Figure 289: PRO59332
Figure 290: DNA323871, XM_165981,
gen.XM_165981
Figure 291: PRO80614
Figure 292: DNA275139, NM_013296,
gen.NM_013296
Figure 293: PRO62849
Figure 294: DNA323872, XM_058702,
gen.XM_058702
Figure 295: DNA323873, XM_054978,
gen.XM_054978
Figure 296: DNA323874, NM_032636,
gen.NM_032636
Figure 297: PRO80617
Figure 298: DNA323875, NM_006513,
gen.NM_006513
Figure 299: PRO80618
Figure 300: DNA323876, NM_006621,
gen.NM_006621
Figure 301: PRO80619
Figure 302A-B: DNA323877, NM_007158,
gen.NM_007158
Figure 303: PRO80620
Figure 304: DNA323878, XM_086132,
gen.XM_086132
Figure 305: PRO80621
Figure 306: DNA323879, NM_004000,
gen.NM_004000
Figure 307: PRO80622
Figure 308: DNA323880, NM_001688,
gen.NM_001688
Figure 309: PRO80623
Figure 310: DNA323881, NM_019099,
gen.NM_019099
Figure 311: PRO80624
Figure 312A-B: DNA323882, NM_000701,
gen.NM_000701
Figure 313: PRO80625

Figure 314A-B: DNA323883, XM_018332,
gen.XM_018332
Figure 315A-B: DNA323884, XM_040709,
gen.XM_040709
Figure 316: PRO80627
Figure 317: DNA323885, XM_086518,
gen.XM_086518
Figure 318A-D: DNA323886, XM_034671,
gen.XM_034671
Figure 319: DNA323887, XM_034662,
gen.XM_034662
Figure 320: PRO80630
Figure 321: DNA323888, XM_039721,
gen.XM_039721
Figure 322: PRO80631
Figure 323A-B: DNA323889, XM_086397,
gen.XM_086397
Figure 324A-B: DNA323890, XM_086515,
gen.XM_086515
Figure 325: PRO80633
Figure 326: DNA323891, XM_016480,
gen.XM_016480
Figure 327: DNA323892, XM_165975,
gen.XM_165975
Figure 328: DNA323893, NM_016361,
gen.NM_016361
Figure 329: PRO231
Figure 330: DNA323894, XM_059210,
gen.XM_059210
Figure 331: DNA323895, XM_086296,
gen.XM_086296
Figure 332: DNA323896, NM_030920,
gen.NM_030920
Figure 333: PRO80638
Figure 334: DNA323897, NM_016022,
gen.NM_016022
Figure 335: PRO80639
Figure 336: DNA323898, NM_031901,
gen.NM_031901
Figure 337: PRO80640
Figure 338A-B: DNA323899, XM_088788,
gen.XM_088788
Figure 339: PRO80641
Figure 340: DNA274759, NM_005620,
gen.NM_005620
Figure 341: PRO62529
Figure 342: DNA323900, XM_001468,
gen.XM_001468
Figure 343: PRO49642
Figure 344: DNA323901, NM_006862,
gen.NM_006862
Figure 345: PRO80642
Figure 346: DNA227529, NM_002796,
gen.NM_002796
Figure 347: PRO37992
Figure 348: DNA323902, NM_002810,

gen.NM_002810
Figure 349: PRO61638
Figure 350: DNA290284, NM_005997,
gen.NM_005997
Figure 351: PRO70433
Figure 352: DNA323903, XM_097639,
gen.XM_097639
Figure 353: DNA323904, XM_041879,
gen.XM_041879
Figure 354: DNA323905, XM_041884,
gen.XM_041884
Figure 355: PRO80644
Figure 356: DNA225809, NM_000396,
gen.NM_000396
Figure 357: PRO36272
Figure 358: DNA323906, NM_025150,
gen.NM_025150
Figure 359: PRO80645
Figure 360: DNA323907, XM_114098,
gen.XM_114098
Figure 361: DNA323908, XM_113369,
gen.XM_113369
Figure 362: PRO80646
Figure 363: DNA323909, XM_099467,
gen.XM_099467
Figure 364: DNA323910, NM_002965,
gen.NM_002965
Figure 365: PRO80648
Figure 366: DNA323911, XM_086400,
gen.XM_086400
Figure 367: DNA210134, NM_014624,
gen.NM_014624
Figure 368: PRO33679
Figure 369: DNA304666, NM_002961,
gen.NM_002961
Figure 370: PRO71093
Figure 371: DNA304720, NM_019554,
gen.NM_019554
Figure 372: PRO71146
Figure 373: DNA323912, XM_165976,
gen.XM_165976
Figure 374: DNA227577, NM_006271,
gen.NM_006271
Figure 375: PRO38040
Figure 376: DNA323913, XM_114097,
gen.XM_114097
Figure 377: DNA323914, XM_040009,
gen.XM_040009
Figure 378: PRO80651
Figure 379: DNA323915, NM_024330,
gen.NM_024330
Figure 380: PRO703
Figure 381: DNA323916, NM_012437,
gen.NM_012437
Figure 382: PRO80652
Figure 383: DNA323917, XM_086271,

gen.XM_086271
Figure 384: DNA323918, XM_114055,
gen.XM_114055
Figure 385: PRO37535
Figure 386: DNA323919, XM_113360,
gen.XM_113360
Figure 387: PRO80654
Figure 388: DNA323920, XM_086564,
gen.XM_086564
Figure 389: DNA323921, NM_005973,
gen.NM_005973
Figure 390: PRO80656
Figure 391: DNA323922, XM_044077,
gen.XM_044077
Figure 392: DNA323923, NM_001878,
gen.NM_001878
Figure 393: PRO80657
Figure 394: DNA323924, NM_021948,
gen.NM_021948
Figure 395: PRO6018
Figure 396: DNA273088, NM_006365,
gen.NM_006365
Figure 397: PRO61146
Figure 398: DNA323925, XM_044127,
gen.XM_044127
Figure 399: PRO80658
Figure 400: DNA323926, XM_053245,
gen.XM_053245
Figure 401: PRO80659
Figure 402: DNA257916, NM_032323,
gen.NM_032323
Figure 403: PRO52449
Figure 404: DNA323927, NM_005572,
gen.NM_005572
Figure 405: PRO80660
Figure 406: DNA323928, XM_044166,
gen.XM_044166
Figure 407: PRO80661
Figure 408: DNA323929, XM_044128,
gen.XM_044128
Figure 409: DNA226125, NM_003145,
gen.NM_003145
Figure 410: PRO36588
Figure 411A-B: DNA323930, XM_044172,
gen.XM_044172
Figure 412: DNA323931, NM_032292,
gen.NM_032292
Figure 413: PRO80664
Figure 414: DNA323932, NM_004632,
gen.NM_004632
Figure 415: PRO80665
Figure 416: DNA323933, XM_044075,
gen.XM_044075
Figure 417: PRO80666
Figure 418: DNA323934, NM_018253,
gen.NM_018253

Figure 419: PRO80667
Figure 420: DNA323935, NM_018116,
gen.NM_018116
Figure 421: PRO80668
Figure 422: DNA323936, NM_002004,
gen.NM_002004
Figure 423: PRO80669
Figure 424: DNA323937, NM_005698,
gen.NM_005698
Figure 425: PRO80670
Figure 426: DNA323938, NM_052837,
gen.NM_052837
Figure 427: PRO80671
Figure 428: DNA194600, NM_006589,
gen.NM_006589
Figure 429: PRO23942
Figure 430: DNA323939, XM_086567,
gen.XM_086567
Figure 431: PRO80672
Figure 432: DNA323940, XM_086552,
gen.XM_086552
Figure 433: DNA323941, XM_036744,
gen.XM_036744
Figure 434: DNA323942, NM_130898,
gen.NM_130898
Figure 435: PRO80675
Figure 436: DNA226793, NM_006694,
gen.NM_006694
Figure 437: PRO37256
Figure 438: DNA294794, NM_002870,
gen.NM_002870
Figure 439: PRO70754
Figure 440: DNA323943, NM_001030,
gen.NM_001030
Figure 441: PRO80676
Figure 442: DNA323944, XM_036829,
gen.XM_036829
Figure 443: PRO80677
Figure 444: DNA323945, NM_015449,
gen.NM_015449
Figure 445: PRO80678
Figure 446: DNA323946, NM_014847,
gen.NM_014847
Figure 447: PRO80679
Figure 448: DNA323947, XM_036934,
gen.XM_036934
Figure 449: PRO80680
Figure 450A-B: DNA323948, XM_036845,
gen.XM_036845
Figure 451: DNA323949, XM_010636,
gen.XM_010636
Figure 452: DNA323950, NM_006556,
gen.NM_006556
Figure 453: PRO62574
Figure 454: DNA323951, XM_034082,
gen.XM_034082

Figure 455: DNA323952, NM_025207,
gen.NM_025207
Figure 456: PRO80684
Figure 457: DNA103436, NM_003815,
gen.NM_003815
Figure 458: PRO4763
Figure 459: DNA323953, NM_003516,
gen.NM_003516
Figure 460: PRO80685
Figure 461: DNA323954, NM_005850,
gen.NM_005850
Figure 462: PRO59725
Figure 463A-B: DNA323955, NM_014849,
gen.NM_014849
Figure 464: PRO80686
Figure 465: DNA323956, XM_059094,
gen.XM_059094
Figure 466: DNA323957, XM_058247,
gen.XM_058247
Figure 467: PRO80688
Figure 468: DNA323958, NM_003779,
gen.NM_003779
Figure 469: PRO80689
Figure 470: DNA323959, NM_004550,
gen.NM_004550
Figure 471: PRO58974
Figure 472: DNA323960, XM_085581,
gen.XM_085581
Figure 473: DNA323961, XM_113379,
gen.XM_113379
Figure 474: DNA226619, NM_003564,
gen.NM_003564
Figure 475: PRO37082
Figure 476A-B: DNA323962, XM_049680,
gen.XM_049680
Figure 477: DNA323963, XM_165443,
gen.XM_165443
Figure 478: PRO80693
Figure 479: DNA323964, XM_086381,
gen.XM_086381
Figure 480: PRO80694
Figure 481A-B: DNA323965, NM_002857,
gen.NM_002857
Figure 482: PRO80695
Figure 483A-B: DNA323966, XM_049690,
gen.XM_049690
Figure 484: DNA323967, XM_114153,
gen.XM_114153
Figure 485: DNA323968, XM_086378,
gen.XM_086378
Figure 486: DNA323969, XM_001897,
gen.XM_001897
Figure 487: PRO10002
Figure 488: DNA323970, NM_052862,
gen.NM_052862
Figure 489: PRO80699

Figure 490: DNA323971, XM_086481,
gen.XM_086481
Figure 491: PRO80700
Figure 492: DNA323972, XM_059191,
gen.XM_059191
Figure 493: DNA323973, XM_086485,
gen.XM_086485
Figure 494: DNA323974, XM_086484,
gen.XM_086484
Figure 495: DNA323975, XM_047479,
gen.XM_047479
Figure 496: PRO80704
Figure 497: DNA323976, NM_003617,
gen.NM_003617
Figure 498: PRO37806
Figure 499: DNA254298, NM_025226,
gen.NM_025226
Figure 500: PRO49409
Figure 501: DNA323977, XM_034000,
gen.XM_034000
Figure 502: PRO80705
Figure 503: DNA323978, NM_032738,
gen.NM_032738
Figure 504: PRO329
Figure 505: DNA323979, NM_000569,
gen.NM_000569
Figure 506: PRO80706
Figure 507: DNA323980, XM_088945,
gen.XM_088945
Figure 508: PRO80707
Figure 509: DNA323981, XM_060331,
gen.XM_060331
Figure 510: PRO80708
Figure 511: DNA323982, NM_004905,
gen.NM_004905
Figure 512: PRO80709
Figure 513: DNA323983, NM_017847,
gen.NM_017847
Figure 514: PRO80710
Figure 515A-B: DNA323984, XM_051877,
gen.XM_051877
Figure 516: PRO62077
Figure 517: DNA323985, NM_005717,
gen.NM_005717
Figure 518: PRO80711
Figure 519A-B: DNA271986, NM_014837,
gen.NM_014837
Figure 520: PRO60261
Figure 521A-B: DNA323986, XM_056923,
gen.XM_056923
Figure 522: DNA323987, XM_046464,
gen.XM_046464
Figure 523: DNA323988, XM_002068,
gen.XM_002068
Figure 524A-B: DNA323989, XM_001289,
gen.XM_001289

Figure 525: DNA323990, XM_114109,
gen.XM_114109
Figure 526: PRO80714
Figure 527: DNA323991, NM_022371,
gen.NM_022371
Figure 528: PRO80715
Figure 529: DNA323992, NM_004673,
gen.NM_004673
Figure 530: PRO188
Figure 531: DNA323993, XM_060517,
gen.XM_060517
Figure 532: DNA323994, XM_165978,
gen.XM_165978
Figure 533: PRO80717
Figure 534: DNA323995, XM_117181,
gen.XM_117181
Figure 535: DNA323996, NM_018122,
gen.NM_018122
Figure 536: PRO80719
Figure 537: DNA323997, XM_042967,
gen.XM_042967
Figure 538: DNA323998, XM_086494,
gen.XM_086494
Figure 539: PRO80720
Figure 540: DNA290234, NM_002923,
gen.NM_002923
Figure 541: PRO70333
Figure 542: DNA323999, XM_086328,
gen.XM_086328
Figure 543: DNA324000, XM_086282,
gen.XM_086282
Figure 544: DNA324001, XM_053633,
gen.XM_053633
Figure 545: DNA256905, NM_138391,
gen.NM_138391
Figure 546: PRO51836
Figure 547: DNA324002, XM_015434,
gen.XM_015434
Figure 548: DNA324003, NM_006763,
gen.NM_006763
Figure 549: PRO80725
Figure 550: DNA227246, NM_005686,
gen.NM_005686
Figure 551: PRO37709
Figure 552: DNA324004, XM_058405,
gen.XM_058405
Figure 553A-B: DNA226005, NM_000228,
gen.NM_000228
Figure 554: PRO36468
Figure 555: DNA324005, NM_015714,
gen.NM_015714
Figure 556: PRO11582
Figure 557: DNA324006, XM_086142,
gen.XM_086142
Figure 558: DNA83046, NM_000574, gen.NM_000574
Figure 559: PRO2569

Figure 560A-B: DNA324007, XM_114030,
gen.XM_114030
Figure 561: DNA324008, XM_097519,
gen.XM_097519
Figure 562: DNA324009, XM_059120,
gen.XM_059120
Figure 563: PRO80730
Figure 564: DNA324010, NM_016456,
gen.NM_016456
Figure 565: PRO1248
Figure 566: DNA324011, XM_036556,
gen.XM_036556
Figure 567: DNA324012, XM_001914,
gen.XM_001914
Figure 568: DNA324013, XM_001916,
gen.XM_001916
Figure 569: DNA324014, NM_018085,
gen.NM_018085
Figure 570: PRO80734
Figure 571: DNA324015, NM_006335,
gen.NM_006335
Figure 572: PRO80735
Figure 573: DNA324016, XM_036500,
gen.XM_036500
Figure 574: PRO80736
Figure 575: DNA324017, XM_036507,
gen.XM_036507
Figure 576: DNA196344, NM_004767,
gen.NM_004767
Figure 577: PRO24851
Figure 578: DNA247474, NM_014176,
gen.NM_014176
Figure 579: PRO44999
Figure 580A-B: DNA324018, XM_084055,
gen.XM_084055
Figure 581: DNA324019, XM_010682,
gen.XM_010682
Figure 582: DNA324020, XM_117185,
gen.XM_117185
Figure 583: DNA324021, XM_055880,
gen.XM_055880
Figure 584: PRO80740
Figure 585: DNA193882, NM_014184,
gen.NM_014184
Figure 586: PRO23300
Figure 587: DNA324022, NM_018212,
gen.NM_018212
Figure 588: PRO80741
Figure 589: DNA324023, XM_086431,
gen.XM_086431
Figure 590: PRO80742
Figure 591: DNA324024, XM_037329,
gen.XM_037329
Figure 592: DNA324025, XM_086432,
gen.XM_086432
Figure 593A-B: DNA324026, XM_010732,

gen.XM_010732
Figure 594: DNA227504, NM_000447,
gen.NM_000447
Figure 595: PRO37967
Figure 596: DNA324027, NM_012486,
gen.NM_012486
Figure 597: PRO80745
Figure 598A-B: DNA324028, XM_113361,
gen.XM_113361
Figure 599A-B: DNA324029, XM_001958,
gen.XM_001958
Figure 600: DNA324030, XM_016199,
gen.XM_016199
Figure 601: DNA324031, XM_086244,
gen.XM_086244
Figure 602: DNA324032, XM_086245,
gen.XM_086245
Figure 603: DNA254346, NM_024709,
gen.NM_024709
Figure 604: PRO49457
Figure 605: DNA324033, XM_088107,
gen.XM_088107
Figure 606: DNA324034, NM_032890,
gen.NM_032890
Figure 607: PRO80752
Figure 608: DNA324035, XM_052974,
gen.XM_052974
Figure 609: PRO80753
Figure 610: DNA324036, XM_047499,
gen.XM_047499
Figure 611: PRO80754
Figure 612: DNA324037, NM_000858,
gen.NM_000858
Figure 613: PRO80755
Figure 614: DNA324038, NM_024319,
gen.NM_024319
Figure 615: PRO80756
Figure 616: DNA324039, XM_047545,
gen.XM_047545
Figure 617: PRO4914
Figure 618A-B: DNA324040, XM_056884,
gen.XM_056884
Figure 619: DNA324041, XM_098599,
gen.XM_098599
Figure 620: DNA324042, XM_165439,
gen.XM_165439
Figure 621: PRO80759
Figure 622: DNA324043, XM_089030,
gen.XM_089030
Figure 623: PRO80760
Figure 624: DNA82328, NM_000029, gen.NM_000029
Figure 625: PRO1707
Figure 626: DNA324044, NM_014236,
gen.NM_014236
Figure 627: PRO80761
Figure 628: DNA324045, XM_056970,

gen.XM_056970
Figure 629: PRO80762
Figure 630: DNA324046, NM_032324,
gen.NM_032324
Figure 631: PRO80763
Figure 632: DNA324047, XM_086257,
gen.XM_086257
Figure 633: PRO80764
Figure 634: DNA324048, XM_114137,
gen.XM_114137
Figure 635: PRO80765
Figure 636: DNA324049, NM_000143,
gen.NM_000143
Figure 637: PRO62607
Figure 638: DNA324050, XM_090833,
gen.XM_090833
Figure 639: DNA324051, NM_130398,
gen.NM_130398
Figure 640: PRO80767
Figure 641: DNA324052, XM_117196,
gen.XM_117196
Figure 642: DNA324053, XM_018041,
gen.XM_018041
Figure 643: DNA324054, NM_001011,
gen.NM_001011
Figure 644: PRO10692
Figure 645: DNA324055, NM_024027,
gen.NM_024027
Figure 646: PRO1182
Figure 647: DNA324056, NM_016030,
gen.NM_016030
Figure 648: PRO80770
Figure 649: DNA103217, NM_003310,
gen.NM_003310
Figure 650: PRO4547
Figure 651: DNA275195, NM_001034,
gen.NM_001034
Figure 652: PRO62893
Figure 653: DNA324057, XM_059368,
gen.XM_059368
Figure 654: PRO80771
Figure 655: DNA324058, NM_006826,
gen.NM_006826
Figure 656: PRO70258
Figure 657: DNA324059, NM_005378,
gen.NM_005378
Figure 658: PRO80772
Figure 659: DNA324060, NM_002539,
gen.NM_002539
Figure 660: PRO80773
Figure 661: DNA324061, XM_096149,
gen.XM_096149
Figure 662: DNA275049, NM_004939,
gen.NM_004939
Figure 663: PRO62770
Figure 664A-B: DNA324062, XM_036450,

gen.XM_036450
Figure 665: DNA324063, XM_103946,
gen.XM_103946
Figure 666: PRO80775
Figure 667: DNA324064, NM_014713,
gen.NM_014713
Figure 668: PRO80776
Figure 669: DNA324065, XM_087206,
gen.XM_087206
Figure 670: DNA324066, NM_106552,
gen.NM_106552
Figure 671: PRO80778
Figure 672: DNA324067, XM_092135,
gen.XM_092135
Figure 673: PRO80779
Figure 674: DNA324068, NM_017910,
gen.NM_017910
Figure 675: PRO80780
Figure 676: DNA324069, XM_092517,
gen.XM_092517
Figure 677: PRO80781
Figure 678A-B: DNA324070, NM_025203,
gen.NM_025203
Figure 679: PRO80782
Figure 680: DNA324071, XM_002480,
gen.XM_002480
Figure 681: DNA324072, NM_002707,
gen.NM_002707
Figure 682: PRO12199
Figure 683: DNA324073, XM_087151,
gen.XM_087151
Figure 684: DNA227165, NM_014748,
gen.NM_014748
Figure 685: PRO37628
Figure 686: DNA324074, NM_015636,
gen.NM_015636
Figure 687: PRO80785
Figure 688: DNA273800, NM_001521,
gen.NM_001521
Figure 689: PRO61761
Figure 690: DNA324075, XM_047175,
gen.XM_047175
Figure 691: PRO80786
Figure 692A-B: DNA324076, NM_004341,
gen.NM_004341
Figure 693: PRO80787
Figure 694: DNA324077, NM_016085,
gen.NM_016085
Figure 695: PRO80788
Figure 696: DNA324078, NM_080592,
gen.NM_080592
Figure 697: PRO80789
Figure 698: DNA227545, NM_021095,
gen.NM_021095
Figure 699: PRO38008
Figure 700: DNA324079, XM_002435,

gen.XM_002435
Figure 701: DNA324080, NM_000221,
gen.NM_000221
Figure 702: PRO80790
Figure 703: DNA271243, NM_006488,
gen.NM_006488
Figure 704: PRO59558
Figure 705: DNA324081, NM_007046,
gen.NM_007046
Figure 706: PRO9886
Figure 707: DNA324082, NM_021831,
gen.NM_021831
Figure 708: PRO80791
Figure 709: DNA324083, NM_020134,
gen.NM_020134
Figure 710: PRO80792
Figure 711: DNA103593, NM_000183,
gen.NM_000183
Figure 712: PRO4917
Figure 713: DNA324084, NM_000182,
gen.NM_000182
Figure 714: PRO80793
Figure 715: DNA324085, XM_097976,
gen.XM_097976
Figure 716A-B: DNA324086, XM_039712,
gen.XM_039712
Figure 717: DNA324087, NM_022552,
gen.NM_022552
Figure 718: PRO80796
Figure 719: DNA324088, NM_024572,
gen.NM_024572
Figure 720: PRO80797
Figure 721: DNA324089, NM_018607,
gen.NM_018607
Figure 722: PRO80798
Figure 723: DNA324090, XM_165448,
gen.XM_165448
Figure 724: PRO80799
Figure 725: DNA324091, XM_087195,
gen.XM_087195
Figure 726: DNA324092, XM_087193,
gen.XM_087193
Figure 727: DNA324093, NM_138801,
gen.NM_138801
Figure 728: PRO80802
Figure 729: DNA324094, XM_098004,
gen.XM_098004
Figure 730: PRO80803
Figure 731: DNA324095, XM_031519,
gen.XM_031519
Figure 732: PRO80804
Figure 733A-B: DNA324096, XM_031527,
gen.XM_031527
Figure 734: DNA324097, XM_038576,
gen.XM_038576
Figure 735: PRO80806

Figure 736: DNA324098, XM_117264,
gen.XM_117264
Figure 737: PRO80807
Figure 738A-B: DNA324099, XM_031626,
gen.XM_031626
Figure 739: PRO80808
Figure 740: DNA324100, XM_057664,
gen.XM_057664
Figure 741: DNA226428, NM_000251,
gen.NM_000251
Figure 742: PRO36891
Figure 743: DNA324101, XM_087211,
gen.XM_087211
Figure 744A-B: DNA275066, NM_000179,
gen.NM_000179
Figure 745: PRO62786
Figure 746A-C: DNA270154, NM_003128,
gen.NM_003128
Figure 747: PRO58543
Figure 748: DNA324102, XM_087051,
gen.XM_087051
Figure 749: DNA324103, NM_002954,
gen.NM_002954
Figure 750: PRO62239
Figure 751: DNA271060, NM_002453,
gen.NM_002453
Figure 752: PRO59384
Figure 753: DNA324104, XM_048088,
gen.XM_048088
Figure 754: PRO80811
Figure 755: DNA324105, XM_010886,
gen.XM_010886
Figure 756: PRO80812
Figure 757: DNA324106, XM_045283,
gen.XM_045283
Figure 758: PRO80813
Figure 759: DNA324107, NM_006430,
gen.NM_006430
Figure 760: PRO80814
Figure 761A-B: DNA324108, NM_003400,
gen.NM_003400
Figure 762: PRO59544
Figure 763: DNA324109, XM_018301,
gen.XM_018301
Figure 764: DNA324110, NM_005917,
gen.NM_005917
Figure 765: PRO4918
Figure 766: DNA324111, XM_016843,
gen.XM_016843
Figure 767: PRO80816
Figure 768: DNA324112, XM_088638,
gen.XM_088638
Figure 769: PRO80817
Figure 770: DNA324113, XM_002647,
gen.XM_002647
Figure 771: DNA324114, XM_010881,

gen.XM_010881
Figure 772: DNA324115, XM_087069,
gen.XM_087069
Figure 773: DNA324116, XM_016625,
gen.XM_016625
Figure 774: PRO80820
Figure 775: DNA324117, XM_087068,
gen.XM_087068
Figure 776: DNA324118, XM_002674,
gen.XM_002674
Figure 777: DNA324119, XM_065884,
gen.XM_065884
Figure 778: PRO80823
Figure 779A-B: DNA324120, XM_002739,
gen.XM_002739
Figure 780: DNA324121, XM_031596,
gen.XM_031596
Figure 781: PRO61325
Figure 782: DNA324122, XM_031585,
gen.XM_031585
Figure 783: DNA324123, XM_031586,
gen.XM_031586
Figure 784: DNA324124, XM_018039,
gen.XM_018039
Figure 785: DNA324125, NM_032822,
gen.NM_032822
Figure 786: PRO80827
Figure 787A-B: DNA324126, XM_096172,
gen.XM_096172
Figure 788A-B: DNA324127, XM_002727,
gen.XM_002727
Figure 789: DNA324128, NM_003124,
gen.NM_003124
Figure 790: PRO80830
Figure 791: DNA324129, XM_086980,
gen.XM_086980
Figure 792: DNA227795, NM_006429,
gen.NM_006429
Figure 793: PRO38258
Figure 794: DNA287167, NM_006636,
gen.NM_006636
Figure 795: PRO59136
Figure 796: DNA324130, NM_033046,
gen.NM_033046
Figure 797: PRO80832
Figure 798: DNA324131, NM_133637,
gen.NM_133637
Figure 799: PRO80833
Figure 800: DNA324132, XM_035220,
gen.XM_035220
Figure 801: DNA324133, NM_013247,
gen.NM_013247
Figure 802: PRO80835
Figure 803: DNA227528, NM_021103,
gen.NM_021103
Figure 804: PRO37991

Figure 805: DNA324134, XM_086920,
gen.XM_086920
Figure 806: DNA150725, NM_001747,
gen.NM_001747
Figure 807: PRO12792
Figure 808: DNA324135, NM_005911,
gen.NM_005911
Figure 809: PRO80837
Figure 810: DNA324136, NM_032827,
gen.NM_032827
Figure 811: PRO80838
Figure 812: DNA324137, NM_017952,
gen.NM_017952
Figure 813: PRO80839
Figure 814: DNA227190, NM_006839,
gen.NM_006839
Figure 815: PRO37653
Figure 816: DNA324138, XM_114215,
gen.XM_114215
Figure 817: DNA324139, XM_052989,
gen.XM_052989
Figure 818: DNA324140, XM_049116,
gen.XM_049116
Figure 819: PRO80842
Figure 820A-B: DNA324141, XM_049108,
gen.XM_049108
Figure 821: PRO80843
Figure 822: DNA324142, XM_049113,
gen.XM_049113
Figure 823: DNA324143, XM_002611,
gen.XM_002611
Figure 824A-B: DNA324144, XM_114247,
gen.XM_114247
Figure 825: DNA324145, NM_017789,
gen.NM_017789
Figure 826: PRO80846
Figure 827: DNA324146, NM_001862,
gen.NM_001862
Figure 828: PRO80847
Figure 829: DNA324147, NM_005783,
gen.NM_005783
Figure 830: PRO80848
Figure 831A-B: DNA324148, XM_037108,
gen.XM_037108
Figure 832: DNA324149, NM_000993,
gen.NM_000993
Figure 833: PRO11197
Figure 834: DNA324150, NM_017546,
gen.NM_017546
Figure 835: PRO80850
Figure 836: DNA324151, NM_001450,
gen.NM_001450
Figure 837: PRO80851
Figure 838: DNA324152, XM_114229,
gen.XM_114229
Figure 839: DNA324153, XM_087122,

gen.XM_087122
Figure 840: PRO80853
Figure 841: DNA324154, XM_018540,
gen.XM_018540
Figure 842: DNA324155, XM_087040,
gen.XM_087040
Figure 843: DNA324156, NM_032212,
gen.NM_032212
Figure 844: PRO80856
Figure 845: DNA324157, XM_002217,
gen.XM_002217
Figure 846: PRO80857
Figure 847: DNA324158, NM_000576,
gen.NM_000576
Figure 848: PRO65
Figure 849: DNA324159, XM_086923,
gen.XM_086923
Figure 850: DNA324160, XM_086925,
gen.XM_086925
Figure 851A-B: DNA324161, XM_114266,
gen.XM_114266
Figure 852: PRO80860
Figure 853: DNA324162, XM_002704,
gen.XM_002704
Figure 854: DNA194740, NM_005291,
gen.NM_005291
Figure 855: PRO24028
Figure 856A-B: DNA324163, XM_114267,
gen.XM_114267
Figure 857: DNA324164, XM_034952,
gen.XM_034952
Figure 858: DNA324165, XM_086950,
gen.XM_086950
Figure 859A-B: DNA255531, NM_017751,
gen.NM_017751
Figure 860: PRO50596
Figure 861: DNA324166, XM_017698,
gen.XM_017698
Figure 862: DNA324167, XM_030529,
gen.XM_030529
Figure 863: PRO80866
Figure 864: DNA275240, NM_005915,
gen.NM_005915
Figure 865: PRO62927
Figure 866: DNA324168, XM_043173,
gen.XM_043173
Figure 867: DNA324169, XM_092489,
gen.XM_092489
Figure 868: PRO80868
Figure 869: DNA324170, XM_115672,
gen.XM_115672
Figure 870: PRO80869
Figure 871: DNA324171, NM_020548,
gen.NM_020548
Figure 872: PRO60753
Figure 873: DNA324172, XM_037101,

gen.XM_037101
Figure 874: PRO80870
Figure 875: DNA324173, NM_032390,
gen.NM_032390
Figure 876: PRO80871
Figure 877: DNA324174, XM_002447,
gen.XM_002447
Figure 878: DNA324175, NM_033416,
gen.NM_033416
Figure 879: PRO80873
Figure 880: DNA324176, XM_016288,
gen.XM_016288
Figure 881: DNA272127, NM_003937,
gen.NM_003937
Figure 882: PRO60397
Figure 883: DNA324177, XM_030582,
gen.XM_030582
Figure 884: PRO80875
Figure 885: DNA324178, NM_015702,
gen.NM_015702
Figure 886: PRO80876
Figure 887: DNA324179, NM_016838,
gen.NM_016838
Figure 888: PRO80877
Figure 889: DNA324180, NM_016839,
gen.NM_016839
Figure 890: PRO80878
Figure 891: DNA324181, XM_087118,
gen.XM_087118
Figure 892: PRO80879
Figure 893: DNA324182, XM_165998,
gen.XM_165998
Figure 894: DNA324183, NM_001935,
gen.NM_001935
Figure 895: PRO80881
Figure 896: DNA324184, NM_020675,
gen.NM_020675
Figure 897: PRO80882
Figure 898: DNA88051, NM_000079, gen.NM_000079
Figure 899: PRO2146
Figure 900: DNA324185, XM_166008,
gen.XM_166008
Figure 901: DNA324186, XM_087240,
gen.XM_087240
Figure 902: PRO11403
Figure 903: DNA324187, NM_013341,
gen.NM_013341
Figure 904: PRO80883
Figure 905: DNA304805, NM_031942,
gen.NM_031942
Figure 906: PRO69531
Figure 907: DNA324188, XM_059465,
gen.XM_059465
Figure 908: PRO80884
Figure 909: DNA324189, XM_015920,
gen.XM_015920

Figure 910: DNA324190, XM_166007,
gen.XM_166007
Figure 911: DNA324191, XM_015922,
gen.XM_015922
Figure 912: DNA324192, XM_087061,
gen.XM_087061
Figure 913: PRO80888
Figure 914: DNA324193, XM_087062,
gen.XM_087062
Figure 915: PRO80889
Figure 916: DNA324194, NM_001463,
gen.NM_001463
Figure 917: PRO80890
Figure 918: DNA324195, XM_092158,
gen.XM_092158
Figure 919: PRO80891
Figure 920: DNA324196, XM_059351,
gen.XM_059351
Figure 921A-B: DNA324197, NM_000090,
gen.NM_000090
Figure 922: PRO2665
Figure 923: DNA324198, NM_014585,
gen.NM_014585
Figure 924: PRO37675
Figure 925: DNA324199, XM_010778,
gen.XM_010778
Figure 926: DNA324200, XM_086961,
gen.XM_086961
Figure 927: DNA324201, XM_165994,
gen.XM_165994
Figure 928: DNA324202, XM_045170,
gen.XM_045170
Figure 929: DNA324203, XM_113390,
gen.XM_113390
Figure 930: DNA299899, NM_002157,
gen.NM_002157
Figure 931: PRO62760
Figure 932: DNA324204, XM_087045,
gen.XM_087045
Figure 933: DNA324205, XM_086944,
gen.XM_086944
Figure 934: DNA271608, NM_014670,
gen.NM_014670
Figure 935: PRO59895
Figure 936: DNA324206, XM_027963,
gen.XM_027963
Figure 937: PRO80900
Figure 938: DNA324207, XM_010852,
gen.XM_010852
Figure 939: PRO80901
Figure 940: DNA324208, XM_028034,
gen.XM_028034
Figure 941: DNA324209, NM_015934,
gen.NM_015934
Figure 942: DNA324210, XM_087028,
gen.XM_087028

Figure 943: PRO80903
Figure 944: DNA324211, XM_092346,
gen.XM_092346
Figure 945: PRO80904
Figure 946: DNA324212, XM_002669,
gen.XM_002669
Figure 947: PRO80905
Figure 948: DNA324213, NM_021121,
gen.NM_021121
Figure 949: PRO23124
Figure 950: DNA324214, NM_001959,
gen.NM_001959
Figure 951: PRO23124
Figure 952: DNA324215, XM_030834,
gen.XM_030834
Figure 953: PRO80906
Figure 954A-C: DNA324216, XM_055254,
gen.XM_055254
Figure 955: DNA324217, NM_004044,
gen.NM_004044
Figure 956: PRO80908
Figure 957: DNA324218, XM_114298,
gen.XM_114298
Figure 958: DNA324219, NM_021141,
gen.NM_021141
Figure 959: PRO59313
Figure 960A-B: DNA324220, XM_098048,
gen.XM_098048
Figure 961: PRO80910
Figure 962: DNA324221, XM_098047,
gen.XM_098047
Figure 963: PRO80911
Figure 964: DNA324222, XM_002636,
gen.XM_002636
Figure 965: DNA324223, XM_087181,
gen.XM_087181
Figure 966: DNA324224, NM_000998,
gen.NM_000998
Figure 967: PRO10498
Figure 968: DNA324225, XM_059422,
gen.XM_059422
Figure 969: PRO9984
Figure 970: DNA324226, XM_092545,
gen.XM_092545
Figure 971: DNA324227, XM_059461,
gen.XM_059461
Figure 972: PRO80915
Figure 973: DNA324228, NM_018674,
gen.NM_018674
Figure 974: PRO80916
Figure 975: DNA324229, XM_050962,
gen.XM_050962
Figure 976: PRO80917
Figure 977: DNA194827, NM_012100,
gen.NM_012100
Figure 978: PRO24091

Figure 979: DNA324230, XM_050638,
gen.XM_050638
Figure 980A-B: DNA324231, NM_002846,
gen.NM_002846
Figure 981: PRO2610
Figure 982: DNA324232, NM_006000,
gen.NM_006000
Figure 983: PRO26228
Figure 984: DNA324233, XM_050891,
gen.XM_050891
Figure 985: DNA324234, XM_087162,
gen.XM_087162
Figure 986: DNA324235, XM_058098,
gen.XM_058098
Figure 987: PRO80920
Figure 988: DNA324236, NM_022453,
gen.NM_022453
Figure 989: PRO80921
Figure 990: DNA324237, NM_032726,
gen.NM_032726
Figure 991: PRO70675
Figure 992: DNA324238, XM_010866,
gen.XM_010866
Figure 993: DNA324239, XM_087166,
gen.XM_087166
Figure 994: DNA254204, NM_001087,
gen.NM_001087
Figure 995: PRO49316
Figure 996: DNA324240, NM_005731,
gen.NM_005731
Figure 997: PRO80924
Figure 998: DNA189697, NM_004846,
gen.NM_004846
Figure 999: PRO23123
Figure 1000: DNA324241, NM_025202,
gen.NM_025202
Figure 1001: PRO80925
Figure 1002: DNA324242, XM_115825,
gen.XM_115825
Figure 1003: PRO80926
Figure 1004: DNA324243, XM_010858,
gen.XM_010858
Figure 1005: PRO80927
Figure 1006: DNA324244, XM_002540,
gen.XM_002540
Figure 1007: DNA324245, XM_048690,
gen.XM_048690
Figure 1008: PRO80929
Figure 1009: DNA324246, NM_030926,
gen.NM_030926
Figure 1010: PRO80930
Figure 1011: DNA324247, XM_087218,
gen.XM_087218
Figure 1012: DNA324248, NM_004509,
gen.NM_004509
Figure 1013: PRO80932

Figure 1014: DNA324249, NM_004510,
gen.NM_004510
Figure 1015: PRO80933
Figure 1016: DNA324250, NM_080424,
gen.NM_080424
Figure 1017: PRO80934
Figure 1018: DNA324251, NM_018410,
gen.NM_018410
Figure 1019: PRO80935
Figure 1020: DNA324252, NM_017974,
gen.NM_017974
Figure 1021: PRO80936
Figure 1022A-B: DNA324253, XM_096169,
gen.XM_096169
Figure 1023: PRO80937
Figure 1024: DNA150884, NM_005855,
gen.NM_005855
Figure 1025: PRO12520
Figure 1026A-B: DNA324254, NM_004735,
gen.NM_004735
Figure 1027: PRO80938
Figure 1028A-C: DNA324255, XM_030203,
gen.XM_030203
Figure 1029: DNA324256, XM_059372,
gen.XM_059372
Figure 1030: DNA324257, NM_002712,
gen.NM_002712
Figure 1031: PRO80941
Figure 1032A-B: DNA324258, XM_042326,
gen.XM_042326
Figure 1033: PRO80942
Figure 1034: DNA324259, NM_004404,
gen.NM_004404
Figure 1035: PRO80943
Figure 1036: DNA324260, XM_002742,
gen.XM_002742
Figure 1037: DNA324261, NM_138483,
gen.NM_138483
Figure 1038: PRO80945
Figure 1039: DNA324262, XM_115706,
gen.XM_115706
Figure 1040: DNA324263, XM_115722,
gen.XM_115722
Figure 1041: DNA324264, XM_084141,
gen.XM_084141
Figure 1042: DNA324265, XM_005086,
gen.XM_005086
Figure 1043: DNA324266, NM_015453,
gen.NM_015453
Figure 1044: PRO80949
Figure 1045: DNA324267, NM_022485,
gen.NM_022485
Figure 1046: PRO80950
Figure 1047A-B: DNA324268, XM_054520,
gen.XM_054520
Figure 1048: PRO80951

Figure 1049: DNA324269, NM_006354,
gen.NM_006354
Figure 1050: PRO80952
Figure 1051: DNA324270, NM_133480,
gen.NM_133480
Figure 1052: PRO80953
Figure 1053: DNA324271, NM_133481,
gen.NM_133481
Figure 1054: PRO80954
Figure 1055: DNA324272, NM_005718,
gen.NM_005718
Figure 1056: PRO80955
Figure 1057: DNA324273, NM_015644,
gen.NM_015644
Figure 1058: PRO80956
Figure 1059: DNA324274, XM_059561,
gen.XM_059561
Figure 1060: DNA324275, XM_052310,
gen.XM_052310
Figure 1061: PRO80958
Figure 1062: DNA269910, NM_006395,
gen.NM_006395
Figure 1063: PRO58308
Figure 1064: DNA324276, NM_000994,
gen.NM_000994
Figure 1065: PRO80959
Figure 1066: DNA151017, NM_004844,
gen.NM_004844
Figure 1067: PRO12841
Figure 1068: DNA324277, XM_059557,
gen.XM_059557
Figure 1069: PRO80960
Figure 1070A-B: DNA324278, XM_042860,
gen.XM_042860
Figure 1071: PRO80961
Figure 1072: DNA324279, XM_042841,
gen.XM_042841
Figure 1073: PRO80962
Figure 1074: DNA324280, XM_053712,
gen.XM_053712
Figure 1075: DNA324281, XM_087284,
gen.XM_087284
Figure 1076: DNA324282, NM_002948,
gen.NM_002948
Figure 1077: PRO6360
Figure 1078: DNA324283, XM_053323,
gen.XM_053323
Figure 1079A-B: DNA324284, NM_001068,
gen.NM_001068
Figure 1080: PRO80966
Figure 1081: DNA252367, NM_017801,
gen.NM_017801
Figure 1082: PRO48357
Figure 1083: DNA324285, XM_093624,
gen.XM_093624
Figure 1084: PRO80967

Figure 1085: DNA324286, XM_046401,
gen.XM_046401
Figure 1086: DNA324287, NM_022461,
gen.NM_022461
Figure 1087: PRO80969
Figure 1088: DNA324288, XM_113410,
gen.XM_113410
Figure 1089: DNA88100, NM_000404,
gen.NM_000404
Figure 1090: PRO2172
Figure 1091: DNA324289, XM_091076,
gen.XM_091076
Figure 1092: PRO80970
Figure 1093A-B: DNA271187, NM_005109,
gen.NM_005109
Figure 1094: PRO59504
Figure 1095: DNA324290, NM_002468,
gen.NM_002468
Figure 1096: PRO36735
Figure 1097: DNA269930, NM_001607,
gen.NM_001607
Figure 1098: PRO58328
Figure 1099: DNA270401, NM_003149,
gen.NM_003149
Figure 1100: PRO58784
Figure 1101: DNA324291, XM_087370,
gen.XM_087370
Figure 1102: PRO80971
Figure 1103: DNA324292, XM_098158,
gen.XM_098158
Figure 1104: PRO80972
Figure 1105: DNA324293, XM_017364,
gen.XM_017364
Figure 1106: DNA324294, XM_087349,
gen.XM_087349
Figure 1107: PRO80974
Figure 1108: DNA226547, NM_002295,
gen.NM_002295
Figure 1109: PRO37010
Figure 1110: DNA324295, NM_003973,
gen.NM_003973
Figure 1111: PRO80975
Figure 1112: DNA324296, XM_030417,
gen.XM_030417
Figure 1113: DNA324297, NM_020347,
gen.NM_020347
Figure 1114: PRO80977
Figure 1115: DNA324298, XM_087346,
gen.XM_087346
Figure 1116: PRO80978
Figure 1117: DNA324299, XM_096198,
gen.XM_096198
Figure 1118: PRO80979
Figure 1119: DNA324300, XM_003222,
gen.XM_003222
Figure 1120: DNA324301, XM_087588,

gen.XM_087588
Figure 1121: DNA324302, XM_166011,
gen.XM_166011
Figure 1122A-B: DNA324303, XM_114364,
gen.XM_114364
Figure 1123A-B: DNA324304, XM_033294,
gen.XM_033294
Figure 1124: PRO80983
Figure 1125: DNA324305, NM_138614,
gen.NM_138614
Figure 1126: PRO80984
Figure 1127: DNA324306, XM_002899,
gen.XM_002899
Figure 1128: DNA225910, NM_004345,
gen.NM_004345
Figure 1129: PRO36373
Figure 1130: DNA324307, XM_010953,
gen.XM_010953
Figure 1131: DNA324308, XM_051518,
gen.XM_051518
Figure 1132A-D: DNA324309, NM_001407,
gen.NM_001407
Figure 1133: PRO50095
Figure 1134: DNA324310, NM_003365,
gen.NM_003365
Figure 1135: PRO80988
Figure 1136: DNA324311, XM_003245,
gen.XM_003245
Figure 1137: DNA324312, XM_047561,
gen.XM_047561
Figure 1138: PRO80990
Figure 1139: DNA324313, XM_116853,
gen.XM_116853
Figure 1140A-B: DNA324314, XM_113405,
gen.XM_113405
Figure 1141: DNA324315, XM_114323,
gen.XM_114323
Figure 1142: PRO80993
Figure 1143: DNA324316, XM_002828,
gen.XM_002828
Figure 1144: PRO80994
Figure 1145: DNA150976, NM_022171,
gen.NM_022171
Figure 1146: PRO12565
Figure 1147: DNA324317, XM_041507,
gen.XM_041507
Figure 1148: PRO71103
Figure 1149: DNA103505, NM_004636,
gen.NM_004636
Figure 1150: PRO4832
Figure 1151: DNA324318, NM_006764,
gen.NM_006764
Figure 1152: PRO80995
Figure 1153: DNA150562, NM_007275,
gen.NM_007275
Figure 1154: PRO12779

Figure 1155: DNA254582, NM_004635, gen.NM_004635
Figure 1156: PRO49685
Figure 1157: DNA324319, NM_052859, gen.NM_052859
Figure 1158: PRO80996
Figure 1159: DNA324320, NM_001064, gen.NM_001064
Figure 1160: PRO80997
Figure 1161: DNA324321, XM_041211, gen.XM_041211
Figure 1162: DNA324322, XM_003213, gen.XM_003213
Figure 1163A-C: DNA324323, XM_037423, gen.XM_037423
Figure 1164: PRO80999
Figure 1165A-B: DNA227307, NM_007184, gen.NM_007184
Figure 1166: PRO37770
Figure 1167: DNA324324, NM_000688, gen.NM_000688
Figure 1168: PRO81000
Figure 1169: DNA324325, XM_067715, gen.XM_067715
Figure 1170: DNA324326, NM_000992, gen.NM_000992
Figure 1171: PRO62153
Figure 1172: DNA324327, NM_000666, gen.NM_000666
Figure 1173: PRO81002
Figure 1174: DNA324328, NM_032750, gen.NM_032750
Figure 1175: PRO81003
Figure 1176: DNA324329, NM_033008, gen.NM_033008
Figure 1177: PRO81004
Figure 1178: DNA324330, NM_033010, gen.NM_033010
Figure 1179: PRO81005
Figure 1180: DNA324331, NM_020418, gen.NM_020418
Figure 1181: PRO81006
Figure 1182: DNA273919, NM_004704, gen.NM_004704
Figure 1183: PRO61870
Figure 1184A-B: DNA324332, XM_087448, gen.XM_087448
Figure 1185: PRO81007
Figure 1186: DNA324333, XM_002855, gen.XM_002855
Figure 1187: DNA324334, XM_002854, gen.XM_002854
Figure 1188: DNA0, NM_002854, gen.NM_002854
Figure 1189: PRO
Figure 1190: DNA324335, XM_096195, gen.XM_096195

Figure 1191: PRO81010
Figure 1192: DNA324336, XM_166015, gen.XM_166015
Figure 1193: DNA324337, XM_113395, gen.XM_113395
Figure 1194: PRO81012
Figure 1195: DNA269730, NM_014814, gen.NM_014814
Figure 1196: PRO58140
Figure 1197: DNA324338, XM_036938, gen.XM_036938
Figure 1198: DNA324339, XM_029369, gen.XM_029369
Figure 1199: DNA324340, XM_076414, gen.XM_076414
Figure 1200: PRO81015
Figure 1201: DNA324341, XM_093546, gen.XM_093546
Figure 1202: DNA324342, XM_113409, gen.XM_113409
Figure 1203: DNA324343, XM_087268, gen.XM_087268
Figure 1204: DNA324344, XM_116071, gen.XM_116071
Figure 1205: DNA324345, XM_116072, gen.XM_116072
Figure 1206: DNA324346, NM_000986, gen.NM_000986
Figure 1207: PRO10602
Figure 1208: DNA324347, XM_015462, gen.XM_015462
Figure 1209: DNA324348, XM_167366, gen.XM_167366
Figure 1210: PRO81022
Figure 1211: DNA324349, XM_087331, gen.XM_087331
Figure 1212: PRO81023
Figure 1213: DNA324350, XM_039952, gen.XM_039952
Figure 1214: DNA324351, XM_045290, gen.XM_045290
Figure 1215: PRO81025
Figure 1216A-B: DNA324352, NM_007085, gen.NM_007085
Figure 1217: PRO2077
Figure 1218: DNA324353, NM_004547, gen.NM_004547
Figure 1219: PRO81026
Figure 1220: DNA324354, XM_027161, gen.XM_027161
Figure 1221A-B: DNA324355, XM_032269, gen.XM_032269
Figure 1222: PRO81028
Figure 1223: DNA88547, NM_006810, gen.NM_006810
Figure 1224: PRO2837

Figure 1225: DNA324356, XM_114301, gen.XM_114301
Figure 1226: PRO81029
Figure 1227: DNA324357, XM_098173, gen.XM_098173
Figure 1228: PRO81030
Figure 1229: DNA324358, XM_042618, gen.XM_042618
Figure 1230: PRO81031
Figure 1231: DNA324359, XM_084129, gen.XM_084129
Figure 1232: DNA324360, XM_098154, gen.XM_098154
Figure 1233: PRO81033
Figure 1234: DNA324361, XM_050552, gen.XM_050552
Figure 1235: DNA324362, NM_032343, gen.NM_032343
Figure 1236: PRO81034
Figure 1237: DNA324363, XM_051264, gen.XM_051264
Figure 1238A-B: DNA324364, NM_013336, gen.NM_013336
Figure 1239: PRO1314
Figure 1240: DNA324365, XM_067264, gen.XM_067264
Figure 1241: PRO81036
Figure 1242: DNA324366, XM_114309, gen.XM_114309
Figure 1243: DNA324367, XM_084111, gen.XM_084111
Figure 1244: DNA324368, XM_113397, gen.XM_113397
Figure 1245: DNA324369, XM_098111, gen.XM_098111
Figure 1246: DNA324370, NM_004637, gen.NM_004637
Figure 1247: PRO81040
Figure 1248: DNA324371, NM_020701, gen.NM_020701
Figure 1249: PRO81041
Figure 1250: DNA324372, NM_003418, gen.NM_003418
Figure 1251: PRO81042
Figure 1252: DNA324373, XM_059583, gen.XM_059583
Figure 1253: PRO81043
Figure 1254: DNA324374, XM_113417, gen.XM_113417
Figure 1255: DNA324375, XM_093487, gen.XM_093487
Figure 1256A-B: DNA324376, XM_030812, gen.XM_030812
Figure 1257: PRO58177
Figure 1258A-B: DNA324377, XM_039805, gen.XM_039805

Figure 1259: PRO81046
Figure 1260: DNA324378, NM_000532, gen.NM_000532
Figure 1261: PRO81047
Figure 1262: DNA324379, XM_036118, gen.XM_036118
Figure 1263: DNA324380, XM_084123, gen.XM_084123
Figure 1264: DNA324381, XM_018149, gen.XM_018149
Figure 1265: DNA324382, XM_087342, gen.XM_087342
Figure 1266: DNA324383, XM_059516, gen.XM_059516
Figure 1267: DNA324384, XM_087341, gen.XM_087341
Figure 1268: DNA324385, XM_165451, gen.XM_165451
Figure 1269: PRO81053
Figure 1270: DNA269858, NM_004766, gen.NM_004766
Figure 1271: PRO58259
Figure 1272: DNA324386, NM_030921, gen.NM_030921
Figure 1273: PRO51109
Figure 1274: DNA324387, XM_002859, gen.XM_002859
Figure 1275: DNA324388, XM_166014, gen.XM_166014
Figure 1276: DNA324389, NM_013363, gen.NM_013363
Figure 1277: PRO287
Figure 1278: DNA324390, XM_058267, gen.XM_058267
Figure 1279: PRO81056
Figure 1280A-B: DNA324391, NM_032383, gen.NM_032383
Figure 1281: PRO81057
Figure 1282: DNA324392, NM_015472, gen.NM_015472
Figure 1283: PRO81058
Figure 1284: DNA324393, NM_014445, gen.NM_014445
Figure 1285: PRO11048
Figure 1286: DNA324394, XM_042168, gen.XM_042168
Figure 1287: PRO81059
Figure 1288A-B: DNA324395, XM_114356, gen.XM_114356
Figure 1289: DNA324396, XM_105236, gen.XM_105236
Figure 1290: DNA324397, XM_010978, gen.XM_010978
Figure 1291: DNA324398, XM_017356, gen.XM_017356
Figure 1292A-B: DNA324399, XM_039796,

gen.XM_039796
Figure 1293: PRO81064
Figure 1294: DNA324400, XM_016334,
gen.XM_016334
Figure 1295: DNA324401, XM_116058,
gen.XM_116058
Figure 1296: DNA324402, XM_113408,
gen.XM_113408
Figure 1297: DNA324403, NM_002492,
gen.NM_002492
Figure 1298: PRO81068
Figure 1299: DNA324404, XM_037381,
gen.XM_037381
Figure 1300: DNA324405, XM_037377,
gen.XM_037377
Figure 1301: PRO69681
Figure 1302A-B: DNA324406, XM_087254,
gen.XM_087254
Figure 1303: PRO81070
Figure 1304: DNA324407, XM_037600,
gen.XM_037600
Figure 1305: PRO81071
Figure 1306: DNA324408, NM_018023,
gen.NM_018023
Figure 1307: PRO81072
Figure 1308: DNA324409, XM_093423,
gen.XM_093423
Figure 1309: PRO81073
Figure 1310: DNA324410, XM_029136,
gen.XM_029136
Figure 1311: PRO81074
Figure 1312: DNA324411, XM_087322,
gen.XM_087322
Figure 1313A-B: DNA324412, XM_029132,
gen.XM_029132
Figure 1314A-B: DNA324413, XM_029104,
gen.XM_029104
Figure 1315: DNA324414, XM_084120,
gen.XM_084120
Figure 1316: DNA254620, NM_005787,
gen.NM_005787
Figure 1317: PRO49722
Figure 1318: DNA324415, NM_032331,
gen.NM_032331
Figure 1319: PRO81079
Figure 1320: DNA324416, XM_011074,
gen.XM_011074
Figure 1321: PRO81080
Figure 1322: DNA324417, XM_087295,
gen.XM_087295
Figure 1323: DNA324418, XM_087289,
gen.XM_087289
Figure 1324: PRO81082
Figure 1325: DNA324419, XM_105658,
gen.XM_105658
Figure 1326: PRO81083

Figure 1327: DNA89239, NM_000893,
gen.NM_000893
Figure 1328: PRO2906
Figure 1329: DNA324420, XM_113422,
gen.XM_113422
Figure 1330: DNA225592, NM_001622,
gen.NM_001622
Figure 1331: PRO36055
Figure 1332: DNA324421, XM_005180,
gen.XM_005180
Figure 1333: DNA324422, XM_087392,
gen.XM_087392
Figure 1334: PRO81086
Figure 1335A-B: DNA272605, NM_003722,
gen.NM_003722
Figure 1336: PRO60741
Figure 1337: DNA324423, XM_117311,
gen.XM_117311
Figure 1338: DNA324424, XM_116034,
gen.XM_116034
Figure 1339: PRO81088
Figure 1340A-B: DNA324425, XM_084110,
gen.XM_084110
Figure 1341: DNA324426, XM_038243,
gen.XM_038243
Figure 1342: PRO81090
Figure 1343: DNA324427, XM_087359,
gen.XM_087359
Figure 1344: DNA324428, XM_114328,
gen.XM_114328
Figure 1345: DNA324429, XM_098109,
gen.XM_098109
Figure 1346: PRO81093
Figure 1347: DNA324430, XM_087410,
gen.XM_087410
Figure 1348: DNA324431, NM_033316,
gen.NM_033316
Figure 1349: PRO81095
Figure 1350: DNA324432, XM_166017,
gen.XM_166017
Figure 1351: PRO81096
Figure 1352: DNA79129, NM_001647,
gen.NM_001647
Figure 1353: PRO2551
Figure 1354: DNA324433, NM_032288,
gen.NM_032288
Figure 1355: PRO81097
Figure 1356: DNA324434, XM_086228,
gen.XM_086228
Figure 1357: PRO81098
Figure 1358: DNA324435, XM_087278,
gen.XM_087278
Figure 1359: DNA324436, XM_018523,
gen.XM_018523
Figure 1360: DNA324437, XM_087297,
gen.XM_087297

Figure 1361: DNA324438, XM_002255,
gen.XM_002255
Figure 1362: PRO81102
Figure 1363: DNA324439, XM_053122,
gen.XM_053122
Figure 1364: DNA324440, XM_042695,
gen.XM_042695
Figure 1365: DNA324441, XM_011160,
gen.XM_011160
Figure 1366: DNA324442, NM_007100,
gen.NM_007100
Figure 1367: PRO81106
Figure 1368: DNA139747, NM_002477,
gen.NM_002477
Figure 1369: PRO9785
Figure 1370: DNA253804, NM_032219,
gen.NM_032219
Figure 1371: PRO49209
Figure 1372: DNA324443, NM_138385,
gen.NM_138385
Figure 1373: PRO81107
Figure 1374: DNA324444, NM_006342,
gen.NM_006342
Figure 1375: PRO81108
Figure 1376A-C: DNA324445, NM_133330,
gen.NM_133330
Figure 1377: PRO81109
Figure 1378A-C: DNA324446, NM_014919,
gen.NM_014919
Figure 1379: PRO81110
Figure 1380A-C: DNA324447, NM_133332,
gen.NM_133332
Figure 1381: PRO81111
Figure 1382: DNA324448, NM_005663,
gen.NM_005663
Figure 1383: PRO81112
Figure 1384A-B: DNA324449, XM_098248,
gen.XM_098248
Figure 1385: PRO81113
Figure 1386: DNA270615, NM_002938,
gen.NM_002938
Figure 1387: PRO58986
Figure 1388A-B: DNA324450, NM_014190,
gen.NM_014190
Figure 1389: PRO81114
Figure 1390A-B: DNA324451, NM_014189,
gen.NM_014189
Figure 1391: PRO81115
Figure 1392: DNA324452, XM_035572,
gen.XM_035572
Figure 1393: PRO81116
Figure 1394A-B: DNA324453, NM_014556,
gen.NM_014556
Figure 1395: PRO81117
Figure 1396: DNA324454, NM_001313,
gen.NM_001313

Figure 1397: PRO60542
Figure 1398A-B: DNA324455, XM_052626,
gen.XM_052626
Figure 1399: PRO81118
Figure 1400: DNA324456, NM_016930,
gen.NM_016930
Figure 1401: PRO81119
Figure 1402: DNA324457, XM_035824,
gen.XM_035824
Figure 1403: PRO81120
Figure 1404: DNA324458, NM_033296,
gen.NM_033296
Figure 1405: PRO81121
Figure 1406: DNA324459, NM_138699,
gen.NM_138699
Figure 1407: PRO81122
Figure 1408: DNA324460, XM_116285,
gen.XM_116285
Figure 1409: PRO81123
Figure 1410: DNA324461, XM_041221,
gen.XM_041221
Figure 1411: PRO81124
Figure 1412: DNA324462, XM_117351,
gen.XM_117351
Figure 1413: DNA324463, XM_039165,
gen.XM_039165
Figure 1414: DNA324464, NM_025205,
gen.NM_025205
Figure 1415: PRO81127
Figure 1416: DNA324465, XM_039173,
gen.XM_039173
Figure 1417: DNA324466, XM_039176,
gen.XM_039176
Figure 1418: DNA324467, XM_087583,
gen.XM_087583
Figure 1419: DNA324468, NM_017491,
gen.NM_017491
Figure 1420: PRO12077
Figure 1421: DNA324469, NM_005112,
gen.NM_005112
Figure 1422: PRO81131
Figure 1423: DNA324470, XM_011129,
gen.XM_011129
Figure 1424A-B: DNA324471, XM_052530,
gen.XM_052530
Figure 1425: DNA324472, NM_000661,
gen.NM_000661
Figure 1426: PRO81134
Figure 1427A-B: DNA324473, NM_002913,
gen.NM_002913
Figure 1428: PRO81135
Figure 1429A-B: DNA324474, XM_047477,
gen.XM_047477
Figure 1430: DNA324475, NM_004181,
gen.NM_004181
Figure 1431: PRO81137

Figure 1432: DNA324476, XM_003435,
gen.XM_003435
Figure 1433: DNA324478, XM_010941,
gen.XM_010941
Figure 1434: DNA324479, XM_059593,
gen.XM_059593
Figure 1435: DNA324480, NM_001553,
gen.NM_001553
Figure 1436: PRO81141
Figure 1437: DNA257511, NM_032313,
gen.NM_032313
Figure 1438: PRO52083
Figure 1439: DNA324481, XM_071623,
gen.XM_071623
Figure 1440A-B: DNA324482, XM_036002,
gen.XM_036002
Figure 1441: DNA324483, XM_058927,
gen.XM_058927
Figure 1442: DNA324484, XM_059628,
gen.XM_059628
Figure 1443: DNA324485, XM_046057,
gen.XM_046057
Figure 1444: PRO81146
Figure 1445: DNA324486, XM_031320,
gen.XM_031320
Figure 1446: DNA225919, NM_001134,
gen.NM_001134
Figure 1447: PRO36382
Figure 1448A-B: DNA324487, XM_003511,
gen.XM_003511
Figure 1449: DNA324488, NM_006835,
gen.NM_006835
Figure 1450: PRO4605
Figure 1451: DNA324489, XM_003305,
gen.XM_003305
Figure 1452: DNA324490, XM_113425,
gen.XM_113425
Figure 1453: DNA324491, XM_001389,
gen.XM_001389
Figure 1454: PRO81148
Figure 1455: DNA324492, XM_087527,
gen.XM_087527
Figure 1456: DNA324493, XM_035986,
gen.XM_035986
Figure 1457A-B: DNA324494, NM_014933,
gen.NM_014933
Figure 1458: PRO81150
Figure 1459: DNA290585, NM_000582,
gen.NM_000582
Figure 1460: PRO70536
Figure 1461: DNA324495, XM_055551,
gen.XM_055551
Figure 1462: PRO81151
Figure 1463: DNA324496, XM_087498,
gen.XM_087498
Figure 1464: DNA324497, XM_096203,

gen.XM_096203
Figure 1465: DNA324498, XM_084158,
gen.XM_084158
Figure 1466: DNA324499, XM_034710,
gen.XM_034710
Figure 1467: PRO81156
Figure 1468: DNA324500, XM_034713,
gen.XM_034713
Figure 1469: DNA324501, XM_059633,
gen.XM_059633
Figure 1470: DNA324502, XM_114426,
gen.XM_114426
Figure 1471: DNA324503, XM_056957,
gen.XM_056957
Figure 1472: DNA324504, XM_088472,
gen.XM_088472
Figure 1473: DNA324505, XM_114424,
gen.XM_114424
Figure 1474A-B: DNA324506, XM_042301,
gen.XM_042301
Figure 1475: PRO81163
Figure 1476: DNA324507, XM_017925,
gen.XM_017925
Figure 1477: DNA324508, XM_052336,
gen.XM_052336
Figure 1478: DNA324509, NM_002106,
gen.NM_002106
Figure 1479: PRO10297
Figure 1480: DNA324510, XM_085068,
gen.XM_085068
Figure 1481: PRO81166
Figure 1482: DNA324511, XM_165473,
gen.XM_165473
Figure 1483: DNA324512, XM_087514,
gen.XM_087514
Figure 1484: DNA324513, XM_116247,
gen.XM_116247
Figure 1485: DNA324514, NM_002358,
gen.NM_002358
Figure 1486: PRO81169
Figure 1487: DNA324515, XM_050200,
gen.XM_050200
Figure 1488: PRO81170
Figure 1489: DNA225584, NM_001154,
gen.NM_001154
Figure 1490: PRO36047
Figure 1491: DNA324516, NM_024900,
gen.NM_024900
Figure 1492: PRO81171
Figure 1493: DNA324517, XM_040752,
gen.XM_040752
Figure 1494: DNA324518, NM_002413,
gen.NM_002413
Figure 1495: PRO60956
Figure 1496: DNA324519, XM_114401,
gen.XM_114401

Figure 1497: DNA324520, XM_068164, gen.XM_068164
Figure 1498: PRO81174
Figure 1499: DNA324521, XM_060067, gen.XM_060067
Figure 1500: DNA324522, XM_003555, gen.XM_003555
Figure 1501: PRO81176
Figure 1502: DNA324523, XM_034321, gen.XM_034321
Figure 1503: PRO81177
Figure 1504: DNA324524, NM_006439, gen.NM_006439
Figure 1505: PRO81178
Figure 1506: DNA324525, NM_001006, gen.NM_001006
Figure 1507: PRO81179
Figure 1508: DNA227575, NM_005141, gen.NM_005141
Figure 1509: PRO38038
Figure 1510: DNA324526, XM_114368, gen.XM_114368
Figure 1511A-B: DNA225920, NM_000508, gen.NM_000508
Figure 1512: PRO36383
Figure 1513: DNA324527, NM_021871, gen.NM_021871
Figure 1514: PRO81181
Figure 1515: DNA225921, NM_000509, gen.NM_000509
Figure 1516: PRO36384
Figure 1517: DNA324528, NM_021870, gen.NM_021870
Figure 1518: PRO81182
Figure 1519: DNA324529, XM_059623, gen.XM_059623
Figure 1520: DNA324530, XM_106246, gen.XM_106246
Figure 1521: PRO81184
Figure 1522: DNA324531, NM_002129, gen.NM_002129
Figure 1523: PRO81185
Figure 1524: DNA324532, XM_040321, gen.XM_040321
Figure 1525: DNA324533, XM_015563, gen.XM_015563
Figure 1526: DNA324534, NM_024748, gen.NM_024748
Figure 1527: PRO81188
Figure 1528: DNA324535, XM_165470, gen.XM_165470
Figure 1529: PRO81189
Figure 1530A-E: DNA324536, XM_003477, gen.XM_003477
Figure 1531: DNA324537, XM_165465, gen.XM_165465

Figure 1532: DNA324538, XM_116204, gen.XM_116204
Figure 1533: DNA324539, XM_116205, gen.XM_116205
Figure 1534: DNA324540, XM_098405, gen.XM_098405
Figure 1535: DNA324541, XM_052313, gen.XM_052313
Figure 1536: PRO81195
Figure 1537: DNA324542, XM_087659, gen.XM_087659
Figure 1538: PRO81196
Figure 1539: DNA324543, XM_029096, gen.XM_029096
Figure 1540: DNA324544, XM_003825, gen.XM_003825
Figure 1541: DNA324545, XM_057994, gen.XM_057994
Figure 1542: PRO81199
Figure 1543: DNA324546, XM_087686, gen.XM_087686
Figure 1544: DNA324547, XM_017641, gen.XM_017641
Figure 1545: DNA324548, NM_030782, gen.NM_030782
Figure 1546: PRO81202
Figure 1547: DNA324549, XM_084168, gen.XM_084168
Figure 1548: DNA324550, XM_057492, gen.XM_057492
Figure 1549: DNA324551, XM_087597, gen.XM_087597
Figure 1550: DNA324552, XM_087601, gen.XM_087601
Figure 1551: DNA324554, XM_087599, gen.XM_087599
Figure 1552: DNA324555, XM_114435, gen.XM_114435
Figure 1553: DNA324556, XM_087600, gen.XM_087600
Figure 1554: DNA324557, XM_016170, gen.XM_016170
Figure 1555: DNA324558, XM_114434, gen.XM_114434
Figure 1556: DNA324559, XM_113452, gen.XM_113452
Figure 1557: DNA324560, XM_071580, gen.XM_071580
Figure 1558: PRO81213
Figure 1559: DNA324561, XM_087713, gen.XM_087713
Figure 1560: PRO81214
Figure 1561: DNA324562, XM_094440, gen.XM_094440
Figure 1562: DNA324563, XM_106739, gen.XM_106739

Figure 1563: PRO81216
Figure 1564: DNA324564, XM_087614,
gen.XM_087614
Figure 1565: DNA324565, XM_004009,
gen.XM_004009
Figure 1566: PRO81219
Figure 1567: DNA324566, XM_114437,
gen.XM_114437
Figure 1568: DNA324567, XM_043771,
gen.XM_043771
Figure 1569: PRO81221
Figure 1570: DNA324568, NM_000997,
gen.NM_000997
Figure 1571: PRO11077
Figure 1572: DNA324569, XM_003869,
gen.XM_003869
Figure 1573: DNA227173, NM_001465,
gen.NM_001465
Figure 1574: PRO37636
Figure 1575: DNA324570, NM_018034,
gen.NM_018034
Figure 1576: PRO81223
Figure 1577: DNA324571, NM_032637,
gen.NM_032637
Figure 1578: PRO81224
Figure 1579: DNA324572, NM_005983,
gen.NM_005983
Figure 1580: PRO81225
Figure 1581A-B: DNA324573, XM_003896,
gen.XM_003896
Figure 1582: DNA287282, NM_002130,
gen.NM_002130
Figure 1583: PRO69554
Figure 1584: DNA324574, XM_114442,
gen.XM_114442
Figure 1585: PRO81227
Figure 1586: DNA324575, XM_114439,
gen.XM_114439
Figure 1587: DNA324576, XM_114440,
gen.XM_114440
Figure 1588A-B: DNA324577, XM_032902,
gen.XM_032902
Figure 1589: PRO81230
Figure 1590: DNA324578, XM_032895,
gen.XM_032895
Figure 1591: DNA324579, XM_084179,
gen.XM_084179
Figure 1592: DNA324580, XM_041712,
gen.XM_041712
Figure 1593: DNA324581, XM_116439,
gen.XM_116439
Figure 1594: PRO81234
Figure 1595: DNA324582, XM_087611,
gen.XM_087611
Figure 1596: DNA324583, XM_059653,
gen.XM_059653

Figure 1597: DNA324584, XM_087610,
gen.XM_087610
Figure 1598: DNA288259, NM_031966,
gen.NM_031966
Figure 1599: PRO4676
Figure 1600: DNA324585, XM_042025,
gen.XM_042025
Figure 1601: PRO81238
Figure 1602: DNA324586, NM_005713,
gen.NM_005713
Figure 1603: PRO81239
Figure 1604: DNA324587, XM_059709,
gen.XM_059709
Figure 1605: PRO81240
Figure 1606: DNA324588, XM_116447,
gen.XM_116447
Figure 1607: PRO81241
Figure 1608: DNA324589, XM_037260,
gen.XM_037260
Figure 1609: DNA324590, XM_098351,
gen.XM_098351
Figure 1610: DNA324591, XM_098354,
gen.XM_098354
Figure 1611: DNA324592, XM_098352,
gen.XM_098352
Figure 1612: DNA324593, XM_166037,
gen.XM_166037
Figure 1613: PRO81246
Figure 1614: DNA324594, XM_041694,
gen.XM_041694
Figure 1615: DNA324595, XM_165488,
gen.XM_165488
Figure 1616: PRO81248
Figure 1617: DNA324596, XM_059669,
gen.XM_059669
Figure 1618: PRO81249
Figure 1619: DNA324597, XM_027964,
gen.XM_027964
Figure 1620: PRO81250
Figure 1621: DNA324598, XM_088020,
gen.XM_088020
Figure 1622: DNA324599, XM_117387,
gen.XM_117387
Figure 1623: DNA324600, XM_114469,
gen.XM_114469
Figure 1624: DNA324601, NM_001207,
gen.NM_001207
Figure 1625: PRO22771
Figure 1626A-B: DNA324602, XM_032553,
gen.XM_032553
Figure 1627: DNA254147, NM_000521,
gen.NM_000521
Figure 1628: PRO49262
Figure 1629: DNA324603, NM_031482,
gen.NM_031482
Figure 1630: PRO81254

Figure 1631: DNA324604, XM_087790,
gen.XM_087790
Figure 1632: DNA324605, NM_001025,
gen.NM_001025
Figure 1633: PRO10685
Figure 1634: DNA324606, XM_098362,
gen.XM_098362
Figure 1635: PRO81256
Figure 1636: DNA324607, NM_003401,
gen.NM_003401
Figure 1637: PRO70327
Figure 1638: DNA290231, NM_022550,
gen.NM_022550
Figure 1639: PRO70327
Figure 1640: DNA324608, XM_017857,
gen.XM_017857
Figure 1641: DNA324609, XM_117398,
gen.XM_117398
Figure 1642A-B: DNA257253, NM_032280,
gen.NM_032280
Figure 1643: PRO51851
Figure 1644: DNA324610, XM_003771,
gen.XM_003771
Figure 1645: PRO81259
Figure 1646A-B: DNA269816, NM_002397,
gen.NM_002397
Figure 1647: PRO58219
Figure 1648: DNA324611, XM_116427,
gen.XM_116427
Figure 1649: PRO81260
Figure 1650: DNA324612, NM_004772,
gen.NM_004772
Figure 1651: PRO81261
Figure 1652: DNA324613, XM_016674,
gen.XM_016674
Figure 1653: PRO81262
Figure 1654: DNA324614, XM_113463,
gen.XM_113463
Figure 1655: DNA324615, XM_034744,
gen.XM_034744
Figure 1656: DNA324616, XM_087745,
gen.XM_087745
Figure 1657: PRO81264
Figure 1658: DNA324617, XM_018473,
gen.XM_018473
Figure 1659: PRO81265
Figure 1660: DNA324618, XM_087635,
gen.XM_087635
Figure 1661: PRO81266
Figure 1662: DNA324619, XM_087637,
gen.XM_087637
Figure 1663: DNA324620, XM_166027,
gen.XM_166027
Figure 1664: DNA324621, NM_014035,
gen.NM_014035
Figure 1665: PRO1285

Figure 1666: DNA324622, XM_003830,
gen.XM_003830
Figure 1667: PRO81269
Figure 1668: DNA324623, XM_037002,
gen.XM_037002
Figure 1669: DNA324624, XM_166026,
gen.XM_166026
Figure 1670: DNA324625, XM_041059,
gen.XM_041059
Figure 1671: DNA83020, NM_000358,
gen.NM_000358
Figure 1672: PRO2561
Figure 1673: DNA324626, NM_003687,
gen.NM_003687
Figure 1674: PRO81272
Figure 1675: DNA324627, XM_034862,
gen.XM_034862
Figure 1676: PRO34544
Figure 1677: DNA103380, NM_003374,
gen.NM_003374
Figure 1678: PRO4710
Figure 1679: DNA324628, XM_017474,
gen.XM_017474
Figure 1680: PRO63082
Figure 1681A-B: DNA324629, NM_014829,
gen.NM_014829
Figure 1682: PRO81273
Figure 1683A-B: DNA324630, XM_114482,
gen.XM_114482
Figure 1684: PRO81274
Figure 1685: DNA324631, NM_004893,
gen.NM_004893
Figure 1686: PRO81275
Figure 1687: DNA269809, NM_006805,
gen.NM_006805
Figure 1688: PRO58213
Figure 1689: DNA226872, NM_001964,
gen.NM_001964
Figure 1690: PRO37335
Figure 1691: DNA324632, XM_116307,
gen.XM_116307
Figure 1692: PRO81276
Figure 1693: DNA324633, NM_004134,
gen.NM_004134
Figure 1694: PRO81277
Figure 1695: DNA324634, XM_038221,
gen.XM_038221
Figure 1696: PRO81278
Figure 1697: DNA271931, NM_005754,
gen.NM_005754
Figure 1698: PRO60207
Figure 1699: DNA324635, XM_003841,
gen.XM_003841
Figure 1700: DNA324636, XM_032759,
gen.XM_032759
Figure 1701: DNA324637, XM_017591,

gen.XM_017591
Figure 1702: DNA324638, NM_006058,
gen.NM_006058
Figure 1703: PRO81280
Figure 1704: DNA324639, NM_002084,
gen.NM_002084
Figure 1705: PRO81281
Figure 1706: DNA324640, NM_018047,
gen.NM_018047
Figure 1707: PRO81282
Figure 1708: DNA324641, NM_005617,
gen.NM_005617
Figure 1709: PRO10849
Figure 1710: DNA324642, XM_003937,
gen.XM_003937
Figure 1711: DNA324643, XM_087621,
gen.XM_087621
Figure 1712A-B: DNA324644, XM_003789,
gen.XM_003789
Figure 1713: DNA324645, XM_087652,
gen.XM_087652
Figure 1714: DNA324646, XM_068853,
gen.XM_068853
Figure 1715: PRO81286
Figure 1716: DNA324647, XM_116465,
gen.XM_116465
Figure 1717: PRO81287
Figure 1718: DNA302020, NM_005573,
gen.NM_005573
Figure 1719: PRO70993
Figure 1720: DNA324648, XM_113467,
gen.XM_113467
Figure 1721: DNA271626, NM_014773,
gen.NM_014773
Figure 1722: PRO59913
Figure 1723A-B: DNA324649, XM_056315,
gen.XM_056315
Figure 1724: DNA324650, NM_024668,
gen.NM_024668
Figure 1725: PRO81289
Figure 1726: DNA324651, NM_080670,
gen.NM_080670
Figure 1727: PRO81290
Figure 1728A-B: DNA324652, NM_002588,
gen.NM_002588
Figure 1729: PRO81291
Figure 1730A-B: DNA324653, NM_003735,
gen.NM_003735
Figure 1731: PRO81292
Figure 1732A-B: DNA150679, NM_003736,
gen.NM_003736
Figure 1733: PRO12416
Figure 1734A-B: DNA324654, NM_018912,
gen.NM_018912
Figure 1735: PRO36058
Figure 1736A-B: DNA324655, NM_018913,

gen.NM_018913
Figure 1737: PRO81293
Figure 1738A-B: DNA324656, NM_018914,
gen.NM_018914
Figure 1739: PRO81294
Figure 1740A-B: DNA324657, NM_018915,
gen.NM_018915
Figure 1741: PRO36020
Figure 1742A-B: DNA324658, NM_018916,
gen.NM_018916
Figure 1743: PRO81295
Figure 1744A-B: DNA324659, NM_018917,
gen.NM_018917
Figure 1745: PRO81296
Figure 1746A-B: DNA324660, NM_018918,
gen.NM_018918
Figure 1747: PRO81297
Figure 1748A-B: DNA324661, NM_018919,
gen.NM_018919
Figure 1749: PRO81298
Figure 1750A-B: DNA324662, NM_018920,
gen.NM_018920
Figure 1751: PRO81299
Figure 1752A-B: DNA324663, NM_018921,
gen.NM_018921
Figure 1753: PRO81300
Figure 1754A-B: DNA324664, NM_018922,
gen.NM_018922
Figure 1755: PRO81301
Figure 1756A-B: DNA324665, NM_018923,
gen.NM_018923
Figure 1757: PRO81302
Figure 1758A-B: DNA324666, NM_018924,
gen.NM_018924
Figure 1759: PRO81303
Figure 1760A-B: DNA324667, NM_018925,
gen.NM_018925
Figure 1761: PRO81304
Figure 1762A-B: DNA324668, NM_018926,
gen.NM_018926
Figure 1763: PRO81305
Figure 1764A-B: DNA324669, NM_018927,
gen.NM_018927
Figure 1765: PRO37091
Figure 1766A-B: DNA324670, NM_018928,
gen.NM_018928
Figure 1767: PRO81306
Figure 1768A-B: DNA324671, NM_018929,
gen.NM_018929
Figure 1769: PRO81307
Figure 1770A-B: DNA324672, NM_032088,
gen.NM_032088
Figure 1771: PRO81308
Figure 1772A-B: DNA324673, NM_032092,
gen.NM_032092
Figure 1773: PRO81309

Figure 1774: DNA324674, NM_032403,
gen.NM_032403
Figure 1775: PRO81310
Figure 1776: DNA324675, NM_032402,
gen.NM_032402
Figure 1777: PRO81311
Figure 1778: DNA324676, XM_098387,
gen.XM_098387
Figure 1779: DNA324677, NM_002109,
gen.NM_002109
Figure 1780: PRO4908
Figure 1781: DNA324678, XM_084180,
gen.XM_084180
Figure 1782: PRO81313
Figure 1783: DNA324679, XM_039975,
gen.XM_039975
Figure 1784: PRO81314
Figure 1785: DNA324680, NM_033551,
gen.NM_033551
Figure 1786: PRO81315
Figure 1787: DNA324681, NM_004821,
gen.NM_004821
Figure 1788: PRO81316
Figure 1789: DNA324682, XM_068395,
gen.XM_068395
Figure 1790: PRO81317
Figure 1791: DNA226418, NM_004060,
gen.NM_004060
Figure 1792: PRO36881
Figure 1793A-B: DNA324683, XM_056963,
gen.XM_056963
Figure 1794: PRO81318
Figure 1795: DNA324684, NM_004219,
gen.NM_004219
Figure 1796: PRO81319
Figure 1797: DNA324685, XM_094243,
gen.XM_094243
Figure 1798A-B: DNA324686, XM_047964,
gen.XM_047964
Figure 1799: DNA324687, XM_016345,
gen.XM_016345
Figure 1800: DNA324688, NM_002887,
gen.NM_002887
Figure 1801: PRO81323
Figure 1802: DNA324689, XM_166029,
gen.XM_166029
Figure 1803: DNA324690, NM_002520,
gen.NM_002520
Figure 1804: PRO58993
Figure 1805: DNA324691, XM_043340,
gen.XM_043340
Figure 1806: PRO81325
Figure 1807: DNA324692, XM_116340,
gen.XM_116340
Figure 1808A-B: DNA324693, XM_043388,
gen.XM_043388

Figure 1809: PRO81327
Figure 1810: DNA324694, XM_116856,
gen.XM_116856
Figure 1811: DNA324695, XM_003716,
gen.XM_003716
Figure 1812: DNA227320, NM_003714,
gen.NM_003714
Figure 1813: PRO37783
Figure 1814: DNA324696, NM_032361,
gen.NM_032361
Figure 1815: PRO81330
Figure 1816: DNA324697, XM_087773,
gen.XM_087773
Figure 1817: DNA324698, XM_114457,
gen.XM_114457
Figure 1818: DNA324699, XM_165483,
gen.XM_165483
Figure 1819: DNA324700, XM_114453,
gen.XM_114453
Figure 1820: DNA324701, XM_165484,
gen.XM_165484
Figure 1821: DNA324702, XM_030771,
gen.XM_030771
Figure 1822: PRO19615
Figure 1823: DNA324703, XM_030777,
gen.XM_030777
Figure 1824: DNA324704, XM_030782,
gen.XM_030782
Figure 1825: PRO81336
Figure 1826: DNA324705, NM_030567,
gen.NM_030567
Figure 1827: PRO81337
Figure 1828: DNA225909, NM_000505,
gen.NM_000505
Figure 1829: PRO36372
Figure 1830: DNA274206, NM_006816,
gen.NM_006816
Figure 1831: PRO62135
Figure 1832: DNA324706, NM_031300,
gen.NM_031300
Figure 1833: PRO81338
Figure 1834: DNA324707, NM_013237,
gen.NM_013237
Figure 1835: PRO81339
Figure 1836: DNA324708, NM_002011,
gen.NM_002011
Figure 1837: PRO81340
Figure 1838: DNA324709, NM_022963,
gen.NM_022963
Figure 1839: PRO81341
Figure 1840: DNA324710, XM_038946,
gen.XM_038946
Figure 1841: DNA324711, XM_113454,
gen.XM_113454
Figure 1842: DNA324712, XM_166028,
gen.XM_166028

Figure 1843: DNA324713, NM_015043,
gen.NM_015043
Figure 1844: PRO81345
Figure 1845: DNA324714, XM_113468,
gen.XM_113468
Figure 1846: DNA324715, NM_014275,
gen.NM_014275
Figure 1847: PRO1927
Figure 1848: DNA324716, NM_054013,
gen.NM_054013
Figure 1849: PRO81347
Figure 1850: DNA270675, NM_005520,
gen.NM_005520
Figure 1851: PRO59040
Figure 1852: DNA324717, NM_006098,
gen.NM_006098
Figure 1853: PRO25849
Figure 1854: DNA269593, NM_005110,
gen.NM_005110
Figure 1855: PRO58006
Figure 1856: DNA324718, XM_116365,
gen.XM_116365
Figure 1857: DNA324719, XM_116511,
gen.XM_116511
Figure 1858: DNA324720, XM_087823,
gen.XM_087823
Figure 1859A-C: DNA324721, XM_053955,
gen.XM_053955
Figure 1860: DNA324722, XM_113476,
gen.XM_113476
Figure 1861: DNA324723, XM_116514,
gen.XM_116514
Figure 1862: DNA324724, XM_094741,
gen.XM_094741
Figure 1863: DNA324725, NM_025168,
gen.NM_025168
Figure 1864: PRO81354
Figure 1865A-B: DNA324726, XM_165740,
gen.XM_165740
Figure 1866: DNA272171, NM_002388,
gen.NM_002388
Figure 1867: PRO60438
Figure 1868: DNA324727, XM_167169,
gen.XM_167169
Figure 1869: PRO81355
Figure 1870: DNA324728, NM_014452,
gen.NM_014452
Figure 1871: PRO868
Figure 1872: DNA324729, XM_166349,
gen.XM_166349
Figure 1873: PRO81356
Figure 1874: DNA304680, NM_007355,
gen.NM_007355
Figure 1875: PRO71106
Figure 1876: DNA324730, XM_165772,
gen.XM_165772

Figure 1877: DNA324731, XM_168123,
gen.XM_168123
Figure 1878: DNA324732, XM_166457,
gen.XM_166457
Figure 1879: DNA324733, XM_166469,
gen.XM_166469
Figure 1880: DNA324734, NM_018135,
gen.NM_018135
Figure 1881: PRO81359
Figure 1882A-B: DNA324735, XM_166340,
gen.XM_166340
Figure 1883: DNA324736, XM_087960,
gen.XM_087960
Figure 1884: DNA324737, XM_166362,
gen.XM_166362
Figure 1885: PRO81362
Figure 1886: DNA227204, NM_015388,
gen.NM_015388
Figure 1887: PRO37667
Figure 1888: DNA324738, XM_166425,
gen.XM_166425
Figure 1889: PRO81363
Figure 1890: DNA324739, NM_057161,
gen.NM_057161
Figure 1891: PRO81364
Figure 1892: DNA270613, NM_006245,
gen.NM_006245
Figure 1893: PRO58984
Figure 1894: DNA324740, NM_006586,
gen.NM_006586
Figure 1895: PRO81365
Figure 1896: DNA324741, XM_166402,
gen.XM_166402
Figure 1897: PRO81366
Figure 1898: DNA324742, NM_001760,
gen.NM_001760
Figure 1899: PRO81367
Figure 1900: DNA287246, NM_004053,
gen.NM_004053
Figure 1901: PRO69521
Figure 1902: DNA324743, NM_017601,
gen.NM_017601
Figure 1903: PRO81368
Figure 1904: DNA275630, NM_006708,
gen.NM_006708
Figure 1905: PRO63253
Figure 1906: DNA324744, NM_014341,
gen.NM_014341
Figure 1907: PRO81369
Figure 1908: DNA304460, NM_016059,
gen.NM_016059
Figure 1909: PRO4984
Figure 1910: DNA324745, XM_166412,
gen.XM_166412
Figure 1911: PRO81370
Figure 1912: DNA304716, NM_078467,

gen.NM_078467
Figure 1913: PRO71142
Figure 1914: DNA324746, XM_166417,
gen.XM_166417
Figure 1915: PRO81371
Figure 1916A-B: DNA324747, NM_003137,
gen.NM_003137
Figure 1917: PRO81372
Figure 1918A-B: DNA324748, NM_004117,
gen.NM_004117
Figure 1919: PRO36841
Figure 1920: DNA324749, XM_166419,
gen.XM_166419
Figure 1921: DNA324750, XM_165794,
gen.XM_165794
Figure 1922: DNA324751, NM_007104,
gen.NM_007104
Figure 1923: PRO10360
Figure 1924: DNA324752, NM_024294,
gen.NM_024294
Figure 1925: PRO81375
Figure 1926: DNA324753, NM_022758,
gen.NM_022758
Figure 1927: PRO50582
Figure 1928: DNA324754, XM_168070,
gen.XM_168070
Figure 1929: DNA324755, NM_012391,
gen.NM_012391
Figure 1930: PRO81377
Figure 1931: DNA324756, XM_166459,
gen.XM_166459
Figure 1932: DNA324757, XM_166333,
gen.XM_166333
Figure 1933: PRO81379
Figure 1934: DNA324758, XM_058039,
gen.XM_058039
Figure 1935: PRO81380
Figure 1936: DNA324759, XM_087990,
gen.XM_087990
Figure 1937: DNA324760, XM_165743,
gen.XM_165743
Figure 1938: DNA324761, XM_166360,
gen.XM_166360
Figure 1939: DNA324763, XM_059801,
gen.XM_059801
Figure 1940: DNA324764, XM_166363,
gen.XM_166363
Figure 1941: DNA324765, XM_016857,
gen.XM_016857
Figure 1942: DNA227442, NM_001350,
gen.NM_001350
Figure 1943: PRO37905
Figure 1944: DNA324766, NM_005452,
gen.NM_005452
Figure 1945: PRO81387
Figure 1946: DNA304661, NM_022551,

gen.NM_022551
Figure 1947: PRO71088
Figure 1948: DNA324767, XM_165747,
gen.XM_165747
Figure 1949: DNA324768, XM_165698,
gen.XM_165698
Figure 1950: PRO4884
Figure 1951A-B: DNA324769, XM_165770,
gen.XM_165770
Figure 1952: DNA287227, NM_004159,
gen.NM_004159
Figure 1953: PRO69506
Figure 1954: DNA324770, XM_165717,
gen.XM_165717
Figure 1955: DNA324771, XM_166480,
gen.XM_166480
Figure 1956: DNA324772, XM_165801,
gen.XM_165801
Figure 1957A-B: DNA324773, NM_000592,
gen.NM_000592
Figure 1958: PRO36316
Figure 1959: DNA324774, NM_001710,
gen.NM_001710
Figure 1960: PRO36305
Figure 1961: DNA227607, NM_005346,
gen.NM_005346
Figure 1962: PRO38070
Figure 1963: DNA304668, NM_005345,
gen.NM_005345
Figure 1964: PRO71095
Figure 1965: DNA324775, NM_021177,
gen.NM_021177
Figure 1966: PRO81394
Figure 1967A-B: DNA272263, NM_006295,
gen.NM_006295
Figure 1968: PRO70138
Figure 1969: DNA287319, NM_001288,
gen.NM_001288
Figure 1970: PRO69584
Figure 1971: DNA324776, NM_001320,
gen.NM_001320
Figure 1972: PRO63052
Figure 1973A-B: DNA324777, NM_004639,
gen.NM_004639
Figure 1974: PRO81395
Figure 1975A-B: DNA324778, NM_080703,
gen.NM_080703
Figure 1976: PRO81396
Figure 1977A-B: DNA324779, NM_080702,
gen.NM_080702
Figure 1978: PRO81397
Figure 1979A-B: DNA324780, NM_004638,
gen.NM_004638
Figure 1980: PRO81398
Figure 1981A-B: DNA324781, NM_080686,
gen.NM_080686

Figure 1982: PRO81399
Figure 1983: DNA324782, XM_165771,
gen.XM_165771
Figure 1984: DNA324783, NM_080598,
gen.NM_080598
Figure 1985: PRO71125
Figure 1986: DNA304699, NM_004640,
gen.NM_004640
Figure 1987: PRO71125
Figure 1988: DNA324784, XM_165765,
gen.XM_165765
Figure 1989: PRO81400
Figure 1990: DNA324785, XM_087945,
gen.XM_087945
Figure 1991: PRO81401
Figure 1992: DNA324786, XM_166381,
gen.XM_166381
Figure 1993: PRO81402
Figure 1994: DNA324787, XM_168104,
gen.XM_168104
Figure 1995: DNA324788, XM_166401,
gen.XM_166401
Figure 1996: PRO81404
Figure 1997: DNA271040, NM_001517,
gen.NM_001517
Figure 1998: PRO59365
Figure 1999A-B: DNA324789, XM_165738,
gen.XM_165738
Figure 2000: DNA324790, XM_087939,
gen.XM_087939
Figure 2001: PRO81406
Figure 2002: DNA324791, XM_166353,
gen.XM_166353
Figure 2003: PRO1112
Figure 2004A-B: DNA324792, XM_166376,
gen.XM_166376
Figure 2005: PRO81407
Figure 2006A-B: DNA324793, XM_165799,
gen.XM_165799
Figure 2007: DNA290264, NM_025263,
gen.NM_025263
Figure 2008: PRO70393
Figure 2009: DNA324794, XM_166361,
gen.XM_166361
Figure 2010: PRO81409
Figure 2011: DNA324795, XM_165764,
gen.XM_165764
Figure 2012: PRO81410
Figure 2013: DNA324796, XM_165758,
gen.XM_165758
Figure 2014: PRO81411
Figure 2015: DNA324797, XM_166406,
gen.XM_166406
Figure 2016: DNA324798, XM_165809,
gen.XM_165809
Figure 2017: DNA324799, NM_018950,

gen.NM_018950
Figure 2018: PRO81414
Figure 2019: DNA324800, XM_166392,
gen.XM_166392
Figure 2020: PRO81415
Figure 2021: DNA324801, XM_166336,
gen.XM_166336
Figure 2022: PRO81416
Figure 2023: DNA324802, XM_167128,
gen.XM_167128
Figure 2024: PRO23797
Figure 2025: DNA324803, XM_167161,
gen.XM_167161
Figure 2026: PRO81417
Figure 2027: DNA324804, NM_013375,
gen.NM_013375
Figure 2028: PRO81418
Figure 2029: DNA324805, NM_007047,
gen.NM_007047
Figure 2030: PRO81419
Figure 2031: DNA324806, XM_167179,
gen.XM_167179
Figure 2032: DNA290785, NM_003107,
gen.NM_003107
Figure 2033: PRO70544
Figure 2034: DNA150772, NM_003472,
gen.NM_003472
Figure 2035: PRO12797
Figure 2036A-B: DNA324807, XM_165728,
gen.XM_165728
Figure 2037: DNA324808, XM_165749,
gen.XM_165749
Figure 2038: PRO81421
Figure 2039A-B: DNA324809, NM_004973,
gen.NM_004973
Figure 2040: PRO81422
Figure 2041: DNA324810, XM_167196,
gen.XM_167196
Figure 2042: DNA324811, XM_166446,
gen.XM_166446
Figure 2043: PRO81424
Figure 2044A-C: DNA324812, XM_165777,
gen.XM_165777
Figure 2045: DNA324813, XM_037875,
gen.XM_037875
Figure 2046: PRO81426
Figure 2047: DNA324814, XM_167225,
gen.XM_167225
Figure 2048: PRO81427
Figure 2049: DNA324815, XM_166357,
gen.XM_166357
Figure 2050: DNA324816, NM_001069,
gen.NM_001069
Figure 2051: PRO81429
Figure 2052: DNA324817, NM_001500,
gen.NM_001500

Figure 2053: PRO81430
Figure 2054A-B: DNA324818, XM_166042,
gen.XM_166042
Figure 2055: PRO51389
Figure 2056: DNA324819, XM_052721,
gen.XM_052721
Figure 2057: DNA324820, XM_165499,
gen.XM_165499
Figure 2058: DNA324821, XM_114497,
gen.XM_114497
Figure 2059: DNA324822, XM_011117,
gen.XM_011117
Figure 2060: DNA324823, XM_094855,
gen.XM_094855
Figure 2061: PRO81435
Figure 2062: DNA324824, XM_059776,
gen.XM_059776
Figure 2063: PRO81436
Figure 2064: DNA324825, XM_055641,
gen.XM_055641
Figure 2065: DNA324826, XM_004151,
gen.XM_004151
Figure 2066: DNA324827, NM_133645,
gen.NM_133645
Figure 2067: PRO81439
Figure 2068: DNA324828, XM_097453,
gen.XM_097453
Figure 2069: DNA324829, XM_029228,
gen.XM_029228
Figure 2070: DNA103471, NM_006670,
gen.NM_006670
Figure 2071: PRO4798
Figure 2072: DNA324830, XM_068963,
gen.XM_068963
Figure 2073: PRO81441
Figure 2074: DNA324831, XM_040623,
gen.XM_040623
Figure 2075: DNA324832, NM_020320,
gen.NM_020320
Figure 2076: PRO81443
Figure 2077: DNA324833, NM_014107,
gen.NM_014107
Figure 2078: PRO81444
Figure 2079A-B: DNA324834, XM_084204,
gen.XM_084204
Figure 2080: DNA324835, XM_017517,
gen.XM_017517
Figure 2081: DNA324836, NM_032929,
gen.NM_032929
Figure 2082: PRO81446
Figure 2083: DNA324837, XM_003611,
gen.XM_003611
Figure 2084: PRO81447
Figure 2085: DNA324838, XM_068919,
gen.XM_068919
Figure 2086: PRO81448

Figure 2087: DNA324839, XM_167016,
gen.XM_167016
Figure 2088: PRO81449
Figure 2089: DNA324840, XM_087855,
gen.XM_087855
Figure 2090: DNA324841, XM_087853,
gen.XM_087853
Figure 2091: DNA324842, XM_165669,
gen.XM_165669
Figure 2092: DNA324843, XM_166303,
gen.XM_166303
Figure 2093: PRO81453
Figure 2094: DNA324844, XM_167027,
gen.XM_167027
Figure 2095: PRO81454
Figure 2096: DNA324845, XM_167037,
gen.XM_167037
Figure 2097: PRO81455
Figure 2098: DNA324846, XM_018182,
gen.XM_018182
Figure 2099: DNA227924, NM_000165,
gen.NM_000165
Figure 2100: PRO38387
Figure 2101: DNA324847, XM_166310,
gen.XM_166310
Figure 2102: PRO81457
Figure 2103: DNA324848, XM_168054,
gen.XM_168054
Figure 2104: DNA271418, NM_003287,
gen.NM_003287
Figure 2105: PRO59717
Figure 2106: DNA324849, XM_114492,
gen.XM_114492
Figure 2107: DNA324850, XM_037056,
gen.XM_037056
Figure 2108: DNA324851, XM_098468,
gen.XM_098468
Figure 2109: PRO19933
Figure 2110: DNA324852, XM_004526,
gen.XM_004526
Figure 2111: DNA324853, NM_001016,
gen.NM_001016
Figure 2112: PRO81462
Figure 2113: DNA324854, XM_004297,
gen.XM_004297
Figure 2114: DNA324855, XM_004256,
gen.XM_004256
Figure 2115: PRO81464
Figure 2116: DNA324856, NM_014320,
gen.NM_014320
Figure 2117: PRO81465
Figure 2118: DNA324857, XM_059741,
gen.XM_059741
Figure 2119: DNA324858, XM_017831,
gen.XM_017831
Figure 2120: PRO81467

Figure 2121: DNA324859, XM_049899,
gen.XM_049899
Figure 2122: DNA324860, XM_004379,
gen.XM_004379
Figure 2123A-C: DNA324861, XM_087834,
gen.XM_087834
Figure 2124A-B: DNA324862, XM_087836,
gen.XM_087836
Figure 2125: PRO81471
Figure 2126: DNA324863, NM_005389,
gen.NM_005389
Figure 2127: PRO66279
Figure 2128A-C: DNA324864, XM_029746,
gen.XM_029746
Figure 2129: PRO66282
Figure 2130: DNA324865, XM_004383,
gen.XM_004383
Figure 2131: DNA324866, XM_059745,
gen.XM_059745
Figure 2132: DNA324867, XM_033912,
gen.XM_033912
Figure 2133: PRO81474
Figure 2134: DNA324868, XM_033910,
gen.XM_033910
Figure 2135: DNA324870, NM_003181,
gen.NM_003181
Figure 2136: PRO81476
Figure 2137: DNA324871, NM_002793,
gen.NM_002793
Figure 2138: PRO81477
Figure 2139: DNA324872, XM_044866,
gen.XM_044866
Figure 2140: DNA324873, XM_116524,
gen.XM_116524
Figure 2141: DNA324874, XM_059773,
gen.XM_059773
Figure 2142: DNA324875, XM_084998,
gen.XM_084998
Figure 2143: PRO81481
Figure 2144: DNA324876, XM_058266,
gen.XM_058266
Figure 2145: DNA324877, XM_042422,
gen.XM_042422
Figure 2146A-B: DNA324878, XM_054706,
gen.XM_054706
Figure 2147: DNA324879, XM_166049,
gen.XM_166049
Figure 2148: DNA324880, XM_042473,
gen.XM_042473
Figure 2149: PRO81486
Figure 2150: DNA324881, XM_167046,
gen.XM_167046
Figure 2151: PRO23797
Figure 2152: DNA324882, XM_071937,
gen.XM_071937
Figure 2153: PRO81487

Figure 2154: DNA324883, XM_087991,
gen.XM_087991
Figure 2155: DNA324884, NM_005514,
gen.NM_005514
Figure 2156: PRO81490
Figure 2157: DNA324885, XM_166327,
gen.XM_166327
Figure 2158: PRO81491
Figure 2159: DNA324886, XM_165692,
gen.XM_165692
Figure 2160: DNA324887, XM_117449,
gen.XM_117449
Figure 2161: DNA324888, XM_086428,
gen.XM_086428
Figure 2162: PRO81494
Figure 2163: DNA324889, NM_032350,
gen.NM_032350
Figure 2164: PRO81495
Figure 2165: DNA324890, NM_013393,
gen.NM_013393
Figure 2166: PRO81496
Figure 2167: DNA324891, XM_165860,
gen.XM_165860
Figure 2168: DNA324892, XM_166541,
gen.XM_166541
Figure 2169: PRO81498
Figure 2170A-B: DNA324893, XM_166523,
gen.XM_166523
Figure 2171: PRO81499
Figure 2172: DNA324894, NM_016003,
gen.NM_016003
Figure 2173: PRO81500
Figure 2174: DNA225631, NM_001101,
gen.NM_001101
Figure 2175: PRO36094
Figure 2176: DNA274326, NM_003088,
gen.NM_003088
Figure 2177: PRO62244
Figure 2178: DNA324895, NM_006303,
gen.NM_006303
Figure 2179: PRO81501
Figure 2180: DNA324896, NM_014413,
gen.NM_014413
Figure 2181: PRO60579
Figure 2182: DNA247595, NM_006908,
gen.NM_006908
Figure 2183: PRO45014
Figure 2184: DNA324897, NM_006854,
gen.NM_006854
Figure 2185: PRO12468
Figure 2186: DNA324898, NM_024067,
gen.NM_024067
Figure 2187: PRO81502
Figure 2188: DNA324899, NM_002947,
gen.NM_002947
Figure 2189: PRO81503

Figure 2190: DNA324900, XM_166531,
gen.XM_166531
Figure 2191: DNA324901, XM_166540,
gen.XM_166540
Figure 2192: PRO81505
Figure 2193: DNA193955, NM_002489,
gen.NM_002489
Figure 2194: PRO23362
Figure 2195: DNA324902, XM_088264,
gen.XM_088264
Figure 2196: PRO81506
Figure 2197: DNA324903, XM_165841,
gen.XM_165841
Figure 2198: DNA324904, XM_166521,
gen.XM_166521
Figure 2199: PRO81508
Figure 2200: DNA324905, XM_166506,
gen.XM_166506
Figure 2201: PRO81509
Figure 2202: DNA324906, XM_166505,
gen.XM_166505
Figure 2203: DNA324907, XM_166514,
gen.XM_166514
Figure 2204: DNA324908, XM_166515,
gen.XM_166515
Figure 2205: DNA324909, XM_166512,
gen.XM_166512
Figure 2206: DNA227929, NM_019059,
gen.NM_019059
Figure 2207: PRO38392
Figure 2208A-B: DNA324910, NM_018947,
gen.NM_018947
Figure 2209: PRO81514
Figure 2210: DNA324911, NM_002137,
gen.NM_002137
Figure 2211: PRO81515
Figure 2212: DNA324912, NM_031243,
gen.NM_031243
Figure 2213: PRO6373
Figure 2214: DNA324913, NM_007276,
gen.NM_007276
Figure 2215: PRO81516
Figure 2216: DNA324914, NM_016587,
gen.NM_016587
Figure 2217: PRO81517
Figure 2218: DNA324915, XM_040853,
gen.XM_040853
Figure 2219: DNA324916, XM_166509,
gen.XM_166509
Figure 2220: DNA324917, XM_166513,
gen.XM_166513
Figure 2221: PRO81520
Figure 2222: DNA324918, XM_166504,
gen.XM_166504
Figure 2223: PRO81521
Figure 2224: DNA324919, XM_166494,

gen.XM_166494
Figure 2225: DNA324920, XM_107825,
gen.XM_107825
Figure 2226A-B: DNA324921, NM_022748,
gen.NM_022748
Figure 2227: PRO81523
Figure 2228: DNA324922, NM_000598,
gen.NM_000598
Figure 2229: PRO119
Figure 2230A-B: DNA324923, XM_166594,
gen.XM_166594
Figure 2231: PRO81524
Figure 2232A-B: DNA275334, NM_030900,
gen.NM_030900
Figure 2233: PRO63009
Figure 2234: DNA324924, NM_031443,
gen.NM_031443
Figure 2235: PRO81525
Figure 2236: DNA324925, NM_012412,
gen.NM_012412
Figure 2237: PRO61812
Figure 2238: DNA324926, NM_021130,
gen.NM_021130
Figure 2239: PRO7427
Figure 2240A-B: DNA324927, XM_165877,
gen.XM_165877
Figure 2241: PRO81526
Figure 2242: DNA227268, NM_019082,
gen.NM_019082
Figure 2243: PRO37731
Figure 2244: DNA324928, XM_015258,
gen.XM_015258
Figure 2245: DNA324929, XM_165870,
gen.XM_165870
Figure 2246: DNA273865, NM_006230,
gen.NM_006230
Figure 2247: PRO61824
Figure 2248A-B: DNA324930, XM_165882,
gen.XM_165882
Figure 2249: DNA324931, XM_165867,
gen.XM_165867
Figure 2250: PRO61688
Figure 2251: DNA324932, NM_014063,
gen.NM_014063
Figure 2252: PRO81529
Figure 2253: DNA324933, XM_165872,
gen.XM_165872
Figure 2254: DNA304707, NM_002787,
gen.NM_002787
Figure 2255: PRO71133
Figure 2256: DNA324934, XM_016733,
gen.XM_016733
Figure 2257: PRO81531
Figure 2258: DNA324935, XM_165876,
gen.XM_165876
Figure 2259A-B: DNA324936, NM_014800,

gen.NM_014800
Figure 2260: DNA324937, NM_130442,
gen.NM_130442
Figure 2261: PRO81534
Figure 2262: DNA226416, NM_000385,
gen.NM_000385
Figure 2263: PRO36879
Figure 2264A-B: DNA324938, XM_167339,
gen.XM_167339
Figure 2265: DNA287189, NM_002047,
gen.NM_002047
Figure 2266: PRO69475
Figure 2267: DNA324939, XM_170195,
gen.XM_170195
Figure 2268: PRO81536
Figure 2269: DNA324940, XM_168378,
gen.XM_168378
Figure 2270: PRO81537
Figure 2271: DNA324941, XM_168354,
gen.XM_168354
Figure 2272: PRO81538
Figure 2273: DNA324942, XM_167494,
gen.XM_167494
Figure 2274: DNA103588, NM_001762,
gen.NM_001762
Figure 2275: PRO4912
Figure 2276: DNA324943, XM_037741,
gen.XM_037741
Figure 2277: PRO81540
Figure 2278: DNA324944, XM_050265,
gen.XM_050265
Figure 2279: PRO81541
Figure 2280: DNA324945, XM_017483,
gen.XM_017483
Figure 2281A-B: DNA324946, XM_018359,
gen.XM_018359
Figure 2282: DNA324947, XM_059876,
gen.XM_059876
Figure 2283: PRO81544
Figure 2284: DNA324948, NM_032951,
gen.NM_032951
Figure 2285: PRO81545
Figure 2286: DNA324949, NM_032953,
gen.NM_032953
Figure 2287: PRO81546
Figure 2288: DNA324950, NM_022170,
gen.NM_022170
Figure 2289: PRO81547
Figure 2290: DNA324951, NM_031992,
gen.NM_031992
Figure 2291: PRO81548
Figure 2292: DNA324952, XM_004901,
gen.XM_004901
Figure 2293: DNA324953, NM_016328,
gen.NM_016328
Figure 2294: PRO81550

Figure 2295A-B: DNA324954, NM_032999,
gen.NM_032999
Figure 2296: PRO81551
Figure 2297: DNA324955, XM_088239,
gen.XM_088239
Figure 2298: PRO81552
Figure 2299A-B: DNA324956, XM_167500,
gen.XM_167500
Figure 2300A-B: DNA324957, XM_167504,
gen.XM_167504
Figure 2301: DNA324958, XM_167498,
gen.XM_167498
Figure 2302: DNA324959, XM_168454,
gen.XM_168454
Figure 2303: PRO81556
Figure 2304: DNA324960, NM_031925,
gen.NM_031925
Figure 2305: PRO81557
Figure 2306: DNA324961, NM_005918,
gen.NM_005918
Figure 2307: PRO81558
Figure 2308: DNA304710, NM_001540,
gen.NM_001540
Figure 2309: PRO71136
Figure 2310: DNA324962, XM_168470,
gen.XM_168470
Figure 2311: DNA324963, XM_168461,
gen.XM_168461
Figure 2312A-B: DNA324964, XM_167502,
gen.XM_167502
Figure 2313: DNA324965, XM_017442,
gen.XM_017442
Figure 2314: PRO81561
Figure 2315: DNA324966, XM_168450,
gen.XM_168450
Figure 2316: DNA324967, XM_168435,
gen.XM_168435
Figure 2317: DNA324968, XM_168464,
gen.XM_168464
Figure 2318: DNA324969, XM_170427,
gen.XM_170427
Figure 2319A-B: DNA324971, NM_015068,
gen.NM_015068
Figure 2320: PRO81566
Figure 2321A-B: DNA324972, XM_167476,
gen.XM_167476
Figure 2322: DNA324973, XM_168181,
gen.XM_168181
Figure 2323: DNA324974, XM_168251,
gen.XM_168251
Figure 2324: PRO81569
Figure 2325: DNA324975, XM_167477,
gen.XM_167477
Figure 2326: DNA324976, NM_005837,
gen.NM_005837
Figure 2327: PRO81571

Figure 2328: DNA324977, XM_167483,
gen.XM_167483
Figure 2329: DNA324978, XM_167484,
gen.XM_167484
Figure 2330: PRO81572
Figure 2331: DNA324979, NM_030935,
gen.NM_030935
Figure 2332: PRO81573
Figure 2333: DNA324980, NM_019606,
gen.NM_019606
Figure 2334: PRO81574
Figure 2335: DNA324981, NM_024070,
gen.NM_024070
Figure 2336: PRO81575
Figure 2337: DNA324982, XM_084241,
gen.XM_084241
Figure 2338: DNA324983, NM_006833,
gen.NM_006833
Figure 2339: PRO22897
Figure 2340: DNA324984, NM_032164,
gen.NM_032164
Figure 2341: PRO81578
Figure 2342: DNA304801, NM_004889,
gen.NM_004889
Figure 2343: PRO71211
Figure 2344: DNA324985, NM_006693,
gen.NM_006693
Figure 2345: PRO81579
Figure 2346: DNA324986, XM_165839,
gen.XM_165839
Figure 2347: PRO81580
Figure 2348: DNA272090, NM_005720,
gen.NM_005720
Figure 2349: PRO60360
Figure 2350: DNA324987, XM_165836,
gen.XM_165836
Figure 2351A-B: DNA324988, XM_166482,
gen.XM_166482
Figure 2352: DNA324989, XM_088180,
gen.XM_088180
Figure 2353A-B: DNA324990, XM_166485,
gen.XM_166485
Figure 2354: PRO81584
Figure 2355: DNA324991, NM_001673,
gen.NM_001673
Figure 2356: PRO81585
Figure 2357: DNA324992, NM_133436,
gen.NM_133436
Figure 2358: PRO81586
Figure 2359: DNA324993, XM_168586,
gen.XM_168586
Figure 2360: PRO81587
Figure 2361: DNA83141, NM_000602,
gen.NM_000602
Figure 2362: PRO2604
Figure 2363: DNA324994, NM_057089,

gen.NM_057089
Figure 2364: PRO81588
Figure 2365: DNA324995, NM_001283,
gen.NM_001283
Figure 2366: PRO41882
Figure 2367: DNA324996, NM_003378,
gen.NM_003378
Figure 2368: PRO81589
Figure 2369: DNA324997, NM_001084,
gen.NM_001084
Figure 2370: PRO58437
Figure 2371: DNA270711, NM_006349,
gen.NM_006349
Figure 2372: PRO59074
Figure 2373: DNA324998, NM_024653,
gen.NM_024653
Figure 2374: PRO81590
Figure 2375: DNA324999, XM_168548,
gen.XM_168548
Figure 2376: DNA325000, NM_032958,
gen.NM_032958
Figure 2377: PRO81591
Figure 2378: DNA325001, NM_002803,
gen.NM_002803
Figure 2379: PRO81592
Figure 2380: DNA325002, XM_168572,
gen.XM_168572
Figure 2381: DNA325003, XM_071605,
gen.XM_071605
Figure 2382: PRO81594
Figure 2383: DNA325004, XM_033876,
gen.XM_033876
Figure 2384: PRO81595
Figure 2385A-B: DNA325005, XM_027214,
gen.XM_027214
Figure 2386: DNA325006, XM_088073,
gen.XM_088073
Figure 2387: DNA325007, XM_072430,
gen.XM_072430
Figure 2388: PRO81598
Figure 2389: DNA325008, XM_050430,
gen.XM_050430
Figure 2390: PRO81599
Figure 2391: DNA325009, NM_001753,
gen.NM_001753
Figure 2392: PRO81600
Figure 2393: DNA226560, NM_006136,
gen.NM_006136
Figure 2394: PRO37023
Figure 2395: DNA325010, XM_012284,
gen.XM_012284
Figure 2396: DNA325011, NM_005000,
gen.NM_005000
Figure 2397: PRO59380
Figure 2398: DNA325012, NM_001662,
gen.NM_001662

Figure 2399: PRO39773
Figure 2400: DNA325013, XM_011618,
gen.XM_011618
Figure 2401: PRO81602
Figure 2402: DNA325014, XM_004627,
gen.XM_004627
Figure 2403: DNA325015, XM_045401,
gen.XM_045401
Figure 2404: DNA325016, XM_114602,
gen.XM_114602
Figure 2405: PRO81605
Figure 2406: DNA325017, XM_117481,
gen.XM_117481
Figure 2407A-C: DNA325018, XM_045856,
gen.XM_045856
Figure 2408: PRO81607
Figure 2409A-B: DNA325019, XM_088105,
gen.XM_088105
Figure 2410: PRO81608
Figure 2411: DNA325020, XM_011548,
gen.XM_011548
Figure 2412: PRO81609
Figure 2413: DNA325021, XM_045952,
gen.XM_045952
Figure 2414: DNA325022, XM_046001,
gen.XM_046001
Figure 2415: PRO81611
Figure 2416: DNA325023, XM_088099,
gen.XM_088099
Figure 2417: DNA325024, XM_040498,
gen.XM_040498
Figure 2418: DNA325025, XM_088103,
gen.XM_088103
Figure 2419: PRO81614
Figure 2420: DNA325026, XM_088122,
gen.XM_088122
Figure 2421: PRO81615
Figure 2422: DNA325027, XM_088119,
gen.XM_088119
Figure 2423: DNA325028, NM_001628,
gen.NM_001628
Figure 2424: PRO81617
Figure 2425: DNA325029, NM_020299,
gen.NM_020299
Figure 2426: PRO81618
Figure 2427: DNA325030, NM_024033,
gen.NM_024033
Figure 2428: PRO81619
Figure 2429: DNA325031, XM_114555,
gen.XM_114555
Figure 2430: DNA325032, XM_059839,
gen.XM_059839
Figure 2431: PRO81621
Figure 2432: DNA325033, XM_095146,
gen.XM_095146
Figure 2433: DNA325034, XM_016700,

gen.XM_016700
Figure 2434: DNA325035, XM_042781,
gen.XM_042781
Figure 2435: DNA304685, NM_003143,
gen.NM_003143
Figure 2436: PRO71111
Figure 2437: DNA325036, NM_018238,
gen.NM_018238
Figure 2438: PRO81625
Figure 2439: DNA325037, XM_035107,
gen.XM_035107
Figure 2440: DNA325038, NM_003461,
gen.NM_003461
Figure 2441: PRO10194
Figure 2442: DNA325039, NM_004911,
gen.NM_004911
Figure 2443: PRO2733
Figure 2444A-B: DNA325040, XM_114578,
gen.XM_114578
Figure 2445: PRO81627
Figure 2446: DNA325041, XM_088135,
gen.XM_088135
Figure 2447: DNA325042, XM_098654,
gen.XM_098654
Figure 2448: PRO81629
Figure 2449: DNA325043, NM_023942,
gen.NM_023942
Figure 2450: PRO81630
Figure 2451: DNA325044, NM_138434,
gen.NM_138434
Figure 2452: PRO81631
Figure 2453: DNA325045, XM_084238,
gen.XM_084238
Figure 2454A-B: DNA325046, XM_032216,
gen.XM_032216
Figure 2455A-B: DNA325047, XM_032121,
gen.XM_032121
Figure 2456: DNA325048, NM_031434,
gen.NM_031434
Figure 2457: PRO1555
Figure 2458: DNA226337, NM_005692,
gen.NM_005692
Figure 2459: PRO36800
Figure 2460: DNA325049, NM_005614,
gen.NM_005614
Figure 2461: PRO37938
Figure 2462A-B: DNA325050, NM_053043,
gen.NM_053043
Figure 2463: PRO81634
Figure 2464: DNA325051, NM_022458,
gen.NM_022458
Figure 2465: PRO81635
Figure 2466: DNA325052, XM_098669,
gen.XM_098669
Figure 2467: DNA325053, NM_017760,
gen.NM_017760

Figure 2468: PRO81637
Figure 2469: DNA325054, XM_036413, gen.XM_036413
Figure 2470A-B: DNA325055, XM_032944, gen.XM_032944
Figure 2471: DNA325056, XM_117444, gen.XM_117444
Figure 2472: DNA325057, XM_117452, gen.XM_117452
Figure 2473: DNA325058, XM_070203, gen.XM_070203
Figure 2474: PRO81641
Figure 2475: DNA325059, XM_095371, gen.XM_095371
Figure 2476: DNA325060, NM_004084, gen.NM_004084
Figure 2477: PRO2570
Figure 2478: DNA325061, NM_005217, gen.NM_005217
Figure 2479: PRO9980
Figure 2480: DNA325062, XM_070188, gen.XM_070188
Figure 2481: PRO81643
Figure 2482: DNA325063, XM_035680, gen.XM_035680
Figure 2483: DNA325064, XM_035662, gen.XM_035662
Figure 2484: PRO3344
Figure 2485: DNA325065, XM_005305, gen.XM_005305
Figure 2486: PRO81645
Figure 2487: DNA325066, XM_050293, gen.XM_050293
Figure 2488A-B: DNA325067, XM_027679, gen.XM_027679
Figure 2489: PRO81647
Figure 2490A-B: DNA325068, XM_027651, gen.XM_027651
Figure 2491: DNA274178, NM_005775, gen.NM_005775
Figure 2492: PRO62108
Figure 2493: DNA325069, XM_113557, gen.XM_113557
Figure 2494: PRO81649
Figure 2495: DNA83022, NM_001199, gen.NM_001199
Figure 2496: PRO2042
Figure 2497: DNA325070, NM_006128, gen.NM_006128
Figure 2498: PRO81650
Figure 2499: DNA325071, NM_006131, gen.NM_006131
Figure 2500: PRO81651
Figure 2501: DNA325072, NM_006132, gen.NM_006132
Figure 2502: PRO81652

Figure 2503: DNA325073, NM_025232, gen.NM_025232
Figure 2504: PRO81653
Figure 2505: DNA325074, XM_027440, gen.XM_027440
Figure 2506: DNA225671, NM_001831, gen.NM_001831
Figure 2507: PRO36134
Figure 2508: DNA325075, NM_024567, gen.NM_024567
Figure 2509: PRO81654
Figure 2510: DNA325076, NM_018250, gen.NM_018250
Figure 2511: PRO81655
Figure 2512: DNA227267, NM_018660, gen.NM_018660
Figure 2513: PRO37730
Figure 2514A-B: DNA325077, XM_095545, gen.XM_095545
Figure 2515: DNA325078, XM_088338, gen.XM_088338
Figure 2516: PRO81657
Figure 2517: DNA325079, XM_114617, gen.XM_114617
Figure 2518: PRO81658
Figure 2519: DNA325080, XM_088336, gen.XM_088336
Figure 2520: PRO81659
Figure 2521: DNA325081, XM_047083, gen.XM_047083
Figure 2522: PRO81660
Figure 2523: DNA325082, XM_114618, gen.XM_114618
Figure 2524: PRO81661
Figure 2525: DNA325083, XM_050215, gen.XM_050215
Figure 2526: DNA325084, XM_113531, gen.XM_113531
Figure 2527: DNA325085, NM_018310, gen.NM_018310
Figure 2528: PRO81664
Figure 2529: DNA325086, XM_088294, gen.XM_088294
Figure 2530: DNA325087, XM_013112, gen.XM_013112
Figure 2531: DNA325088, XM_059933, gen.XM_059933
Figure 2532: PRO1108
Figure 2533: DNA325089, XM_011629, gen.XM_011629
Figure 2534: DNA325090, NM_000930, gen.NM_000930
Figure 2535: PRO4
Figure 2536: DNA325091, NM_000931, gen.NM_000931
Figure 2537: PRO81668

Figure 2538: DNA325092, NM_033011,
gen.NM_033011
Figure 2539: PRO81669
Figure 2540: DNA325093, XM_166063,
gen.XM_166063
Figure 2541: DNA325094, NM_025070,
gen.NM_025070
Figure 2542: PRO81671
Figure 2543A-B: DNA325095, XM_030268,
gen.XM_030268
Figure 2544: DNA325096, XM_030274,
gen.XM_030274
Figure 2545: PRO81673
Figure 2546: DNA151010, NM_003350,
gen.NM_003350
Figure 2547: PRO12838
Figure 2548: DNA325097, XM_113540,
gen.XM_113540
Figure 2549: PRO81674
Figure 2550: DNA325098, NM_006330,
gen.NM_006330
Figure 2551: PRO59230
Figure 2552: DNA325099, NM_001023,
gen.NM_001023
Figure 2553: PRO58263
Figure 2554: DNA325100, XM_095667,
gen.XM_095667
Figure 2555: PRO81675
Figure 2556: DNA325101, XM_114640,
gen.XM_114640
Figure 2557: DNA325102, XM_057780,
gen.XM_057780
Figure 2558: DNA325103, XM_166064,
gen.XM_166064
Figure 2559: DNA325104, XM_088399,
gen.XM_088399
Figure 2560: DNA325105, XM_088401,
gen.XM_088401
Figure 2561: DNA325106, XM_042658,
gen.XM_042658
Figure 2562: DNA325107, XM_011769,
gen.XM_011769
Figure 2563: DNA325108, XM_044627,
gen.XM_044627
Figure 2564: DNA325109, XM_098761,
gen.XM_098761
Figure 2565: DNA226496, NM_006837,
gen.NM_006837
Figure 2566: PRO36959
Figure 2567: DNA325110, NM_014294,
gen.NM_014294
Figure 2568: PRO23248
Figure 2569: DNA325111, NM_000971,
gen.NM_000971
Figure 2570: PRO81685
Figure 2571: DNA325112, XM_050731,

gen.XM_050731
Figure 2572: DNA325113, XM_088325,
gen.XM_088325
Figure 2573: PRO81687
Figure 2574: DNA325114, XM_088323,
gen.XM_088323
Figure 2575: DNA325115, NM_001444,
gen.NM_001444
Figure 2576: PRO81689
Figure 2577: DNA325116, XM_013127,
gen.XM_013127
Figure 2578: PRO81690
Figure 2579: DNA325117, XM_165514,
gen.XM_165514
Figure 2580: PRO81691
Figure 2581: DNA325118, XM_017816,
gen.XM_017816
Figure 2582: DNA325119, XM_098747,
gen.XM_098747
Figure 2583: DNA325120, XM_050506,
gen.XM_050506
Figure 2584: DNA325121, NM_024613,
gen.NM_024613
Figure 2585: PRO81695
Figure 2586: DNA325122, XM_011642,
gen.XM_011642
Figure 2587: PRO81696
Figure 2588: DNA325123, NM_000989,
gen.NM_000989
Figure 2589: PRO11265
Figure 2590: DNA325124, NM_003406,
gen.NM_003406
Figure 2591: PRO71091
Figure 2592: DNA325125, XM_011657,
gen.XM_011657
Figure 2593: DNA131588, NM_002568,
gen.NM_002568
Figure 2594: PRO7445
Figure 2595: DNA325126, XM_018287,
gen.XM_018287
Figure 2596: DNA325127, NM_001568,
gen.NM_001568
Figure 2597: PRO81699
Figure 2598: DNA325128, NM_003756,
gen.NM_003756
Figure 2599: PRO81700
Figure 2600A-B: DNA272050, NM_006265,
gen.NM_006265
Figure 2601: PRO60321
Figure 2602: DNA325129, NM_052886,
gen.NM_052886
Figure 2603: PRO81701
Figure 2604: DNA325130, XM_016047,
gen.XM_016047
Figure 2605: DNA325131, XM_005060,
gen.XM_005060

Figure 2606: DNA325132, NM_005005,
gen.NM_005005
Figure 2607: PRO81704
Figure 2608: DNA325133, XM_037657,
gen.XM_037657
Figure 2609: DNA325134, XM_029567,
gen.XM_029567
Figure 2610: PRO81705
Figure 2611: DNA325135, XM_088316,
gen.XM_088316
Figure 2612: DNA325136, XM_051298,
gen.XM_051298
Figure 2613: DNA325137, XM_088370,
gen.XM_088370
Figure 2614: DNA325138, NM_016647,
gen.NM_016647
Figure 2615: PRO23201
Figure 2616: DNA325139, NM_052963,
gen.NM_052963
Figure 2617: PRO81708
Figure 2618: DNA325140, XM_049247,
gen.XM_049247
Figure 2619: DNA325141, XM_058968,
gen.XM_058968
Figure 2620: DNA325143, NM_023078,
gen.NM_023078
Figure 2621: PRO81711
Figure 2622: DNA325144, XM_117487,
gen.XM_117487
Figure 2623: DNA325145, XM_049226,
gen.XM_049226
Figure 2624: PRO81714
Figure 2625: DNA325146, XM_114613,
gen.XM_114613
Figure 2626: DNA325147, XM_035368,
gen.XM_035368
Figure 2627: DNA325148, XM_113532,
gen.XM_113532
Figure 2628: DNA325149, XM_088321,
gen.XM_088321
Figure 2629: DNA325150, XM_035373,
gen.XM_035373
Figure 2630: PRO81719
Figure 2631: DNA325151, XM_035370,
gen.XM_035370
Figure 2632: PRO81720
Figure 2633: DNA325152, NM_000973,
gen.NM_000973
Figure 2634: PRO22907
Figure 2635: DNA325153, NM_033301,
gen.NM_033301
Figure 2636: PRO22907
Figure 2637: DNA325154, XM_049421,
gen.XM_049421
Figure 2638: DNA325155, XM_034640,
gen.XM_034640

Figure 2639: PRO81722
Figure 2640: DNA325156, XM_088550,
gen.XM_088550
Figure 2641: DNA325157, XM_088552,
gen.XM_088552
Figure 2642: DNA325158, XM_088553,
gen.XM_088553
Figure 2643: PRO81725
Figure 2644: DNA325159, XM_059979,
gen.XM_059979
Figure 2645: DNA325160, XM_167558,
gen.XM_167558
Figure 2646: DNA325161, XM_039654,
gen.XM_039654
Figure 2647: DNA325162, XM_060006,
gen.XM_060006
Figure 2648: PRO81729
Figure 2649: DNA325163, NM_001122,
gen.NM_001122
Figure 2650: PRO81730
Figure 2651: DNA325164, NM_001010,
gen.NM_001010
Figure 2652: PRO10824
Figure 2653: DNA325165, NM_058195,
gen.NM_058195
Figure 2654: PRO81731
Figure 2655: DNA325166, NM_000077,
gen.NM_000077
Figure 2656: PRO36693
Figure 2657: DNA325167, NM_058196,
gen.NM_058196
Figure 2658: PRO81732
Figure 2659: DNA325168, XM_017931,
gen.XM_017931
Figure 2660: DNA271847, NM_001539,
gen.NM_001539
Figure 2661: PRO60127
Figure 2662: DNA270991, NM_004323,
gen.NM_004323
Figure 2663: PRO59321
Figure 2664: DNA325169, NM_016410,
gen.NM_016410
Figure 2665: PRO81734
Figure 2666: DNA325170, XM_005543,
gen.XM_005543
Figure 2667: PRO38028
Figure 2668: DNA325171, NM_001842,
gen.NM_001842
Figure 2669: PRO21481
Figure 2670: DNA226345, NM_005866,
gen.NM_005866
Figure 2671: PRO36808
Figure 2672: DNA325172, XM_088563,
gen.XM_088563
Figure 2673: DNA325173, XM_059998,
gen.XM_059998

Figure 2674: PRO59579
Figure 2675: DNA325174, NM_013442,
gen.NM_013442
Figure 2676: PRO9819
Figure 2677: DNA325175, XM_114661,
gen.XM_114661
Figure 2678: PRO81736
Figure 2679: DNA325176, XM_048479,
gen.XM_048479
Figure 2680: DNA290319, NM_003289,
gen.NM_003289
Figure 2681: PRO70595
Figure 2682A-C: DNA325177, NM_006289,
gen.NM_006289
Figure 2683: PRO81738
Figure 2684: DNA325178, XM_048518,
gen.XM_048518
Figure 2685: PRO81739
Figure 2686: DNA325179, XM_048539,
gen.XM_048539
Figure 2687: PRO81740
Figure 2688: DNA325180, XM_114662,
gen.XM_114662
Figure 2689: DNA325181, NM_001833,
gen.NM_001833
Figure 2690: PRO81742
Figure 2691: DNA227491, NM_007096,
gen.NM_007096
Figure 2692: PRO37954
Figure 2693: DNA254771, NM_012203,
gen.NM_012203
Figure 2694: PRO49869
Figure 2695: DNA89242, NM_000700,
gen.NM_000700
Figure 2696: PRO2907
Figure 2697: DNA325182, XM_041020,
gen.XM_041020
Figure 2698: PRO81743
Figure 2699: DNA325183, XM_114686,
gen.XM_114686
Figure 2700: DNA325184, XM_088637,
gen.XM_088637
Figure 2701: DNA287216, NM_021154,
gen.NM_021154
Figure 2702: PRO69496
Figure 2703: DNA288247, NM_058179,
gen.NM_058179
Figure 2704: PRO70011
Figure 2705: DNA325185, XM_071178,
gen.XM_071178
Figure 2706: PRO81746
Figure 2707: DNA325186, XM_005490,
gen.XM_005490
Figure 2708: DNA325187, NM_031263,
gen.NM_031263
Figure 2709: PRO81748

Figure 2710: DNA325188, XM_018006,
gen.XM_018006
Figure 2711: DNA325189, XM_017996,
gen.XM_017996
Figure 2712: DNA325190, XM_016113,
gen.XM_016113
Figure 2713: PRO81751
Figure 2714: DNA272655, NM_001827,
gen.NM_001827
Figure 2715: PRO60781
Figure 2716A-B: DNA325191, NM_002161,
gen.NM_002161
Figure 2717: PRO81752
Figure 2718A-B: DNA325192, NM_013417,
gen.NM_013417
Figure 2719: PRO81753
Figure 2720A-B: DNA325193, XM_046863,
gen.XM_046863
Figure 2721: PRO81754
Figure 2722: DNA325194, XM_046836,
gen.XM_046836
Figure 2723: DNA275322, NM_003837,
gen.NM_003837
Figure 2724: PRO63000
Figure 2725A-B: DNA325195, XM_098943,
gen.XM_098943
Figure 2726: DNA325196, XM_016308,
gen.XM_016308
Figure 2727: DNA325197, XM_005525,
gen.XM_005525
Figure 2728: DNA325198, NM_003389,
gen.NM_003389
Figure 2729: PRO81759
Figure 2730: DNA325199, NM_033219,
gen.NM_033219
Figure 2731: PRO81760
Figure 2732: DNA325200, NM_006401,
gen.NM_006401
Figure 2733: PRO81761
Figure 2734: DNA272213, NM_002486,
gen.NM_002486
Figure 2735: PRO60475
Figure 2736: DNA325201, NM_001333,
gen.NM_001333
Figure 2737: PRO81762
Figure 2738: DNA325202, XM_116818,
gen.XM_116818
Figure 2739: PRO81763
Figure 2740: DNA254543, NM_006808,
gen.NM_006808
Figure 2741: PRO49648
Figure 2742: DNA325203, XM_070873,
gen.XM_070873
Figure 2743: PRO81764
Figure 2744: DNA325204, XM_042788,
gen.XM_042788

Figure 2745: PRO81765
Figure 2746: DNA257309, NM_032342,
gen.NM_032342
Figure 2747: PRO51901
Figure 2748: DNA325205, XM_088569,
gen.XM_088569
Figure 2749: PRO81766
Figure 2750: DNA325206, XM_088571,
gen.XM_088571
Figure 2751: DNA271722, NM_004697,
gen.NM_004697
Figure 2752: PRO60006
Figure 2753: DNA325207, NM_017443,
gen.NM_017443
Figure 2754: PRO81768
Figure 2755A-C: DNA325208, XM_005348,
gen.XM_005348
Figure 2756: DNA325209, XM_114646,
gen.XM_114646
Figure 2757: DNA325210, XM_038391,
gen.XM_038391
Figure 2758: PRO81771
Figure 2759A-B: DNA325211, XM_045296,
gen.XM_045296
Figure 2760: DNA325212, XM_005365,
gen.XM_005365
Figure 2761: DNA289530, NM_004435,
gen.NM_004435
Figure 2762: PRO70290
Figure 2763: DNA287271, NM_032799,
gen.NM_032799
Figure 2764: PRO69542
Figure 2765: DNA325213, XM_026987,
gen.XM_026987
Figure 2766: DNA325214, XM_026985,
gen.XM_026985
Figure 2767: DNA225630, NM_016174,
gen.NM_016174
Figure 2768: PRO36093
Figure 2769: DNA325215, XM_026968,
gen.XM_026968
Figure 2770: PRO81775
Figure 2771: DNA325216, XM_026951,
gen.XM_026951
Figure 2772: DNA325217, NM_025072,
gen.NM_025072
Figure 2773: PRO33818
Figure 2774: DNA325218, XM_033424,
gen.XM_033424
Figure 2775: DNA325219, NM_004957,
gen.NM_004957
Figure 2776: PRO81778
Figure 2777: DNA325220, XM_033457,
gen.XM_033457
Figure 2778A-B: DNA325221, XM_033460,
gen.XM_033460

Figure 2779: PRO81780
Figure 2780: DNA325222, NM_000976,
gen.NM_000976
Figure 2781: PRO62236
Figure 2782: DNA218841, NM_012098,
gen.NM_012098
Figure 2783: PRO34473
Figure 2784A-B: DNA325223, XM_052725,
gen.XM_052725
Figure 2785: PRO81781
Figure 2786: DNA325224, XM_011752,
gen.XM_011752
Figure 2787: DNA325225, XM_026944,
gen.XM_026944
Figure 2788: PRO81783
Figure 2789: DNA325226, XM_116806,
gen.XM_116806
Figure 2790A-B: DNA325227, NM_005347,
gen.NM_005347
Figure 2791: PRO81785
Figure 2792: DNA325228, NM_005833,
gen.NM_005833
Figure 2793: PRO81786
Figure 2794: DNA325229, NM_007209,
gen.NM_007209
Figure 2795: PRO61897
Figure 2796: DNA88350, NM_000177,
gen.NM_000177
Figure 2797: PRO2758
Figure 2798A-B: DNA325230, XM_011749,
gen.XM_011749
Figure 2799: DNA325231, XM_114679,
gen.XM_114679
Figure 2800: DNA325232, XM_087041,
gen.XM_087041
Figure 2801: DNA325233, XM_114678,
gen.XM_114678
Figure 2802: DNA325234, XM_114677,
gen.XM_114677
Figure 2803: DNA325235, XM_087038,
gen.XM_087038
Figure 2804: DNA325236, XM_059637,
gen.XM_059637
Figure 2805: PRO81792
Figure 2806: DNA325237, NM_000368,
gen.NM_000368
Figure 2807: PRO60115
Figure 2808: DNA325238, XM_033385,
gen.XM_033385
Figure 2809A-B: DNA325239, XM_033380,
gen.XM_033380
Figure 2810: PRO81794
Figure 2811: DNA325240, XM_033362,
gen.XM_033362
Figure 2812: PRO81795
Figure 2813: DNA325241, XM_059986,

gen.XM_059986
Figure 2814: PRO81796
Figure 2815A-B: DNA325242, XM_033361,
gen.XM_033361
Figure 2816: PRO81797
Figure 2817A-B: DNA325243, XM_033360,
gen.XM_033360
Figure 2818: DNA325244, XM_033359,
gen.XM_033359
Figure 2819A-B: DNA325245, XM_033355,
gen.XM_033355
Figure 2820: DNA325246, NM_014285,
gen.NM_014285
Figure 2821: PRO81800
Figure 2822: DNA325247, NM_054012,
gen.NM_054012
Figure 2823: PRO81801
Figure 2824: DNA325248, XM_035103,
gen.XM_035103
Figure 2825: DNA325249, XM_035109,
gen.XM_035109
Figure 2826: DNA325250, NM_000972,
gen.NM_000972
Figure 2827: PRO81804
Figure 2828: DNA325251, NM_033161,
gen.NM_033161
Figure 2829: PRO81805
Figure 2830: DNA325252, NM_000787,
gen.NM_000787
Figure 2831: PRO81806
Figure 2832A-B: DNA325253, XM_011778,
gen.XM_011778
Figure 2833: DNA325254, XM_088426,
gen.XM_088426
Figure 2834: DNA325255, NM_002003,
gen.NM_002003
Figure 2835: PRO1910
Figure 2836: DNA325256, NM_058199,
gen.NM_058199
Figure 2837: PRO81809
Figure 2838: DNA325257, XM_059945,
gen.XM_059945
Figure 2839: DNA325258, XM_088422,
gen.XM_088422
Figure 2840: PRO81811
Figure 2841: DNA325259, XM_029168,
gen.XM_029168
Figure 2842: PRO81812
Figure 2843: DNA325260, XM_098913,
gen.XM_098913
Figure 2844: PRO81813
Figure 2845: DNA325261, XM_114669,
gen.XM_114669
Figure 2846: DNA325262, XM_113564,
gen.XM_113564
Figure 2847A-B: DNA325263, XM_088459,

gen.XM_088459
Figure 2848: PRO81815
Figure 2849: DNA325264, XM_054752,
gen.XM_054752
Figure 2850: PRO81816
Figure 2851: DNA325265, XM_084270,
gen.XM_084270
Figure 2852: DNA325266, XM_054763,
gen.XM_054763
Figure 2853: PRO81817
Figure 2854: DNA325267, XM_114655,
gen.XM_114655
Figure 2855: DNA325268, XM_038030,
gen.XM_038030
Figure 2856: PRO59351
Figure 2857: DNA325269, XM_072526,
gen.XM_072526
Figure 2858: PRO81819
Figure 2859: DNA325270, XM_059961,
gen.XM_059961
Figure 2860: DNA325271, NM_032928,
gen.NM_032928
Figure 2861: PRO81821
Figure 2862: DNA325272, NM_014172,
gen.NM_014172
Figure 2863: PRO81822
Figure 2864: DNA325273, XM_038049,
gen.XM_038049
Figure 2865: PRO62069
Figure 2866: DNA325274, XM_038063,
gen.XM_038063
Figure 2867: PRO81823
Figure 2868: DNA325275, NM_000954,
gen.NM_000954
Figure 2869: PRO81824
Figure 2870: DNA325276, XM_088461,
gen.XM_088461
Figure 2871: DNA325277, XM_059966,
gen.XM_059966
Figure 2872: PRO81826
Figure 2873: DNA325278, XM_114649,
gen.XM_114649
Figure 2874: DNA325279, XM_117519,
gen.XM_117519
Figure 2875: DNA325280, XM_053206,
gen.XM_053206
Figure 2876: DNA325281, XM_040272,
gen.XM_040272
Figure 2877: PRO58939
Figure 2878: DNA325282, XM_005724,
gen.XM_005724
Figure 2879: DNA325283, XM_040267,
gen.XM_040267
Figure 2880: PRO81831
Figure 2881: DNA325284, XM_048859,
gen.XM_048859

Figure 2882: PRO62617
Figure 2883: DNA325285, NM_003739,
gen.NM_003739
Figure 2884: PRO81832
Figure 2885: DNA325286, XM_060976,
gen.XM_060976
Figure 2886: PRO81833
Figure 2887: DNA325287, XM_167626,
gen.XM_167626
Figure 2888: PRO81834
Figure 2889: DNA325288, XM_165555,
gen.XM_165555
Figure 2890: PRO81835
Figure 2891: DNA325289, NM_001494,
gen.NM_001494
Figure 2892: PRO81836
Figure 2893: DNA325290, NM_032905,
gen.NM_032905
Figure 2894: PRO81837
Figure 2895: DNA325291, NM_005174,
gen.NM_005174
Figure 2896: PRO81838
Figure 2897: DNA325292, XM_165557,
gen.XM_165557
Figure 2898: DNA325293, XM_167374,
gen.XM_167374
Figure 2899: DNA273759, NM_006023,
gen.NM_006023
Figure 2900: PRO61721
Figure 2901: DNA325294, XM_167411,
gen.XM_167411
Figure 2902: DNA325295, NM_031453,
gen.NM_031453
Figure 2903: PRO81841
Figure 2904: DNA325296, XM_167414,
gen.XM_167414
Figure 2905: PRO12851
Figure 2906: DNA325297, XM_166717,
gen.XM_166717
Figure 2907: PRO81842
Figure 2908: DNA325298, XM_005100,
gen.XM_005100
Figure 2909: DNA325299, XM_038536,
gen.XM_038536
Figure 2910A-B: DNA325300, XM_084420,
gen.XM_084420
Figure 2911: DNA325301, XM_084429,
gen.XM_084429
Figure 2912: PRO81846
Figure 2913A-C: DNA325302, XM_165551,
gen.XM_165551
Figure 2914: DNA325303, XM_059720,
gen.XM_059720
Figure 2915: PRO81848
Figure 2916A-B: DNA325304, NM_019619,
gen.NM_019619

Figure 2917: PRO81849
Figure 2918: DNA325305, XM_166665,
gen.XM_166665
Figure 2919A-B: DNA325306, NM_002211,
gen.NM_002211
Figure 2920: PRO81851
Figure 2921A-B: DNA325307, XM_165567,
gen.XM_165567
Figure 2922: DNA325308, XM_166157,
gen.XM_166157
Figure 2923: DNA325309, NM_032023,
gen.NM_032023
Figure 2924: PRO52537
Figure 2925: DNA325310, XM_165560,
gen.XM_165560
Figure 2926: DNA325311, XM_165563,
gen.XM_165563
Figure 2927: DNA325312, XM_113615,
gen.XM_113615
Figure 2928: PRO81855
Figure 2929: DNA325313, XM_165890,
gen.XM_165890
Figure 2930: DNA325314, XM_061126,
gen.XM_061126
Figure 2931: DNA325315, XM_061125,
gen.XM_061125
Figure 2932: PRO81858
Figure 2933: DNA325316, XM_054474,
gen.XM_054474
Figure 2934: DNA325317, XM_165888,
gen.XM_165888
Figure 2935: DNA325318, XM_054475,
gen.XM_054475
Figure 2936: PRO81861
Figure 2937: DNA325319, XM_015652,
gen.XM_015652
Figure 2938: PRO81862
Figure 2939: DNA325320, XM_036593,
gen.XM_036593
Figure 2940: PRO81863
Figure 2941: DNA325321, XM_165891,
gen.XM_165891
Figure 2942: DNA325322, XM_084450,
gen.XM_084450
Figure 2943: PRO81865
Figure 2944: DNA325323, XM_084385,
gen.XM_084385
Figure 2945: DNA325324, NM_021226,
gen.NM_021226
Figure 2946: PRO81867
Figure 2947: DNA193957, NM_003055,
gen.NM_003055
Figure 2948: PRO23364
Figure 2949: DNA325325, NM_032997,
gen.NM_032997
Figure 2950: PRO81868

Figure 2951: DNA287642, NM_018464,
gen.NM_018464
Figure 2952: PRO9902
Figure 2953: DNA325326, XM_084451,
gen.XM_084451
Figure 2954: PRO81869
Figure 2955: DNA325327, NM_012207,
gen.NM_012207
Figure 2956: PRO81870
Figure 2957: DNA325328, NM_024045,
gen.NM_024045
Figure 2958: PRO81871
Figure 2959: DNA325329, NM_004728,
gen.NM_004728
Figure 2960: PRO81872
Figure 2961: DNA88562, NM_002727,
gen.NM_002727
Figure 2962: PRO2842
Figure 2963: DNA325330, XM_167395,
gen.XM_167395
Figure 2964: DNA227172, NM_021129,
gen.NM_021129
Figure 2965: PRO37635
Figure 2966A-B: DNA325331, XM_166125,
gen.XM_166125
Figure 2967: PRO81874
Figure 2968: DNA325332, XM_044354,
gen.XM_044354
Figure 2969: PRO81875
Figure 2970: DNA325333, XM_032520,
gen.XM_032520
Figure 2971: DNA325334, NM_019058,
gen.NM_019058
Figure 2972: PRO81877
Figure 2973: DNA325335, XM_045140,
gen.XM_045140
Figure 2974: PRO2875
Figure 2975: DNA325336, XM_116863,
gen.XM_116863
Figure 2976: DNA325337, XM_032476,
gen.XM_032476
Figure 2977: DNA325338, XM_114894,
gen.XM_114894
Figure 2978: DNA325339, NM_033022,
gen.NM_033022
Figure 2979: PRO81881
Figure 2980: DNA325340, NM_001026,
gen.NM_001026
Figure 2981: PRO11139
Figure 2982: DNA103421, NM_003375,
gen.NM_003375
Figure 2983: PRO4749
Figure 2984A-B: DNA325341, XM_166093,
gen.XM_166093
Figure 2985: PRO81882
Figure 2986: DNA304459, NM_005729,

gen.NM_005729
Figure 2987: PRO37073
Figure 2988: DNA325342, XM_166629,
gen.XM_166629
Figure 2989: PRO81883
Figure 2990: DNA103506, NM_001157,
gen.NM_001157
Figure 2991: PRO4833
Figure 2992: DNA325343, XM_016093,
gen.XM_016093
Figure 2993: PRO81884
Figure 2994: DNA325344, XM_084467,
gen.XM_084467
Figure 2995: PRO81885
Figure 2996: DNA304488, NM_032333,
gen.NM_032333
Figure 2997: PRO71057
Figure 2998: DNA325345, XM_043589,
gen.XM_043589
Figure 2999: DNA325346, XM_043605,
gen.XM_043605
Figure 3000: DNA325347, XM_087480,
gen.XM_087480
Figure 3001: PRO81887
Figure 3002: DNA325348, NM_002921,
gen.NM_002921
Figure 3003: PRO81888
Figure 3004: DNA226217, NM_005271,
gen.NM_005271
Figure 3005: PRO36680
Figure 3006: DNA325349, XM_089551,
gen.XM_089551
Figure 3007: PRO81889
Figure 3008: DNA287237, NM_001613,
gen.NM_001613
Figure 3009: PRO39648
Figure 3010: DNA325350, XM_084477,
gen.XM_084477
Figure 3011: PRO69523
Figure 3012: DNA325351, XM_084480,
gen.XM_084480
Figure 3013A-B: DNA325352, NM_013451,
gen.NM_013451
Figure 3014: PRO12813
Figure 3015: DNA325353, XM_018167,
gen.XM_018167
Figure 3016: DNA325354, XM_084372,
gen.XM_084372
Figure 3017: DNA325355, NM_020992,
gen.NM_020992
Figure 3018: PRO81893
Figure 3019: DNA325356, XM_089514,
gen.XM_089514
Figure 3020A-B: DNA325357, XM_058343,
gen.XM_058343
Figure 3021: PRO81895

Figure 3022: DNA325358, XM_058602,
gen.XM_058602
Figure 3023: PRO81896
Figure 3024A-B: DNA325359, NM_015179,
gen.NM_015179
Figure 3025: PRO81897
Figure 3026: DNA325360, XM_083842,
gen.XM_083842
Figure 3027: PRO69473
Figure 3028: DNA325361, XM_084413,
gen.XM_084413
Figure 3029: DNA325362, NM_022362,
gen.NM_022362
Figure 3030: PRO81899
Figure 3031: DNA325363, NM_032112,
gen.NM_032112
Figure 3032: PRO81900
Figure 3033: DNA325364, NM_021830,
gen.NM_021830
Figure 3034: PRO81901
Figure 3035A-B: DNA325365, XM_046743,
gen.XM_046743
Figure 3036: PRO81902
Figure 3037: DNA325366, NM_013274,
gen.NM_013274
Figure 3038: PRO81903
Figure 3039: DNA325367, NM_022039,
gen.NM_022039
Figure 3040: PRO81904
Figure 3041A-B: DNA325368, XM_031866,
gen.XM_031866
Figure 3042A-B: DNA325369, NM_015062,
gen.NM_015062
Figure 3043: PRO81905
Figure 3044A-B: DNA325370, XM_031890,
gen.XM_031890
Figure 3045A-B: DNA325371, NM_004193,
gen.NM_004193
Figure 3046: PRO81907
Figure 3047: DNA325372, NM_024040,
gen.NM_024040
Figure 3048: PRO81908
Figure 3049: DNA325373, XM_031949,
gen.XM_031949
Figure 3050: PRO4900
Figure 3051A-B: DNA144601, NM_016169,
gen.NM_016169
Figure 3052: PRO34073
Figure 3053: DNA325374, XM_005698,
gen.XM_005698
Figure 3054: PRO81909
Figure 3055: DNA325375, NM_006523,
gen.NM_006523
Figure 3056: PRO59043
Figure 3057: DNA325376, XM_018279,
gen.XM_018279

Figure 3058A-B: DNA325377, XM_005938,
gen.XM_005938
Figure 3059A-B: DNA325378, XM_031992,
gen.XM_031992
Figure 3060: PRO81912
Figure 3061: DNA325379, NM_032747,
gen.NM_032747
Figure 3062: PRO81913
Figure 3063: DNA325380, NM_005004,
gen.NM_005004
Figure 3064: PRO81914
Figure 3065: DNA325381, XM_030447,
gen.XM_030447
Figure 3066: DNA273521, NM_002079,
gen.NM_002079
Figure 3067: PRO61502
Figure 3068A-B: DNA325382, NM_032211,
gen.NM_032211
Figure 3069: PRO81916
Figure 3070: DNA325383, NM_031484,
gen.NM_031484
Figure 3071: PRO81917
Figure 3072: DNA325384, XM_084632,
gen.XM_084632
Figure 3073: DNA325385, XM_084359,
gen.XM_084359
Figure 3074A-D: DNA325386, XM_045667,
gen.XM_045667
Figure 3075: DNA325387, XM_109162,
gen.XM_109162
Figure 3076: DNA227509, NM_000274,
gen.NM_000274
Figure 3077: PRO37972
Figure 3078: DNA325388, XM_058361,
gen.XM_058361
Figure 3079: PRO81922
Figure 3080: DNA325389, XM_084505,
gen.XM_084505
Figure 3081: PRO81923
Figure 3082A-B: DNA325390, XM_049795,
gen.XM_049795
Figure 3083: PRO81924
Figure 3084: DNA325391, XM_058406,
gen.XM_058406
Figure 3085: PRO81925
Figure 3086: DNA325392, XM_055573,
gen.XM_055573
Figure 3087: PRO60991
Figure 3088: DNA325393, XM_005969,
gen.XM_005969
Figure 3089: DNA325394, NM_007190,
gen.NM_007190
Figure 3090: PRO81926
Figure 3091: DNA325395, NM_000982,
gen.NM_000982
Figure 3092: PRO81927

Figure 3093: DNA269952, NM_004725,
gen.NM_004725
Figure 3094: PRO58348
Figure 3095: DNA325396, NM_024942,
gen.NM_024942
Figure 3096: PRO81928
Figure 3097: DNA325397, NM_016567,
gen.NM_016567
Figure 3098: PRO81929
Figure 3099: DNA325398, NM_004092,
gen.NM_004092
Figure 3100: PRO81930
Figure 3101: DNA269431, NM_006659,
gen.NM_006659
Figure 3102: PRO57854
Figure 3103: DNA325399, XM_005675,
gen.XM_005675
Figure 3104: DNA325400, XM_114862,
gen.XM_114862
Figure 3105: PRO81932
Figure 3106: DNA325401, XM_088009,
gen.XM_088009
Figure 3107: DNA325402, NM_016526,
gen.NM_016526
Figure 3108: PRO81934
Figure 3109: DNA255696, NM_021932,
gen.NM_021932
Figure 3110: PRO50756
Figure 3111: DNA325403, XM_043220,
gen.XM_043220
Figure 3112: PRO81935
Figure 3113: DNA255078, NM_006435,
gen.NM_006435
Figure 3114: PRO50165
Figure 3115: DNA325404, NM_002339,
gen.NM_002339
Figure 3116: PRO81936
Figure 3117: DNA325405, XM_028192,
gen.XM_028192
Figure 3118: PRO81937
Figure 3119: DNA325406, XM_096544,
gen.XM_096544
Figure 3120: DNA325407, NM_000612,
gen.NM_000612
Figure 3121: PRO124
Figure 3122: DNA325408, XM_084742,
gen.XM_084742
Figure 3123: PRO81939
Figure 3124: DNA325409, XM_084739,
gen.XM_084739
Figure 3125: DNA325410, XM_058505,
gen.XM_058505
Figure 3126: PRO81941
Figure 3127: DNA325411, XM_006139,
gen.XM_006139
Figure 3128: PRO81942

Figure 3129: DNA325412, XM_044932,
gen.XM_044932
Figure 3130: PRO81943
Figure 3131A-B: DNA325413, XM_044957,
gen.XM_044957
Figure 3132: PRO81944
Figure 3133: DNA325414, NM_001909,
gen.NM_001909
Figure 3134: PRO292
Figure 3135: DNA325415, XM_006475,
gen.XM_006475
Figure 3136: DNA325416, XM_006483,
gen.XM_006483
Figure 3137: DNA325417, NM_001751,
gen.NM_001751
Figure 3138: PRO69635
Figure 3139: DNA325418, XM_114981,
gen.XM_114981
Figure 3140: PRO81945
Figure 3141: DNA325419, XM_083852,
gen.XM_083852
Figure 3142: DNA325420, NM_000559,
gen.NM_000559
Figure 3143: PRO81946
Figure 3144: DNA325421, NM_000184,
gen.NM_000184
Figure 3145: PRO81947
Figure 3146: DNA325422, NM_005330,
gen.NM_005330
Figure 3147: PRO81948
Figure 3148: DNA325423, XM_015243,
gen.XM_015243
Figure 3149: DNA325424, NM_015324,
gen.NM_015324
Figure 3150: PRO81950
Figure 3151: DNA325425, XM_006424,
gen.XM_006424
Figure 3152: DNA325426, XM_113238,
gen.XM_113238
Figure 3153A-C: DNA325427, XM_052786,
gen.XM_052786
Figure 3154: PRO81953
Figure 3155: DNA325428, NM_000990,
gen.NM_000990
Figure 3156: PRO25985
Figure 3157A-B: DNA325429, XM_045750,
gen.XM_045750
Figure 3158: PRO81954
Figure 3159: DNA325430, XM_058414,
gen.XM_058414
Figure 3160: PRO81955
Figure 3161A-B: DNA325431, XM_049197,
gen.XM_049197
Figure 3162: PRO81956
Figure 3163A-B: DNA325432, NM_001418,
gen.NM_001418

Figure 3164: PRO81957
Figure 3165: DNA325433, XM_096520, gen.XM_096520
Figure 3166: PRO81958
Figure 3167: DNA325434, XM_006212, gen.XM_006212
Figure 3168: PRO81959
Figure 3169: DNA325435, XM_084527, gen.XM_084527
Figure 3170: DNA325436, XM_016139, gen.XM_016139
Figure 3171: DNA325437, NM_001017, gen.NM_001017
Figure 3172: PRO11262
Figure 3173: DNA325438, NM_014267, gen.NM_014267
Figure 3174: PRO81962
Figure 3175: DNA97285, NM_005566, gen.NM_005566
Figure 3176: PRO3632
Figure 3177: DNA325439, XM_115081, gen.XM_115081
Figure 3178: DNA325440, XM_036339, gen.XM_036339
Figure 3179: PRO81964
Figure 3180: DNA325441, XM_084514, gen.XM_084514
Figure 3181: PRO81965
Figure 3182: DNA325442, XM_084516, gen.XM_084516
Figure 3183: DNA325443, XM_084515, gen.XM_084515
Figure 3184: DNA325444, XM_084517, gen.XM_084517
Figure 3185: DNA325445, XM_034431, gen.XM_034431
Figure 3186: PRO11691
Figure 3187: DNA325446, XM_030326, gen.XM_030326
Figure 3188: DNA325447, NM_057174, gen.NM_057174
Figure 3189: PRO81970
Figure 3190: DNA325448, NM_004813, gen.NM_004813
Figure 3191: PRO81971
Figure 3192: DNA325449, XM_167437, gen.XM_167437
Figure 3193: DNA325450, XM_054856, gen.XM_054856
Figure 3194: DNA325451, XM_004330, gen.XM_004330
Figure 3195: DNA325452, XM_084681, gen.XM_084681
Figure 3196: DNA325453, XM_006297, gen.XM_006297
Figure 3197: DNA325454, NM_003646,

gen.NM_003646
Figure 3198: PRO81977
Figure 3199: DNA325455, NM_004551, gen.NM_004551
Figure 3200: PRO81978
Figure 3201: DNA325456, XM_006170, gen.XM_006170
Figure 3202: DNA325457, XM_037173, gen.XM_037173
Figure 3203: PRO81980
Figure 3204: DNA150974, NM_005693, gen.NM_005693
Figure 3205: PRO12224
Figure 3206: DNA226080, NM_001610, gen.NM_001610
Figure 3207: PRO36543
Figure 3208: DNA270134, NM_000107, gen.NM_000107
Figure 3209: PRO58523
Figure 3210: DNA325458, NM_016223, gen.NM_016223
Figure 3211: PRO81981
Figure 3212: DNA325459, XM_037147, gen.XM_037147
Figure 3213: PRO81982
Figure 3214: DNA325460, XM_015705, gen.XM_015705
Figure 3215: DNA272728, NM_003146, gen.NM_003146
Figure 3216: PRO60847
Figure 3217: DNA325461, XM_165611, gen.XM_165611
Figure 3218: DNA287417, NM_024098, gen.NM_024098
Figure 3219: PRO69674
Figure 3220: DNA227088, NM_014502, gen.NM_014502
Figure 3221: PRO37551
Figure 3222: DNA325462, XM_165610, gen.XM_165610
Figure 3223A-B: DNA325463, XM_165612, gen.XM_165612
Figure 3224: DNA325464, XM_166234, gen.XM_166234
Figure 3225: DNA325465, NM_015533, gen.NM_015533
Figure 3226: PRO81988
Figure 3227: DNA325466, XM_166232, gen.XM_166232
Figure 3228A-B: DNA325467, XM_167748, gen.XM_167748
Figure 3229: PRO81990
Figure 3230: DNA325468, NM_004739, gen.NM_004739
Figure 3231: PRO81991
Figure 3232: DNA325469, NM_014610,

gen.NM_014610
Figure 3233: PRO81992
Figure 3234: DNA325470, XM_167747,
gen.XM_167747
Figure 3235: PRO81993
Figure 3236: DNA287254, NM_024099,
gen.NM_024099
Figure 3237: PRO69528
Figure 3238: DNA325471, NM_015853,
gen.NM_015853
Figure 3239: PRO81994
Figure 3240: DNA325472, NM_032667,
gen.NM_032667
Figure 3241: PRO81995
Figure 3242: DNA325473, NM_006362,
gen.NM_006362
Figure 3243: PRO81996
Figure 3244: DNA325474, XM_167716,
gen.XM_167716
Figure 3245: DNA75863, NM_002411,
gen.NM_002411
Figure 3246: PRO2018
Figure 3247: DNA325475, XM_087710,
gen.XM_087710
Figure 3248: DNA325476, XM_167726,
gen.XM_167726
Figure 3249: DNA325477, NM_004265,
gen.NM_004265
Figure 3250: PRO12878
Figure 3251A-B: DNA325478, NM_013402,
gen.NM_013402
Figure 3252: PRO81999
Figure 3253: DNA325479, NM_004111,
gen.NM_004111
Figure 3254: PRO69568
Figure 3255: DNA325480, XM_048286,
gen.XM_048286
Figure 3256: DNA325481, NM_004322,
gen.NM_004322
Figure 3257: PRO20117
Figure 3258: DNA325482, NM_032989,
gen.NM_032989
Figure 3259: PRO20117
Figure 3260: DNA325483, XM_011988,
gen.XM_011988
Figure 3261: DNA325484, NM_031472,
gen.NM_031472
Figure 3262: PRO82002
Figure 3263: DNA325485, XM_037808,
gen.XM_037808
Figure 3264: DNA325486, NM_004074,
gen.NM_004074
Figure 3265: PRO82004
Figure 3266: DNA325487, NM_017670,
gen.NM_017670
Figure 3267: PRO82005

Figure 3268: DNA325488, XM_113223,
gen.XM_113223
Figure 3269: DNA325489, XM_045642,
gen.XM_045642
Figure 3270: DNA325490, XM_006533,
gen.XM_006533
Figure 3271: DNA325491, XM_045613,
gen.XM_045613
Figure 3272: PRO59721
Figure 3273A-B: DNA325492, XM_045612,
gen.XM_045612
Figure 3274: PRO82009
Figure 3275: DNA325493, XM_113224,
gen.XM_113224
Figure 3276: DNA325494, XM_045499,
gen.XM_045499
Figure 3277: PRO82011
Figure 3278: DNA325495, XM_045525,
gen.XM_045525
Figure 3279: DNA325496, NM_013265,
gen.NM_013265
Figure 3280: PRO82013
Figure 3281: DNA325497, XM_006529,
gen.XM_006529
Figure 3282: PRO60008
Figure 3283: DNA325498, XM_053787,
gen.XM_053787
Figure 3284: DNA269803, NM_001667,
gen.NM_001667
Figure 3285: PRO58207
Figure 3286: DNA325499, XM_115031,
gen.XM_115031
Figure 3287: DNA325500, XM_084702,
gen.XM_084702
Figure 3288: DNA325501, XM_053796,
gen.XM_053796
Figure 3289: DNA325502, NM_002689,
gen.NM_002689
Figure 3290: PRO82018
Figure 3291A-D: DNA325503, XM_167804,
gen.XM_167804
Figure 3292: PRO82019
Figure 3293: DNA325504, XM_166235,
gen.XM_166235
Figure 3294: DNA325505, XM_166236,
gen.XM_166236
Figure 3295: DNA270721, NM_006842,
gen.NM_006842
Figure 3296: PRO59084
Figure 3297: DNA189687, NM_000852,
gen.NM_000852
Figure 3298: PRO25845
Figure 3299: DNA325506, NM_007103,
gen.NM_007103
Figure 3300: PRO58606
Figure 3301: DNA325507, NM_005851,

gen.NM_005851
Figure 3302: PRO69461
Figure 3303A-B: DNA325508, XM_165598,
gen.XM_165598
Figure 3304: DNA325509, NM_006019,
gen.NM_006019
Figure 3305: PRO82023
Figure 3306: DNA325510, NM_006053,
gen.NM_006053
Figure 3307: PRO24831
Figure 3308: DNA325511, XM_166196,
gen.XM_166196
Figure 3309: PRO82024
Figure 3310: DNA325512, XM_165600,
gen.XM_165600
Figure 3311A-B: DNA325513, NM_053056,
gen.NM_053056
Figure 3312: PRO4870
Figure 3313: DNA103474, NM_003824,
gen.NM_003824
Figure 3314: PRO4801
Figure 3315: DNA325514, XM_096486,
gen.XM_096486
Figure 3316A-B: DNA325515, NM_003626,
gen.NM_003626
Figure 3317: PRO82027
Figure 3318A-B: DNA325516, XM_167853,
gen.XM_167853
Figure 3319: PRO82028
Figure 3320: DNA325517, NM_014042,
gen.NM_014042
Figure 3321: PRO82029
Figure 3322A-B: DNA325518, NM_001567,
gen.NM_001567
Figure 3323: PRO61238
Figure 3324: DNA325519, XM_167433,
gen.XM_167433
Figure 3325: DNA325520, XM_165616,
gen.XM_165616
Figure 3326: DNA325521, NM_032871,
gen.NM_032871
Figure 3327: PRO57307
Figure 3328: DNA325522, XM_165631,
gen.XM_165631
Figure 3329: DNA254186, NM_014752,
gen.NM_014752
Figure 3330: PRO49298
Figure 3331: DNA325523, NM_001005,
gen.NM_001005
Figure 3332: PRO82032
Figure 3333: DNA88176, NM_001235,
gen.NM_001235
Figure 3334: PRO2685
Figure 3335A-B: DNA325524, XM_165627,
gen.XM_165627
Figure 3336: DNA325525, XM_166253,

gen.XM_166253
Figure 3337: DNA325526, NM_001293,
gen.NM_001293
Figure 3338: PRO82034
Figure 3339: DNA325527, XM_042852,
gen.XM_042852
Figure 3340: PRO82035
Figure 3341: DNA325528, XM_165628,
gen.XM_165628
Figure 3342A-B: DNA325529, NM_080491,
gen.NM_080491
Figure 3343: PRO82037
Figure 3344A-B: DNA325530, NM_012296,
gen.NM_012296
Figure 3345: PRO60311
Figure 3346: DNA325531, NM_032379,
gen.NM_032379
Figure 3347: PRO82038
Figure 3348: DNA325532, NM_007173,
gen.NM_007173
Figure 3349: DNA325533, XM_166239,
gen.XM_166239
Figure 3350: DNA325534, XM_084610,
gen.XM_084610
Figure 3351: PRO82040
Figure 3352: DNA325535, XM_058450,
gen.XM_058450
Figure 3353: DNA325536, XM_084601,
gen.XM_084601
Figure 3354: PRO82042
Figure 3355A-B: DNA325537, XM_006464,
gen.XM_006464
Figure 3356: PRO82043
Figure 3357: DNA325538, XM_084570,
gen.XM_084570
Figure 3358: DNA325539, XM_051435,
gen.XM_051435
Figure 3359: DNA325540, NM_001467,
gen.NM_001467
Figure 3360: PRO82045
Figure 3361: DNA325541, NM_001028,
gen.NM_001028
Figure 3362: PRO82046
Figure 3363: DNA325542, XM_113230,
gen.XM_113230
Figure 3364: DNA325543, XM_115062,
gen.XM_115062
Figure 3365: DNA325544, XM_115063,
gen.XM_115063
Figure 3366: DNA325545, XM_113229,
gen.XM_113229
Figure 3367A-B: DNA325546, XM_051489,
gen.XM_051489
Figure 3368: PRO82050
Figure 3369: DNA325547, NM_022003,
gen.NM_022003

Figure 3370: PRO82051
Figure 3371: DNA325548, XM_006432, gen.XM_006432
Figure 3372: PRO82052
Figure 3373: DNA325549, XM_051716, gen.XM_051716
Figure 3374: DNA325550, NM_025164, gen.NM_025164
Figure 3375: PRO82054
Figure 3376: DNA225752, NM_000039, gen.NM_000039
Figure 3377: PRO36215
Figure 3378: DNA325551, XM_052113, gen.XM_052113
Figure 3379: PRO82055
Figure 3380: DNA271324, NM_006169, gen.NM_006169
Figure 3381: PRO59629
Figure 3382: DNA325552, XM_084658, gen.XM_084658
Figure 3383: PRO82056
Figure 3384: DNA325553, NM_000795, gen.NM_000795
Figure 3385: PRO12448
Figure 3386: DNA325554, NM_017868, gen.NM_017868
Figure 3387: PRO82057
Figure 3388: DNA325555, XM_084654, gen.XM_084654
Figure 3389: PRO82058
Figure 3390: DNA272413, NM_003002, gen.NM_003002
Figure 3391: PRO60666
Figure 3392: DNA271843, NM_004398, gen.NM_004398
Figure 3393: PRO60123
Figure 3394: DNA325556, XM_017369, gen.XM_017369
Figure 3395: DNA325557, NM_032299, gen.NM_032299
Figure 3396: PRO82060
Figure 3397: DNA325558, XM_055369, gen.XM_055369
Figure 3398: DNA325559, XM_051430, gen.XM_051430
Figure 3399: DNA325560, XM_006467, gen.XM_006467
Figure 3400: DNA325561, XM_113226, gen.XM_113226
Figure 3401: DNA325562, XM_165592, gen.XM_165592
Figure 3402: PRO82064
Figure 3403: DNA325563, XM_166181, gen.XM_166181
Figure 3404: DNA325564, XM_052862, gen.XM_052862

Figure 3405: PRO82066
Figure 3406: DNA325565, XM_166177, gen.XM_166177
Figure 3407: DNA325566, XM_165571, gen.XM_165571
Figure 3408: PRO82068
Figure 3409: DNA325567, XM_166174, gen.XM_166174
Figure 3410: PRO82069
Figure 3411: DNA325568, NM_001274, gen.NM_001274
Figure 3412: PRO12187
Figure 3413: DNA325569, XM_165586, gen.XM_165586
Figure 3414: DNA325570, XM_165584, gen.XM_165584
Figure 3415: DNA257965, NM_032873, gen.NM_032873
Figure 3416: PRO52492
Figure 3417: DNA325571, XM_167780, gen.XM_167780
Figure 3418: DNA325572, XM_166743, gen.XM_166743
Figure 3419: PRO82072
Figure 3420: DNA325573, NM_012101, gen.NM_012101
Figure 3421: PRO82073
Figure 3422: DNA325574, NM_058193, gen.NM_058193
Figure 3423: PRO82074
Figure 3424: DNA325575, XM_084522, gen.XM_084522
Figure 3425: PRO82075
Figure 3426: DNA325576, XM_091786, gen.XM_091786
Figure 3427: DNA325577, XM_165390, gen.XM_165390
Figure 3428: DNA325578, XM_084525, gen.XM_084525
Figure 3429A-B: DNA325579, XM_010494, gen.XM_010494
Figure 3430A-B: DNA325580, NM_015064, gen.NM_015064
Figure 3431: PRO82078
Figure 3432: DNA325581, NM_030775, gen.NM_030775
Figure 3433: PRO71031
Figure 3434: DNA297398, NM_032642, gen.NM_032642
Figure 3435: PRO71031
Figure 3436: DNA325582, XM_017080, gen.XM_017080
Figure 3437: DNA325583, XM_113739, gen.XM_113739
Figure 3438: PRO82080
Figure 3439: DNA325584, NM_002014, gen.NM_002014

gen.NM_002014
Figure 3440: PRO59262
Figure 3441: DNA325585, XM_096661,
gen.XM_096661
Figure 3442: DNA325586, NM_018463,
gen.NM_018463
Figure 3443: PRO82082
Figure 3444: DNA325587, NM_021953,
gen.NM_021953
Figure 3445: PRO82083
Figure 3446: DNA325588, NM_031465,
gen.NM_031465
Figure 3447: PRO82084
Figure 3448: DNA325589, NM_005002,
gen.NM_005002
Figure 3449: PRO82085
Figure 3450: DNA325590, XM_033227,
gen.XM_033227
Figure 3451: DNA325591, XM_116926,
gen.XM_116926
Figure 3452: DNA88114, NM_001734,
gen.NM_001734
Figure 3453: PRO2660
Figure 3454: DNA325592, XM_058574,
gen.XM_058574
Figure 3455: DNA325593, NM_007273,
gen.NM_007273
Figure 3456: PRO36970
Figure 3457A-B: DNA325594, XM_032588,
gen.XM_032588
Figure 3458: DNA325595, NM_001975,
gen.NM_001975
Figure 3459: PRO38010
Figure 3460: DNA325596, NM_000365,
gen.NM_000365
Figure 3461: PRO69549
Figure 3462: DNA325597, XM_032614,
gen.XM_032614
Figure 3463: DNA325598, NM_002075,
gen.NM_002075
Figure 3464: PRO82091
Figure 3465: DNA325599, XM_165910,
gen.XM_165910
Figure 3466: DNA151827, NM_005439,
gen.NM_005439
Figure 3467: PRO12902
Figure 3468A-B: DNA254624, NM_001273,
gen.NM_001273
Figure 3469: PRO49726
Figure 3470: DNA325600, NM_015438,
gen.NM_015438
Figure 3471: PRO82093
Figure 3472: DNA325601, XM_033263,
gen.XM_033263
Figure 3473: DNA225632, NM_002046,
gen.NM_002046

Figure 3474: PRO36095
Figure 3475A-B: DNA325602, XM_006958,
gen.XM_006958
Figure 3476: DNA83180, NM_002342,
gen.NM_002342
Figure 3477: PRO2622
Figure 3478: DNA103514, NM_001038,
gen.NM_001038
Figure 3479: PRO4841
Figure 3480: DNA188396, NM_001065,
gen.NM_001065
Figure 3481: PRO21924
Figure 3482A-C: DNA325603, XM_006947,
gen.XM_006947
Figure 3483A-B: DNA325604, XM_006936,
gen.XM_006936
Figure 3484: PRO82097
Figure 3485A-B: DNA325605, XM_006925,
gen.XM_006925
Figure 3486: DNA325606, XM_096630,
gen.XM_096630
Figure 3487: PRO82099
Figure 3488: DNA325607, XM_084901,
gen.XM_084901
Figure 3489: DNA226028, NM_002355,
gen.NM_002355
Figure 3490: PRO36491
Figure 3491: DNA325608, XM_031807,
gen.XM_031807
Figure 3492: PRO82101
Figure 3493A-B: DNA325609, XM_049663,
gen.XM_049663
Figure 3494: DNA325610, XM_012159,
gen.XM_012159
Figure 3495: DNA325611, XM_084922,
gen.XM_084922
Figure 3496: DNA325612, NM_031289,
gen.NM_031289
Figure 3497: PRO82104
Figure 3498: DNA226771, NM_003979,
gen.NM_003979
Figure 3499: PRO37234
Figure 3500: DNA325613, XM_084918,
gen.XM_084918
Figure 3501: DNA325614, NM_007178,
gen.NM_007178
Figure 3502: PRO82106
Figure 3503: DNA325615, XM_041100,
gen.XM_041100
Figure 3504A-B: DNA325616, XM_058567,
gen.XM_058567
Figure 3505: PRO82107
Figure 3506A-B: DNA325617, XM_166605,
gen.XM_166605
Figure 3507: DNA325618, XM_029805,
gen.XM_029805

Figure 3508: PRO82109
Figure 3509: DNA325619, NM_005889,
gen.NM_005889
Figure 3510: PRO82110
Figure 3511: DNA256072, NM_001644,
gen.NM_001644
Figure 3512: PRO51121
Figure 3513: DNA325620, NM_018686,
gen.NM_018686
Figure 3514: PRO82111
Figure 3515: DNA325621, XM_084770,
gen.XM_084770
Figure 3516: PRO82112
Figure 3517: DNA325622, NM_018048,
gen.NM_018048
Figure 3518: PRO82113
Figure 3519: DNA325623, XM_113730,
gen.XM_113730
Figure 3520: DNA150978, NM_007244,
gen.NM_007244
Figure 3521: PRO11601
Figure 3522: DNA325624, NM_006250,
gen.NM_006250
Figure 3523: PRO82115
Figure 3524: DNA79313, NM_005042,
gen.NM_005042
Figure 3525: PRO2555
Figure 3526: DNA150997, NM_004982,
gen.NM_004982
Figure 3527: PRO12573
Figure 3528: DNA325625, XM_050074,
gen.XM_050074
Figure 3529: DNA325626, NM_024854,
gen.NM_024854
Figure 3530: PRO82117
Figure 3531: DNA325627, XM_084807,
gen.XM_084807
Figure 3532: DNA325628, XM_165906,
gen.XM_165906
Figure 3533A-B: DNA325629, XM_038659,
gen.XM_038659
Figure 3534: PRO82120
Figure 3535: DNA325630, XM_006694,
gen.XM_006694
Figure 3536: DNA325631, XM_006748,
gen.XM_006748
Figure 3537: PRO82122
Figure 3538: DNA325632, XM_016640,
gen.XM_016640
Figure 3539: DNA325633, XM_096146,
gen.XM_096146
Figure 3540A-B: DNA325634, XM_084841,
gen.XM_084841
Figure 3541: PRO82125
Figure 3542: DNA325635, XM_090218,
gen.XM_090218

Figure 3543: DNA325636, XM_012272,
gen.XM_012272
Figure 3544: PRO82127
Figure 3545A-B: DNA325637, XM_056481,
gen.XM_056481
Figure 3546: DNA325638, NM_006262,
gen.NM_006262
Figure 3547: PRO82129
Figure 3548: DNA325639, NM_018113,
gen.NM_018113
Figure 3549: PRO82130
Figure 3550: DNA271344, NM_001659,
gen.NM_001659
Figure 3551: PRO59647
Figure 3552: DNA325640, NM_017822,
gen.NM_017822
Figure 3553: PRO82131
Figure 3554A-E: DNA325641, XM_028760,
gen.XM_028760
Figure 3555: DNA272379, NM_002733,
gen.NM_002733
Figure 3556: PRO60634
Figure 3557: DNA325642, XM_084866,
gen.XM_084866
Figure 3558: PRO82133
Figure 3559: DNA325643, XM_006826,
gen.XM_006826
Figure 3560: DNA325644, XM_113719,
gen.XM_113719
Figure 3561: DNA325645, XM_028662,
gen.XM_028662
Figure 3562: DNA325646, XM_035497,
gen.XM_035497
Figure 3563: PRO82137
Figure 3564: DNA325647, XM_035490,
gen.XM_035490
Figure 3565: PRO82138
Figure 3566: DNA325648, NM_013277,
gen.NM_013277
Figure 3567: PRO82139
Figure 3568: DNA325649, NM_003076,
gen.NM_003076
Figure 3569: PRO82140
Figure 3570: DNA325650, XM_115117,
gen.XM_115117
Figure 3571: DNA325651, XM_035485,
gen.XM_035485
Figure 3572A-B: DNA325652, NM_016357,
gen.NM_016357
Figure 3573: PRO82143
Figure 3574: DNA325653, NM_005171,
gen.NM_005171
Figure 3575: PRO60924
Figure 3576: DNA325654, NM_014033,
gen.NM_014033
Figure 3577: PRO4348

Figure 3578: DNA325655, XM_096620, gen.XM_096620
Figure 3579: DNA325656, XM_165905, gen.XM_165905
Figure 3580: DNA325657, XM_015481, gen.XM_015481
Figure 3581: DNA325658, XM_049148, gen.XM_049148
Figure 3582: DNA325659, XM_084885, gen.XM_084885
Figure 3583: DNA325660, XM_084884, gen.XM_084884
Figure 3584: DNA325661, XM_113726, gen.XM_113726
Figure 3585: DNA325662, XM_015476, gen.XM_015476
Figure 3586: DNA325663, XM_049141, gen.XM_049141
Figure 3587: PRO82152
Figure 3588: DNA227191, NM_021934, gen.NM_021934
Figure 3589: PRO37654
Figure 3590: DNA325664, XM_083868, gen.XM_083868
Figure 3591: DNA270458, NM_002273, gen.NM_002273
Figure 3592: PRO58837
Figure 3593: DNA227092, NM_000224, gen.NM_000224
Figure 3594: PRO37555
Figure 3595: DNA325665, XM_029728, gen.XM_029728
Figure 3596: DNA325666, XM_015468, gen.XM_015468
Figure 3597: PRO82155
Figure 3598: DNA325667, XM_012162, gen.XM_012162
Figure 3599: DNA325668, XM_084789, gen.XM_084789
Figure 3600: DNA196351, NM_002178, gen.NM_002178
Figure 3601: PRO3449
Figure 3602A-B: DNA325669, XM_029631, gen.XM_029631
Figure 3603: PRO82158
Figure 3604: DNA325670, NM_015665, gen.NM_015665
Figure 3605: PRO82159
Figure 3606: DNA325671, NM_014311, gen.NM_014311
Figure 3607: PRO82160
Figure 3608: DNA325672, XM_096606, gen.XM_096606
Figure 3609: PRO82161
Figure 3610: DNA325673, NM_018457, gen.NM_018457

Figure 3611: PRO82162
Figure 3612: DNA325674, NM_031157, gen.NM_031157
Figure 3613: PRO82163
Figure 3614: DNA325675, NM_004178, gen.NM_004178
Figure 3615: PRO82164
Figure 3616: DNA325676, NM_134323, gen.NM_134323
Figure 3617: PRO82165
Figure 3618: DNA325677, NM_134324, gen.NM_134324
Figure 3619: PRO82166
Figure 3620: DNA290294, NM_005016, gen.NM_005016
Figure 3621: PRO70453
Figure 3622: DNA325678, NM_031989, gen.NM_031989
Figure 3623: PRO82167
Figure 3624: DNA325679, XM_028643, gen.XM_028643
Figure 3625: PRO82168
Figure 3626: DNA325680, XM_006710, gen.XM_006710
Figure 3627: PRO82169
Figure 3628: DNA227094, NM_005594, gen.NM_005594
Figure 3629: PRO37557
Figure 3630: DNA325681, XM_084824, gen.XM_084824
Figure 3631: DNA304783, NM_014255, gen.NM_014255
Figure 3632: PRO4426
Figure 3633: DNA325682, XM_165903, gen.XM_165903
Figure 3634: DNA325683, XM_115140, gen.XM_115140
Figure 3635: DNA325684, XM_113712, gen.XM_113712
Figure 3636: DNA325685, NM_006601, gen.NM_006601
Figure 3637: PRO82174
Figure 3638: DNA325686, XM_012182, gen.XM_012182
Figure 3639: PRO82175
Figure 3640: DNA325687, XM_048943, gen.XM_048943
Figure 3641: DNA325688, XM_053164, gen.XM_053164
Figure 3642: DNA325689, XM_048991, gen.XM_048991
Figure 3643: DNA325690, NM_024068, gen.NM_024068
Figure 3644: PRO82179
Figure 3645A-B: DNA325691, XM_056346, gen.XM_056346

Figure 3646: DNA325692, NM_021019,
gen.NM_021019
Figure 3647: PRO82181
Figure 3648: DNA325693, NM_079423,
gen.NM_079423
Figure 3649: PRO82182
Figure 3650: DNA325694, NM_079425,
gen.NM_079425
Figure 3651: PRO82183
Figure 3652: DNA325695, XM_049048,
gen.XM_049048
Figure 3653: PRO82184
Figure 3654: DNA325696, NM_021104,
gen.NM_021104
Figure 3655: PRO11213
Figure 3656: DNA325697, NM_001029,
gen.NM_001029
Figure 3657: PRO10838
Figure 3658: DNA325698, XM_001482,
gen.XM_001482
Figure 3659: DNA325699, XM_049150,
gen.XM_049150
Figure 3660: DNA325700, NM_006928,
gen.NM_006928
Figure 3661: PRO2846
Figure 3662: DNA325701, XM_056353,
gen.XM_056353
Figure 3663: DNA325702, NM_001780,
gen.NM_001780
Figure 3664: PRO283
Figure 3665: DNA325703, NM_031479,
gen.NM_031479
Figure 3666: PRO21773
Figure 3667A-: DNA137231, NM_005269,
gen.NM_005269
Figure 3668: PRO9112
Figure 3669: DNA325704, NM_004990,
gen.NM_004990
Figure 3670: PRO82188
Figure 3671: DNA325705, XM_058528,
gen.XM_058528
Figure 3672: DNA325706, XM_084801,
gen.XM_084801
Figure 3673: PRO82190
Figure 3674: DNA325707, XM_048603,
gen.XM_048603
Figure 3675: PRO82191
Figure 3676: DNA325708, NM_133483,
gen.NM_133483
Figure 3677: PRO82192
Figure 3678: DNA79101, NM_006812,
gen.NM_006812
Figure 3679: PRO2549
Figure 3680: DNA325709, XM_096566,
gen.XM_096566
Figure 3681: DNA325710, NM_005981,

gen.NM_005981
Figure 3682: PRO4666
Figure 3683: DNA325711, NM_000075,
gen.NM_000075
Figure 3684: PRO4873
Figure 3685: DNA325712, NM_052984,
gen.NM_052984
Figure 3686: PRO82194
Figure 3687: DNA325713, NM_000785,
gen.NM_000785
Figure 3688: PRO58440
Figure 3689: DNA325714, NM_005371,
gen.NM_005371
Figure 3690: PRO82195
Figure 3691: DNA325715, NM_023032,
gen.NM_023032
Figure 3692: PRO82196
Figure 3693: DNA325716, NM_023033,
gen.NM_023033
Figure 3694: PRO82197
Figure 3695: DNA325717, NM_005726,
gen.NM_005726
Figure 3696: PRO82198
Figure 3697: DNA325718, NM_006576,
gen.NM_006576
Figure 3698: PRO82199
Figure 3699A-B: DNA325719, XM_096038,
gen.XM_096038
Figure 3700: DNA325720, XM_056681,
gen.XM_056681
Figure 3701: PRO82201
Figure 3702: DNA325721, XM_084909,
gen.XM_084909
Figure 3703: PRO82202
Figure 3704: DNA325722, XM_004098,
gen.XM_004098
Figure 3705: DNA325723, XM_084912,
gen.XM_084912
Figure 3706: PRO82204
Figure 3707: DNA325724, XM_040221,
gen.XM_040221
Figure 3708: DNA325725, XM_016605,
gen.XM_016605
Figure 3709: PRO82206
Figure 3710: DNA325726, XM_017508,
gen.XM_017508
Figure 3711: PRO82207
Figure 3712: DNA325727, NM_032338,
gen.NM_032338
Figure 3713: PRO82208
Figure 3714A-B: DNA325728, XM_052460,
gen.XM_052460
Figure 3715: DNA325729, XM_083866,
gen.XM_083866
Figure 3716: PRO82210
Figure 3717: DNA304694, NM_020401,

gen.NM_020401
Figure 3718: PRO71120
Figure 3719: DNA325730, XM_052474,
gen.XM_052474
Figure 3720: DNA227474, NM_015646,
gen.NM_015646
Figure 3721: PRO37937
Figure 3722: DNA325731, XM_053952,
gen.XM_053952
Figure 3723: PRO82212
Figure 3724: DNA227171, NM_014515,
gen.NM_014515
Figure 3725: PRO37634
Figure 3726: DNA325732, XM_046041,
gen.XM_046041
Figure 3727: DNA271492, NM_006530,
gen.NM_006530
Figure 3728: PRO59785
Figure 3729: DNA226014, NM_000239,
gen.NM_000239
Figure 3730: PRO36477
Figure 3731: DNA325733, XM_084645,
gen.XM_084645
Figure 3732A-B: DNA325734, XM_039395,
gen.XM_039395
Figure 3733: PRO82213
Figure 3734: DNA325736, XM_040644,
gen.XM_040644
Figure 3735: PRO82214
Figure 3736A-B: DNA325737, XM_006578,
gen.XM_006578
Figure 3737: DNA325738, XM_038308,
gen.XM_038308
Figure 3738: PRO82215
Figure 3739: DNA325739, XM_096597,
gen.XM_096597
Figure 3740: DNA325740, NM_001920,
gen.NM_001920
Figure 3741: PRO2841
Figure 3742: DNA325741, NM_133503,
gen.NM_133503
Figure 3743: PRO2841
Figure 3744: DNA325742, NM_133504,
gen.NM_133504
Figure 3745: PRO82218
Figure 3746: DNA325743, NM_133505,
gen.NM_133505
Figure 3747: PRO82219
Figure 3748: DNA325744, NM_133507,
gen.NM_133507
Figure 3749: PRO82220
Figure 3750: DNA325745, NM_133506,
gen.NM_133506
Figure 3751: PRO82221
Figure 3752: DNA325746, NM_002345,
gen.NM_002345

Figure 3753: PRO9987
Figure 3754: DNA325747, XM_167518,
gen.XM_167518
Figure 3755: DNA325748, XM_052542,
gen.XM_052542
Figure 3756: PRO82223
Figure 3757: DNA325749, NM_003877,
gen.NM_003877
Figure 3758: PRO12839
Figure 3759: DNA325750, XM_012219,
gen.XM_012219
Figure 3760: PRO69473
Figure 3761: DNA325751, XM_012145,
gen.XM_012145
Figure 3762: PRO82224
Figure 3763: DNA274361, NM_000895,
gen.NM_000895
Figure 3764: PRO62273
Figure 3765: DNA325752, XM_006887,
gen.XM_006887
Figure 3766: DNA325753, XM_006589,
gen.XM_006589
Figure 3767: DNA325754, XM_090458,
gen.XM_090458
Figure 3768: PRO82227
Figure 3769: DNA325755, XM_052641,
gen.XM_052641
Figure 3770: PRO82228
Figure 3771A-B: DNA325756, XM_049211,
gen.XM_049211
Figure 3772: DNA325757, XM_049201,
gen.XM_049201
Figure 3773: DNA325758, XM_058556,
gen.XM_058556
Figure 3774: DNA325759, XM_083864,
gen.XM_083864
Figure 3775: DNA325760, XM_062437,
gen.XM_062437
Figure 3776: PRO82232
Figure 3777: DNA254777, NM_014325,
gen.NM_014325
Figure 3778: PRO49875
Figure 3779: DNA325761, XM_090413,
gen.XM_090413
Figure 3780: PRO82233
Figure 3781: DNA325762, NM_000970,
gen.NM_000970
Figure 3782: PRO82234
Figure 3783: DNA325763, XM_084800,
gen.XM_084800
Figure 3784: PRO82235
Figure 3785: DNA325764, NM_006817,
gen.NM_006817
Figure 3786: PRO70694
Figure 3787A-C: DNA325765, XM_083892,
gen.XM_083892

Figure 3788A-B: DNA325766, XM_084941,
gen.XM_084941
Figure 3789: PRO82237
Figure 3790A-B: DNA325767, NM_057169,
gen.NM_057169
Figure 3791: PRO82238
Figure 3792A-B: DNA325768, NM_014776,
gen.NM_014776
Figure 3793: PRO82239
Figure 3794: DNA325769, NM_032904,
gen.NM_032904
Figure 3795: PRO82240
Figure 3796A-B: DNA325770, XM_007003,
gen.XM_007003
Figure 3797: DNA325771, XM_007002,
gen.XM_007002
Figure 3798: DNA325772, XM_056996,
gen.XM_056996
Figure 3799: PRO82243
Figure 3800: DNA325773, XM_084946,
gen.XM_084946
Figure 3801: PRO82244
Figure 3802: DNA325775, XM_027102,
gen.XM_027102
Figure 3803: PRO82245
Figure 3804: DNA325776, XM_084948,
gen.XM_084948
Figure 3805: DNA325777, NM_007062,
gen.NM_007062
Figure 3806: PRO82247
Figure 3807: DNA325778, NM_006825,
gen.NM_006825
Figure 3808: PRO82248
Figure 3809: DNA325779, XM_115197,
gen.XM_115197
Figure 3810: DNA325780, NM_017901,
gen.NM_017901
Figure 3811: PRO82250
Figure 3812: DNA325781, NM_032814,
gen.NM_032814
Figure 3813: PRO82252
Figure 3814: DNA325782, XM_084889,
gen.XM_084889
Figure 3815: PRO82253
Figure 3816: DNA325783, NM_002567,
gen.NM_002567
Figure 3817: PRO59001
Figure 3818: DNA325784, XM_084808,
gen.XM_084808
Figure 3819: DNA325785, XM_096572,
gen.XM_096572
Figure 3820: PRO82255
Figure 3821: DNA325786, XM_045010,
gen.XM_045010
Figure 3822: PRO82256
Figure 3823: DNA270677, NM_014868,

gen.NM_014868
Figure 3824: PRO59042
Figure 3825: DNA325787, XM_052893,
gen.XM_052893
Figure 3826A-B: DNA325788, XM_045802,
gen.XM_045802
Figure 3827: DNA302016, NM_001002,
gen.NM_001002
Figure 3828: PRO70989
Figure 3829: DNA325789, NM_053275,
gen.NM_053275
Figure 3830: PRO70989
Figure 3831: DNA325790, NM_006253,
gen.NM_006253
Figure 3832: PRO82259
Figure 3833: DNA325791, XM_045187,
gen.XM_045187
Figure 3834: DNA325792, XM_045963,
gen.XM_045963
Figure 3835: DNA325793, XM_006595,
gen.XM_006595
Figure 3836: DNA325794, XM_012124,
gen.XM_012124
Figure 3837: DNA325795, NM_002813,
gen.NM_002813
Figure 3838: PRO82263
Figure 3839: DNA325796, NM_019887,
gen.NM_019887
Figure 3840: PRO69471
Figure 3841A-B: DNA325797, XM_038791,
gen.XM_038791
Figure 3842: PRO82264
Figure 3843: DNA325798, NM_016638,
gen.NM_016638
Figure 3844: PRO82265
Figure 3845: DNA325799, XM_116913,
gen.XM_116913
Figure 3846: PRO82266
Figure 3847: DNA325800, NM_006815,
gen.NM_006815
Figure 3848: PRO4793
Figure 3849: DNA325801, XM_006566,
gen.XM_006566
Figure 3850: PRO82267
Figure 3851: DNA325802, NM_032656,
gen.NM_032656
Figure 3852: PRO82268
Figure 3853: DNA325803, XM_055013,
gen.XM_055013
Figure 3854: PRO82269
Figure 3855: DNA325804, XM_113737,
gen.XM_113737
Figure 3856A-C: DNA325805, XM_045602,
gen.XM_045602
Figure 3857: DNA325806, XM_087955,
gen.XM_087955

Figure 3858: PRO82272
Figure 3859A-B: DNA325807, XM_044334,
gen.XM_044334
Figure 3860: PRO82273
Figure 3861: DNA325808, XM_012184,
gen.XM_012184
Figure 3862: DNA325809, XM_113702,
gen.XM_113702
Figure 3863: PRO82275
Figure 3864A-B: DNA270015, NM_003453,
gen.NM_003453
Figure 3865: PRO58410
Figure 3866: DNA226853, NM_004004,
gen.NM_004004
Figure 3867: PRO37316
Figure 3868: DNA325810, XM_167911,
gen.XM_167911
Figure 3869: DNA325811, XM_167918,
gen.XM_167918
Figure 3870: DNA325812, XM_084982,
gen.XM_084982
Figure 3871: PRO82278
Figure 3872: DNA325813, NM_024026,
gen.NM_024026
Figure 3873: PRO82279
Figure 3874: DNA325814, XM_012638,
gen.XM_012638
Figure 3875: PRO82280
Figure 3876: DNA325815, XM_167439,
gen.XM_167439
Figure 3877: DNA325816, XM_167906,
gen.XM_167906
Figure 3878A-B: DNA325817, NM_014778,
gen.NM_014778
Figure 3879: PRO82283
Figure 3880: DNA325818, XM_169414,
gen.XM_169414
Figure 3881A-B: DNA325819, NM_006646,
gen.NM_006646
Figure 3882: PRO82285
Figure 3883: DNA325820, XM_167892,
gen.XM_167892
Figure 3884: DNA325821, NM_015932,
gen.NM_015932
Figure 3885: PRO82287
Figure 3886: DNA325822, XM_166273,
gen.XM_166273
Figure 3887: DNA304669, NM_002128,
gen.NM_002128
Figure 3888: PRO71096
Figure 3889: DNA325823, NM_014887,
gen.NM_014887
Figure 3890: PRO82289
Figure 3891: DNA325824, NM_002915,
gen.NM_002915
Figure 3892: PRO82290

Figure 3893: DNA325825, XM_085017,
gen.XM_085017
Figure 3894: PRO82291
Figure 3895: DNA325826, XM_017432,
gen.XM_017432
Figure 3896A-B: DNA270254, NM_002015,
gen.NM_002015
Figure 3897: PRO58642
Figure 3898: DNA325827, NM_005830,
gen.NM_005830
Figure 3899: PRO58092
Figure 3900: DNA281436, NM_003295,
gen.NM_003295
Figure 3901: PRO66275
Figure 3902: DNA325828, XM_038371,
gen.XM_038371
Figure 3903A-B: DNA325829, XM_165636,
gen.XM_165636
Figure 3904: DNA325830, XM_166266,
gen.XM_166266
Figure 3905: PRO82295
Figure 3906: DNA325831, NM_014166,
gen.NM_014166
Figure 3907: PRO82296
Figure 3908: DNA325832, NM_021999,
gen.NM_021999
Figure 3909: PRO1869
Figure 3910: DNA325833, NM_030925,
gen.NM_030925
Figure 3911: PRO82297
Figure 3912: DNA274058, NM_016119,
gen.NM_016119
Figure 3913: PRO61999
Figure 3914: DNA325834, NM_032565,
gen.NM_032565
Figure 3915: PRO11982
Figure 3916: DNA325835, XM_085044,
gen.XM_085044
Figure 3917: DNA325836, XM_165639,
gen.XM_165639
Figure 3918: DNA325837, XM_018399,
gen.XM_018399
Figure 3919: PRO82300
Figure 3920: DNA325838, XM_058977,
gen.XM_058977
Figure 3921: DNA325839, XM_015840,
gen.XM_015840
Figure 3922: PRO82302
Figure 3923: DNA325840, XM_007199,
gen.XM_007199
Figure 3924: DNA325841, XM_016351,
gen.XM_016351
Figure 3925: DNA325842, XM_041209,
gen.XM_041209
Figure 3926: DNA325843, XM_058611,
gen.XM_058611

Figure 3927: PRO82305
Figure 3928: DNA325844, XM_041473, gen.XM_041473
Figure 3929: PRO82306
Figure 3930: DNA325845, XM_032443, gen.XM_032443
Figure 3931: DNA325847, XM_048957, gen.XM_048957
Figure 3932: DNA325848, XM_015842, gen.XM_015842
Figure 3933: DNA325849, XM_084997, gen.XM_084997
Figure 3934: PRO82311
Figure 3935: DNA325850, NM_024089, gen.NM_024089
Figure 3936: PRO82312
Figure 3937A-B: DNA325851, XM_049904, gen.XM_049904
Figure 3938: DNA325852, NM_024537, gen.NM_024537
Figure 3939: PRO82314
Figure 3940: DNA325853, NM_023011, gen.NM_023011
Figure 3941: PRO82315
Figure 3942: DNA325854, NM_080687, gen.NM_080687
Figure 3943: PRO82316
Figure 3944: DNA325855, XM_041484, gen.XM_041484
Figure 3945: PRO82317
Figure 3946A-B: DNA325856, XM_113752, gen.XM_113752
Figure 3947: PRO82318
Figure 3948: DNA325857, XM_115215, gen.XM_115215
Figure 3949: DNA325858, XM_046651, gen.XM_046651
Figure 3950: DNA325859, XM_046648, gen.XM_046648
Figure 3951: DNA325860, XM_046642, gen.XM_046642
Figure 3952: PRO10404
Figure 3953: DNA325861, XM_017914, gen.XM_017914
Figure 3954: PRO82321
Figure 3955: DNA325862, XM_085166, gen.XM_085166
Figure 3956: PRO82322
Figure 3957: DNA325863, XM_007316, gen.XM_007316
Figure 3958: DNA325864, XM_007315, gen.XM_007315
Figure 3959: DNA325865, XM_033251, gen.XM_033251
Figure 3960: DNA325866, NM_024658, gen.NM_024658

Figure 3961: PRO82325
Figure 3962: DNA210180, NM_005132, gen.NM_005132
Figure 3963: PRO33717
Figure 3964: DNA325867, XM_033337, gen.XM_033337
Figure 3965: PRO82326
Figure 3966: DNA325868, XM_096772, gen.XM_096772
Figure 3967: DNA325869, XM_007293, gen.XM_007293
Figure 3968: DNA325870, XM_007288, gen.XM_007288
Figure 3969A-B: DNA325871, XM_033391, gen.XM_033391
Figure 3970: PRO82329
Figure 3971: DNA325872, NM_017815, gen.NM_017815
Figure 3972: PRO82330
Figure 3973: DNA325873, NM_006109, gen.NM_006109
Figure 3974: PRO82331
Figure 3975: DNA325874, XM_033435, gen.XM_033435
Figure 3976: DNA225865, NM_004995, gen.NM_004995
Figure 3977: PRO36328
Figure 3978: DNA325875, XM_058647, gen.XM_058647
Figure 3979: PRO82333
Figure 3980: DNA325876, XM_033445, gen.XM_033445
Figure 3981: DNA325877, NM_005015, gen.NM_005015
Figure 3982: PRO82334
Figure 3983: DNA325878, XM_012377, gen.XM_012377
Figure 3984: DNA227321, NM_001344, gen.NM_001344
Figure 3985: PRO37784
Figure 3986: DNA325879, XM_058646, gen.XM_058646
Figure 3987: DNA325880, XM_085106, gen.XM_085106
Figure 3988: DNA325881, NM_019852, gen.NM_019852
Figure 3989: PRO82338
Figure 3990: DNA325882, XM_012376, gen.XM_012376
Figure 3991: DNA325883, XM_033553, gen.XM_033553
Figure 3992: DNA226105, NM_002934, gen.NM_002934
Figure 3993: PRO36568
Figure 3994: DNA325884, XM_033595, gen.XM_033595

Figure 3995: PRO2871
Figure 3996: DNA325885, XM_007491,
gen.XM_007491
Figure 3997: DNA325886, NM_001641,
gen.NM_001641
Figure 3998: PRO82342
Figure 3999: DNA325887, NM_080648,
gen.NM_080648
Figure 4000: PRO82343
Figure 4001: DNA325888, NM_080649,
gen.NM_080649
Figure 4002: PRO82344
Figure 4003: DNA325889, NM_017807,
gen.NM_017807
Figure 4004: PRO82345
Figure 4005A-C: DNA325890, XM_007488,
gen.XM_007488
Figure 4006: DNA325891, NM_021178,
gen.NM_021178
Figure 4007: PRO82347
Figure 4008: DNA325892, XM_041235,
gen.XM_041235
Figure 4009: PRO82348
Figure 4010: DNA325893, NM_002028,
gen.NM_002028
Figure 4011: PRO82349
Figure 4012: DNA325894, NM_002083,
gen.NM_002083
Figure 4013: PRO82350
Figure 4014A-B: DNA325895, XM_085127,
gen.XM_085127
Figure 4015: PRO82351
Figure 4016A-B: DNA325896, NM_001530,
gen.NM_001530
Figure 4017: PRO82352
Figure 4018: DNA325897, XM_058210,
gen.XM_058210
Figure 4019: DNA325898, XM_085141,
gen.XM_085141
Figure 4020: DNA325899, NM_021728,
gen.NM_021728
Figure 4021: PRO82355
Figure 4022: DNA325900, NM_002306,
gen.NM_002306
Figure 4023: PRO82356
Figure 4024: DNA325901, XM_007328,
gen.XM_007328
Figure 4025A-B: DNA325902, XM_051712,
gen.XM_051712
Figure 4026: PRO82357
Figure 4027: DNA325903, XM_007324,
gen.XM_007324
Figure 4028: PRO82358
Figure 4029: DNA325904, NM_002863,
gen.NM_002863
Figure 4030: PRO82359

Figure 4031: DNA325905, XM_085125,
gen.XM_085125
Figure 4032: DNA325906, XM_031025,
gen.XM_031025
Figure 4033: DNA325907, XM_085066,
gen.XM_085066
Figure 4034: DNA325908, XM_096744,
gen.XM_096744
Figure 4035: DNA325909, NM_016445,
gen.NM_016445
Figure 4036: PRO82364
Figure 4037: DNA325910, NM_016026,
gen.NM_016026
Figure 4038: PRO82365
Figure 4039: DNA325911, XM_031074,
gen.XM_031074
Figure 4040: DNA325912, NM_001102,
gen.NM_001102
Figure 4041: PRO82367
Figure 4042: DNA225649, NM_022137,
gen.NM_022137
Figure 4043: PRO36112
Figure 4044: DNA325913, XM_085065,
gen.XM_085065
Figure 4045: DNA325914, XM_007441,
gen.XM_007441
Figure 4046: DNA325915, NM_006821,
gen.NM_006821
Figure 4047: PRO82369
Figure 4048: DNA325916, NM_006432,
gen.NM_006432
Figure 4049: PRO2066
Figure 4050A-B: DNA325917, XM_085151,
gen.XM_085151
Figure 4051: PRO82370
Figure 4052: DNA325918, NM_002632,
gen.NM_002632
Figure 4053: PRO82371
Figure 4054: DNA325919, XM_085162,
gen.XM_085162
Figure 4055: DNA325920, NM_012111,
gen.NM_012111
Figure 4056: PRO82373
Figure 4057: DNA325921, NM_024824,
gen.NM_024824
Figure 4058: PRO82374
Figure 4059: DNA269498, NM_002802,
gen.NM_002802
Figure 4060: PRO57917
Figure 4061: DNA325922, XM_058677,
gen.XM_058677
Figure 4062: PRO82375
Figure 4063: DNA325923, NM_006888,
gen.NM_006888
Figure 4064: PRO4904
Figure 4065: DNA325924, NM_001275,

gen.NM_001275
Figure 4066: PRO2054
Figure 4067: DNA325925, XM_029288,
gen.XM_029288
Figure 4068A-B: DNA325926, XM_016487,
gen.XM_016487
Figure 4069: DNA325927, NM_020414,
gen.NM_020414
Figure 4070: PRO62099
Figure 4071: DNA325928, XM_016486,
gen.XM_016486
Figure 4072: DNA325929, XM_007483,
gen.XM_007483
Figure 4073: DNA325930, XM_028358,
gen.XM_028358
Figure 4074: DNA325931, XM_028347,
gen.XM_028347
Figure 4075: DNA325932, XM_028322,
gen.XM_028322
Figure 4076: PRO82381
Figure 4077: DNA325933, XM_056317,
gen.XM_056317
Figure 4078: PRO82382
Figure 4079: DNA151893, NM_021966,
gen.NM_021966
Figure 4080: PRO12916
Figure 4081: DNA325934, XM_007272,
gen.XM_007272
Figure 4082: DNA325935, XM_090914,
gen.XM_090914
Figure 4083: PRO82383
Figure 4084: DNA325936, NM_022747,
gen.NM_022747
Figure 4085: PRO82384
Figure 4086: DNA325937, XM_041014,
gen.XM_041014
Figure 4087: PRO60575
Figure 4088: DNA325938, NM_003836,
gen.NM_003836
Figure 4089: PRO82385
Figure 4090A-B: DNA325939, XM_040952,
gen.XM_040952
Figure 4091: DNA325940, XM_058618,
gen.XM_058618
Figure 4092: DNA325941, NM_005348,
gen.NM_005348
Figure 4093: PRO82388
Figure 4094: DNA325942, XM_040942,
gen.XM_040942
Figure 4095: DNA226324, NM_014226,
gen.NM_014226
Figure 4096: PRO36787
Figure 4097A-B: DNA325943, XM_007254,
gen.XM_007254
Figure 4098A-B: DNA325944, NM_001969,
gen.NM_001969

Figure 4099: PRO82391
Figure 4100: DNA325945, XM_040898,
gen.XM_040898
Figure 4101: DNA325946, NM_005432,
gen.NM_005432
Figure 4102: PRO60070
Figure 4103A-B: DNA325947, XM_050278,
gen.XM_050278
Figure 4104: PRO82393
Figure 4105: DNA325948, XM_113759,
gen.XM_113759
Figure 4106: DNA325949, NM_006427,
gen.NM_006427
Figure 4107: PRO82395
Figure 4108: DNA325950, NM_021709,
gen.NM_021709
Figure 4109: PRO82396
Figure 4110: DNA103509, NM_005163,
gen.NM_005163
Figure 4111: PRO4836
Figure 4112: DNA325951, NM_017955,
gen.NM_017955
Figure 4113: PRO82397
Figure 4114: DNA325952, XM_088588,
gen.XM_088588
Figure 4115: DNA325953, XM_060012,
gen.XM_060012
Figure 4116: DNA325954, XM_034953,
gen.XM_034953
Figure 4117: PRO82400
Figure 4118: DNA325955, XM_058636,
gen.XM_058636
Figure 4119: DNA325956, XM_035014,
gen.XM_035014
Figure 4120: DNA325957, XM_088587,
gen.XM_088587
Figure 4121: DNA325958, XM_088589,
gen.XM_088589
Figure 4122: DNA325959, XM_071801,
gen.XM_071801
Figure 4123: DNA325960, XM_018054,
gen.XM_018054
Figure 4124: DNA325961, XM_091108,
gen.XM_091108
Figure 4125A-B: DNA325962, XM_039225,
gen.XM_039225
Figure 4126: PRO82408
Figure 4127: DNA325963, XM_165921,
gen.XM_165921
Figure 4128: PRO82409
Figure 4129: DNA325964, XM_007751,
gen.XM_007751
Figure 4130: DNA325965, XM_085203,
gen.XM_085203
Figure 4131: PRO82411
Figure 4132: DNA325966, XM_085204,

gen.XM_085204
Figure 4133: DNA325967, XM_012398,
gen.XM_012398
Figure 4134A-B: DNA325968, XM_036727,
gen.XM_036727
Figure 4135: DNA325969, XM_017240,
gen.XM_017240
Figure 4136: DNA325970, NM_020149,
gen.NM_020149
Figure 4137: PRO82415
Figure 4138A-B: DNA325971, XM_031617,
gen.XM_031617
Figure 4139A-B: DNA325972, NM_001211,
gen.NM_001211
Figure 4140: PRO82417
Figure 4141A-B: DNA151831, NM_004573,
gen.NM_004573
Figure 4142: PRO12198
Figure 4143: DNA325973, NM_130468,
gen.NM_130468
Figure 4144: PRO82418
Figure 4145: DNA325974, XM_031554,
gen.XM_031554
Figure 4146: PRO82419
Figure 4147: DNA325975, XM_031515,
gen.XM_031515
Figure 4148: DNA325976, NM_024111,
gen.NM_024111
Figure 4149: PRO82421
Figure 4150: DNA325977, NM_032196,
gen.NM_032196
Figure 4151: PRO82422
Figure 4152: DNA325978, NM_016359,
gen.NM_016359
Figure 4153: PRO82423
Figure 4154: DNA325979, NM_018454,
gen.NM_018454
Figure 4155: PRO82424
Figure 4156A-B: DNA325980, XM_007545,
gen.XM_007545
Figure 4157: DNA325981, XM_091159,
gen.XM_091159
Figure 4158: PRO82425
Figure 4159: DNA325982, XM_031718,
gen.XM_031718
Figure 4160: DNA325983, XM_085307,
gen.XM_085307
Figure 4161: DNA227559, NM_000070,
gen.NM_000070
Figure 4162: PRO38022
Figure 4163A-B: DNA325984, XM_113823,
gen.XM_113823
Figure 4164: PRO82428
Figure 4165: DNA325985, XM_016713,
gen.XM_016713
Figure 4166: PRO82429

Figure 4167A-B: DNA325986, XM_007531,
gen.XM_007531
Figure 4168: DNA325987, NM_014444,
gen.NM_014444
Figure 4169: PRO82431
Figure 4170A-B: DNA227206, NM_005657,
gen.NM_005657
Figure 4171: PRO37669
Figure 4172: DNA325988, NM_020990,
gen.NM_020990
Figure 4173: PRO82432
Figure 4174: DNA325989, NM_005313,
gen.NM_005313
Figure 4175: PRO2732
Figure 4176: DNA325990, NM_005770,
gen.NM_005770
Figure 4177: PRO82433
Figure 4178: DNA325991, NM_004048,
gen.NM_004048
Figure 4179: PRO4379
Figure 4180: DNA325992, XM_032403,
gen.XM_032403
Figure 4181: PRO82434
Figure 4182: DNA219233, NM_014335,
gen.NM_014335
Figure 4183: PRO34557
Figure 4184A-C: DNA325993, XM_034890,
gen.XM_034890
Figure 4185: PRO82435
Figure 4186: DNA325994, XM_058684,
gen.XM_058684
Figure 4187: DNA325995, NM_003104,
gen.NM_003104
Figure 4188: PRO82437
Figure 4189: DNA325996, XM_007651,
gen.XM_007651
Figure 4190: PRO82438
Figure 4191: DNA325997, XM_090991,
gen.XM_090991
Figure 4192: PRO82439
Figure 4193: DNA325998, NM_016304,
gen.NM_016304
Figure 4194: PRO82440
Figure 4195: DNA325999, NM_017610,
gen.NM_017610
Figure 4196: PRO82441
Figure 4197: DNA326000, NM_004701,
gen.NM_004701
Figure 4198: PRO82442
Figure 4199A-B: DNA326001, XM_012418,
gen.XM_012418
Figure 4200: DNA326002, XM_039702,
gen.XM_039702
Figure 4201: PRO82444
Figure 4202: DNA326003, XM_113266,
gen.XM_113266

Figure 4203: DNA326004, NM_001218,
gen.NM_001218
Figure 4204: PRO54594
Figure 4205: DNA326005, NM_015920,
gen.NM_015920
Figure 4206: PRO82446
Figure 4207: DNA326006, XM_113268,
gen.XM_113268
Figure 4208: DNA255340, NM_017684,
gen.NM_017684
Figure 4209: PRO50409
Figure 4210: DNA326007, NM_002537,
gen.NM_002537
Figure 4211: DNA326008, XM_085283,
gen.XM_085283
Figure 4212: PRO82448
Figure 4213: DNA326009, XM_016985,
gen.XM_016985
Figure 4214: DNA234442, NM_014736,
gen.NM_014736
Figure 4215: PRO38852
Figure 4216: DNA326010, NM_022048,
gen.NM_022048
Figure 4217: PRO82450
Figure 4218: DNA326011, NM_000942,
gen.NM_000942
Figure 4219: PRO2720
Figure 4220: DNA326012, XM_050964,
gen.XM_050964
Figure 4221: DNA326013, XM_007623,
gen.XM_007623
Figure 4222A-B: DNA326014, NM_133375,
gen.NM_133375
Figure 4223: PRO82453
Figure 4224: DNA226646, NM_017882,
gen.NM_017882
Figure 4225: PRO37109
Figure 4226: DNA326015, NM_015322,
gen.NM_015322
Figure 4227: PRO82454
Figure 4228: DNA326016, NM_001003,
gen.NM_001003
Figure 4229: PRO82455
Figure 4230A-B: DNA326017, XM_051463,
gen.XM_051463
Figure 4231: PRO82456
Figure 4232: DNA326018, NM_018357,
gen.NM_018357
Figure 4233: PRO82457
Figure 4234: DNA326019, XM_063639,
gen.XM_063639
Figure 4235: PRO82458
Figure 4236: DNA326020, XM_085249,
gen.XM_085249
Figure 4237: DNA326021, XM_016076,
gen.XM_016076

Figure 4238: PRO82460
Figure 4239: DNA326022, XM_015366,
gen.XM_015366
Figure 4240: PRO82461
Figure 4241: DNA326023, XM_096060,
gen.XM_096060
Figure 4242: DNA287331, NM_002654,
gen.NM_002654
Figure 4243: PRO69595
Figure 4244: DNA326024, XM_037778,
gen.XM_037778
Figure 4245: DNA326025, XM_096842,
gen.XM_096842
Figure 4246: DNA326026, NM_022369,
gen.NM_022369
Figure 4247: PRO82465
Figure 4248: DNA326027, NM_032907,
gen.NM_032907
Figure 4249: PRO82466
Figure 4250: DNA326028, XM_058699,
gen.XM_058699
Figure 4251: DNA326029, XM_118637,
gen.XM_118637
Figure 4252: DNA326030, XM_053585,
gen.XM_053585
Figure 4253: PRO82469
Figure 4254: DNA326031, XM_085239,
gen.XM_085239
Figure 4255: PRO82470
Figure 4256: DNA326032, XM_034897,
gen.XM_034897
Figure 4257A-B: DNA326033, XM_057020,
gen.XM_057020
Figure 4258: PRO82472
Figure 4259: DNA326034, NM_000743,
gen.NM_000743
Figure 4260: PRO61219
Figure 4261: DNA326035, NM_002789,
gen.NM_002789
Figure 4262: PRO60499
Figure 4263: DNA326036, XM_091100,
gen.XM_091100
Figure 4264: PRO82473
Figure 4265: DNA255370, NM_012170,
gen.NM_012170
Figure 4266: PRO50438
Figure 4267: DNA273014, NM_000126,
gen.NM_000126
Figure 4268: PRO61085
Figure 4269: DNA326037, XM_044565,
gen.XM_044565
Figure 4270: DNA326038, NM_025234,
gen.NM_025234
Figure 4271: PRO82475
Figure 4272: DNA326039, XM_044569,
gen.XM_044569

Figure 4273: DNA326040, NM_005724,
gen.NM_005724
Figure 4274: PRO730
Figure 4275: DNA326041, XM_049354,
gen.XM_049354
Figure 4276: PRO82477
Figure 4277: DNA326042, NM_007364,
gen.NM_007364
Figure 4278: DNA326043, XM_044593,
gen.XM_044593
Figure 4279: DNA326044, NM_006791,
gen.NM_006791
Figure 4280: PRO82479
Figure 4281: DNA326045, XM_060042,
gen.XM_060042
Figure 4282: DNA326046, XM_085215,
gen.XM_085215
Figure 4283: DNA326047, NM_001021,
gen.NM_001021
Figure 4284: PRO82482
Figure 4285: DNA326048, XM_031404,
gen.XM_031404
Figure 4286: DNA326049, XM_096844,
gen.XM_096844
Figure 4287: DNA326050, XM_045681,
gen.XM_045681
Figure 4288: PRO82485
Figure 4289: DNA326051, XM_085280,
gen.XM_085280
Figure 4290: DNA326052, NM_022839,
gen.NM_022839
Figure 4291: PRO82487
Figure 4292: DNA326053, XM_031354,
gen.XM_031354
Figure 4293: DNA326054, NM_002168,
gen.NM_002168
Figure 4294: PRO82489
Figure 4295: DNA326055, XM_031292,
gen.XM_031292
Figure 4296: DNA326056, NM_022566,
gen.NM_022566
Figure 4297: PRO82491
Figure 4298A-B: DNA326057, XM_051860,
gen.XM_051860
Figure 4299: PRO82492
Figure 4300: DNA275144, NM_000137,
gen.NM_000137
Figure 4301: PRO62852
Figure 4302: DNA326058, NM_016645,
gen.NM_016645
Figure 4303: PRO82493
Figure 4304: DNA326059, XM_044523,
gen.XM_044523
Figure 4305: DNA150485, NM_006384,
gen.NM_006384
Figure 4306: PRO12774

Figure 4307A-B: DNA326060, XM_044533,
gen.XM_044533
Figure 4308: PRO82495
Figure 4309A-C: DNA326061, XM_054900,
gen.XM_054900
Figure 4310: DNA326062, NM_032162,
gen.NM_032162
Figure 4311A-B: DNA326063, XM_015835,
gen.XM_015835
Figure 4312: DNA326064, NM_018668,
gen.NM_018668
Figure 4313: PRO82499
Figure 4314: DNA326065, XM_085262,
gen.XM_085262
Figure 4315: DNA326066, NM_033544,
gen.NM_033544
Figure 4316: PRO82501
Figure 4317: DNA326067, XM_049372,
gen.XM_049372
Figure 4318: PRO82502
Figure 4319: DNA326068, XM_017971,
gen.XM_017971
Figure 4320: DNA275181, NM_003090,
gen.NM_003090
Figure 4321: PRO62882
Figure 4322: DNA326069, XM_012462,
gen.XM_012462
Figure 4323A-B: DNA326070, XM_085525,
gen.XM_085525
Figure 4324: PRO82505
Figure 4325: DNA326071, XM_165923,
gen.XM_165923
Figure 4326: DNA326072, XM_113836,
gen.XM_113836
Figure 4327: DNA326073, NM_017668,
gen.NM_017668
Figure 4328: PRO82508
Figure 4329: DNA326074, XM_027309,
gen.XM_027309
Figure 4330: PRO82509
Figure 4331: DNA326075, XM_018432,
gen.XM_018432
Figure 4332: PRO82510
Figure 4333: DNA326076, XM_115352,
gen.XM_115352
Figure 4334: DNA326077, XM_027365,
gen.XM_027365
Figure 4335: DNA326078, NM_016641,
gen.NM_016641
Figure 4336: PRO38464
Figure 4337: DNA326079, XM_058796,
gen.XM_058796
Figure 4338: DNA326080, XM_017984,
gen.XM_017984
Figure 4339: PRO82513
Figure 4340: DNA326081, NM_020677,

gen.NM_020677
Figure 4341: PRO82514
Figure 4342: DNA326082, XM_036680,
gen.XM_036680
Figure 4343: PRO37961
Figure 4344A-B: DNA326083, XM_048119,
gen.XM_048119
Figure 4345: PRO82515
Figure 4346: DNA326084, NM_024589,
gen.NM_024589
Figure 4347: PRO82516
Figure 4348: DNA326085, XM_050534,
gen.XM_050534
Figure 4349: PRO82517
Figure 4350: DNA326086, NM_024571,
gen.NM_024571
Figure 4351: PRO82518
Figure 4352: DNA326087, XM_027558,
gen.XM_027558
Figure 4353: DNA326088, XM_008126,
gen.XM_008126
Figure 4354: DNA326089, NM_000517,
gen.NM_000517
Figure 4355: PRO3629
Figure 4356: DNA326090, NM_000558,
gen.NM_000558
Figure 4357: PRO3629
Figure 4358: DNA326091, NM_018032,
gen.NM_018032
Figure 4359: PRO38311
Figure 4360: DNA273839, NM_006428,
gen.NM_006428
Figure 4361: PRO61799
Figure 4362A-B: DNA256844, NM_005632,
gen.NM_005632
Figure 4363: PRO51775
Figure 4364: DNA326092, XM_083939,
gen.XM_083939
Figure 4365: PRO82521
Figure 4366: DNA326093, NM_058192,
gen.NM_058192
Figure 4367: PRO82522
Figure 4368: DNA326094, XM_027412,
gen.XM_027412
Figure 4369: PRO82523
Figure 4370: DNA256886, NM_014587,
gen.NM_014587
Figure 4371: PRO51815
Figure 4372A-B: DNA326095, NM_001287,
gen.NM_001287
Figure 4373: PRO38480
Figure 4374: DNA254781, NM_016111,
gen.NM_016111
Figure 4375: PRO49879
Figure 4376: DNA326096, XM_034586,
gen.XM_034586

Figure 4377: PRO82524
Figure 4378: DNA326097, NM_023936,
gen.NM_023936
Figure 4379: PRO82525
Figure 4380: DNA326098, XM_034590,
gen.XM_034590
Figure 4381: PRO82526
Figure 4382: DNA326099, NM_002952,
gen.NM_002952
Figure 4383: PRO82527
Figure 4384: DNA326100, NM_006453,
gen.NM_006453
Figure 4385: PRO82528
Figure 4386: DNA326101, NM_014353,
gen.NM_014353
Figure 4387: PRO82529
Figure 4388: DNA326102, NM_032271,
gen.NM_032271
Figure 4389: PRO82530
Figure 4390: DNA326103, XM_028848,
gen.XM_028848
Figure 4391: PRO82531
Figure 4392: DNA326104, NM_006711,
gen.NM_006711
Figure 4393: PRO82532
Figure 4394: DNA326105, NM_080594,
gen.NM_080594
Figure 4395: PRO82533
Figure 4396: DNA326106, NM_024339,
gen.NM_024339
Figure 4397: PRO82534
Figure 4398: DNA326107, NM_016639,
gen.NM_016639
Figure 4399: PRO12683
Figure 4400: DNA326108, NM_021195,
gen.NM_021195
Figure 4401: PRO82535
Figure 4402: DNA326109, NM_004203,
gen.NM_004203
Figure 4403: PRO82536
Figure 4404: DNA326110, XM_058784,
gen.XM_058784
Figure 4405: PRO82537
Figure 4406: DNA326111, NM_024507,
gen.NM_024507
Figure 4407: PRO82538
Figure 4408: DNA326112, NM_006799,
gen.NM_006799
Figure 4409: PRO303
Figure 4410A-C: DNA326113, XM_036528,
gen.XM_036528
Figure 4411: DNA326114, NM_025108,
gen.NM_025108
Figure 4412: PRO82540
Figure 4413A-C: DNA326115, XM_165411,
gen.XM_165411

Figure 4414: DNA326116, NM_016292,
gen.NM_016292
Figure 4415: PRO82542
Figure 4416: DNA326117, NM_002484,
gen.NM_002484
Figure 4417: PRO82543
Figure 4418: DNA326118, XM_113845,
gen.XM_113845
Figure 4419: PRO82544
Figure 4420: DNA326119, XM_113843,
gen.XM_113843
Figure 4421: DNA97293, NM_003366,
gen.NM_003366
Figure 4422: PRO3640
Figure 4423: DNA326120, NM_006110,
gen.NM_006110
Figure 4424: PRO82546
Figure 4425: DNA326121, XM_085445,
gen.XM_085445
Figure 4426: DNA326122, XM_113876,
gen.XM_113876
Figure 4427A-B: DNA326123, XM_055195,
gen.XM_055195
Figure 4428: PRO82548
Figure 4429: DNA326124, XM_113291,
gen.XM_113291
Figure 4430A-B: DNA326125, XM_007988,
gen.XM_007988
Figure 4431: DNA326126, XM_113874,
gen.XM_113874
Figure 4432: DNA326127, XM_102377,
gen.XM_102377
Figure 4433: PRO82551
Figure 4434: DNA326128, XM_086278,
gen.XM_086278
Figure 4435: DNA326129, XM_085452,
gen.XM_085452
Figure 4436: DNA326130, NM_018054,
gen.NM_018054
Figure 4437: PRO82554
Figure 4438A-B: DNA326131, XM_056260,
gen.XM_056260
Figure 4439: PRO82555
Figure 4440: DNA326132, NM_032626,
gen.NM_032626
Figure 4441: PRO82556
Figure 4442: DNA326133, NM_005030,
gen.NM_005030
Figure 4443: PRO82557
Figure 4444: DNA326134, NM_032486,
gen.NM_032486
Figure 4445: PRO82558
Figure 4446: DNA289522, NM_005003,
gen.NM_005003
Figure 4447: PRO70276
Figure 4448: DNA326135, XM_085340,

gen.XM_085340
Figure 4449: DNA326136, NM_003752,
gen.NM_003752
Figure 4450: PRO60325
Figure 4451: DNA326137, NM_012248,
gen.NM_012248
Figure 4452: PRO82560
Figure 4453A-B: DNA326138, XM_046035,
gen.XM_046035
Figure 4454: DNA326139, NM_024671,
gen.NM_024671
Figure 4455: PRO82562
Figure 4456: DNA326140, NM_033410,
gen.NM_033410
Figure 4457: PRO82563
Figure 4458: DNA326141, NM_024031,
gen.NM_024031
Figure 4459: PRO82564
Figure 4460A-B: DNA326142, XM_034375,
gen.XM_034375
Figure 4461: DNA326143, XM_012569,
gen.XM_012569
Figure 4462: DNA326144, XM_050194,
gen.XM_050194
Figure 4463: DNA326145, XM_008106,
gen.XM_008106
Figure 4464: PRO82567
Figure 4465: DNA326146, NM_004960,
gen.NM_004960
Figure 4466: PRO82568
Figure 4467: DNA326147, XM_113293,
gen.XM_113293
Figure 4468: DNA326148, NM_022744,
gen.NM_022744
Figure 4469: PRO82570
Figure 4470: DNA326149, NM_024048,
gen.NM_024048
Figure 4471: PRO82571
Figure 4472: DNA326150, XM_018088,
gen.XM_018088
Figure 4473: PRO82572
Figure 4474: DNA326151, XM_007963,
gen.XM_007963
Figure 4475: PRO82573
Figure 4476: DNA274002, NM_014321,
gen.NM_014321
Figure 4477: PRO61948
Figure 4478: DNA326152, XM_015700,
gen.XM_015700
Figure 4479: DNA326153, XM_051219,
gen.XM_051219
Figure 4480: DNA326154, XM_085393,
gen.XM_085393
Figure 4481: PRO82576
Figure 4482: DNA326155, XM_085395,
gen.XM_085395

Figure 4483: DNA326156, XM_091270, gen.XM_091270
Figure 4484: DNA326157, XM_165656, gen.XM_165656
Figure 4485: DNA326158, NM_032330, gen.NM_032330
Figure 4486: PRO82579
Figure 4487: DNA254532, NM_001043, gen.NM_001043
Figure 4488: PRO49639
Figure 4489: DNA326159, XM_165658, gen.XM_165658
Figure 4490: DNA326160, XM_166285, gen.XM_166285
Figure 4491: DNA326161, XM_166282, gen.XM_166282
Figure 4492: PRO82582
Figure 4493: DNA326162, XM_165657, gen.XM_165657
Figure 4494: PRO82583
Figure 4495: DNA326163, NM_032038, gen.NM_032038
Figure 4496: PRO82584
Figure 4497: DNA326164, XM_008065, gen.XM_008065
Figure 4498: DNA326165, NM_017458, gen.NM_017458
Figure 4499: PRO82585
Figure 4500: DNA326166, NM_005115, gen.NM_005115
Figure 4501: PRO82586
Figure 4502: DNA326167, NM_024516, gen.NM_024516
Figure 4503: PRO82587
Figure 4504: DNA326168, XM_113299, gen.XM_113299
Figure 4505: DNA326169, XM_055771, gen.XM_055771
Figure 4506: PRO82589
Figure 4507: DNA271171, NM_007317, gen.NM_007317
Figure 4508: PRO59491
Figure 4509: DNA326170, XM_008064, gen.XM_008064
Figure 4510: PRO82590
Figure 4511: DNA326171, NM_003123, gen.NM_003123
Figure 4512: PRO2355
Figure 4513: DNA326172, XM_085442, gen.XM_085442
Figure 4514: DNA326173, XM_055132, gen.XM_055132
Figure 4515: PRO82592
Figure 4516: DNA274180, NM_007074, gen.NM_007074
Figure 4517: PRO62110

Figure 4518: DNA326174, NM_002720, gen.NM_002720
Figure 4519: PRO42208
Figure 4520: DNA287355, NM_000034, gen.NM_000034
Figure 4521: PRO69617
Figure 4522: DNA326175, NM_031478, gen.NM_031478
Figure 4523: PRO82593
Figure 4524: DNA326176, XM_085434, gen.XM_085434
Figure 4525: PRO82594
Figure 4526: DNA326177, XM_058116, gen.XM_058116
Figure 4527: DNA326178, XM_165649, gen.XM_165649
Figure 4528: DNA326179, XM_165647, gen.XM_165647
Figure 4529: PRO82597
Figure 4530: DNA194805, NM_014685, gen.NM_014685
Figure 4531: PRO24075
Figure 4532: DNA326180, XM_166277, gen.XM_166277
Figure 4533: PRO82598
Figure 4534: DNA326181, XM_165645, gen.XM_165645
Figure 4535: DNA326182, NM_018110, gen.NM_018110
Figure 4536: PRO82599
Figure 4537: DNA326183, XM_165648, gen.XM_165648
Figure 4538: DNA326184, XM_167453, gen.XM_167453
Figure 4539: DNA326185, NM_022770, gen.NM_022770
Figure 4540: PRO82602
Figure 4541: DNA326186, XM_167456, gen.XM_167456
Figure 4542: PRO82603
Figure 4543: DNA326187, XM_058745, gen.XM_058745
Figure 4544: DNA326188, XM_091420, gen.XM_091420
Figure 4545: DNA326189, NM_004691, gen.NM_004691
Figure 4546: PRO82606
Figure 4547: DNA326190, NM_000196, gen.NM_000196
Figure 4548: PRO82607
Figure 4549A-B: DNA326191, NM_004360, gen.NM_004360
Figure 4550: PRO2672
Figure 4551: DNA326192, XM_039306, gen.XM_039306
Figure 4552: PRO82608

Figure 4553: DNA326193, NM_030579,
gen.NM_030579
Figure 4554: PRO82609
Figure 4555: DNA326194, XM_012487,
gen.XM_012487
Figure 4556: DNA326195, NM_014062,
gen.NM_014062
Figure 4557: PRO82611
Figure 4558: DNA326196, XM_085471,
gen.XM_085471
Figure 4559: PRO82612
Figure 4560: DNA326197, XM_113855,
gen.XM_113855
Figure 4561: DNA326198, XM_085475,
gen.XM_085475
Figure 4562: DNA326199, XM_028151,
gen.XM_028151
Figure 4563: PRO82615
Figure 4564: DNA275408, NM_001605,
gen.NM_001605
Figure 4565: PRO63068
Figure 4566: DNA326200, NM_007242,
gen.NM_007242
Figure 4567: PRO82616
Figure 4568: DNA189703, NM_005548,
gen.NM_005548
Figure 4569: PRO22637
Figure 4570: DNA326201, XM_113853,
gen.XM_113853
Figure 4571: DNA326202, NM_032140,
gen.NM_032140
Figure 4572: PRO82618
Figure 4573: DNA326203, NM_030819,
gen.NM_030819
Figure 4574: PRO82619
Figure 4575: DNA304704, NM_005796,
gen.NM_005796
Figure 4576: PRO71130
Figure 4577: DNA326204, XM_043047,
gen.XM_043047
Figure 4578: PRO49967
Figure 4579: DNA88261, NM_001907,
gen.NM_001907
Figure 4580: PRO2719
Figure 4581A-B: DNA326205, NM_005072,
gen.NM_005072
Figure 4582: PRO4814
Figure 4583: DNA326206, XM_165410,
gen.XM_165410
Figure 4584: DNA326207, NM_017803,
gen.NM_017803
Figure 4585: PRO82621
Figure 4586A-B: DNA326208, NM_004555,
gen.NM_004555
Figure 4587: PRO82622
Figure 4588A-B: DNA326209, NM_018124,

gen.NM_018124
Figure 4589: PRO82623
Figure 4590: DNA326210, XM_091399,
gen.XM_091399
Figure 4591: PRO82624
Figure 4592A-B: DNA326211, NM_014003,
gen.NM_014003
Figure 4593: PRO82625
Figure 4594: DNA326212, NM_017853,
gen.NM_017853
Figure 4595: PRO82626
Figure 4596: DNA326213, XM_042621,
gen.XM_042621
Figure 4597: DNA326214, XM_064091,
gen.XM_064091
Figure 4598: PRO82627
Figure 4599: DNA326215, XM_085981,
gen.XM_085981
Figure 4600A-B: DNA326216, XM_051778,
gen.XM_051778
Figure 4601: PRO82629
Figure 4602: DNA326217, NM_004483,
gen.NM_004483
Figure 4603: PRO82630
Figure 4604: DNA326218, NM_020188,
gen.NM_020188
Figure 4605: PRO82631
Figure 4606: DNA326219, XM_033922,
gen.XM_033922
Figure 4607: PRO82632
Figure 4608: DNA326220, XM_113840,
gen.XM_113840
Figure 4609: PRO82633
Figure 4610: DNA326221, NM_016095,
gen.NM_016095
Figure 4611: PRO82634
Figure 4612: DNA326222, NM_006067,
gen.NM_006067
Figure 4613: PRO50658
Figure 4614: DNA326223, NM_001861,
gen.NM_001861
Figure 4615: PRO82635
Figure 4616A-B: DNA326224, XM_085483,
gen.XM_085483
Figure 4617: DNA326225, NM_017566,
gen.NM_017566
Figure 4618: PRO82637
Figure 4619: DNA326226, XM_057150,
gen.XM_057150
Figure 4620: PRO82638
Figure 4621: DNA326227, XM_058739,
gen.XM_058739
Figure 4622: DNA326228, XM_085327,
gen.XM_085327
Figure 4623: PRO82640
Figure 4624: DNA326229, XM_047436,

gen.XM_047436
Figure 4625: PRO82641
Figure 4626: DNA227234, NM_002386,
gen.NM_002386
Figure 4627: PRO37697
Figure 4628: DNA326230, NM_014972,
gen.NM_014972
Figure 4629: PRO82642
Figure 4630: DNA326231, XM_071873,
gen.XM_071873
Figure 4631: PRO82643
Figure 4632: DNA326232, XM_047525,
gen.XM_047525
Figure 4633: DNA326233, NM_000977,
gen.NM_000977
Figure 4634: PRO82645
Figure 4635: DNA326234, NM_033251,
gen.NM_033251
Figure 4636: PRO82646
Figure 4637: DNA326235, XM_085408,
gen.XM_085408
Figure 4638: DNA326236, NM_004933,
gen.NM_004933
Figure 4639: PRO2198
Figure 4640: DNA326237, XM_113882,
gen.XM_113882
Figure 4641: DNA326238, XM_010938,
gen.XM_010938
Figure 4642: DNA326239, NM_006761,
gen.NM_006761
Figure 4643: PRO39530
Figure 4644A-B: DNA326240, XM_017096,
gen.XM_017096
Figure 4645: DNA326241, XM_033714,
gen.XM_033714
Figure 4646A-B: DNA326242, XM_033689,
gen.XM_033689
Figure 4647: DNA326243, NM_002615,
gen.NM_002615
Figure 4648: DNA326244, XM_056082,
gen.XM_056082
Figure 4649: PRO82654
Figure 4650: DNA326245, XM_008557,
gen.XM_008557
Figure 4651: DNA326246, XM_045183,
gen.XM_045183
Figure 4652: PRO82656
Figure 4653: DNA326247, XM_113901,
gen.XM_113901
Figure 4654: DNA326248, NM_080822,
gen.NM_080822
Figure 4655: PRO82658
Figure 4656A-B: DNA326249, XM_029438,
gen.XM_029438
Figure 4657: PRO82659
Figure 4658: DNA326250, XM_008509,

gen.XM_008509
Figure 4659: DNA326251, XM_085687,
gen.XM_085687
Figure 4660: PRO82661
Figure 4661: DNA326252, XM_027825,
gen.XM_027825
Figure 4662: PRO82662
Figure 4663: DNA326253, XM_053717,
gen.XM_053717
Figure 4664: PRO82663
Figure 4665: DNA326254, NM_005022,
gen.NM_005022
Figure 4666: PRO62780
Figure 4667A-B: DNA326255, XM_028398,
gen.XM_028398
Figure 4668: PRO82664
Figure 4669: DNA326256, NM_000018,
gen.NM_000018
Figure 4670: PRO66265
Figure 4671: DNA326257, XM_008334,
gen.XM_008334
Figure 4672: DNA326258, NM_024297,
gen.NM_024297
Figure 4673: PRO82665
Figure 4674: DNA326259, XM_113324,
gen.XM_113324
Figure 4675: DNA326260, XM_012676,
gen.XM_012676
Figure 4676: PRO82667
Figure 4677: DNA326261, XM_085691,
gen.XM_085691
Figure 4678: DNA326262, XM_028417,
gen.XM_028417
Figure 4679: PRO82669
Figure 4680A-B: DNA326263, XM_041964,
gen.XM_041964
Figure 4681: PRO82670
Figure 4682: DNA326264, NM_019013,
gen.NM_019013
Figure 4683: PRO82671
Figure 4684: DNA326265, XM_008538,
gen.XM_008538
Figure 4685: PRO82672
Figure 4686: DNA326266, XM_008441,
gen.XM_008441
Figure 4687: DNA97300, NM_001416,
gen.NM_001416
Figure 4688: PRO3647
Figure 4689: DNA326267, NM_004870,
gen.NM_004870
Figure 4690: PRO82674
Figure 4691: DNA326268, NM_006942,
gen.NM_006942
Figure 4692: PRO82675
Figure 4693: DNA326269, XM_008679,
gen.XM_008679

Figure 4694: DNA326270, XM_008231,
gen.XM_008231
Figure 4695: DNA326271, XM_113328,
gen.XM_113328
Figure 4696: DNA326272, XM_113929,
gen.XM_113929
Figure 4697: DNA326273, NM_001970,
gen.NM_001970
Figure 4698: PRO82678
Figure 4699: DNA297388, NM_004217,
gen.NM_004217
Figure 4700: PRO70812
Figure 4701: DNA326274, XM_165421,
gen.XM_165421
Figure 4702: PRO82679
Figure 4703: DNA326275, XM_113325,
gen.XM_113325
Figure 4704: DNA326276, XM_165422,
gen.XM_165422
Figure 4705: PRO49182
Figure 4706: DNA326277, XM_113931,
gen.XM_113931
Figure 4707: DNA326278, XM_036659,
gen.XM_036659
Figure 4708: DNA103401, NM_003876,
gen.NM_003876
Figure 4709: PRO4729
Figure 4710A-B: DNA326279, XM_042698,
gen.XM_042698
Figure 4711: PRO82683
Figure 4712A-B: DNA326280, XM_017234,
gen.XM_017234
Figure 4713: DNA326281, XM_165418,
gen.XM_165418
Figure 4714: DNA304715, NM_000987,
gen.NM_000987
Figure 4715: PRO71141
Figure 4716A-B: DNA326282, NM_004618,
gen.NM_004618
Figure 4717: PRO62981
Figure 4718: DNA326283, XM_085743,
gen.XM_085743
Figure 4719A-B: DNA254198, NM_002018,
gen.NM_002018
Figure 4720: PRO49310
Figure 4721A-B: DNA326284, XM_039910,
gen.XM_039910
Figure 4722: PRO82687
Figure 4723A-C: DNA326285, XM_113310,
gen.XM_113310
Figure 4724: DNA326286, XM_085613,
gen.XM_085613
Figure 4725: DNA326287, NM_006470,
gen.NM_006470
Figure 4726: PRO82689
Figure 4727: DNA326288, XM_051763,

gen.XM_051763
Figure 4728: DNA290292, NM_018955,
gen.NM_018955
Figure 4729: PRO70449
Figure 4730: DNA326289, XM_058900,
gen.XM_058900
Figure 4731: PRO82691
Figure 4732: DNA326290, XM_039921,
gen.XM_039921
Figure 4733: PRO82692
Figure 4734: DNA326291, XM_012549,
gen.XM_012549
Figure 4735: DNA326292, XM_085548,
gen.XM_085548
Figure 4736: PRO82694
Figure 4737: DNA326293, NM_018019,
gen.NM_018019
Figure 4738: PRO82695
Figure 4739: DNA326294, NM_138427,
gen.NM_138427
Figure 4740: PRO82696
Figure 4741: DNA326295, XM_085545,
gen.XM_085545
Figure 4742A-B: DNA227084, NM_004176,
gen.NM_004176
Figure 4743: PRO37547
Figure 4744: DNA326296, XM_012615,
gen.XM_012615
Figure 4745: DNA326297, XM_085722,
gen.XM_085722
Figure 4746: PRO82699
Figure 4747: DNA255414, NM_018242,
gen.NM_018242
Figure 4748: PRO50481
Figure 4749: DNA326298, XM_045044,
gen.XM_045044
Figure 4750: DNA326299, XM_008323,
gen.XM_008323
Figure 4751: DNA326300, XM_045535,
gen.XM_045535
Figure 4752A-B: DNA326301, XM_045551,
gen.XM_045551
Figure 4753: PRO82702
Figure 4754: DNA326302, XM_097204,
gen.XM_097204
Figure 4755: DNA326303, XM_058867,
gen.XM_058867
Figure 4756: PRO82704
Figure 4757: DNA326304, XM_085672,
gen.XM_085672
Figure 4758: DNA326305, XM_031536,
gen.XM_031536
Figure 4759: PRO82706
Figure 4760: DNA326306, XM_008486,
gen.XM_008486
Figure 4761: DNA326307, NM_015584,

gen.NM_015584
Figure 4762: PRO82707
Figure 4763: DNA326308, NM_000638,
gen.NM_000638
Figure 4764: PRO82708
Figure 4765A-B: DNA326309, XM_031466,
gen.XM_031466
Figure 4766: PRO82709
Figure 4767: DNA326310, XM_031415,
gen.XM_031415
Figure 4768: DNA326311, XM_117066,
gen.XM_117066
Figure 4769: DNA326312, XM_031427,
gen.XM_031427
Figure 4770: PRO82712
Figure 4771: DNA326313, NM_032322,
gen.NM_032322
Figure 4772: PRO82713
Figure 4773A-B: DNA326314, XM_050101,
gen.XM_050101
Figure 4774: PRO82714
Figure 4775: DNA326315, XM_056730,
gen.XM_056730
Figure 4776: PRO82715
Figure 4777: DNA326316, XM_008462,
gen.XM_008462
Figure 4778: DNA287427, NM_002815,
gen.NM_002815
Figure 4779: PRO69684
Figure 4780: DNA326317, NM_015544,
gen.NM_015544
Figure 4781: PRO82717
Figure 4782: DNA188351, NM_005623,
gen.NM_005623
Figure 4783: PRO21887
Figure 4784: DNA326318, NM_002878,
gen.NM_002878
Figure 4785: PRO82718
Figure 4786: DNA326319, NM_133627,
gen.NM_133627
Figure 4787: PRO82719
Figure 4788: DNA326320, NM_133630,
gen.NM_133630
Figure 4789: PRO82720
Figure 4790: DNA326321, NM_133629,
gen.NM_133629
Figure 4791: PRO82721
Figure 4792: DNA326322, NM_018096,
gen.NM_018096
Figure 4793: PRO37791
Figure 4794A-B: DNA326323, XM_039474,
gen.XM_039474
Figure 4795: PRO82722
Figure 4796A-B: DNA66475, NM_004448,
gen.NM_004448
Figure 4797: PRO1204

Figure 4798: DNA326324, NM_000981,
gen.NM_000981
Figure 4799: PRO4738
Figure 4800A-B: DNA326325, XM_008150,
gen.XM_008150
Figure 4801: DNA326326, NM_000978,
gen.NM_000978
Figure 4802: PRO82724
Figure 4803: DNA326327, XM_058830,
gen.XM_058830
Figure 4804: PRO82725
Figure 4805: DNA270979, NM_002809,
gen.NM_002809
Figure 4806: PRO59309
Figure 4807: DNA326328, NM_000422,
gen.NM_000422
Figure 4808: PRO82726
Figure 4809: DNA326329, XM_008579,
gen.XM_008579
Figure 4810: DNA326330, NM_002276,
gen.NM_002276
Figure 4811: PRO82728
Figure 4812: DNA272889, NM_002275,
gen.NM_002275
Figure 4813: PRO60979
Figure 4814: DNA326331, NM_002274,
gen.NM_002274
Figure 4815: PRO82729
Figure 4816: DNA326332, NM_000526,
gen.NM_000526
Figure 4817: PRO82730
Figure 4818: DNA326333, XM_049937,
gen.XM_049937
Figure 4819A-B: DNA326334, XM_113334,
gen.XM_113334
Figure 4820: DNA226389, NM_000964,
gen.NM_000964
Figure 4821: PRO36852
Figure 4822: DNA326335, NM_006455,
gen.NM_006455
Figure 4823: PRO82732
Figure 4824: DNA326336, XM_113938,
gen.XM_113938
Figure 4825: DNA326337, XM_036465,
gen.XM_036465
Figure 4826: DNA326338, XM_055061,
gen.XM_055061
Figure 4827A-B: DNA326339, XM_036462,
gen.XM_036462
Figure 4828: PRO82736
Figure 4829: DNA326340, XM_048654,
gen.XM_048654
Figure 4830: DNA326341, NM_025197,
gen.NM_025197
Figure 4831: PRO82737
Figure 4832: DNA326342, XM_054038,

gen.XM_054038
Figure 4833: PRO82738
Figure 4834: DNA326343, NM_002265,
gen.NM_002265
Figure 4835: PRO82739
Figure 4836: DNA326344, XM_032201,
gen.XM_032201
Figure 4837: PRO82740
Figure 4838: DNA326345, NM_012138,
gen.NM_012138
Figure 4839: PRO82741
Figure 4840: DNA326346, XM_018534,
gen.XM_018534
Figure 4841: DNA227873, NM_001050,
gen.NM_001050
Figure 4842: PRO38336
Figure 4843: DNA270975, NM_000386,
gen.NM_000386
Figure 4844: PRO59305
Figure 4845: DNA88378, NM_002087,
gen.NM_002087
Figure 4846: PRO2769
Figure 4847: DNA326347, NM_016016,
gen.NM_016016
Figure 4848: PRO82743
Figure 4849: DNA326348, XM_012642,
gen.XM_012642
Figure 4850A-B: DNA326349, NM_005474,
gen.NM_005474
Figure 4851: PRO82745
Figure 4852: DNA326350, XM_045901,
gen.XM_045901
Figure 4853: PRO82746
Figure 4854: DNA257428, NM_032376,
gen.NM_032376
Figure 4855: PRO52010
Figure 4856: DNA326351, XM_008351,
gen.XM_008351
Figure 4857: DNA326352, XM_032852,
gen.XM_032852
Figure 4858: PRO82748
Figure 4859: DNA326353, NM_025233,
gen.NM_025233
Figure 4860: PRO82749
Figure 4861: DNA326354, XM_032817,
gen.XM_032817
Figure 4862: PRO82750
Figure 4863: DNA326355, XM_032813,
gen.XM_032813
Figure 4864: DNA326356, XM_032766,
gen.XM_032766
Figure 4865: DNA326357, NM_003766,
gen.NM_003766
Figure 4866: PRO82753
Figure 4867: DNA326358, XM_008401,
gen.XM_008401

Figure 4868: PRO82754
Figure 4869: DNA326359, XM_008402,
gen.XM_008402
Figure 4870: PRO82755
Figure 4871: DNA326360, NM_017595,
gen.NM_017595
Figure 4872: PRO82756
Figure 4873: DNA326361, XM_085636,
gen.XM_085636
Figure 4874: PRO82757
Figure 4875: DNA326362, NM_006373,
gen.NM_006373
Figure 4876: PRO82758
Figure 4877: DNA196642, NM_005440,
gen.NM_005440
Figure 4878: PRO25115
Figure 4879A-B: DNA270901, NM_004247,
gen.NM_004247
Figure 4880: DNA326363, XM_050159,
gen.XM_050159
Figure 4881: DNA326364, XM_083983,
gen.XM_083983
Figure 4882: PRO82760
Figure 4883A-B: DNA326365, NM_021079,
gen.NM_021079
Figure 4884: PRO82761
Figure 4885: DNA326366, NM_133373,
gen.NM_133373
Figure 4886: PRO82762
Figure 4887: DNA97290, NM_002512,
gen.NM_002512
Figure 4888: PRO3637
Figure 4889: DNA227071, NM_000269,
gen.NM_000269
Figure 4890: PRO37534
Figure 4891: DNA227764, NM_003971,
gen.NM_003971
Figure 4892: PRO38227
Figure 4893A-B: DNA326367, NM_020038,
gen.NM_020038
Figure 4894: PRO82763
Figure 4895A-B: DNA326368, NM_020037,
gen.NM_020037
Figure 4896: PRO82764
Figure 4897: DNA326369, XM_037971,
gen.XM_037971
Figure 4898: DNA254791, NM_018346,
gen.NM_018346
Figure 4899: PRO49888
Figure 4900: DNA287425, NM_018509,
gen.NM_018509
Figure 4901: PRO69682
Figure 4902A-B: DNA326370, XM_008432,
gen.XM_008432
Figure 4903: DNA88554, NM_000250,
gen.NM_000250

Figure 4904: PRO2839
Figure 4905: DNA326371, XM_113919,
gen.XM_113919
Figure 4906: DNA326372, NM_017777,
gen.NM_017777
Figure 4907: PRO82768
Figure 4908: DNA326373, NM_006924,
gen.NM_006924
Figure 4909: PRO82769
Figure 4910: DNA326374, XM_115480,
gen.XM_115480
Figure 4911: DNA326375, NM_005831,
gen.NM_005831
Figure 4912: PRO59328
Figure 4913: DNA326376, XM_117061,
gen.XM_117061
Figure 4914: PRO82771
Figure 4915: DNA326377, XM_008459,
gen.XM_008459
Figure 4916A-B: DNA326378, XM_012651,
gen.XM_012651
Figure 4917: DNA326379, NM_021626,
gen.NM_021626
Figure 4918: PRO302
Figure 4919: DNA287291, NM_021213,
gen.NM_021213
Figure 4920: PRO69561
Figure 4921A-B: DNA326380, NM_004859,
gen.NM_004859
Figure 4922: PRO82774
Figure 4923: DNA326381, XM_083966,
gen.XM_083966
Figure 4924: DNA326382, XM_044426,
gen.XM_044426
Figure 4925: PRO82776
Figure 4926: DNA326383, XM_008253,
gen.XM_008253
Figure 4927: DNA326384, XM_044394,
gen.XM_044394
Figure 4928: PRO10400
Figure 4929: DNA326385, NM_017647,
gen.NM_017647
Figure 4930: PRO82778
Figure 4931: DNA326386, NM_007372,
gen.NM_007372
Figure 4932: PRO82779
Figure 4933: DNA326387, NM_002401,
gen.NM_002401
Figure 4934: PRO37764
Figure 4935: DNA326388, XM_044376,
gen.XM_044376
Figure 4936A-B: DNA150457, NM_006039,
gen.NM_006039
Figure 4937: PRO12265
Figure 4938: DNA326389, XM_044367,
gen.XM_044367

Figure 4939: DNA227055, NM_002634,
gen.NM_002634
Figure 4940: PRO37518
Figure 4941: DNA326390, XM_011118,
gen.XM_011118
Figure 4942: DNA326391, XM_055199,
gen.XM_055199
Figure 4943A-B: DNA326392, XM_044372,
gen.XM_044372
Figure 4944: DNA326393, XM_113315,
gen.XM_113315
Figure 4945: DNA326394, XM_012609,
gen.XM_012609
Figure 4946: DNA326395, NM_005220,
gen.NM_005220
Figure 4947: PRO82787
Figure 4948: DNA326396, XM_085589,
gen.XM_085589
Figure 4949: PRO82788
Figure 4950: DNA326397, XM_012634,
gen.XM_012634
Figure 4951: DNA326398, XM_085627,
gen.XM_085627
Figure 4952: PRO82790
Figure 4953: DNA150814, NM_002086,
gen.NM_002086
Figure 4954: PRO12806
Figure 4955: DNA326399, NM_024844,
gen.NM_024844
Figure 4956: PRO82791
Figure 4957: DNA326400, XM_041583,
gen.XM_041583
Figure 4958: DNA326401, XM_046932,
gen.XM_046932
Figure 4959: PRO82792
Figure 4960: DNA326402, NM_004524,
gen.NM_004524
Figure 4961: PRO82793
Figure 4962A-B: DNA326403, XM_113951,
gen.XM_113951
Figure 4963A-B: DNA88430, NM_000213,
gen.NM_000213
Figure 4964: PRO2788
Figure 4965A-B: DNA326404, XM_036104,
gen.XM_036104
Figure 4966: PRO82794
Figure 4967: DNA326405, NM_000154,
gen.NM_000154
Figure 4968: PRO82795
Figure 4969: DNA326406, NM_005324,
gen.NM_005324
Figure 4970: PRO11403
Figure 4971A-B: DNA326407, XM_036115,
gen.XM_036115
Figure 4972: PRO82796
Figure 4973: DNA326408, XM_054344,

gen.XM_054344
Figure 4974: PRO82797
Figure 4975: DNA274755, NM_002766,
gen.NM_002766
Figure 4976: PRO70703
Figure 4977A-B: DNA326409, XM_085531,
gen.XM_085531
Figure 4978: DNA326410, XM_113892,
gen.XM_113892
Figure 4979: PRO82799
Figure 4980: DNA326411, XM_017578,
gen.XM_017578
Figure 4981: PRO82800
Figure 4982: DNA326412, XM_036785,
gen.XM_036785
Figure 4983: PRO39201
Figure 4984: DNA326413, XM_097043,
gen.XM_097043
Figure 4985: DNA129504, NM_001168,
gen.NM_001168
Figure 4986: PRO7143
Figure 4987: DNA326414, XM_037196,
gen.XM_037196
Figure 4988: DNA326415, XM_037195,
gen.XM_037195
Figure 4989: DNA326416, XM_045104,
gen.XM_045104
Figure 4990: PRO37540
Figure 4991: DNA326417, XM_085563,
gen.XM_085563
Figure 4992A-B: DNA326418, XM_085716,
gen.XM_085716
Figure 4993: PRO82805
Figure 4994A-B: DNA326419, XM_049934,
gen.XM_049934
Figure 4995: DNA326420, XM_049931,
gen.XM_049931
Figure 4996A-B: DNA326421, XM_045581,
gen.XM_045581
Figure 4997: PRO82807
Figure 4998: DNA326422, XM_113945,
gen.XM_113945
Figure 4999: DNA326423, XM_046481,
gen.XM_046481
Figure 5000: DNA326424, XM_097195,
gen.XM_097195
Figure 5001: DNA326425, XM_097193,
gen.XM_097193
Figure 5002: DNA326426, NM_004309,
gen.NM_004309
Figure 5003: PRO61246
Figure 5004: DNA326427, XM_046472,
gen.XM_046472
Figure 5005: PRO82812
Figure 5006: DNA326428, NM_016286,
gen.NM_016286

Figure 5007: PRO82813
Figure 5008: DNA326429, NM_004127,
gen.NM_004127
Figure 5009: PRO82814
Figure 5010A-C: DNA326430, XM_113943,
gen.XM_113943
Figure 5011: DNA326431, XM_113330,
gen.XM_113330
Figure 5012: PRO82816
Figure 5013: DNA326432, XM_113303,
gen.XM_113303
Figure 5014: DNA287234, NM_031968,
gen.NM_031968
Figure 5015: PRO69513
Figure 5016: DNA326433, NM_022158,
gen.NM_022158
Figure 5017: PRO82818
Figure 5018: DNA326434, XM_038424,
gen.XM_038424
Figure 5019: DNA326435, XM_085735,
gen.XM_085735
Figure 5020: DNA326436, XM_046765,
gen.XM_046765
Figure 5021: DNA326437, XM_046769,
gen.XM_046769
Figure 5022: DNA326438, XM_046767,
gen.XM_046767
Figure 5023: DNA273694, NM_006101,
gen.NM_006101
Figure 5024: PRO61661
Figure 5025A-B: DNA326439, XM_028744,
gen.XM_028744
Figure 5026: DNA326440, XM_165954,
gen.XM_165954
Figure 5027: DNA326441, XM_041678,
gen.XM_041678
Figure 5028: DNA326442, XM_113343,
gen.XM_113343
Figure 5029: PRO82825
Figure 5030: DNA326443, XM_067325,
gen.XM_067325
Figure 5031: DNA326444, XM_012741,
gen.XM_012741
Figure 5032: DNA326445, NM_014214,
gen.NM_014214
Figure 5033: PRO82828
Figure 5034A-B: DNA326446, XM_035640,
gen.XM_035640
Figure 5035: PRO82829
Figure 5036: DNA326447, XM_016382,
gen.XM_016382
Figure 5037: DNA326448, NM_032933,
gen.NM_032933
Figure 5038: PRO82831
Figure 5039: DNA274690, NM_006938,
gen.NM_006938

Figure 5040A-B: DNA88457, NM_000227,
gen.NM_000227
Figure 5041: PRO2799
Figure 5042: DNA326449, XM_085791,
gen.XM_085791
Figure 5043: DNA326450, XM_085789,
gen.XM_085789
Figure 5044: PRO82833
Figure 5045: DNA326451, XM_085790,
gen.XM_085790
Figure 5046: DNA326452, XM_015755,
gen.XM_015755
Figure 5047: PRO82835
Figure 5048: DNA326453, XM_097232,
gen.XM_097232
Figure 5049: DNA326454, XM_085788,
gen.XM_085788
Figure 5050: DNA88281, NM_001944,
gen.NM_001944
Figure 5051: PRO2267
Figure 5052: DNA271841, NM_003787,
gen.NM_003787
Figure 5053: PRO60121
Figure 5054: DNA326455, XM_008723,
gen.XM_008723
Figure 5055: DNA326456, XM_084007,
gen.XM_084007
Figure 5056: DNA256813, NM_018255,
gen.NM_018255
Figure 5057: PRO51744
Figure 5058: DNA326457, XM_085775,
gen.XM_085775
Figure 5059: PRO82840
Figure 5060: DNA326458, NM_138443,
gen.NM_138443
Figure 5061: PRO82841
Figure 5062: DNA326459, XM_038872,
gen.XM_038872
Figure 5063: PRO82842
Figure 5064: DNA326460, XM_086779,
gen.XM_086779
Figure 5065: DNA326461, XM_167363,
gen.XM_167363
Figure 5066: DNA326462, XM_031944,
gen.XM_031944
Figure 5067: DNA326463, NM_000985,
gen.NM_000985
Figure 5068: PRO82846
Figure 5069: DNA326464, NM_002396,
gen.NM_002396
Figure 5070: PRO61113
Figure 5071: DNA326465, XM_166288,
gen.XM_166288
Figure 5072: DNA326466, NM_004539,
gen.NM_004539
Figure 5073: PRO60800

Figure 5074: DNA326467, XM_006937,
gen.XM_006937
Figure 5075: DNA326468, XM_085779,
gen.XM_085779
Figure 5076: DNA326469, XM_011089,
gen.XM_011089
Figure 5077: PRO82850
Figure 5078: DNA326470, XM_169540,
gen.XM_169540
Figure 5079: PRO82851
Figure 5080: DNA326471, XM_167008,
gen.XM_167008
Figure 5081: PRO82852
Figure 5082: DNA326472, XM_048471,
gen.XM_048471
Figure 5083A-B: DNA326473, XM_008812,
gen.XM_008812
Figure 5084A-B: DNA326474, XM_117096,
gen.XM_117096
Figure 5085: PRO82855
Figure 5086: DNA326475, NM_002385,
gen.NM_002385
Figure 5087: PRO82856
Figure 5088: DNA326476, XM_015241,
gen.XM_015241
Figure 5089A-B: DNA326477, XM_008695,
gen.XM_008695
Figure 5090A-B: DNA326478, XM_041872,
gen.XM_041872
Figure 5091: PRO82859
Figure 5092: DNA326479, XM_051586,
gen.XM_051586
Figure 5093: DNA326480, NM_003712,
gen.NM_003712
Figure 5094: PRO1077
Figure 5095: DNA326481, XM_042018,
gen.XM_042018
Figure 5096: PRO2560
Figure 5097: DNA326482, XM_114018,
gen.XM_114018
Figure 5098: DNA326483, NM_017876,
gen.NM_017876
Figure 5099: PRO82861
Figure 5100: DNA326484, NM_031990,
gen.NM_031990
Figure 5101: PRO82862
Figure 5102: DNA326485, NM_002819,
gen.NM_002819
Figure 5103: PRO62899
Figure 5104: DNA326486, NM_005224,
gen.NM_005224
Figure 5105: PRO82863
Figure 5106: DNA326487, XM_037565,
gen.XM_037565
Figure 5107: PRO82864
Figure 5108: DNA326488, XM_092042,

gen.XM_092042
Figure 5109: DNA326489, XM_037572,
gen.XM_037572
Figure 5110: DNA326490, XM_009279,
gen.XM_009279
Figure 5111: PRO82867
Figure 5112: DNA326491, NM_002085,
gen.NM_002085
Figure 5113A-B: DNA326492, XM_009277,
gen.XM_009277
Figure 5114: DNA326493, XM_012913,
gen.XM_012913
Figure 5115: DNA274101, NM_001687,
gen.NM_001687
Figure 5116: PRO62039
Figure 5117: DNA326494, XM_028067,
gen.XM_028067
Figure 5118: PRO82871
Figure 5119: DNA326495, XM_028064,
gen.XM_028064
Figure 5120: DNA326496, NM_024407,
gen.NM_024407
Figure 5121: PRO82872
Figure 5122: DNA326497, NM_000156,
gen.NM_000156
Figure 5123: PRO58046
Figure 5124: DNA326498, NM_138924,
gen.NM_138924
Figure 5125: PRO82873
Figure 5126: DNA326499, NM_001018,
gen.NM_001018
Figure 5127: PRO10485
Figure 5128: DNA326500, XM_086101,
gen.XM_086101
Figure 5129: PRO82874
Figure 5130: DNA326501, XM_086102,
gen.XM_086102
Figure 5131: DNA326502, XM_047584,
gen.XM_047584
Figure 5132A-B: DNA326503, XM_047600,
gen.XM_047600
Figure 5133: PRO38496
Figure 5134: DNA326504, XM_097420,
gen.XM_097420
Figure 5135A-B: DNA326505, XM_030721,
gen.XM_030721
Figure 5136: PRO82877
Figure 5137: DNA326506, XM_030720,
gen.XM_030720
Figure 5138: DNA326507, NM_031213,
gen.NM_031213
Figure 5139: PRO82879
Figure 5140: DNA326508, XM_039723,
gen.XM_039723
Figure 5141: DNA326509, NM_001319,
gen.NM_001319

Figure 5142: PRO82881
Figure 5143: DNA326510, NM_017797,
gen.NM_017797
Figure 5144: PRO82882
Figure 5145: DNA326511, XM_030714,
gen.XM_030714
Figure 5146: DNA256555, NM_017572,
gen.NM_017572
Figure 5147: PRO51586
Figure 5148A-B: DNA326512, NM_003938,
gen.NM_003938
Figure 5149: PRO82884
Figure 5150A-B: DNA326513, XM_046822,
gen.XM_046822
Figure 5151: PRO82885
Figure 5152: DNA326514, NM_007165,
gen.NM_007165
Figure 5153: PRO82886
Figure 5154: DNA287636, NM_004152,
gen.NM_004152
Figure 5155: DNA326515, NM_012458,
gen.NM_012458
Figure 5156: PRO82887
Figure 5157: DNA326516, NM_032737,
gen.NM_032737
Figure 5158: PRO82888
Figure 5159: DNA326517, XM_030485,
gen.XM_030485
Figure 5160: DNA326518, XM_046934,
gen.XM_046934
Figure 5161: DNA326519, NM_003021,
gen.NM_003021
Figure 5162: PRO62302
Figure 5163: DNA326520, XM_055686,
gen.XM_055686
Figure 5164: PRO37951
Figure 5165: DNA326521, XM_009222,
gen.XM_009222
Figure 5166: DNA326522, XM_052635,
gen.XM_052635
Figure 5167: PRO82892
Figure 5168: DNA326523, XM_052661,
gen.XM_052661
Figure 5169: DNA326524, NM_016263,
gen.NM_016263
Figure 5170: PRO82893
Figure 5171: DNA326525, NM_006339,
gen.NM_006339
Figure 5172: PRO82894
Figure 5173: DNA326526, NM_032753,
gen.NM_032753
Figure 5174: PRO82895
Figure 5175: DNA326527, XM_056421,
gen.XM_056421
Figure 5176A-B: DNA326528, XM_031917,
gen.XM_031917

Figure 5177: PRO82897
Figure 5178: DNA326529, NM_001961,
gen.NM_001961
Figure 5179: PRO62225
Figure 5180: DNA326530, XM_016871,
gen.XM_016871
Figure 5181: DNA326531, NM_016539,
gen.NM_016539
Figure 5182: PRO82899
Figure 5183: DNA326532, XM_117122,
gen.XM_117122
Figure 5184: DNA326533, XM_031857,
gen.XM_031857
Figure 5185: PRO82901
Figure 5186: DNA326534, NM_024333,
gen.NM_024333
Figure 5187: PRO82902
Figure 5188: DNA326535, NM_003025,
gen.NM_003025
Figure 5189: PRO82903
Figure 5190: DNA326536, NM_025241,
gen.NM_025241
Figure 5191: PRO82904
Figure 5192: DNA326537, XM_035638,
gen.XM_035638
Figure 5193: PRO82905
Figure 5194A-B: DNA326538, XM_035636,
gen.XM_035636
Figure 5195: DNA326539, XM_012862,
gen.XM_012862
Figure 5196A-B: DNA326540, XM_035627,
gen.XM_035627
Figure 5197A-B: DNA326541, XM_035625,
gen.XM_035625
Figure 5198: PRO82909
Figure 5199: DNA274761, NM_014649,
gen.NM_014649
Figure 5200: PRO62531
Figure 5201: DNA272421, NM_006012,
gen.NM_006012
Figure 5202: PRO60674
Figure 5203: DNA326542, NM_003685,
gen.NM_003685
Figure 5204: PRO82910
Figure 5205A-B: DNA326543, XM_009010,
gen.XM_009010
Figure 5206: DNA270315, NM_004240,
gen.NM_004240
Figure 5207: PRO58702
Figure 5208: DNA326544, NM_005490,
gen.NM_005490
Figure 5209: PRO201
Figure 5210: DNA326546, XM_044619,
gen.XM_044619
Figure 5211: PRO82912
Figure 5212: DNA326547, XM_012798,

gen.XM_012798
Figure 5213: DNA326548, XM_044608,
gen.XM_044608
Figure 5214: DNA326549, NM_003624,
gen.NM_003624
Figure 5215: PRO82915
Figure 5216: DNA326550, NM_016579,
gen.NM_016579
Figure 5217: PRO224
Figure 5218A-B: DNA326551, XM_048351,
gen.XM_048351
Figure 5219: DNA326552, XM_048364,
gen.XM_048364
Figure 5220: PRO82917
Figure 5221: DNA326553, XM_091938,
gen.XM_091938
Figure 5222: DNA326554, XM_097300,
gen.XM_097300
Figure 5223: DNA326555, XM_049282,
gen.XM_049282
Figure 5224: PRO82920
Figure 5225: DNA326556, XM_058232,
gen.XM_058232
Figure 5226: DNA326557, XM_045151,
gen.XM_045151
Figure 5227A-B: DNA326558, XM_050435,
gen.XM_050435
Figure 5228: PRO82923
Figure 5229: DNA326559, XM_113988,
gen.XM_113988
Figure 5230: DNA326560, NM_058164,
gen.NM_058164
Figure 5231: PRO82925
Figure 5232: DNA227280, NM_020230,
gen.NM_020230
Figure 5233: PRO37743
Figure 5234: DNA270621, NM_003755,
gen.NM_003755
Figure 5235: PRO58991
Figure 5236: DNA326561, XM_049502,
gen.XM_049502
Figure 5237: DNA326562, NM_007065,
gen.NM_007065
Figure 5238: PRO63226
Figure 5239: DNA326563, XM_049561,
gen.XM_049561
Figure 5240: DNA326564, XM_017204,
gen.XM_017204
Figure 5241: DNA326565, NM_005498,
gen.NM_005498
Figure 5242: PRO62112
Figure 5243: DNA326566, XM_008887,
gen.XM_008887
Figure 5244: DNA326567, XM_085862,
gen.XM_085862
Figure 5245: PRO82930

Figure 5246: DNA326568, XM_084014,
gen.XM_084014
Figure 5247A-B: DNA326569, XM_032710,
gen.XM_032710
Figure 5248: DNA326570, XM_032719,
gen.XM_032719
Figure 5249: PRO82933
Figure 5250: DNA326571, NM_024029,
gen.NM_024029
Figure 5251: PRO23794
Figure 5252: DNA326572, XM_032724,
gen.XM_032724
Figure 5253: PRO82934
Figure 5254A-B: DNA326573, NM_003072,
gen.NM_003072
Figure 5255: PRO82935
Figure 5256A-B: DNA326574, XM_009082,
gen.XM_009082
Figure 5257: DNA326575, XM_032774,
gen.XM_032774
Figure 5258: DNA218271, NM_000121,
gen.NM_000121
Figure 5259: PRO34323
Figure 5260: DNA326576, XM_057074,
gen.XM_057074
Figure 5261: DNA326577, XM_032782,
gen.XM_032782
Figure 5262: DNA326578, NM_032377,
gen.NM_032377
Figure 5263: PRO82939
Figure 5264: DNA326579, XM_015697,
gen.XM_015697
Figure 5265: PRO82940
Figure 5266: DNA326580, XM_010156,
gen.XM_010156
Figure 5267: DNA326581, NM_001930,
gen.NM_001930
Figure 5268: PRO58446
Figure 5269: DNA326582, NM_013406,
gen.NM_013406
Figure 5270: DNA326583, NM_013407,
gen.NM_013407
Figure 5271: PRO82943
Figure 5272: DNA103320, NM_002229,
gen.NM_002229
Figure 5273: PRO4650
Figure 5274: DNA326584, XM_009063,
gen.XM_009063
Figure 5275: PRO82944
Figure 5276: DNA326585, XM_085917,
gen.XM_085917
Figure 5277: DNA274034, NM_006397,
gen.NM_006397
Figure 5278: PRO61977
Figure 5279: DNA287243, NM_004461,
gen.NM_004461

Figure 5280: PRO69518
Figure 5281: DNA326586, XM_032020,
gen.XM_032020
Figure 5282: PRO2718
Figure 5283: DNA326587, NM_005053,
gen.NM_005053
Figure 5284: PRO22613
Figure 5285: DNA326588, XM_085916,
gen.XM_085916
Figure 5286: DNA326589, NM_017722,
gen.NM_017722
Figure 5287: PRO82947
Figure 5288: DNA326590, NM_003765,
gen.NM_003765
Figure 5289: PRO82948
Figure 5290: DNA326591, XM_051364,
gen.XM_051364
Figure 5291: PRO82949
Figure 5292: DNA326592, XM_031345,
gen.XM_031345
Figure 5293: PRO82950
Figure 5294: DNA326593, XM_113352,
gen.XM_113352
Figure 5295: DNA326594, XM_058967,
gen.XM_058967
Figure 5296: PRO82952
Figure 5297: DNA326595, XM_085909,
gen.XM_085909
Figure 5298: DNA269894, NM_002730,
gen.NM_002730
Figure 5299: PRO58292
Figure 5300: DNA326596, NM_018154,
gen.NM_018154
Figure 5301: PRO82954
Figure 5302: DNA326597, XM_031276,
gen.XM_031276
Figure 5303: DNA326598, XM_031273,
gen.XM_031273
Figure 5304: PRO82956
Figure 5305: DNA326599, XM_031263,
gen.XM_031263
Figure 5306: PRO82957
Figure 5307: DNA326600, XM_031251,
gen.XM_031251
Figure 5308: DNA326601, NM_006844,
gen.NM_006844
Figure 5309: PRO82958
Figure 5310A-C: DNA326602, XM_009303,
gen.XM_009303
Figure 5311: DNA326603, XM_086074,
gen.XM_086074
Figure 5312: DNA269630, NM_003290,
gen.NM_003290
Figure 5313: PRO58042
Figure 5314: DNA326604, NM_005370,
gen.NM_005370

Figure 5315: PRO12130
Figure 5316: DNA326605, XM_113348, gen.XM_113348
Figure 5317: DNA326606, NM_032207, gen.NM_032207
Figure 5318: PRO82962
Figure 5319A-B: DNA326607, NM_006387, gen.NM_006387
Figure 5320: PRO82963
Figure 5321: DNA326608, NM_024881, gen.NM_024881
Figure 5322: PRO82964
Figure 5323: DNA326609, NM_024104, gen.NM_024104
Figure 5324: PRO82965
Figure 5325A-C: DNA326610, XM_008854, gen.XM_008854
Figure 5326: DNA326611, NM_014173, gen.NM_014173
Figure 5327: PRO82967
Figure 5328: DNA287240, NM_004335, gen.NM_004335
Figure 5329: PRO29371
Figure 5330: DNA326612, XM_050660, gen.XM_050660
Figure 5331: DNA326613, XM_086116, gen.XM_086116
Figure 5332: DNA326614, NM_018174, gen.NM_018174
Figure 5333: PRO82970
Figure 5334: DNA326615, NM_000980, gen.NM_000980
Figure 5335: PRO82971
Figure 5336: DNA326616, XM_055230, gen.XM_055230
Figure 5337: DNA326617, XM_012179, gen.XM_012179
Figure 5338A-B: DNA326618, XM_009293, gen.XM_009293
Figure 5339: DNA326619, XM_038146, gen.XM_038146
Figure 5340: PRO82975
Figure 5341: DNA326620, XM_092046, gen.XM_092046
Figure 5342: PRO82976
Figure 5343: DNA326621, XM_038098, gen.XM_038098
Figure 5344: PRO82977
Figure 5345: DNA326622, NM_032627, gen.NM_032627
Figure 5346: PRO82978
Figure 5347: DNA326623, XM_165960, gen.XM_165960
Figure 5348: PRO82979
Figure 5349: DNA326624, XM_114004, gen.XM_114004

Figure 5350: DNA326625, NM_012181, gen.NM_012181
Figure 5351: PRO82980
Figure 5352: DNA227249, NM_007263, gen.NM_007263
Figure 5353: PRO37712
Figure 5354: DNA326626, XM_018515, gen.XM_018515
Figure 5355: DNA326627, NM_033415, gen.NM_033415
Figure 5356: PRO82982
Figure 5357: DNA326628, XM_009330, gen.XM_009330
Figure 5358: DNA326629, NM_134440, gen.NM_134440
Figure 5359: PRO82983
Figure 5360: DNA326630, NM_003721, gen.NM_003721
Figure 5361: PRO59220
Figure 5362: DNA326631, NM_015965, gen.NM_015965
Figure 5363: PRO82984
Figure 5364: DNA326632, XM_016378, gen.XM_016378
Figure 5365: PRO82985
Figure 5366: DNA326633, XM_114027, gen.XM_114027
Figure 5367: DNA326634, XM_165963, gen.XM_165963
Figure 5368: PRO82987
Figure 5369: DNA326635, XM_015769, gen.XM_015769
Figure 5370: DNA326636, XM_012812, gen.XM_012812
Figure 5371: DNA326637, XM_085971, gen.XM_085971
Figure 5372: DNA326638, XM_037662, gen.XM_037662
Figure 5373: PRO82991
Figure 5374: DNA326639, NM_001238, gen.NM_001238
Figure 5375: PRO82992
Figure 5376: DNA326640, NM_057182, gen.NM_057182
Figure 5377: PRO4756
Figure 5378: DNA326641, XM_009180, gen.XM_009180
Figure 5379: DNA326642, XM_117118, gen.XM_117118
Figure 5380: DNA326643, XM_092049, gen.XM_092049
Figure 5381: PRO82995
Figure 5382: DNA326644, XM_028672, gen.XM_028672
Figure 5383: DNA326645, XM_028666, gen.XM_028666

Figure 5384: DNA326646, XM_009338,
gen.XM_009338
Figure 5385: DNA326647, XM_048258,
gen.XM_048258
Figure 5386: PRO82998
Figure 5387: DNA256836, NM_018468,
gen.NM_018468
Figure 5388: PRO51767
Figure 5389: DNA326648, NM_024321,
gen.NM_024321
Figure 5390: PRO82999
Figure 5391A-B: DNA326649, XM_049237,
gen.XM_049237
Figure 5392: PRO83000
Figure 5393: DNA326650, NM_032635,
gen.NM_032635
Figure 5394: PRO23845
Figure 5395: DNA326651, XM_115615,
gen.XM_115615
Figure 5396A-B: DNA326652, XM_091984,
gen.XM_091984
Figure 5397: PRO83002
Figure 5398: DNA326653, XM_085986,
gen.XM_085986
Figure 5399: DNA326654, XM_032285,
gen.XM_032285
Figure 5400: PRO83004
Figure 5401: DNA326655, NM_002812,
gen.NM_002812
Figure 5402: PRO83005
Figure 5403A-E: DNA326656, XM_029455,
gen.XM_029455
Figure 5404: DNA326657, XM_029450,
gen.XM_029450
Figure 5405: PRO83007
Figure 5406: DNA326658, XM_009149,
gen.XM_009149
Figure 5407: PRO62500
Figure 5408: DNA326659, XM_056602,
gen.XM_056602
Figure 5409: DNA326660, NM_012237,
gen.NM_012237
Figure 5410: PRO83008
Figure 5411: DNA326661, NM_030593,
gen.NM_030593
Figure 5412: PRO83009
Figure 5413: DNA326662, NM_017827,
gen.NM_017827
Figure 5414: PRO83010
Figure 5415: DNA326663, NM_021107,
gen.NM_021107
Figure 5416: PRO83011
Figure 5417: DNA326664, NM_033363,
gen.NM_033363
Figure 5418: PRO83012
Figure 5419: DNA326665, XM_059045,

gen.XM_059045
Figure 5420: PRO83013
Figure 5421: DNA273474, NM_005884,
gen.NM_005884
Figure 5422: PRO61458
Figure 5423: DNA326666, XM_046090,
gen.XM_046090
Figure 5424: PRO83014
Figure 5425: DNA326667, XM_086004,
gen.XM_086004
Figure 5426: DNA272347, NM_001020,
gen.NM_001020
Figure 5427: PRO60603
Figure 5428A-B: DNA326668, NM_003169,
gen.NM_003169
Figure 5429: PRO12822
Figure 5430: DNA326669, XM_053074,
gen.XM_053074
Figure 5431: PRO83016
Figure 5432: DNA326670, NM_016941,
gen.NM_016941
Figure 5433: PRO83017
Figure 5434: DNA256840, NM_004714,
gen.NM_004714
Figure 5435: PRO51771
Figure 5436: DNA326671, NM_001436,
gen.NM_001436
Figure 5437: PRO83018
Figure 5438: DNA326672, XM_016410,
gen.XM_016410
Figure 5439: DNA326673, XM_012860,
gen.XM_012860
Figure 5440: DNA326674, XM_097365,
gen.XM_097365
Figure 5441: DNA274139, NM_006503,
gen.NM_006503
Figure 5442: PRO62075
Figure 5443: DNA326675, XM_009203,
gen.XM_009203
Figure 5444: DNA326676, XM_047409,
gen.XM_047409
Figure 5445: DNA326677, XM_047376,
gen.XM_047376
Figure 5446A-B: DNA326678, XM_047374,
gen.XM_047374
Figure 5447: DNA326679, XM_059052,
gen.XM_059052
Figure 5448: DNA273600, NM_004596,
gen.NM_004596
Figure 5449: PRO61575
Figure 5450: DNA326680, XM_030914,
gen.XM_030914
Figure 5451: DNA326681, NM_052848,
gen.NM_052848
Figure 5452: PRO83027
Figure 5453: DNA326682, XM_008912,

gen.XM_008912
 Figure 5454: DNA326683, NM_020158,
 gen.NM_020158
 Figure 5455: PRO83029
 Figure 5456: DNA326684, XM_030901,
 gen.XM_030901
 Figure 5457: PRO83030
 Figure 5458: DNA326685, NM_018035,
 gen.NM_018035
 Figure 5459: PRO83031
 Figure 5460: DNA326686, XM_085874,
 gen.XM_085874
 Figure 5461: DNA326687, XM_085875,
 gen.XM_085875
 Figure 5462: DNA326688, XM_085876,
 gen.XM_085876
 Figure 5463: DNA326689, XM_058949,
 gen.XM_058949
 Figure 5464: PRO83035
 Figure 5465: DNA326690, XM_030895,
 gen.XM_030895
 Figure 5466: DNA326691, XM_115603,
 gen.XM_115603
 Figure 5467: PRO83037
 Figure 5468: DNA326692, NM_001022,
 gen.NM_001022
 Figure 5469: PRO83038
 Figure 5470: DNA326693, NM_004706,
 gen.NM_004706
 Figure 5471: PRO83039
 Figure 5472: DNA326694, XM_008878,
 gen.XM_008878
 Figure 5473: PRO83040
 Figure 5474: DNA326695, NM_022752,
 gen.NM_022752
 Figure 5475: PRO83041
 Figure 5476: DNA151808, NM_006494,
 gen.NM_006494
 Figure 5477: PRO12892
 Figure 5478: DNA326696, NM_001816,
 gen.NM_001816
 Figure 5479: PRO34151
 Figure 5480: DNA326697, NM_000554,
 gen.NM_000554
 Figure 5481: PRO83042
 Figure 5482: DNA326698, XM_049920,
 gen.XM_049920
 Figure 5483: DNA326699, XM_055859,
 gen.XM_055859
 Figure 5484A-B: DNA326700, XM_009125,
 gen.XM_009125
 Figure 5485: DNA326701, XM_008860,
 gen.XM_008860
 Figure 5486: DNA326702, XM_009036,
 gen.XM_009036
 Figure 5487: DNA326703, XM_085950,

gen.XM_085950
 Figure 5488: DNA326704, XM_028263,
 gen.XM_028263
 Figure 5489: DNA326705, XM_085928,
 gen.XM_085928
 Figure 5490: PRO36963
 Figure 5491: DNA326706, XM_028267,
 gen.XM_028267
 Figure 5492: DNA326707, NM_013403,
 gen.NM_013403
 Figure 5493: PRO83050
 Figure 5494: DNA103580, NM_001743,
 gen.NM_001743
 Figure 5495: PRO4904
 Figure 5496: DNA326708, XM_009126,
 gen.XM_009126
 Figure 5497: DNA326709, NM_006247,
 gen.NM_006247
 Figure 5498: PRO25881
 Figure 5499: DNA326710, NM_003370,
 gen.NM_003370
 Figure 5500: PRO83052
 Figure 5501: DNA326711, XM_085856,
 gen.XM_085856
 Figure 5502: DNA150784, NM_001983,
 gen.NM_001983
 Figure 5503: PRO12800
 Figure 5504: DNA270931, NM_012099,
 gen.NM_012099
 Figure 5505: PRO59264
 Figure 5506A-B: DNA257531, NM_031417,
 gen.NM_031417
 Figure 5507: PRO52101
 Figure 5508: DNA326712, NM_001294,
 gen.NM_001294
 Figure 5509: PRO83054
 Figure 5510: DNA326713, XM_097274,
 gen.XM_097274
 Figure 5511: DNA88084, NM_000041,
 gen.NM_000041
 Figure 5512: PRO2644
 Figure 5513: DNA256533, NM_006114,
 gen.NM_006114
 Figure 5514: PRO51565
 Figure 5515: DNA251057, NM_002856,
 gen.NM_002856
 Figure 5516: PRO47354
 Figure 5517: DNA226011, NM_005581,
 gen.NM_005581
 Figure 5518: PRO36474
 Figure 5519: DNA326714, NM_012116,
 gen.NM_012116
 Figure 5520: PRO83056
 Figure 5521: DNA326715, XM_097275,
 gen.XM_097275
 Figure 5522: DNA326716, XM_008851,

gen.XM_008851
Figure 5523: DNA274289, NM_016440,
gen.NM_016440
Figure 5524: PRO62212
Figure 5525: DNA326717, NM_012068,
gen.NM_012068
Figure 5526: PRO83059
Figure 5527: DNA326718, XM_085927,
gen.XM_085927
Figure 5528: DNA326719, XM_084023,
gen.XM_084023
Figure 5529: DNA326720, XM_167530,
gen.XM_167530
Figure 5530: DNA326721, XM_114025,
gen.XM_114025
Figure 5531: DNA326722, XM_008985,
gen.XM_008985
Figure 5532: DNA326723, NM_030973,
gen.NM_030973
Figure 5533: PRO83065
Figure 5534: DNA326724, NM_025129,
gen.NM_025129
Figure 5535: PRO83066
Figure 5536: DNA326725, NM_014203,
gen.NM_014203
Figure 5537: DNA326726, XM_085934,
gen.XM_085934
Figure 5538: PRO83068
Figure 5539: DNA326727, NM_001536,
gen.NM_001536
Figure 5540: PRO83069
Figure 5541: DNA326728, XM_165432,
gen.XM_165432
Figure 5542: DNA274823, NM_001571,
gen.NM_001571
Figure 5543: PRO62582
Figure 5544A-B: DNA326729, XM_046313,
gen.XM_046313
Figure 5545: PRO83071
Figure 5546: DNA326730, NM_015953,
gen.NM_015953
Figure 5547: PRO83072
Figure 5548: DNA326731, XM_027904,
gen.XM_027904
Figure 5549: DNA326732, XM_084026,
gen.XM_084026
Figure 5550: DNA290260, NM_012423,
gen.NM_012423
Figure 5551: PRO70385
Figure 5552: DNA326733, XM_058991,
gen.XM_058991
Figure 5553: PRO83073
Figure 5554: DNA326734, NM_017916,
gen.NM_017916
Figure 5555: PRO83074
Figure 5556: DNA326735, NM_003598,

gen.NM_003598
Figure 5557: PRO83075
Figure 5558: DNA326736, NM_006666,
gen.NM_006666
Figure 5559: PRO83076
Figure 5560: DNA326737, XM_114024,
gen.XM_114024
Figure 5561: PRO83077
Figure 5562: DNA304658, NM_000146,
gen.NM_000146
Figure 5563: PRO71085
Figure 5564: DNA326738, NM_004324,
gen.NM_004324
Figure 5565: PRO38101
Figure 5566: DNA326739, NM_006184,
gen.NM_006184
Figure 5567: PRO83078
Figure 5568: DNA273066, NM_001190,
gen.NM_001190
Figure 5569: PRO61129
Figure 5570: DNA326740, XM_058987,
gen.XM_058987
Figure 5571: DNA326741, NM_000979,
gen.NM_000979
Figure 5572: PRO83080
Figure 5573: DNA326742, XM_085935,
gen.XM_085935
Figure 5574: DNA326743, NM_031485,
gen.NM_031485
Figure 5575: PRO61308
Figure 5576: DNA103239, NM_006801,
gen.NM_006801
Figure 5577: PRO4569
Figure 5578: DNA326744, XM_046419,
gen.XM_046419
Figure 5579: PRO83082
Figure 5580: DNA326745, NM_002691,
gen.NM_002691
Figure 5581: PRO83083
Figure 5582: DNA326746, XM_056286,
gen.XM_056286
Figure 5583: PRO83084
Figure 5584: DNA326747, XM_058990,
gen.XM_058990
Figure 5585: PRO83085
Figure 5586: DNA326748, XM_091981,
gen.XM_091981
Figure 5587: PRO83086
Figure 5588: DNA326749, NM_032712,
gen.NM_032712
Figure 5589: PRO23238
Figure 5590: DNA83154, NM_001648,
gen.NM_001648
Figure 5591: PRO2109
Figure 5592: DNA326750, XM_055658,
gen.XM_055658

Figure 5593: DNA269481, NM_001985,
gen.NM_001985
Figure 5594: PRO57901
Figure 5595: DNA326751, XM_091886,
gen.XM_091886
Figure 5596: PRO83087
Figure 5597: DNA326752, XM_008830,
gen.XM_008830
Figure 5598: DNA326753, XM_039908,
gen.XM_039908
Figure 5599: PRO83089
Figure 5600: DNA326754, NM_015629,
gen.NM_015629
Figure 5601: PRO83090
Figure 5602: DNA326755, XM_050236,
gen.XM_050236
Figure 5603: DNA326756, XM_050589,
gen.XM_050589
Figure 5604: PRO83092
Figure 5605: DNA326757, XM_117128,
gen.XM_117128
Figure 5606: PRO83093
Figure 5607: DNA326758, XM_059321,
gen.XM_059321
Figure 5608: DNA326759, NM_003283,
gen.NM_003283
Figure 5609: PRO83095
Figure 5610A-B: DNA326760, NM_014931,
gen.NM_014931
Figure 5611: PRO83096
Figure 5612: DNA326761, XM_035919,
gen.XM_035919
Figure 5613: DNA326762, NM_000991,
gen.NM_000991
Figure 5614: PRO83098
Figure 5615: DNA273346, NM_014501,
gen.NM_014501
Figure 5616: PRO61349
Figure 5617: DNA326763, NM_013333,
gen.NM_013333
Figure 5618: PRO83099
Figure 5619: DNA326764, NM_007279,
gen.NM_007279
Figure 5620: PRO83100
Figure 5621: DNA326765, NM_016202,
gen.NM_016202
Figure 5622: PRO83101
Figure 5623: DNA326766, XM_034377,
gen.XM_034377
Figure 5624: PRO83102
Figure 5625: DNA272062, NM_014453,
gen.NM_014453
Figure 5626: PRO60333
Figure 5627: DNA254548, NM_005762,
gen.NM_005762
Figure 5628: PRO49653

Figure 5629: DNA326767, XM_085972,
gen.XM_085972
Figure 5630: PRO83103
Figure 5631: DNA326768, NM_032792,
gen.NM_032792
Figure 5632: PRO83104
Figure 5633: DNA326769, NM_001009,
gen.NM_001009
Figure 5634: PRO83105
Figure 5635: DNA326770, XM_058125,
gen.XM_058125
Figure 5636: DNA326771, NM_024691,
gen.NM_024691
Figure 5637: PRO83107
Figure 5638: DNA297288, NM_021158,
gen.NM_021158
Figure 5639: PRO70810
Figure 5640: DNA304662, NM_031229,
gen.NM_031229
Figure 5641: PRO71089
Figure 5642: DNA326772, NM_031228,
gen.NM_031228
Figure 5643: PRO83108
Figure 5644: DNA326773, XM_097749,
gen.XM_097749
Figure 5645: PRO83109
Figure 5646: DNA326774, XM_055993,
gen.XM_055993
Figure 5647: DNA326775, XM_009622,
gen.XM_009622
Figure 5648: DNA326776, NM_000801,
gen.NM_000801
Figure 5649: PRO59142
Figure 5650: DNA326777, NM_054014,
gen.NM_054014
Figure 5651: PRO59142
Figure 5652: DNA326778, NM_016143,
gen.NM_016143
Figure 5653: PRO83112
Figure 5654: DNA287270, NM_003091,
gen.NM_003091
Figure 5655: PRO69541
Figure 5656: DNA326779, NM_052881,
gen.NM_052881
Figure 5657: PRO83113
Figure 5658: DNA326780, XM_044914,
gen.XM_044914
Figure 5659: PRO83114
Figure 5660: DNA326781, XM_044915,
gen.XM_044915
Figure 5661: DNA326782, NM_006899,
gen.NM_006899
Figure 5662: PRO83116
Figure 5663: DNA326783, NM_019609,
gen.NM_019609
Figure 5664: PRO83117

Figure 5665: DNA326784, NM_021826, gen.NM_021826
Figure 5666: PRO83118
Figure 5667: DNA326785, XM_045418, gen.XM_045418
Figure 5668: DNA287261, NM_017874, gen.NM_017874
Figure 5669: PRO69533
Figure 5670: DNA326786, XM_086710, gen.XM_086710
Figure 5671: DNA326787, XM_045451, gen.XM_045451
Figure 5672: PRO83121
Figure 5673: DNA326788, XM_114174, gen.XM_114174
Figure 5674: DNA326789, XM_045460, gen.XM_045460
Figure 5675: DNA326790, XM_059268, gen.XM_059268
Figure 5676A-B: DNA271010, NM_014737, gen.NM_014737
Figure 5677: PRO59339
Figure 5678: DNA326791, XM_056035, gen.XM_056035
Figure 5679: DNA83170, NM_001819, gen.NM_001819
Figure 5680: PRO2615
Figure 5681: DNA227348, NM_019095, gen.NM_019095
Figure 5682: PRO37811
Figure 5683: DNA326792, NM_003092, gen.NM_003092
Figure 5684: PRO83125
Figure 5685: DNA287290, NM_014426, gen.NM_014426
Figure 5686: PRO69560
Figure 5687: DNA326793, XM_086701, gen.XM_086701
Figure 5688: DNA326794, XM_117209, gen.XM_117209
Figure 5689A-B: DNA326795, XM_046520, gen.XM_046520
Figure 5690: PRO83128
Figure 5691: DNA326796, XM_115846, gen.XM_115846
Figure 5692: PRO83129
Figure 5693: DNA326797, NM_080820, gen.NM_080820
Figure 5694: PRO83130
Figure 5695: DNA326798, XM_086715, gen.XM_086715
Figure 5696: DNA326799, XM_092760, gen.XM_092760
Figure 5697: PRO83132
Figure 5698: DNA326800, NM_012255, gen.NM_012255

Figure 5699: PRO83133
Figure 5700: DNA326801, XM_012970, gen.XM_012970
Figure 5701: DNA326802, XM_042765, gen.XM_042765
Figure 5702: PRO83135
Figure 5703: DNA150548, NM_001247, gen.NM_001247
Figure 5704: PRO12324
Figure 5705A-B: DNA326803, XM_009436, gen.XM_009436
Figure 5706: DNA326804, XM_114178, gen.XM_114178
Figure 5707: PRO83137
Figure 5708: DNA326805, XM_046160, gen.XM_046160
Figure 5709: PRO83138
Figure 5710: DNA326806, XM_046179, gen.XM_046179
Figure 5711: PRO83139
Figure 5712: DNA326807, XM_086745, gen.XM_086745
Figure 5713: DNA326808, NM_138578, gen.NM_138578
Figure 5714: PRO83141
Figure 5715: DNA326809, NM_012112, gen.NM_012112
Figure 5716: PRO83142
Figure 5717: DNA326810, XM_086736, gen.XM_086736
Figure 5718: PRO83143
Figure 5719: DNA326811, NM_030815, gen.NM_030815
Figure 5720: PRO83144
Figure 5721A-B: DNA150767, NM_014742, gen.NM_014742
Figure 5722: PRO12460
Figure 5723A-B: DNA326812, XM_047007, gen.XM_047007
Figure 5724: PRO83145
Figure 5725A-B: DNA326813, XM_047011, gen.XM_047011
Figure 5726: PRO83146
Figure 5727A-B: DNA326814, XM_047018, gen.XM_047018
Figure 5728: DNA326815, XM_009450, gen.XM_009450
Figure 5729: DNA326816, NM_033197, gen.NM_033197
Figure 5730: PRO83149
Figure 5731: DNA326817, XM_097772, gen.XM_097772
Figure 5732: PRO83150
Figure 5733: DNA326818, NM_016732, gen.NM_016732
Figure 5734: DNA97298, NM_003908,

gen.NM_003908
Figure 5735: PRO3645
Figure 5736: DNA326819, NM_000687,
gen.NM_000687
Figure 5737: PRO83152
Figure 5738: DNA273517, NM_000178,
gen.NM_000178
Figure 5739: PRO61498
Figure 5740: DNA326820, NM_018217,
gen.NM_018217
Figure 5741: PRO83153
Figure 5742: DNA326821, NM_002212,
gen.NM_002212
Figure 5743: PRO60945
Figure 5744A-C: DNA326822, NM_007186,
gen.NM_007186
Figure 5745: DNA226758, NM_015966,
gen.NM_015966
Figure 5746: PRO37221
Figure 5747: DNA194701, NM_003915,
gen.NM_003915
Figure 5748: PRO24002
Figure 5749: DNA326823, XM_113380,
gen.XM_113380
Figure 5750: DNA326824, NM_016558,
gen.NM_016558
Figure 5751: PRO83155
Figure 5752: DNA326825, NM_015511,
gen.NM_015511
Figure 5753: PRO83156
Figure 5754: DNA326826, XM_009501,
gen.XM_009501
Figure 5755: PRO83157
Figure 5756: DNA326827, XM_057236,
gen.XM_057236
Figure 5757: DNA326828, NM_024918,
gen.NM_024918
Figure 5758: PRO83159
Figure 5759: DNA326829, XM_009642,
gen.XM_009642
Figure 5760: DNA194807, NM_006698,
gen.NM_006698
Figure 5761: PRO24077
Figure 5762: DNA326830, XM_009686,
gen.XM_009686
Figure 5763: DNA326831, NM_030877,
gen.NM_030877
Figure 5764: PRO83161
Figure 5765: DNA326832, XM_028806,
gen.XM_028806
Figure 5766A-B: DNA326833, XM_028810,
gen.XM_028810
Figure 5767: PRO83163
Figure 5768: DNA326834, XM_012931,
gen.XM_012931
Figure 5769: DNA326835, NM_024855,

gen.NM_024855
Figure 5770: PRO83165
Figure 5771A-B: DNA227472, NM_002660,
gen.NM_002660
Figure 5772: PRO37935
Figure 5773: DNA326836, XM_097727,
gen.XM_097727
Figure 5774: DNA103525, NM_002466,
gen.NM_002466
Figure 5775: PRO4852
Figure 5776: DNA326837, XM_029810,
gen.XM_029810
Figure 5777: PRO83167
Figure 5778: DNA326838, XM_029822,
gen.XM_029822
Figure 5779: DNA326839, NM_002638,
gen.NM_002638
Figure 5780: PRO2065
Figure 5781: DNA326840, NM_003064,
gen.NM_003064
Figure 5782: PRO1720
Figure 5783: DNA326841, NM_015937,
gen.NM_015937
Figure 5784: PRO83169
Figure 5785: DNA273320, NM_007019,
gen.NM_007019
Figure 5786: PRO61327
Figure 5787: DNA326842, NM_033421,
gen.NM_033421
Figure 5788: PRO83170
Figure 5789: DNA88569, NM_006227,
gen.NM_006227
Figure 5790: PRO2420
Figure 5791: DNA88239, NM_004994,
gen.NM_004994
Figure 5792: PRO2711
Figure 5793: DNA326843, XM_057374,
gen.XM_057374
Figure 5794: DNA326844, XM_114163,
gen.XM_114163
Figure 5795A-B: DNA326845, XM_097731,
gen.XM_097731
Figure 5796A-B: DNA326846, XM_030044,
gen.XM_030044
Figure 5797: PRO83174
Figure 5798: DNA326847, NM_017895,
gen.NM_017895
Figure 5799: PRO83175
Figure 5800: DNA326848, XM_097713,
gen.XM_097713
Figure 5801: PRO83176
Figure 5802: DNA326849, NM_005985,
gen.NM_005985
Figure 5803: PRO83177
Figure 5804: DNA326850, NM_003349,
gen.NM_003349

Figure 5805: PRO83178
Figure 5806: DNA326851, NM_022442, gen.NM_022442
Figure 5807: PRO83179
Figure 5808: DNA326852, NM_005194, gen.NM_005194
Figure 5809: DNA326853, NM_002827, gen.NM_002827
Figure 5810: PRO38066
Figure 5811: DNA326854, NM_003859, gen.NM_003859
Figure 5812: PRO83180
Figure 5813: DNA326855, XM_114165, gen.XM_114165
Figure 5814: DNA269526, NM_001324, gen.NM_001324
Figure 5815: PRO57942
Figure 5816: DNA326856, XM_009549, gen.XM_009549
Figure 5817: PRO83182
Figure 5818: DNA326857, XM_030621, gen.XM_030621
Figure 5819: DNA326858, XM_086648, gen.XM_086648
Figure 5820: PRO83183
Figure 5821: DNA326859, XM_009672, gen.XM_009672
Figure 5822: PRO83184
Figure 5823A-B: DNA326860, XM_009671, gen.XM_009671
Figure 5824: DNA326861, NM_004738, gen.NM_004738
Figure 5825: PRO983
Figure 5826: DNA326862, NM_016592, gen.NM_016592
Figure 5827: PRO83185
Figure 5828: DNA326863, NM_080425, gen.NM_080425
Figure 5829: PRO83186
Figure 5830: DNA304670, NM_000516, gen.NM_000516
Figure 5831: PRO71097
Figure 5832: DNA326864, NM_080426, gen.NM_080426
Figure 5833: PRO83187
Figure 5834: DNA326865, XM_030699, gen.XM_030699
Figure 5835: PRO83188
Figure 5836: DNA188229, NM_000114, gen.NM_000114
Figure 5837: PRO21728
Figure 5838: DNA326866, NM_002792, gen.NM_002792
Figure 5839: PRO83189
Figure 5840A-B: DNA326867, XM_037202, gen.XM_037202

Figure 5841: PRO83190
Figure 5842: DNA326868, XM_037206, gen.XM_037206
Figure 5843: PRO83191
Figure 5844: DNA103486, NM_007002, gen.NM_007002
Figure 5845: PRO4813
Figure 5846A-D: DNA326869, XM_037217, gen.XM_037217
Figure 5847: DNA326870, NM_001024, gen.NM_001024
Figure 5848: PRO83193
Figure 5849: DNA326871, NM_018270, gen.NM_018270
Figure 5850: PRO83194
Figure 5851: DNA326872, XM_028783, gen.XM_028783
Figure 5852: PRO83195
Figure 5853: DNA326873, NM_001853, gen.NM_001853
Figure 5854: PRO83196
Figure 5855: DNA326874, NM_080796, gen.NM_080796
Figure 5856: PRO83197
Figure 5857: DNA326875, NM_022105, gen.NM_022105
Figure 5858: PRO83198
Figure 5859: DNA326876, NM_080797, gen.NM_080797
Figure 5860: PRO83199
Figure 5861: DNA326877, NM_018209, gen.NM_018209
Figure 5862: PRO83200
Figure 5863A-C: DNA326878, XM_028834, gen.XM_028834
Figure 5864: PRO83201
Figure 5865: DNA326879, NM_024299, gen.NM_024299
Figure 5866: PRO83202
Figure 5867A-C: DNA326880, XM_028918, gen.XM_028918
Figure 5868: PRO83203
Figure 5869: DNA326881, NM_032527, gen.NM_032527
Figure 5870: PRO83204
Figure 5871A-B: DNA326882, XM_028966, gen.XM_028966
Figure 5872: PRO83205
Figure 5873: DNA269746, NM_012469, gen.NM_012469
Figure 5874: PRO58155
Figure 5875: DNA326883, XM_114154, gen.XM_114154
Figure 5876: DNA326884, XM_072173, gen.XM_072173
Figure 5877: DNA326885, XM_086759,

gen.XM_086759
 Figure 5878: DNA326886, XM_086760,
 gen.XM_086760
 Figure 5879: DNA326887, NM_021219,
 gen.NM_021219
 Figure 5880: PRO28687
 Figure 5881: DNA188732, NM_000484,
 gen.NM_000484
 Figure 5882: PRO25302
 Figure 5883: DNA326888, NM_016940,
 gen.NM_016940
 Figure 5884: PRO83210
 Figure 5885: DNA254572, NM_006585,
 gen.NM_006585
 Figure 5886: PRO49675
 Figure 5887: DNA326889, NM_005806,
 gen.NM_005806
 Figure 5888: PRO83211
 Figure 5889: DNA326890, XM_114185,
 gen.XM_114185
 Figure 5890: DNA254994, NM_017613,
 gen.NM_017613
 Figure 5891: PRO50083
 Figure 5892: DNA274129, NM_001697,
 gen.NM_001697
 Figure 5893: PRO62065
 Figure 5894: DNA326891, NM_001757,
 gen.NM_001757
 Figure 5895: PRO83212
 Figure 5896A-C: DNA151898, NM_003316,
 gen.NM_003316
 Figure 5897: PRO12135
 Figure 5898: DNA326892, NM_003720,
 gen.NM_003720
 Figure 5899: PRO83213
 Figure 5900: DNA326893, NM_002606,
 gen.NM_002606
 Figure 5901: PRO83214
 Figure 5902: DNA326894, XM_033015,
 gen.XM_033015
 Figure 5903: DNA326895, XM_033016,
 gen.XM_033016
 Figure 5904: PRO59669
 Figure 5905: DNA326896, NM_003681,
 gen.NM_003681
 Figure 5906: PRO69486
 Figure 5907: DNA326897, XM_035999,
 gen.XM_035999
 Figure 5908: DNA326898, NM_020132,
 gen.NM_020132
 Figure 5909: PRO83217
 Figure 5910: DNA326899, XM_036011,
 gen.XM_036011
 Figure 5911: DNA326900, NM_013369,
 gen.NM_013369
 Figure 5912: PRO83219

Figure 5913: DNA326901, XM_036042,
 gen.XM_036042
 Figure 5914: DNA326902, XM_086770,
 gen.XM_086770
 Figure 5915: DNA326903, NM_004928,
 gen.NM_004928
 Figure 5916: PRO83222
 Figure 5917: DNA326904, XM_036087,
 gen.XM_036087
 Figure 5918: PRO83223
 Figure 5919: DNA326905, XM_009805,
 gen.XM_009805
 Figure 5920: PRO83224
 Figure 5921: DNA226409, NM_004339,
 gen.NM_004339
 Figure 5922: PRO36872
 Figure 5923: DNA326906, XM_036107,
 gen.XM_036107
 Figure 5924A-B: DNA326907, XM_036175,
 gen.XM_036175
 Figure 5925: DNA326908, XM_097817,
 gen.XM_097817
 Figure 5926A-B: DNA326909, XM_054566,
 gen.XM_054566
 Figure 5927: DNA326910, XM_036755,
 gen.XM_036755
 Figure 5928: DNA326911, XM_086773,
 gen.XM_086773
 Figure 5929: DNA326912, XM_097807,
 gen.XM_097807
 Figure 5930: DNA326913, XM_086777,
 gen.XM_086777
 Figure 5931: DNA326914, NM_002340,
 gen.NM_002340
 Figure 5932: PRO83233
 Figure 5933A-B: DNA326915, NM_003906,
 gen.NM_003906
 Figure 5934: PRO83234
 Figure 5935: DNA226617, NM_006272,
 gen.NM_006272
 Figure 5936: PRO37080
 Figure 5937: DNA326916, NM_033070,
 gen.NM_033070
 Figure 5938: PRO83235
 Figure 5939: DNA255046, NM_017829,
 gen.NM_017829
 Figure 5940: PRO50134
 Figure 5941: DNA326917, NM_001696,
 gen.NM_001696
 Figure 5942: PRO83236
 Figure 5943A-B: DNA326918, XM_032996,
 gen.XM_032996
 Figure 5944: PRO83237
 Figure 5945: DNA326919, XM_167538,
 gen.XM_167538
 Figure 5946: DNA326920, XM_033090,

gen.XM_033090
Figure 5947: DNA225954, NM_000407,
gen.NM_000407
Figure 5948: PRO36417
Figure 5949: DNA326921, XM_058918,
gen.XM_058918
Figure 5950: DNA326922, XM_097833,
gen.XM_097833
Figure 5951: DNA326923, NM_024627,
gen.NM_024627
Figure 5952: PRO83242
Figure 5953: DNA326924, XM_086809,
gen.XM_086809
Figure 5954: DNA326925, NM_006440,
gen.NM_006440
Figure 5955: PRO83244
Figure 5956: DNA226561, NM_000754,
gen.NM_000754
Figure 5957: PRO37024
Figure 5958: DNA326926, NM_007310,
gen.NM_007310
Figure 5959: PRO83245
Figure 5960A-B: DNA326927, XM_033813,
gen.XM_033813
Figure 5961: DNA326928, NM_022727,
gen.NM_022727
Figure 5962: PRO83247
Figure 5963: DNA326929, XM_086805,
gen.XM_086805
Figure 5964: DNA326930, XM_086873,
gen.XM_086873
Figure 5965: DNA257549, NM_030573,
gen.NM_030573
Figure 5966: PRO52119
Figure 5967: DNA326931, XM_096155,
gen.XM_096155
Figure 5968: DNA326932, XM_096156,
gen.XM_096156
Figure 5969A-B: DNA326933, XM_036937,
gen.XM_036937
Figure 5970: PRO83252
Figure 5971: DNA326934, XM_097886,
gen.XM_097886
Figure 5972: PRO83253
Figure 5973: DNA304835, NM_022044,
gen.NM_022044
Figure 5974: PRO71242
Figure 5975: DNA326935, NM_006115,
gen.NM_006115
Figure 5976: PRO37012
Figure 5977: DNA326936, XM_037682,
gen.XM_037682
Figure 5978: PRO83254
Figure 5979: DNA326937, NM_002415,
gen.NM_002415
Figure 5980: PRO83255

Figure 5981A-B: DNA326938, XM_037797,
gen.XM_037797
Figure 5982: PRO83256
Figure 5983: DNA326939, NM_004175,
gen.NM_004175
Figure 5984: PRO83257
Figure 5985: DNA326940, XM_086821,
gen.XM_086821
Figure 5986: DNA326941, XM_092888,
gen.XM_092888
Figure 5987: DNA326942, NM_005080,
gen.NM_005080
Figure 5988: PRO83260
Figure 5989: DNA269830, NM_005243,
gen.NM_005243
Figure 5990: PRO58232
Figure 5991: DNA326943, NM_006478,
gen.NM_006478
Figure 5992: PRO83261
Figure 5993A-B: DNA326944, XM_037945,
gen.XM_037945
Figure 5994: DNA103462, NM_000268,
gen.NM_000268
Figure 5995: PRO4789
Figure 5996: DNA326945, NM_032204,
gen.NM_032204
Figure 5997: PRO83263
Figure 5998: DNA326946, XM_066291,
gen.XM_066291
Figure 5999: DNA326947, NM_005877,
gen.NM_005877
Figure 6000: PRO62328
Figure 6001: DNA326948, NM_016498,
gen.NM_016498
Figure 6002: PRO83265
Figure 6003: DNA254141, NM_014303,
gen.NM_014303
Figure 6004: PRO49256
Figure 6005A-B: DNA151882, NM_014941,
gen.NM_014941
Figure 6006: PRO12134
Figure 6007: DNA326949, NM_006932,
gen.NM_006932
Figure 6008: PRO83266
Figure 6009: DNA326950, NM_134269,
gen.NM_134269
Figure 6010: PRO83267
Figure 6011: DNA270697, NM_004147,
gen.NM_004147
Figure 6012: PRO59061
Figure 6013: DNA326951, XM_059335,
gen.XM_059335
Figure 6014: DNA326952, XM_018539,
gen.XM_018539
Figure 6015: DNA326953, NM_014306,
gen.NM_014306

Figure 6016: PRO83270
Figure 6017: DNA326954, NM_012179,
gen.NM_012179
Figure 6018: PRO83271
Figure 6019A-B: DNA326955, XM_038584,
gen.XM_038584
Figure 6020: DNA151752, NM_002133,
gen.NM_002133
Figure 6021: PRO12886
Figure 6022: DNA326956, XM_009947,
gen.XM_009947
Figure 6023: PRO12845
Figure 6024: DNA326957, XM_114209,
gen.XM_114209
Figure 6025A-B: DNA326958, NM_002473,
gen.NM_002473
Figure 6026: PRO83273
Figure 6027: DNA188740, NM_003753,
gen.NM_003753
Figure 6028: PRO22481
Figure 6029: DNA326959, NM_021126,
gen.NM_021126
Figure 6030: PRO70331
Figure 6031: DNA326960, XM_009967,
gen.XM_009967
Figure 6032: DNA326961, NM_013365,
gen.NM_013365
Figure 6033: PRO83274
Figure 6034: DNA290259, NM_018957,
gen.NM_018957
Figure 6035: PRO70383
Figure 6036: DNA326962, NM_020315,
gen.NM_020315
Figure 6037: PRO83275
Figure 6038: DNA304719, NM_002305,
gen.NM_002305
Figure 6039: PRO71145
Figure 6040: DNA326963, NM_007032,
gen.NM_007032
Figure 6041: PRO83276
Figure 6042: DNA326964, XM_009973,
gen.XM_009973
Figure 6043: DNA326965, XM_086830,
gen.XM_086830
Figure 6044: PRO83278
Figure 6045: DNA254240, NM_016091,
gen.NM_016091
Figure 6046: PRO49352
Figure 6047A-B: DNA326966, XM_039236,
gen.XM_039236
Figure 6048: PRO83279
Figure 6049: DNA326967, NM_006941,
gen.NM_006941
Figure 6050: PRO83280
Figure 6051: DNA326968, XM_039248,
gen.XM_039248

Figure 6052: DNA326969, NM_012323,
gen.NM_012323
Figure 6053: PRO83282
Figure 6054: DNA326970, NM_012264,
gen.NM_012264
Figure 6055: PRO12490
Figure 6056: DNA326971, NM_015373,
gen.NM_015373
Figure 6057: PRO83283
Figure 6058: DNA326972, NM_020243,
gen.NM_020243
Figure 6059: PRO23231
Figure 6060: DNA326973, XM_039339,
gen.XM_039339
Figure 6061: DNA326974, NM_000967,
gen.NM_000967
Figure 6062: PRO83285
Figure 6063: DNA326975, XM_010000,
gen.XM_010000
Figure 6064: DNA326976, XM_010002,
gen.XM_010002
Figure 6065: DNA326977, XM_039372,
gen.XM_039372
Figure 6066: DNA326978, XM_013010,
gen.XM_013010
Figure 6067: PRO83288
Figure 6068: DNA254165, NM_000026,
gen.NM_000026
Figure 6069: PRO49278
Figure 6070: DNA326979, NM_003932,
gen.NM_003932
Figure 6071: PRO4586
Figure 6072: DNA326980, NM_014248,
gen.NM_014248
Figure 6073: PRO83289
Figure 6074: DNA326981, XM_086844,
gen.XM_086844
Figure 6075: DNA219225, NM_002883,
gen.NM_002883
Figure 6076: PRO34531
Figure 6077: DNA326982, NM_003216,
gen.NM_003216
Figure 6078: PRO83291
Figure 6079: DNA270954, NM_001098,
gen.NM_001098
Figure 6080: PRO59285
Figure 6081: DNA326983, NM_001469,
gen.NM_001469
Figure 6082: PRO4872
Figure 6083: DNA326984, NM_005008,
gen.NM_005008
Figure 6084: PRO83292
Figure 6085A-B: DNA326985, NM_004599,
gen.NM_004599
Figure 6086: PRO83293
Figure 6087A-B: DNA326986, XM_010024,

gen.XM_010024
Figure 6088: DNA326987, XM_040066,
gen.XM_040066
Figure 6089: DNA326988, XM_013015,
gen.XM_013015
Figure 6090A-B: DNA326989, XM_084084,
gen.XM_084084
Figure 6091: DNA326990, XM_040095,
gen.XM_040095
Figure 6092: PRO83297
Figure 6093: DNA326991, XM_086875,
gen.XM_086875
Figure 6094: DNA326992, XM_010029,
gen.XM_010029
Figure 6095: DNA326993, NM_007311,
gen.NM_007311
Figure 6096: PRO83300
Figure 6097: DNA326994, NM_015140,
gen.NM_015140
Figure 6098: PRO83301
Figure 6099: DNA326995, XM_043614,
gen.XM_043614
Figure 6100: PRO83302
Figure 6101: DNA256070, NM_022141,
gen.NM_022141
Figure 6102: PRO51119
Figure 6103: DNA326996, XM_010040,
gen.XM_010040
Figure 6104: DNA237931, NM_005036,
gen.NM_005036
Figure 6105: PRO39030
Figure 6106A-B: DNA326997, XM_027143,
gen.XM_027143
Figure 6107: PRO83304
Figure 6108A-B: DNA326998, XM_010055,
gen.XM_010055
Figure 6109: DNA326999, NM_025204,
gen.NM_025204
Figure 6110: PRO83306
Figure 6111: DNA327000, XM_041248,
gen.XM_041248
Figure 6112: PRO83307
Figure 6113: DNA327001, XM_092966,
gen.XM_092966
Figure 6114: DNA327002, XM_037468,
gen.XM_037468
Figure 6115: PRO83309
Figure 6116: DNA327003, XM_037474,
gen.XM_037474
Figure 6117: PRO83310
Figure 6118: DNA327004, XM_013029,
gen.XM_013029
Figure 6119: DNA327005, XM_114724,
gen.XM_114724
Figure 6120: PRO83312
Figure 6121: DNA327006, XM_115924,

gen.XM_115924
Figure 6122: DNA327007, XM_113585,
gen.XM_113585
Figure 6123A-C: DNA327008, XM_035465,
gen.XM_035465
Figure 6124: DNA327009, NM_002414,
gen.NM_002414
Figure 6125: PRO2373
Figure 6126: DNA269793, NM_005333,
gen.NM_005333
Figure 6127: PRO58198
Figure 6128: DNA327010, XM_088747,
gen.XM_088747
Figure 6129: PRO83316
Figure 6130: DNA327011, XM_114720,
gen.XM_114720
Figure 6131: DNA327012, XM_115886,
gen.XM_115886
Figure 6132: DNA327013, XM_010272,
gen.XM_010272
Figure 6133: PRO83319
Figure 6134: DNA327014, NM_006746,
gen.NM_006746
Figure 6135: PRO83320
Figure 6136: DNA327015, XM_115890,
gen.XM_115890
Figure 6137: PRO83321
Figure 6138: DNA327016, NM_000284,
gen.NM_000284
Figure 6139: PRO59441
Figure 6140: DNA327017, NM_004595,
gen.NM_004595
Figure 6141: PRO61744
Figure 6142: DNA327018, XM_166078,
gen.XM_166078
Figure 6143: DNA327019, NM_001415,
gen.NM_001415
Figure 6144: PRO83323
Figure 6145: DNA327020, XM_013086,
gen.XM_013086
Figure 6146: DNA327021, XM_060030,
gen.XM_060030
Figure 6147: DNA227689, NM_002364,
gen.NM_002364
Figure 6148: PRO38152
Figure 6149: DNA274829, NM_003662,
gen.NM_003662
Figure 6150: PRO62588
Figure 6151: DNA327022, XM_088619,
gen.XM_088619
Figure 6152: DNA327023, XM_088622,
gen.XM_088622
Figure 6153A-B: DNA327024, XM_084288,
gen.XM_084288
Figure 6154: PRO59168
Figure 6155: DNA327025, XM_054221,

gen.XM_054221
Figure 6156: PRO83328
Figure 6157: DNA327026, XM_018019,
gen.XM_018019
Figure 6158: DNA327027, XM_088665,
gen.XM_088665
Figure 6159: DNA327028, NM_005300,
gen.NM_005300
Figure 6160: PRO37083
Figure 6161: DNA327029, XM_018241,
gen.XM_018241
Figure 6162: PRO83331
Figure 6163: DNA327030, NM_014138,
gen.NM_014138
Figure 6164: PRO83332
Figure 6165: DNA327031, NM_005676,
gen.NM_005676
Figure 6166: PRO83333
Figure 6167: DNA327032, NM_003334,
gen.NM_003334
Figure 6168: PRO83334
Figure 6169: DNA327033, XM_010378,
gen.XM_010378
Figure 6170: DNA327034, XM_033884,
gen.XM_033884
Figure 6171: PRO83335
Figure 6172: DNA327035, XM_033878,
gen.XM_033878
Figure 6173: DNA327036, XM_033862,
gen.XM_033862
Figure 6174: DNA327037, NM_004182,
gen.NM_004182
Figure 6175: PRO83337
Figure 6176: DNA327038, XM_047032,
gen.XM_047032
Figure 6177: DNA327039, XM_047024,
gen.XM_047024
Figure 6178: PRO83339
Figure 6179: DNA327040, NM_017883,
gen.NM_017883
Figure 6180: PRO83340
Figure 6181: DNA238039, NM_005710,
gen.NM_005710
Figure 6182: PRO39127
Figure 6183: DNA327041, XM_054098,
gen.XM_054098
Figure 6184: PRO83341
Figure 6185: DNA327042, NM_002668,
gen.NM_002668
Figure 6186: PRO34584
Figure 6187: DNA271580, NM_014008,
gen.NM_014008
Figure 6188: PRO59868
Figure 6189A-B: DNA327043, XM_032930,
gen.XM_032930
Figure 6190: DNA273992, NM_004493,

gen.NM_004493
Figure 6191: PRO61938
Figure 6192A-B: DNA327044, XM_050403,
gen.XM_050403
Figure 6193: PRO83343
Figure 6194: DNA327045, XM_029187,
gen.XM_029187
Figure 6195: PRO83344
Figure 6196: DNA327046, XM_013060,
gen.XM_013060
Figure 6197: DNA227943, NM_006787,
gen.NM_006787
Figure 6198: PRO38406
Figure 6199: DNA327047, NM_014481,
gen.NM_014481
Figure 6200: PRO83345
Figure 6201: DNA327048, XM_034935,
gen.XM_034935
Figure 6202: PRO83346
Figure 6203: DNA327049, XM_084287,
gen.XM_084287
Figure 6204: DNA327050, NM_007268,
gen.NM_007268
Figure 6205: PRO34043
Figure 6206: DNA327051, XM_015516,
gen.XM_015516
Figure 6207A-B: DNA327052, XM_013042,
gen.XM_013042
Figure 6208: PRO83349
Figure 6209: DNA327053, XM_088630,
gen.XM_088630
Figure 6210: DNA327054, NM_031206,
gen.NM_031206
Figure 6211: PRO83351
Figure 6212: DNA327055, XM_093050,
gen.XM_093050
Figure 6213: PRO83352
Figure 6214A-B: DNA225721, NM_018977,
gen.NM_018977
Figure 6215: PRO36184
Figure 6216: DNA327056, XM_010141,
gen.XM_010141
Figure 6217: PRO38021
Figure 6218: DNA327057, XM_088689,
gen.XM_088689
Figure 6219: PRO83353
Figure 6220: DNA327058, XM_088688,
gen.XM_088688
Figure 6221: PRO83354
Figure 6222: DNA327059, NM_018486,
gen.NM_018486
Figure 6223: PRO83355
Figure 6224: DNA327060, NM_001007,
gen.NM_001007
Figure 6225: PRO42022
Figure 6226: DNA327061, XM_093130,

gen.XM_093130
Figure 6227: DNA327062, XM_084296,
gen.XM_084296
Figure 6228: DNA327063, XM_093241,
gen.XM_093241
Figure 6229: DNA327064, XM_084283,
gen.XM_084283
Figure 6230: DNA273254, NM_000291,
gen.NM_000291
Figure 6231: PRO61271
Figure 6232: DNA327065, XM_018142,
gen.XM_018142
Figure 6233: DNA327066, XM_030373,
gen.XM_030373
Figure 6234: PRO83360
Figure 6235: DNA327067, XM_165533,
gen.XM_165533
Figure 6236: PRO83361
Figure 6237: DNA327068, XM_051476,
gen.XM_051476
Figure 6238: DNA327069, XM_051471,
gen.XM_051471
Figure 6239: DNA270496, NM_001325,
gen.NM_001325
Figure 6240: PRO58875
Figure 6241: DNA327070, XM_033147,
gen.XM_033147
Figure 6242: DNA327071, NM_004085,
gen.NM_004085
Figure 6243: PRO59022
Figure 6244: DNA327072, NM_021029,
gen.NM_021029
Figure 6245: PRO10723
Figure 6246: DNA327073, NM_012286,
gen.NM_012286
Figure 6247: PRO83365
Figure 6248: DNA327074, NM_024863,
gen.NM_024863
Figure 6249: PRO83366
Figure 6250: DNA327075, XM_043643,
gen.XM_043643
Figure 6251: DNA327076, NM_052936,
gen.NM_052936
Figure 6252: PRO83368
Figure 6253: DNA327077, XM_088710,
gen.XM_088710
Figure 6254: PRO83369
Figure 6255: DNA327078, XM_166081,
gen.XM_166081
Figure 6256: DNA327079, XM_096303,
gen.XM_096303
Figure 6257: DNA254785, NM_032227,
gen.NM_032227
Figure 6258: PRO49883
Figure 6259: DNA327080, XM_115923,
gen.XM_115923

Figure 6260: PRO83372
Figure 6261: DNA327081, XM_066900,
gen.XM_066900
Figure 6262: PRO83373
Figure 6263: DNA327082, XM_104983,
gen.XM_104983
Figure 6264: PRO83374
Figure 6265: DNA327083, XM_088736,
gen.XM_088736
Figure 6266: PRO83375
Figure 6267: DNA327084, XM_088738,
gen.XM_088738
Figure 6268: DNA327085, XM_088739,
gen.XM_088739
Figure 6269: DNA327086, XM_010117,
gen.XM_010117
Figure 6270A-B: DNA76504, NM_001560,
gen.NM_001560
Figure 6271: PRO2537
Figure 6272: DNA227181, NM_006667,
gen.NM_006667
Figure 6273: PRO37644
Figure 6274: DNA327087, XM_010362,
gen.XM_010362
Figure 6275: DNA327088, XM_016125,
gen.XM_016125
Figure 6276: DNA327089, NM_015129,
gen.NM_015129
Figure 6277: PRO83381
Figure 6278: DNA327090, NM_001000,
gen.NM_001000
Figure 6279: PRO10935
Figure 6280: DNA327091, XM_010436,
gen.XM_010436
Figure 6281: DNA327092, XM_115874,
gen.XM_115874
Figure 6282: DNA327093, XM_029461,
gen.XM_029461
Figure 6283: PRO83383
Figure 6284: DNA327094, XM_017930,
gen.XM_017930
Figure 6285: DNA227656, NM_004208,
gen.NM_004208
Figure 6286: PRO38119
Figure 6287: DNA273487, NM_004794,
gen.NM_004794
Figure 6288: PRO61470
Figure 6289: DNA327095, XM_088745,
gen.XM_088745
Figure 6290: PRO83385
Figure 6291: DNA327096, XM_114708,
gen.XM_114708
Figure 6292: PRO83386
Figure 6293: DNA327097, NM_016267,
gen.NM_016267
Figure 6294: PRO83387

Figure 6295A-B: DNA327098, XM_042963,
gen.XM_042963
Figure 6296: PRO83388
Figure 6297: DNA327099, XM_042968,
gen.XM_042968
Figure 6298: PRO83389
Figure 6299: DNA327100, XM_093219,
gen.XM_093219
Figure 6300: DNA327101, NM_016249,
gen.NM_016249
Figure 6301: PRO83391
Figure 6302: DNA327102, XM_098995,
gen.XM_098995
Figure 6303: PRO83392
Figure 6304: DNA327103, XM_041921,
gen.XM_041921
Figure 6305: PRO83393
Figure 6306: DNA327104, XM_048905,
gen.XM_048905
Figure 6307: PRO83394
Figure 6308: DNA327105, NM_005364,
gen.NM_005364
Figure 6309: PRO83395
Figure 6310: DNA327106, XM_010178,
gen.XM_010178
Figure 6311: DNA327107, XM_088592,
gen.XM_088592
Figure 6312: PRO25245
Figure 6313: DNA327108, XM_018108,
gen.XM_018108
Figure 6314: PRO83397
Figure 6315: DNA327109, XM_018109,
gen.XM_018109
Figure 6316: DNA327110, NM_005362,
gen.NM_005362
Figure 6317: PRO24021
Figure 6318: DNA254783, NM_001363,
gen.NM_001363
Figure 6319: PRO49881
Figure 6320: DNA327111, XM_049337,
gen.XM_049337
Figure 6321: DNA227917, NM_019848,
gen.NM_019848
Figure 6322: PRO38380
Figure 6323: DNA327112, NM_004699,
gen.NM_004699
Figure 6324: PRO83400
Figure 6325: DNA327113, XM_048420,
gen.XM_048420
Figure 6326: DNA327114, NM_006013,

gen.NM_006013
Figure 6327: PRO62466
Figure 6328: DNA327115, XM_048410,
gen.XM_048410
Figure 6329A-C: DNA327116, XM_048404,
gen.XM_048404
Figure 6330A-C: DNA327117, NM_004992,
gen.NM_004992
Figure 6331: PRO83403
Figure 6332: DNA227013, NM_001569,
gen.NM_001569
Figure 6333: PRO37476
Figure 6334A-B: DNA225800, NM_000425,
gen.NM_000425
Figure 6335: PRO36263
Figure 6336A-B: DNA327118, NM_024003,
gen.NM_024003
Figure 6337: PRO83404
Figure 6338: DNA225655, NM_006280,
gen.NM_006280
Figure 6339: PRO36118
Figure 6340: DNA276159, NM_004135,
gen.NM_004135
Figure 6341: PRO63299
Figure 6342A-B: DNA230792, NM_000033,
gen.NM_000033
Figure 6343: PRO38730
Figure 6344: DNA103558, NM_005745,
gen.NM_005745
Figure 6345: PRO4885
Figure 6346: DNA327119, XM_042155,
gen.XM_042155
Figure 6347: PRO83405
Figure 6348: DNA327120, XM_042153,
gen.XM_042153
Figure 6349: DNA327121, XM_117555,
gen.XM_117555
Figure 6350: DNA327122, XM_084311,
gen.XM_084311
Figure 6351: DNA327123, XM_033232,
gen.XM_033232
Figure 6352: DNA327124, XM_117539,
gen.XM_117539
Figure 6353: DNA327125, XM_027952,
gen.XM_027952
Figure 6354: DNA327126, XM_114692,
gen.XM_114692
Figure 6355A-B: DNA327127, XM_165530,
gen.XM_165530

DNA Index (to Figure number)

DNA0, 1188	DNA171408, 48
DNA103214, 218	DNA188229, 5836
DNA103217, 649	DNA188351, 4782
DNA103239, 5576	DNA188396, 3480
DNA103253, 188	DNA188732, 5882
DNA103320, 5272	DNA188740, 6027
DNA103380, 1677	DNA188748, 146
DNA103401, 4708	DNA189315, 167
DNA103421, 2982	DNA189687, 3297
DNA103436, 457	DNA189697, 998
DNA103462, 5994	DNA189703, 4568
DNA103471, 2070	DNA193882, 585
DNA103474, 3313	DNA193955, 2193
DNA103486, 5844	DNA193957, 2947
DNA103505, 1149	DNA194600, 428
DNA103506, 2990	DNA194701, 5747
DNA103509, 4110	DNA194740, 854
DNA103514, 3478	DNA194805, 4530
DNA103525, 5774	DNA194807, 5760
DNA103558, 6344	DNA194827, 977
DNA103580, 5494	DNA196344, 576
DNA103588, 2274	DNA196349, 124
DNA103593, 711	DNA196351, 3600
DNA129504, 4985	DNA196642, 4877
DNA131588, 2593	DNA210134, 367
DNA137231, 3667	DNA210180, 3962
DNA139747, 1368	DNA218271, 5258
DNA144601, 3051	DNA218841, 2782
DNA150457, 4936	DNA219225, 6075
DNA150485, 4305	DNA219233, 4182
DNA150548, 5703	DNA225584, 1489
DNA150562, 1153	DNA225592, 1330
DNA150679, 1732	DNA225630, 2767
DNA150725, 806	DNA225631, 2174
DNA150767, 5721	DNA225632, 3473
DNA150772, 2034	DNA225649, 4042
DNA150784, 5502	DNA225655, 6338
DNA150814, 4953	DNA225671, 2506
DNA150884, 1024	DNA225721, 6214
DNA150974, 3204	DNA225752, 3376
DNA150976, 1145	DNA225800, 6334
DNA150978, 3520	DNA225809, 356
DNA150997, 3526	DNA225865, 3976
DNA151010, 2546	DNA225909, 1828
DNA151017, 1066	DNA225910, 1128
DNA151148, 44	DNA225919, 1446
DNA151752, 6020	DNA225920, 1511
DNA151808, 5476	DNA225921, 1515
DNA151827, 3466	DNA225954, 5947
DNA151831, 4141	DNA226005, 553
DNA151882, 6005	DNA226011, 5517
DNA151893, 4079	DNA226014, 3729
DNA151898, 5896	DNA226028, 3489

DNA226080, 3206
DNA226105, 3992
DNA226125, 409
DNA226217, 3004
DNA226260, 271
DNA226262, 105
DNA226324, 4095
DNA226337, 2458
DNA226345, 2670
DNA226389, 4820
DNA226409, 5921
DNA226416, 2262
DNA226418, 1791
DNA226428, 741
DNA226496, 2565
DNA226547, 1108
DNA226560, 2393
DNA226561, 5956
DNA226617, 5935
DNA226619, 474
DNA226646, 4224
DNA226758, 5745
DNA226771, 3498
DNA226793, 436
DNA226853, 3866
DNA226872, 1689
DNA227013, 6332
DNA227055, 4939
DNA227071, 4889
DNA227084, 4742
DNA227088, 3220
DNA227092, 3593
DNA227094, 3628
DNA227165, 684
DNA227171, 3724
DNA227172, 2964
DNA227173, 1573
DNA227181, 6272
DNA227190, 814
DNA227191, 3588
DNA227204, 1886
DNA227206, 4170
DNA227213, 157
DNA227234, 4626
DNA227246, 550
DNA227249, 5352
DNA227267, 2512
DNA227268, 2242
DNA227280, 5232
DNA227307, 1165
DNA227320, 1812
DNA227321, 3984
DNA227348, 5681
DNA227442, 1942
DNA227472, 5771
DNA227474, 3720

DNA227491, 2691
DNA227504, 594
DNA227509, 3076
DNA227528, 803
DNA227529, 346
DNA227545, 698
DNA227559, 4161
DNA227575, 1508
DNA227577, 374
DNA227607, 1961
DNA227656, 6285
DNA227689, 6147
DNA227764, 4891
DNA227795, 792
DNA227821, 36
DNA227873, 4841
DNA227917, 6321
DNA227924, 2099
DNA227929, 2206
DNA227943, 6197
DNA230792, 6342
DNA234442, 4214
DNA237931, 6104
DNA238039, 6181
DNA247474, 578
DNA247595, 2182
DNA251057, 5515
DNA252367, 1081
DNA253804, 1370
DNA254141, 6003
DNA254147, 1627
DNA254165, 6068
DNA254186, 3329
DNA254198, 4719
DNA254204, 994
DNA254240, 6045
DNA254298, 499
DNA254346, 603
DNA254532, 4487
DNA254543, 2740
DNA254548, 5627
DNA254572, 5885
DNA254582, 1155
DNA254620, 1316
DNA254624, 3468
DNA254771, 2693
DNA254777, 3777
DNA254781, 4374
DNA254783, 6318
DNA254785, 6257
DNA254791, 4898
DNA254994, 5890
DNA255046, 5939
DNA255078, 3113
DNA255340, 4208
DNA255370, 4265

DNA255414, 4747
DNA255531, 859
DNA255696, 3109
DNA256070, 6101
DNA256072, 3511
DNA256503, 199
DNA256533, 5513
DNA256555, 5146
DNA256813, 5056
DNA256836, 5387
DNA256840, 5434
DNA256844, 4362
DNA256886, 4370
DNA256905, 545
DNA257253, 1642
DNA257309, 2746
DNA257428, 4854
DNA257511, 1437
DNA257531, 5506
DNA257549, 5965
DNA257916, 402
DNA257965, 3415
DNA269431, 3101
DNA269481, 5593
DNA269498, 4059
DNA269526, 5814
DNA269593, 1854
DNA269630, 5312
DNA269708, 267
DNA269730, 1195
DNA269746, 5873
DNA269793, 6126
DNA269803, 3284
DNA269809, 1687
DNA269816, 1646
DNA269830, 5989
DNA269858, 1270
DNA269894, 5298
DNA269910, 1062
DNA269930, 1097
DNA269952, 3093
DNA270015, 3864
DNA270134, 3208
DNA270154, 746
DNA270254, 3896
DNA270315, 5206
DNA270401, 1099
DNA270458, 3591
DNA270496, 6239
DNA270613, 1892
DNA270615, 1386
DNA270621, 5234
DNA270675, 1850
DNA270677, 3823
DNA270697, 6011
DNA270711, 2371

DNA270721, 3295
DNA270901, 4879
DNA270931, 5504
DNA270954, 6079
DNA270975, 4843
DNA270979, 4805
DNA270991, 2662
DNA271003, 288
DNA271010, 5676
DNA271040, 1997
DNA271060, 751
DNA271171, 4507
DNA271187, 1093
DNA271243, 703
DNA271324, 3380
DNA271344, 3550
DNA271418, 2104
DNA271492, 3727
DNA271580, 6187
DNA271608, 934
DNA271626, 1721
DNA271722, 2751
DNA271841, 5052
DNA271843, 3392
DNA271847, 2660
DNA271931, 1697
DNA271986, 519
DNA272024, 202
DNA272050, 2600
DNA272062, 5625
DNA272090, 2348
DNA272127, 881
DNA272171, 1866
DNA272213, 2734
DNA272263, 1967
DNA272347, 5426
DNA272379, 3555
DNA272413, 3390
DNA272421, 5201
DNA272605, 1335
DNA272655, 2714
DNA272728, 3215
DNA272748, 235
DNA272889, 4812
DNA273014, 4267
DNA273060, 194
DNA273066, 5568
DNA273088, 396
DNA273254, 6230
DNA273320, 5785
DNA273346, 5615
DNA273474, 5421
DNA273487, 6287
DNA273517, 5738
DNA273521, 3066
DNA273600, 5448

DNA273694, 5023
DNA273712, 42
DNA273759, 2899
DNA273800, 689
DNA273839, 4360
DNA273865, 2246
DNA273919, 1182
DNA273992, 6190
DNA274002, 4476
DNA274034, 5277
DNA274058, 3912
DNA274101, 5115
DNA274129, 5892
DNA274139, 5441
DNA274178, 2491
DNA274180, 4516
DNA274206, 1830
DNA274289, 5523
DNA274326, 2176
DNA274361, 3763
DNA274487, 180
DNA274690, 5039
DNA274745, 192
DNA274755, 4975
DNA274759, 340
DNA274761, 5199
DNA274823, 5542
DNA274829, 6149
DNA275049, 662
DNA275066, 744
DNA275139, 292
DNA275144, 4300
DNA275181, 4320
DNA275195, 651
DNA275240, 864
DNA275322, 2723
DNA275334, 2232
DNA275408, 4564
DNA275630, 1904
DNA276159, 6340
DNA281436, 3900
DNA287167, 794
DNA287173, 31
DNA287189, 2265
DNA287216, 2701
DNA287227, 1952
DNA287234, 5014
DNA287237, 3008
DNA287240, 5328
DNA287243, 5279
DNA287246, 1900
DNA287254, 3236
DNA287261, 5668
DNA287270, 5654
DNA287271, 2763
DNA287282, 1582

DNA287290, 5685
DNA287291, 4919
DNA287319, 1969
DNA287331, 4242
DNA287355, 4520
DNA287417, 3218
DNA287425, 4900
DNA287427, 4778
DNA287636, 5154
DNA287642, 2951
DNA288247, 2703
DNA288259, 1598
DNA289522, 4446
DNA289530, 2761
DNA290231, 1638
DNA290234, 540
DNA290259, 6034
DNA290260, 5550
DNA290264, 2007
DNA290284, 350
DNA290292, 4728
DNA290294, 3620
DNA290319, 2680
DNA290585, 1459
DNA290785, 2032
DNA294794, 438
DNA297288, 5638
DNA297388, 4699
DNA297398, 3434
DNA299899, 930
DNA302016, 3827
DNA302020, 1718
DNA304459, 2986
DNA304460, 1908
DNA304488, 2996
DNA304658, 5562
DNA304661, 1946
DNA304662, 5640
DNA304666, 369
DNA304668, 1963
DNA304669, 3887
DNA304670, 5830
DNA304680, 1874
DNA304685, 2435
DNA304686, 220
DNA304694, 3717
DNA304699, 1986
DNA304704, 4575
DNA304707, 2254
DNA304710, 2308
DNA304715, 4714
DNA304716, 1912
DNA304719, 6038
DNA304720, 371
DNA304783, 3631
DNA304801, 2342

DNA304805, 905
DNA304835, 5973
DNA323717, 1
DNA323718, 2
DNA323719, 3
DNA323720, 4
DNA323721, 6
DNA323722, 8
DNA323723, 10
DNA323724, 12
DNA323725, 14
DNA323726, 15
DNA323727, 17
DNA323728, 19
DNA323729, 20
DNA323730, 22
DNA323731, 24
DNA323732, 26
DNA323733, 28
DNA323734, 29
DNA323735, 33
DNA323736, 34
DNA323737, 38
DNA323738, 40
DNA323739, 41
DNA323740, 46
DNA323741, 50
DNA323742, 52
DNA323743, 54
DNA323744, 55
DNA323745, 57
DNA323746, 58
DNA323747, 59
DNA323748, 60
DNA323749, 62
DNA323750, 64
DNA323751, 66
DNA323752, 67
DNA323753, 68
DNA323754, 69
DNA323755, 71
DNA323756, 73
DNA323757, 75
DNA323758, 76
DNA323759, 77
DNA323760, 78
DNA323761, 79
DNA323762, 81
DNA323763, 83
DNA323764, 85
DNA323765, 87
DNA323766, 89
DNA323767, 91
DNA323768, 93
DNA323769, 95
DNA323770, 97

DNA323771, 98
DNA323772, 99
DNA323773, 101
DNA323774, 102
DNA323775, 103
DNA323776, 107
DNA323777, 109
DNA323778, 110
DNA323779, 112
DNA323780, 113
DNA323781, 114
DNA323782, 116
DNA323783, 118
DNA323784, 120
DNA323785, 122
DNA323788, 126
DNA323789, 127
DNA323790, 129
DNA323791, 130
DNA323792, 131
DNA323793, 133
DNA323794, 134
DNA323795, 135
DNA323796, 136
DNA323797, 137
DNA323798, 139
DNA323799, 140
DNA323800, 141
DNA323801, 142
DNA323802, 144
DNA323803, 145
DNA323804, 148
DNA323805, 150
DNA323806, 152
DNA323807, 154
DNA323808, 155
DNA323809, 159
DNA323810, 161
DNA323811, 163
DNA323812, 165
DNA323813, 169
DNA323814, 171
DNA323815, 175
DNA323816, 176
DNA323817, 178
DNA323818, 182
DNA323819, 183
DNA323820, 185
DNA323821, 187
DNA323822, 190
DNA323823, 196
DNA323824, 198
DNA323825, 201
DNA323826, 204
DNA323827, 206
DNA323828, 208

DNA323829, 210	DNA323885, 317
DNA323830, 212	DNA323886, 318
DNA323831, 213	DNA323887, 319
DNA323832, 214	DNA323888, 321
DNA323833, 216	DNA323889, 323
DNA323834, 222	DNA323890, 324
DNA323835, 224	DNA323891, 326
DNA323836, 226	DNA323892, 327
DNA323837, 228	DNA323893, 328
DNA323838, 229	DNA323894, 330
DNA323839, 231	DNA323895, 331
DNA323840, 233	DNA323896, 332
DNA323841, 237	DNA323897, 334
DNA323842, 239	DNA323898, 336
DNA323843, 241	DNA323899, 338
DNA323844, 243	DNA323900, 342
DNA323845, 244	DNA323901, 344
DNA323846, 245	DNA323902, 348
DNA323847, 247	DNA323903, 352
DNA323848, 249	DNA323904, 353
DNA323849, 250	DNA323905, 354
DNA323850, 251	DNA323906, 358
DNA323851, 253	DNA323907, 360
DNA323852, 254	DNA323908, 361
DNA323853, 256	DNA323909, 363
DNA323854, 257	DNA323910, 364
DNA323855, 259	DNA323911, 366
DNA323856, 260	DNA323912, 373
DNA323857, 262	DNA323913, 376
DNA323858, 264	DNA323914, 377
DNA323859, 265	DNA323915, 379
DNA323860, 269	DNA323916, 381
DNA323861, 273	DNA323917, 383
DNA323862, 275	DNA323918, 384
DNA323863, 276	DNA323919, 386
DNA323864, 277	DNA323920, 388
DNA323865, 279	DNA323921, 389
DNA323866, 280	DNA323922, 391
DNA323867, 281	DNA323923, 392
DNA323868, 282	DNA323924, 394
DNA323869, 284	DNA323925, 398
DNA323870, 286	DNA323926, 400
DNA323871, 290	DNA323927, 404
DNA323872, 294	DNA323928, 406
DNA323873, 295	DNA323929, 408
DNA323874, 296	DNA323930, 411
DNA323875, 298	DNA323931, 412
DNA323876, 300	DNA323932, 414
DNA323877, 302	DNA323933, 416
DNA323878, 304	DNA323934, 418
DNA323879, 306	DNA323935, 420
DNA323880, 308	DNA323936, 422
DNA323881, 310	DNA323937, 424
DNA323882, 312	DNA323938, 426
DNA323883, 314	DNA323939, 430
DNA323884, 315	DNA323940, 432

DNA323941, 433	DNA323997, 537
DNA323942, 434	DNA323998, 538
DNA323943, 440	DNA323999, 542
DNA323944, 442	DNA324000, 543
DNA323945, 444	DNA324001, 544
DNA323946, 446	DNA324002, 547
DNA323947, 448	DNA324003, 548
DNA323948, 450	DNA324004, 552
DNA323949, 451	DNA324005, 555
DNA323950, 452	DNA324006, 557
DNA323951, 454	DNA324007, 560
DNA323952, 455	DNA324008, 561
DNA323953, 459	DNA324009, 562
DNA323954, 461	DNA324010, 564
DNA323955, 463	DNA324011, 566
DNA323956, 465	DNA324012, 567
DNA323957, 466	DNA324013, 568
DNA323958, 468	DNA324014, 569
DNA323959, 470	DNA324015, 571
DNA323960, 472	DNA324016, 573
DNA323961, 473	DNA324017, 575
DNA323962, 476	DNA324018, 580
DNA323963, 477	DNA324019, 581
DNA323964, 479	DNA324020, 582
DNA323965, 481	DNA324021, 583
DNA323966, 483	DNA324022, 587
DNA323967, 484	DNA324023, 589
DNA323968, 485	DNA324024, 591
DNA323969, 486	DNA324025, 592
DNA323970, 488	DNA324026, 593
DNA323971, 490	DNA324027, 596
DNA323972, 492	DNA324028, 598
DNA323973, 493	DNA324029, 599
DNA323974, 494	DNA324030, 600
DNA323975, 495	DNA324031, 601
DNA323976, 497	DNA324032, 602
DNA323977, 501	DNA324033, 605
DNA323978, 503	DNA324034, 606
DNA323979, 505	DNA324035, 608
DNA323980, 507	DNA324036, 610
DNA323981, 509	DNA324037, 612
DNA323982, 511	DNA324038, 614
DNA323983, 513	DNA324039, 616
DNA323984, 515	DNA324040, 618
DNA323985, 517	DNA324041, 619
DNA323986, 521	DNA324042, 620
DNA323987, 522	DNA324043, 622
DNA323988, 523	DNA324044, 626
DNA323989, 524	DNA324045, 628
DNA323990, 525	DNA324046, 630
DNA323991, 527	DNA324047, 632
DNA323992, 529	DNA324048, 634
DNA323993, 531	DNA324049, 636
DNA323994, 532	DNA324050, 638
DNA323995, 534	DNA324051, 639
DNA323996, 535	DNA324052, 641

DNA324053, 642
DNA324054, 643
DNA324055, 645
DNA324056, 647
DNA324057, 653
DNA324058, 655
DNA324059, 657
DNA324060, 659
DNA324061, 661
DNA324062, 664
DNA324063, 665
DNA324064, 667
DNA324065, 669
DNA324066, 670
DNA324067, 672
DNA324068, 674
DNA324069, 676
DNA324070, 678
DNA324071, 680
DNA324072, 681
DNA324073, 683
DNA324074, 686
DNA324075, 690
DNA324076, 692
DNA324077, 694
DNA324078, 696
DNA324079, 700
DNA324080, 701
DNA324081, 705
DNA324082, 707
DNA324083, 709
DNA324084, 713
DNA324085, 715
DNA324086, 716
DNA324087, 717
DNA324088, 719
DNA324089, 721
DNA324090, 723
DNA324091, 725
DNA324092, 726
DNA324093, 727
DNA324094, 729
DNA324095, 731
DNA324096, 733
DNA324097, 734
DNA324098, 736
DNA324099, 738
DNA324100, 740
DNA324101, 743
DNA324102, 748
DNA324103, 749
DNA324104, 753
DNA324105, 755
DNA324106, 757
DNA324107, 759
DNA324108, 761

DNA324109, 763
DNA324110, 764
DNA324111, 766
DNA324112, 768
DNA324113, 770
DNA324114, 771
DNA324115, 772
DNA324116, 773
DNA324117, 775
DNA324118, 776
DNA324119, 777
DNA324120, 779
DNA324121, 780
DNA324122, 782
DNA324123, 783
DNA324124, 784
DNA324125, 785
DNA324126, 787
DNA324127, 788
DNA324128, 789
DNA324129, 791
DNA324130, 796
DNA324131, 798
DNA324132, 800
DNA324133, 801
DNA324134, 805
DNA324135, 808
DNA324136, 810
DNA324137, 812
DNA324138, 816
DNA324139, 817
DNA324140, 818
DNA324141, 820
DNA324142, 822
DNA324143, 823
DNA324144, 824
DNA324145, 825
DNA324146, 827
DNA324147, 829
DNA324148, 831
DNA324149, 832
DNA324150, 834
DNA324151, 836
DNA324152, 838
DNA324153, 839
DNA324154, 841
DNA324155, 842
DNA324156, 843
DNA324157, 845
DNA324158, 847
DNA324159, 849
DNA324160, 850
DNA324161, 851
DNA324162, 853
DNA324163, 856
DNA324164, 857

DNA324165, 858
DNA324166, 861
DNA324167, 862
DNA324168, 866
DNA324169, 867
DNA324170, 869
DNA324171, 871
DNA324172, 873
DNA324173, 875
DNA324174, 877
DNA324175, 878
DNA324176, 880
DNA324177, 883
DNA324178, 885
DNA324179, 887
DNA324180, 889
DNA324181, 891
DNA324182, 893
DNA324183, 894
DNA324184, 896
DNA324185, 900
DNA324186, 901
DNA324187, 903
DNA324188, 907
DNA324189, 909
DNA324190, 910
DNA324191, 911
DNA324192, 912
DNA324193, 914
DNA324194, 916
DNA324195, 918
DNA324196, 920
DNA324197, 921
DNA324198, 923
DNA324199, 925
DNA324200, 926
DNA324201, 927
DNA324202, 928
DNA324203, 929
DNA324204, 932
DNA324205, 933
DNA324206, 936
DNA324207, 938
DNA324208, 940
DNA324209, 941
DNA324210, 942
DNA324211, 944
DNA324212, 946
DNA324213, 948
DNA324214, 950
DNA324215, 952
DNA324216, 954
DNA324217, 955
DNA324218, 957
DNA324219, 958
DNA324220, 960

DNA324221, 962
DNA324222, 964
DNA324223, 965
DNA324224, 966
DNA324225, 968
DNA324226, 970
DNA324227, 971
DNA324228, 973
DNA324229, 975
DNA324230, 979
DNA324231, 980
DNA324232, 982
DNA324233, 984
DNA324234, 985
DNA324235, 986
DNA324236, 988
DNA324237, 990
DNA324238, 992
DNA324239, 993
DNA324240, 996
DNA324241, 1000
DNA324242, 1002
DNA324243, 1004
DNA324244, 1006
DNA324245, 1007
DNA324246, 1009
DNA324247, 1011
DNA324248, 1012
DNA324249, 1014
DNA324250, 1016
DNA324251, 1018
DNA324252, 1020
DNA324253, 1022
DNA324254, 1026
DNA324255, 1028
DNA324256, 1029
DNA324257, 1030
DNA324258, 1032
DNA324259, 1034
DNA324260, 1036
DNA324261, 1037
DNA324262, 1039
DNA324263, 1040
DNA324264, 1041
DNA324265, 1042
DNA324266, 1043
DNA324267, 1045
DNA324268, 1047
DNA324269, 1049
DNA324270, 1051
DNA324271, 1053
DNA324272, 1055
DNA324273, 1057
DNA324274, 1059
DNA324275, 1060
DNA324276, 1064

DNA324277, 1068
DNA324278, 1070
DNA324279, 1072
DNA324280, 1074
DNA324281, 1075
DNA324282, 1076
DNA324283, 1078
DNA324284, 1079
DNA324285, 1083
DNA324286, 1085
DNA324287, 1086
DNA324288, 1088
DNA324289, 1091
DNA324290, 1095
DNA324291, 1101
DNA324292, 1103
DNA324293, 1105
DNA324294, 1106
DNA324295, 1110
DNA324296, 1112
DNA324297, 1113
DNA324298, 1115
DNA324299, 1117
DNA324300, 1119
DNA324301, 1120
DNA324302, 1121
DNA324303, 1122
DNA324304, 1123
DNA324305, 1125
DNA324306, 1127
DNA324307, 1130
DNA324308, 1131
DNA324309, 1132
DNA324310, 1134
DNA324311, 1136
DNA324312, 1137
DNA324313, 1139
DNA324314, 1140
DNA324315, 1141
DNA324316, 1143
DNA324317, 1147
DNA324318, 1151
DNA324319, 1157
DNA324320, 1159
DNA324321, 1161
DNA324322, 1162
DNA324323, 1163
DNA324324, 1167
DNA324325, 1169
DNA324326, 1170
DNA324327, 1172
DNA324328, 1174
DNA324329, 1176
DNA324330, 1178
DNA324331, 1180
DNA324332, 1184

DNA324333, 1186
DNA324334, 1187
DNA324335, 1190
DNA324336, 1192
DNA324337, 1193
DNA324338, 1197
DNA324339, 1198
DNA324340, 1199
DNA324341, 1201
DNA324342, 1202
DNA324343, 1203
DNA324344, 1204
DNA324345, 1205
DNA324346, 1206
DNA324347, 1208
DNA324348, 1209
DNA324349, 1211
DNA324350, 1213
DNA324351, 1214
DNA324352, 1216
DNA324353, 1218
DNA324354, 1220
DNA324355, 1221
DNA324356, 1225
DNA324357, 1227
DNA324358, 1229
DNA324359, 1231
DNA324360, 1232
DNA324361, 1234
DNA324362, 1235
DNA324363, 1237
DNA324364, 1238
DNA324365, 1240
DNA324366, 1242
DNA324367, 1243
DNA324368, 1244
DNA324369, 1245
DNA324370, 1246
DNA324371, 1248
DNA324372, 1250
DNA324373, 1252
DNA324374, 1254
DNA324375, 1255
DNA324376, 1256
DNA324377, 1258
DNA324378, 1260
DNA324379, 1262
DNA324380, 1263
DNA324381, 1264
DNA324382, 1265
DNA324383, 1266
DNA324384, 1267
DNA324385, 1268
DNA324386, 1272
DNA324387, 1274
DNA324388, 1275

DNA324389, 1276
DNA324390, 1278
DNA324391, 1280
DNA324392, 1282
DNA324393, 1284
DNA324394, 1286
DNA324395, 1288
DNA324396, 1289
DNA324397, 1290
DNA324398, 1291
DNA324399, 1292
DNA324400, 1294
DNA324401, 1295
DNA324402, 1296
DNA324403, 1297
DNA324404, 1299
DNA324405, 1300
DNA324406, 1302
DNA324407, 1304
DNA324408, 1306
DNA324409, 1308
DNA324410, 1310
DNA324411, 1312
DNA324412, 1313
DNA324413, 1314
DNA324414, 1315
DNA324415, 1318
DNA324416, 1320
DNA324417, 1322
DNA324418, 1323
DNA324419, 1325
DNA324420, 1329
DNA324421, 1332
DNA324422, 1333
DNA324423, 1337
DNA324424, 1338
DNA324425, 1340
DNA324426, 1341
DNA324427, 1343
DNA324428, 1344
DNA324429, 1345
DNA324430, 1347
DNA324431, 1348
DNA324432, 1350
DNA324433, 1354
DNA324434, 1356
DNA324435, 1358
DNA324436, 1359
DNA324437, 1360
DNA324438, 1361
DNA324439, 1363
DNA324440, 1364
DNA324441, 1365
DNA324442, 1366
DNA324443, 1372
DNA324444, 1374

DNA324445, 1376
DNA324446, 1378
DNA324447, 1380
DNA324448, 1382
DNA324449, 1384
DNA324450, 1388
DNA324451, 1390
DNA324452, 1392
DNA324453, 1394
DNA324454, 1396
DNA324455, 1398
DNA324456, 1400
DNA324457, 1402
DNA324458, 1404
DNA324459, 1406
DNA324460, 1408
DNA324461, 1410
DNA324462, 1412
DNA324463, 1413
DNA324464, 1414
DNA324465, 1416
DNA324466, 1417
DNA324467, 1418
DNA324468, 1419
DNA324469, 1421
DNA324470, 1423
DNA324471, 1424
DNA324472, 1425
DNA324473, 1427
DNA324474, 1429
DNA324475, 1430
DNA324476, 1432
DNA324478, 1433
DNA324479, 1434
DNA324480, 1435
DNA324481, 1439
DNA324482, 1440
DNA324483, 1441
DNA324484, 1442
DNA324485, 1443
DNA324486, 1445
DNA324487, 1448
DNA324488, 1449
DNA324489, 1451
DNA324490, 1452
DNA324491, 1453
DNA324492, 1455
DNA324493, 1456
DNA324494, 1457
DNA324495, 1461
DNA324496, 1463
DNA324497, 1464
DNA324498, 1465
DNA324499, 1466
DNA324500, 1468
DNA324501, 1469

DNA324502, 1470
DNA324503, 1471
DNA324504, 1472
DNA324505, 1473
DNA324506, 1474
DNA324507, 1476
DNA324508, 1477
DNA324509, 1478
DNA324510, 1480
DNA324511, 1482
DNA324512, 1483
DNA324513, 1484
DNA324514, 1485
DNA324515, 1487
DNA324516, 1491
DNA324517, 1493
DNA324518, 1494
DNA324519, 1496
DNA324520, 1497
DNA324521, 1499
DNA324522, 1500
DNA324523, 1502
DNA324524, 1504
DNA324525, 1506
DNA324526, 1510
DNA324527, 1513
DNA324528, 1517
DNA324529, 1519
DNA324530, 1520
DNA324531, 1522
DNA324532, 1524
DNA324533, 1525
DNA324534, 1526
DNA324535, 1528
DNA324536, 1530
DNA324537, 1531
DNA324538, 1532
DNA324539, 1533
DNA324540, 1534
DNA324541, 1535
DNA324542, 1537
DNA324543, 1539
DNA324544, 1540
DNA324545, 1541
DNA324546, 1543
DNA324547, 1544
DNA324548, 1545
DNA324549, 1547
DNA324550, 1548
DNA324551, 1549
DNA324552, 1550
DNA324554, 1551
DNA324555, 1552
DNA324556, 1553
DNA324557, 1554
DNA324558, 1555

DNA324559, 1556
DNA324560, 1557
DNA324561, 1559
DNA324562, 1561
DNA324563, 1562
DNA324564, 1564
DNA324565, 1565
DNA324566, 1567
DNA324567, 1568
DNA324568, 1570
DNA324569, 1572
DNA324570, 1575
DNA324571, 1577
DNA324572, 1579
DNA324573, 1581
DNA324574, 1584
DNA324575, 1586
DNA324576, 1587
DNA324577, 1588
DNA324578, 1590
DNA324579, 1591
DNA324580, 1592
DNA324581, 1593
DNA324582, 1595
DNA324583, 1596
DNA324584, 1597
DNA324585, 1600
DNA324586, 1602
DNA324587, 1604
DNA324588, 1606
DNA324589, 1608
DNA324590, 1609
DNA324591, 1610
DNA324592, 1611
DNA324593, 1612
DNA324594, 1614
DNA324595, 1615
DNA324596, 1617
DNA324597, 1619
DNA324598, 1621
DNA324599, 1622
DNA324600, 1623
DNA324601, 1624
DNA324602, 1626
DNA324603, 1629
DNA324604, 1631
DNA324605, 1632
DNA324606, 1634
DNA324607, 1636
DNA324608, 1640
DNA324609, 1641
DNA324610, 1644
DNA324611, 1648
DNA324612, 1650
DNA324613, 1652
DNA324614, 1654

DNA324615, 1655
DNA324616, 1656
DNA324617, 1658
DNA324618, 1660
DNA324619, 1662
DNA324620, 1663
DNA324621, 1664
DNA324622, 1666
DNA324623, 1668
DNA324624, 1669
DNA324625, 1670
DNA324626, 1673
DNA324627, 1675
DNA324628, 1679
DNA324629, 1681
DNA324630, 1683
DNA324631, 1685
DNA324632, 1691
DNA324633, 1693
DNA324634, 1695
DNA324635, 1699
DNA324636, 1700
DNA324637, 1701
DNA324638, 1702
DNA324639, 1704
DNA324640, 1706
DNA324641, 1708
DNA324642, 1710
DNA324643, 1711
DNA324644, 1712
DNA324645, 1713
DNA324646, 1714
DNA324647, 1716
DNA324648, 1720
DNA324649, 1723
DNA324650, 1724
DNA324651, 1726
DNA324652, 1728
DNA324653, 1730
DNA324654, 1734
DNA324655, 1736
DNA324656, 1738
DNA324657, 1740
DNA324658, 1742
DNA324659, 1744
DNA324660, 1746
DNA324661, 1748
DNA324662, 1750
DNA324663, 1752
DNA324664, 1754
DNA324665, 1756
DNA324666, 1758
DNA324667, 1760
DNA324668, 1762
DNA324669, 1764
DNA324670, 1766

DNA324671, 1768
DNA324672, 1770
DNA324673, 1772
DNA324674, 1774
DNA324675, 1776
DNA324676, 1778
DNA324677, 1779
DNA324678, 1781
DNA324679, 1783
DNA324680, 1785
DNA324681, 1787
DNA324682, 1789
DNA324683, 1793
DNA324684, 1795
DNA324685, 1797
DNA324686, 1798
DNA324687, 1799
DNA324688, 1800
DNA324689, 1802
DNA324690, 1803
DNA324691, 1805
DNA324692, 1807
DNA324693, 1808
DNA324694, 1810
DNA324695, 1811
DNA324696, 1814
DNA324697, 1816
DNA324698, 1817
DNA324699, 1818
DNA324700, 1819
DNA324701, 1820
DNA324702, 1821
DNA324703, 1823
DNA324704, 1824
DNA324705, 1826
DNA324706, 1832
DNA324707, 1834
DNA324708, 1836
DNA324709, 1838
DNA324710, 1840
DNA324711, 1841
DNA324712, 1842
DNA324713, 1843
DNA324714, 1845
DNA324715, 1846
DNA324716, 1848
DNA324717, 1852
DNA324718, 1856
DNA324719, 1857
DNA324720, 1858
DNA324721, 1859
DNA324722, 1860
DNA324723, 1861
DNA324724, 1862
DNA324725, 1863
DNA324726, 1865

DNA324727, 1868
DNA324728, 1870
DNA324729, 1872
DNA324730, 1876
DNA324731, 1877
DNA324732, 1878
DNA324733, 1879
DNA324734, 1880
DNA324735, 1882
DNA324736, 1883
DNA324737, 1884
DNA324738, 1888
DNA324739, 1890
DNA324740, 1894
DNA324741, 1896
DNA324742, 1898
DNA324743, 1902
DNA324744, 1906
DNA324745, 1910
DNA324746, 1914
DNA324747, 1916
DNA324748, 1918
DNA324749, 1920
DNA324750, 1921
DNA324751, 1922
DNA324752, 1924
DNA324753, 1926
DNA324754, 1928
DNA324755, 1929
DNA324756, 1931
DNA324757, 1932
DNA324758, 1934
DNA324759, 1936
DNA324760, 1937
DNA324761, 1938
DNA324763, 1939
DNA324764, 1940
DNA324765, 1941
DNA324766, 1944
DNA324767, 1948
DNA324768, 1949
DNA324769, 1951
DNA324770, 1954
DNA324771, 1955
DNA324772, 1956
DNA324773, 1957
DNA324774, 1959
DNA324775, 1965
DNA324776, 1971
DNA324777, 1973
DNA324778, 1975
DNA324779, 1977
DNA324780, 1979
DNA324781, 1981
DNA324782, 1983
DNA324783, 1984

DNA324784, 1988
DNA324785, 1990
DNA324786, 1992
DNA324787, 1994
DNA324788, 1995
DNA324789, 1999
DNA324790, 2000
DNA324791, 2002
DNA324792, 2004
DNA324793, 2006
DNA324794, 2009
DNA324795, 2011
DNA324796, 2013
DNA324797, 2015
DNA324798, 2016
DNA324799, 2017
DNA324800, 2019
DNA324801, 2021
DNA324802, 2023
DNA324803, 2025
DNA324804, 2027
DNA324805, 2029
DNA324806, 2031
DNA324807, 2036
DNA324808, 2037
DNA324809, 2039
DNA324810, 2041
DNA324811, 2042
DNA324812, 2044
DNA324813, 2045
DNA324814, 2047
DNA324815, 2049
DNA324816, 2050
DNA324817, 2052
DNA324818, 2054
DNA324819, 2056
DNA324820, 2057
DNA324821, 2058
DNA324822, 2059
DNA324823, 2060
DNA324824, 2062
DNA324825, 2064
DNA324826, 2065
DNA324827, 2066
DNA324828, 2068
DNA324829, 2069
DNA324830, 2072
DNA324831, 2074
DNA324832, 2075
DNA324833, 2077
DNA324834, 2079
DNA324835, 2080
DNA324836, 2081
DNA324837, 2083
DNA324838, 2085
DNA324839, 2087

DNA324840, 2089
DNA324841, 2090
DNA324842, 2091
DNA324843, 2092
DNA324844, 2094
DNA324845, 2096
DNA324846, 2098
DNA324847, 2101
DNA324848, 2103
DNA324849, 2106
DNA324850, 2107
DNA324851, 2108
DNA324852, 2110
DNA324853, 2111
DNA324854, 2113
DNA324855, 2114
DNA324856, 2116
DNA324857, 2118
DNA324858, 2119
DNA324859, 2121
DNA324860, 2122
DNA324861, 2123
DNA324862, 2124
DNA324863, 2126
DNA324864, 2128
DNA324865, 2130
DNA324866, 2131
DNA324867, 2132
DNA324868, 2134
DNA324870, 2135
DNA324871, 2137
DNA324872, 2139
DNA324873, 2140
DNA324874, 2141
DNA324875, 2142
DNA324876, 2144
DNA324877, 2145
DNA324878, 2146
DNA324879, 2147
DNA324880, 2148
DNA324881, 2150
DNA324882, 2152
DNA324883, 2154
DNA324884, 2155
DNA324885, 2157
DNA324886, 2159
DNA324887, 2160
DNA324888, 2161
DNA324889, 2163
DNA324890, 2165
DNA324891, 2167
DNA324892, 2168
DNA324893, 2170
DNA324894, 2172
DNA324895, 2178
DNA324896, 2180

DNA324897, 2184
DNA324898, 2186
DNA324899, 2188
DNA324900, 2190
DNA324901, 2191
DNA324902, 2195
DNA324903, 2197
DNA324904, 2198
DNA324905, 2200
DNA324906, 2202
DNA324907, 2203
DNA324908, 2204
DNA324909, 2205
DNA324910, 2208
DNA324911, 2210
DNA324912, 2212
DNA324913, 2214
DNA324914, 2216
DNA324915, 2218
DNA324916, 2219
DNA324917, 2220
DNA324918, 2222
DNA324919, 2224
DNA324920, 2225
DNA324921, 2226
DNA324922, 2228
DNA324923, 2230
DNA324924, 2234
DNA324925, 2236
DNA324926, 2238
DNA324927, 2240
DNA324928, 2244
DNA324929, 2245
DNA324930, 2248
DNA324931, 2249
DNA324932, 2251
DNA324933, 2253
DNA324934, 2256
DNA324935, 2258
DNA324936, 2259
DNA324937, 2260
DNA324938, 2264
DNA324939, 2267
DNA324940, 2269
DNA324941, 2271
DNA324942, 2273
DNA324943, 2276
DNA324944, 2278
DNA324945, 2280
DNA324946, 2281
DNA324947, 2282
DNA324948, 2284
DNA324949, 2286
DNA324950, 2288
DNA324951, 2290
DNA324952, 2292

DNA324953, 2293
DNA324954, 2295
DNA324955, 2297
DNA324956, 2299
DNA324957, 2300
DNA324958, 2301
DNA324959, 2302
DNA324960, 2304
DNA324961, 2306
DNA324962, 2310
DNA324963, 2311
DNA324964, 2312
DNA324965, 2313
DNA324966, 2315
DNA324967, 2316
DNA324968, 2317
DNA324969, 2318
DNA324971, 2319
DNA324972, 2321
DNA324973, 2322
DNA324974, 2323
DNA324975, 2325
DNA324976, 2326
DNA324977, 2328
DNA324978, 2329
DNA324979, 2331
DNA324980, 2333
DNA324981, 2335
DNA324982, 2337
DNA324983, 2338
DNA324984, 2340
DNA324985, 2344
DNA324986, 2346
DNA324987, 2350
DNA324988, 2351
DNA324989, 2352
DNA324990, 2353
DNA324991, 2355
DNA324992, 2357
DNA324993, 2360
DNA324994, 2363
DNA324995, 2365
DNA324996, 2367
DNA324997, 2369
DNA324998, 2373
DNA324999, 2375
DNA325000, 2376
DNA325001, 2378
DNA325002, 2380
DNA325003, 2381
DNA325004, 2383
DNA325005, 2385
DNA325006, 2386
DNA325007, 2387
DNA325008, 2389
DNA325009, 2391

DNA325010, 2395
DNA325011, 2396
DNA325012, 2398
DNA325013, 2400
DNA325014, 2402
DNA325015, 2403
DNA325016, 2404
DNA325017, 2406
DNA325018, 2407
DNA325019, 2409
DNA325020, 2411
DNA325021, 2413
DNA325022, 2414
DNA325023, 2416
DNA325024, 2417
DNA325025, 2418
DNA325026, 2420
DNA325027, 2422
DNA325028, 2423
DNA325029, 2425
DNA325030, 2427
DNA325031, 2429
DNA325032, 2430
DNA325033, 2432
DNA325034, 2433
DNA325035, 2434
DNA325036, 2437
DNA325037, 2439
DNA325038, 2440
DNA325039, 2442
DNA325040, 2444
DNA325041, 2446
DNA325042, 2447
DNA325043, 2449
DNA325044, 2451
DNA325045, 2453
DNA325046, 2454
DNA325047, 2455
DNA325048, 2456
DNA325049, 2460
DNA325050, 2462
DNA325051, 2464
DNA325052, 2466
DNA325053, 2467
DNA325054, 2469
DNA325055, 2470
DNA325056, 2471
DNA325057, 2472
DNA325058, 2473
DNA325059, 2475
DNA325060, 2476
DNA325061, 2478
DNA325062, 2480
DNA325063, 2482
DNA325064, 2483
DNA325065, 2485

DNA325066, 2487
DNA325067, 2488
DNA325068, 2490
DNA325069, 2493
DNA325070, 2497
DNA325071, 2499
DNA325072, 2501
DNA325073, 2503
DNA325074, 2505
DNA325075, 2508
DNA325076, 2510
DNA325077, 2514
DNA325078, 2515
DNA325079, 2517
DNA325080, 2519
DNA325081, 2521
DNA325082, 2523
DNA325083, 2525
DNA325084, 2526
DNA325085, 2527
DNA325086, 2529
DNA325087, 2530
DNA325088, 2531
DNA325089, 2533
DNA325090, 2534
DNA325091, 2536
DNA325092, 2538
DNA325093, 2540
DNA325094, 2541
DNA325095, 2543
DNA325096, 2544
DNA325097, 2548
DNA325098, 2550
DNA325099, 2552
DNA325100, 2554
DNA325101, 2556
DNA325102, 2557
DNA325103, 2558
DNA325104, 2559
DNA325105, 2560
DNA325106, 2561
DNA325107, 2562
DNA325108, 2563
DNA325109, 2564
DNA325110, 2567
DNA325111, 2569
DNA325112, 2571
DNA325113, 2572
DNA325114, 2574
DNA325115, 2575
DNA325116, 2577
DNA325117, 2579
DNA325118, 2581
DNA325119, 2582
DNA325120, 2583
DNA325121, 2584

DNA325122, 2586
DNA325123, 2588
DNA325124, 2590
DNA325125, 2592
DNA325126, 2595
DNA325127, 2596
DNA325128, 2598
DNA325129, 2602
DNA325130, 2604
DNA325131, 2605
DNA325132, 2606
DNA325133, 2608
DNA325134, 2609
DNA325135, 2611
DNA325136, 2612
DNA325137, 2613
DNA325138, 2614
DNA325139, 2616
DNA325140, 2618
DNA325141, 2619
DNA325143, 2620
DNA325144, 2622
DNA325145, 2623
DNA325146, 2625
DNA325147, 2626
DNA325148, 2627
DNA325149, 2628
DNA325150, 2629
DNA325151, 2631
DNA325152, 2633
DNA325153, 2635
DNA325154, 2637
DNA325155, 2638
DNA325156, 2640
DNA325157, 2641
DNA325158, 2642
DNA325159, 2644
DNA325160, 2645
DNA325161, 2646
DNA325162, 2647
DNA325163, 2649
DNA325164, 2651
DNA325165, 2653
DNA325166, 2655
DNA325167, 2657
DNA325168, 2659
DNA325169, 2664
DNA325170, 2666
DNA325171, 2668
DNA325172, 2672
DNA325173, 2673
DNA325174, 2675
DNA325175, 2677
DNA325176, 2679
DNA325177, 2682
DNA325178, 2684

DNA325179, 2686
DNA325180, 2688
DNA325181, 2689
DNA325182, 2697
DNA325183, 2699
DNA325184, 2700
DNA325185, 2705
DNA325186, 2707
DNA325187, 2708
DNA325188, 2710
DNA325189, 2711
DNA325190, 2712
DNA325191, 2716
DNA325192, 2718
DNA325193, 2720
DNA325194, 2722
DNA325195, 2725
DNA325196, 2726
DNA325197, 2727
DNA325198, 2728
DNA325199, 2730
DNA325200, 2732
DNA325201, 2736
DNA325202, 2738
DNA325203, 2742
DNA325204, 2744
DNA325205, 2748
DNA325206, 2750
DNA325207, 2753
DNA325208, 2755
DNA325209, 2756
DNA325210, 2757
DNA325211, 2759
DNA325212, 2760
DNA325213, 2765
DNA325214, 2766
DNA325215, 2769
DNA325216, 2771
DNA325217, 2772
DNA325218, 2774
DNA325219, 2775
DNA325220, 2777
DNA325221, 2778
DNA325222, 2780
DNA325223, 2784
DNA325224, 2786
DNA325225, 2787
DNA325226, 2789
DNA325227, 2790
DNA325228, 2792
DNA325229, 2794
DNA325230, 2798
DNA325231, 2799
DNA325232, 2800
DNA325233, 2801
DNA325234, 2802

DNA325235, 2803
DNA325236, 2804
DNA325237, 2806
DNA325238, 2808
DNA325239, 2809
DNA325240, 2811
DNA325241, 2813
DNA325242, 2815
DNA325243, 2817
DNA325244, 2818
DNA325245, 2819
DNA325246, 2820
DNA325247, 2822
DNA325248, 2824
DNA325249, 2825
DNA325250, 2826
DNA325251, 2828
DNA325252, 2830
DNA325253, 2832
DNA325254, 2833
DNA325255, 2834
DNA325256, 2836
DNA325257, 2838
DNA325258, 2839
DNA325259, 2841
DNA325260, 2843
DNA325261, 2845
DNA325262, 2846
DNA325263, 2847
DNA325264, 2849
DNA325265, 2851
DNA325266, 2852
DNA325267, 2854
DNA325268, 2855
DNA325269, 2857
DNA325270, 2859
DNA325271, 2860
DNA325272, 2862
DNA325273, 2864
DNA325274, 2866
DNA325275, 2868
DNA325276, 2870
DNA325277, 2871
DNA325278, 2873
DNA325279, 2874
DNA325280, 2875
DNA325281, 2876
DNA325282, 2878
DNA325283, 2879
DNA325284, 2881
DNA325285, 2883
DNA325286, 2885
DNA325287, 2887
DNA325288, 2889
DNA325289, 2891
DNA325290, 2893

DNA325291, 2895
DNA325292, 2897
DNA325293, 2898
DNA325294, 2901
DNA325295, 2902
DNA325296, 2904
DNA325297, 2906
DNA325298, 2908
DNA325299, 2909
DNA325300, 2910
DNA325301, 2911
DNA325302, 2913
DNA325303, 2914
DNA325304, 2916
DNA325305, 2918
DNA325306, 2919
DNA325307, 2921
DNA325308, 2922
DNA325309, 2923
DNA325310, 2925
DNA325311, 2926
DNA325312, 2927
DNA325313, 2929
DNA325314, 2930
DNA325315, 2931
DNA325316, 2933
DNA325317, 2934
DNA325318, 2935
DNA325319, 2937
DNA325320, 2939
DNA325321, 2941
DNA325322, 2942
DNA325323, 2944
DNA325324, 2945
DNA325325, 2949
DNA325326, 2953
DNA325327, 2955
DNA325328, 2957
DNA325329, 2959
DNA325330, 2963
DNA325331, 2966
DNA325332, 2968
DNA325333, 2970
DNA325334, 2971
DNA325335, 2973
DNA325336, 2975
DNA325337, 2976
DNA325338, 2977
DNA325339, 2978
DNA325340, 2980
DNA325341, 2984
DNA325342, 2988
DNA325343, 2992
DNA325344, 2994
DNA325345, 2998
DNA325346, 2999

DNA325347, 3000
DNA325348, 3002
DNA325349, 3006
DNA325350, 3010
DNA325351, 3012
DNA325352, 3013
DNA325353, 3015
DNA325354, 3016
DNA325355, 3017
DNA325356, 3019
DNA325357, 3020
DNA325358, 3022
DNA325359, 3024
DNA325360, 3026
DNA325361, 3028
DNA325362, 3029
DNA325363, 3031
DNA325364, 3033
DNA325365, 3035
DNA325366, 3037
DNA325367, 3039
DNA325368, 3041
DNA325369, 3042
DNA325370, 3044
DNA325371, 3045
DNA325372, 3047
DNA325373, 3049
DNA325374, 3053
DNA325375, 3055
DNA325376, 3057
DNA325377, 3058
DNA325378, 3059
DNA325379, 3061
DNA325380, 3063
DNA325381, 3065
DNA325382, 3068
DNA325383, 3070
DNA325384, 3072
DNA325385, 3073
DNA325386, 3074
DNA325387, 3075
DNA325388, 3078
DNA325389, 3080
DNA325390, 3082
DNA325391, 3084
DNA325392, 3086
DNA325393, 3088
DNA325394, 3089
DNA325395, 3091
DNA325396, 3095
DNA325397, 3097
DNA325398, 3099
DNA325399, 3103
DNA325400, 3104
DNA325401, 3106
DNA325402, 3107

DNA325403, 3111
DNA325404, 3115
DNA325405, 3117
DNA325406, 3119
DNA325407, 3120
DNA325408, 3122
DNA325409, 3124
DNA325410, 3125
DNA325411, 3127
DNA325412, 3129
DNA325413, 3131
DNA325414, 3133
DNA325415, 3135
DNA325416, 3136
DNA325417, 3137
DNA325418, 3139
DNA325419, 3141
DNA325420, 3142
DNA325421, 3144
DNA325422, 3146
DNA325423, 3148
DNA325424, 3149
DNA325425, 3151
DNA325426, 3152
DNA325427, 3153
DNA325428, 3155
DNA325429, 3157
DNA325430, 3159
DNA325431, 3161
DNA325432, 3163
DNA325433, 3165
DNA325434, 3167
DNA325435, 3169
DNA325436, 3170
DNA325437, 3171
DNA325438, 3173
DNA325439, 3177
DNA325440, 3178
DNA325441, 3180
DNA325442, 3182
DNA325443, 3183
DNA325444, 3184
DNA325445, 3185
DNA325446, 3187
DNA325447, 3188
DNA325448, 3190
DNA325449, 3192
DNA325450, 3193
DNA325451, 3194
DNA325452, 3195
DNA325453, 3196
DNA325454, 3197
DNA325455, 3199
DNA325456, 3201
DNA325457, 3202
DNA325458, 3210

DNA325459, 3212
DNA325460, 3214
DNA325461, 3217
DNA325462, 3222
DNA325463, 3223
DNA325464, 3224
DNA325465, 3225
DNA325466, 3227
DNA325467, 3228
DNA325468, 3230
DNA325469, 3232
DNA325470, 3234
DNA325471, 3238
DNA325472, 3240
DNA325473, 3242
DNA325474, 3244
DNA325475, 3247
DNA325476, 3248
DNA325477, 3249
DNA325478, 3251
DNA325479, 3253
DNA325480, 3255
DNA325481, 3256
DNA325482, 3258
DNA325483, 3260
DNA325484, 3261
DNA325485, 3263
DNA325486, 3264
DNA325487, 3266
DNA325488, 3268
DNA325489, 3269
DNA325490, 3270
DNA325491, 3271
DNA325492, 3273
DNA325493, 3275
DNA325494, 3276
DNA325495, 3278
DNA325496, 3279
DNA325497, 3281
DNA325498, 3283
DNA325499, 3286
DNA325500, 3287
DNA325501, 3288
DNA325502, 3289
DNA325503, 3291
DNA325504, 3293
DNA325505, 3294
DNA325506, 3299
DNA325507, 3301
DNA325508, 3303
DNA325509, 3304
DNA325510, 3306
DNA325511, 3308
DNA325512, 3310
DNA325513, 3311
DNA325514, 3315

DNA325515, 3316	DNA325571, 3417
DNA325516, 3318	DNA325572, 3418
DNA325517, 3320	DNA325573, 3420
DNA325518, 3322	DNA325574, 3422
DNA325519, 3324	DNA325575, 3424
DNA325520, 3325	DNA325576, 3426
DNA325521, 3326	DNA325577, 3427
DNA325522, 3328	DNA325578, 3428
DNA325523, 3331	DNA325579, 3429
DNA325524, 3335	DNA325580, 3430
DNA325525, 3336	DNA325581, 3432
DNA325526, 3337	DNA325582, 3436
DNA325527, 3339	DNA325583, 3437
DNA325528, 3341	DNA325584, 3439
DNA325529, 3342	DNA325585, 3441
DNA325530, 3344	DNA325586, 3442
DNA325531, 3346	DNA325587, 3444
DNA325532, 3348	DNA325588, 3446
DNA325533, 3349	DNA325589, 3448
DNA325534, 3350	DNA325590, 3450
DNA325535, 3352	DNA325591, 3451
DNA325536, 3353	DNA325592, 3454
DNA325537, 3355	DNA325593, 3455
DNA325538, 3357	DNA325594, 3457
DNA325539, 3358	DNA325595, 3458
DNA325540, 3359	DNA325596, 3460
DNA325541, 3361	DNA325597, 3462
DNA325542, 3363	DNA325598, 3463
DNA325543, 3364	DNA325599, 3465
DNA325544, 3365	DNA325600, 3470
DNA325545, 3366	DNA325601, 3472
DNA325546, 3367	DNA325602, 3475
DNA325547, 3369	DNA325603, 3482
DNA325548, 3371	DNA325604, 3483
DNA325549, 3373	DNA325605, 3485
DNA325550, 3374	DNA325606, 3486
DNA325551, 3378	DNA325607, 3488
DNA325552, 3382	DNA325608, 3491
DNA325553, 3384	DNA325609, 3493
DNA325554, 3386	DNA325610, 3494
DNA325555, 3388	DNA325611, 3495
DNA325556, 3394	DNA325612, 3496
DNA325557, 3395	DNA325613, 3500
DNA325558, 3397	DNA325614, 3501
DNA325559, 3398	DNA325615, 3503
DNA325560, 3399	DNA325616, 3504
DNA325561, 3400	DNA325617, 3506
DNA325562, 3401	DNA325618, 3507
DNA325563, 3403	DNA325619, 3509
DNA325564, 3404	DNA325620, 3513
DNA325565, 3406	DNA325621, 3515
DNA325566, 3407	DNA325622, 3517
DNA325567, 3409	DNA325623, 3519
DNA325568, 3411	DNA325624, 3522
DNA325569, 3413	DNA325625, 3528
DNA325570, 3414	DNA325626, 3529

DNA325627, 3531
DNA325628, 3532
DNA325629, 3533
DNA325630, 3535
DNA325631, 3536
DNA325632, 3538
DNA325633, 3539
DNA325634, 3540
DNA325635, 3542
DNA325636, 3543
DNA325637, 3545
DNA325638, 3546
DNA325639, 3548
DNA325640, 3552
DNA325641, 3554
DNA325642, 3557
DNA325643, 3559
DNA325644, 3560
DNA325645, 3561
DNA325646, 3562
DNA325647, 3564
DNA325648, 3566
DNA325649, 3568
DNA325650, 3570
DNA325651, 3571
DNA325652, 3572
DNA325653, 3574
DNA325654, 3576
DNA325655, 3578
DNA325656, 3579
DNA325657, 3580
DNA325658, 3581
DNA325659, 3582
DNA325660, 3583
DNA325661, 3584
DNA325662, 3585
DNA325663, 3586
DNA325664, 3590
DNA325665, 3595
DNA325666, 3596
DNA325667, 3598
DNA325668, 3599
DNA325669, 3602
DNA325670, 3604
DNA325671, 3606
DNA325672, 3608
DNA325673, 3610
DNA325674, 3612
DNA325675, 3614
DNA325676, 3616
DNA325677, 3618
DNA325678, 3622
DNA325679, 3624
DNA325680, 3626
DNA325681, 3630
DNA325682, 3633

DNA325683, 3634
DNA325684, 3635
DNA325685, 3636
DNA325686, 3638
DNA325687, 3640
DNA325688, 3641
DNA325689, 3642
DNA325690, 3643
DNA325691, 3645
DNA325692, 3646
DNA325693, 3648
DNA325694, 3650
DNA325695, 3652
DNA325696, 3654
DNA325697, 3656
DNA325698, 3658
DNA325699, 3659
DNA325700, 3660
DNA325701, 3662
DNA325702, 3663
DNA325703, 3665
DNA325704, 3669
DNA325705, 3671
DNA325706, 3672
DNA325707, 3674
DNA325708, 3676
DNA325709, 3680
DNA325710, 3681
DNA325711, 3683
DNA325712, 3685
DNA325713, 3687
DNA325714, 3689
DNA325715, 3691
DNA325716, 3693
DNA325717, 3695
DNA325718, 3697
DNA325719, 3699
DNA325720, 3700
DNA325721, 3702
DNA325722, 3704
DNA325723, 3705
DNA325724, 3707
DNA325725, 3708
DNA325726, 3710
DNA325727, 3712
DNA325728, 3714
DNA325729, 3715
DNA325730, 3719
DNA325731, 3722
DNA325732, 3726
DNA325733, 3731
DNA325734, 3732
DNA325736, 3734
DNA325737, 3736
DNA325738, 3737
DNA325739, 3739

DNA325740, 3740
DNA325741, 3742
DNA325742, 3744
DNA325743, 3746
DNA325744, 3748
DNA325745, 3750
DNA325746, 3752
DNA325747, 3754
DNA325748, 3755
DNA325749, 3757
DNA325750, 3759
DNA325751, 3761
DNA325752, 3765
DNA325753, 3766
DNA325754, 3767
DNA325755, 3769
DNA325756, 3771
DNA325757, 3772
DNA325758, 3773
DNA325759, 3774
DNA325760, 3775
DNA325761, 3779
DNA325762, 3781
DNA325763, 3783
DNA325764, 3785
DNA325765, 3787
DNA325766, 3788
DNA325767, 3790
DNA325768, 3792
DNA325769, 3794
DNA325770, 3796
DNA325771, 3797
DNA325772, 3798
DNA325773, 3800
DNA325775, 3802
DNA325776, 3804
DNA325777, 3805
DNA325778, 3807
DNA325779, 3809
DNA325780, 3810
DNA325781, 3812
DNA325782, 3814
DNA325783, 3816
DNA325784, 3818
DNA325785, 3819
DNA325786, 3821
DNA325787, 3825
DNA325788, 3826
DNA325789, 3829
DNA325790, 3831
DNA325791, 3833
DNA325792, 3834
DNA325793, 3835
DNA325794, 3836
DNA325795, 3837
DNA325796, 3839

DNA325797, 3841
DNA325798, 3843
DNA325799, 3845
DNA325800, 3847
DNA325801, 3849
DNA325802, 3851
DNA325803, 3853
DNA325804, 3855
DNA325805, 3856
DNA325806, 3857
DNA325807, 3859
DNA325808, 3861
DNA325809, 3862
DNA325810, 3868
DNA325811, 3869
DNA325812, 3870
DNA325813, 3872
DNA325814, 3874
DNA325815, 3876
DNA325816, 3877
DNA325817, 3878
DNA325818, 3880
DNA325819, 3881
DNA325820, 3883
DNA325821, 3884
DNA325822, 3886
DNA325823, 3889
DNA325824, 3891
DNA325825, 3893
DNA325826, 3895
DNA325827, 3898
DNA325828, 3902
DNA325829, 3903
DNA325830, 3904
DNA325831, 3906
DNA325832, 3908
DNA325833, 3910
DNA325834, 3914
DNA325835, 3916
DNA325836, 3917
DNA325837, 3918
DNA325838, 3920
DNA325839, 3921
DNA325840, 3923
DNA325841, 3924
DNA325842, 3925
DNA325843, 3926
DNA325844, 3928
DNA325845, 3930
DNA325847, 3931
DNA325848, 3932
DNA325849, 3933
DNA325850, 3935
DNA325851, 3937
DNA325852, 3938
DNA325853, 3940

DNA325854, 3942
DNA325855, 3944
DNA325856, 3946
DNA325857, 3948
DNA325858, 3949
DNA325859, 3950
DNA325860, 3951
DNA325861, 3953
DNA325862, 3955
DNA325863, 3957
DNA325864, 3958
DNA325865, 3959
DNA325866, 3960
DNA325867, 3964
DNA325868, 3966
DNA325869, 3967
DNA325870, 3968
DNA325871, 3969
DNA325872, 3971
DNA325873, 3973
DNA325874, 3975
DNA325875, 3978
DNA325876, 3980
DNA325877, 3981
DNA325878, 3983
DNA325879, 3986
DNA325880, 3987
DNA325881, 3988
DNA325882, 3990
DNA325883, 3991
DNA325884, 3994
DNA325885, 3996
DNA325886, 3997
DNA325887, 3999
DNA325888, 4001
DNA325889, 4003
DNA325890, 4005
DNA325891, 4006
DNA325892, 4008
DNA325893, 4010
DNA325894, 4012
DNA325895, 4014
DNA325896, 4016
DNA325897, 4018
DNA325898, 4019
DNA325899, 4020
DNA325900, 4022
DNA325901, 4024
DNA325902, 4025
DNA325903, 4027
DNA325904, 4029
DNA325905, 4031
DNA325906, 4032
DNA325907, 4033
DNA325908, 4034
DNA325909, 4035

DNA325910, 4037
DNA325911, 4039
DNA325912, 4040
DNA325913, 4044
DNA325914, 4045
DNA325915, 4046
DNA325916, 4048
DNA325917, 4050
DNA325918, 4052
DNA325919, 4054
DNA325920, 4055
DNA325921, 4057
DNA325922, 4061
DNA325923, 4063
DNA325924, 4065
DNA325925, 4067
DNA325926, 4068
DNA325927, 4069
DNA325928, 4071
DNA325929, 4072
DNA325930, 4073
DNA325931, 4074
DNA325932, 4075
DNA325933, 4077
DNA325934, 4081
DNA325935, 4082
DNA325936, 4084
DNA325937, 4086
DNA325938, 4088
DNA325939, 4090
DNA325940, 4091
DNA325941, 4092
DNA325942, 4094
DNA325943, 4097
DNA325944, 4098
DNA325945, 4100
DNA325946, 4101
DNA325947, 4103
DNA325948, 4105
DNA325949, 4106
DNA325950, 4108
DNA325951, 4112
DNA325952, 4114
DNA325953, 4115
DNA325954, 4116
DNA325955, 4118
DNA325956, 4119
DNA325957, 4120
DNA325958, 4121
DNA325959, 4122
DNA325960, 4123
DNA325961, 4124
DNA325962, 4125
DNA325963, 4127
DNA325964, 4129
DNA325965, 4130

DNA325966, 4132
DNA325967, 4133
DNA325968, 4134
DNA325969, 4135
DNA325970, 4136
DNA325971, 4138
DNA325972, 4139
DNA325973, 4143
DNA325974, 4145
DNA325975, 4147
DNA325976, 4148
DNA325977, 4150
DNA325978, 4152
DNA325979, 4154
DNA325980, 4156
DNA325981, 4157
DNA325982, 4159
DNA325983, 4160
DNA325984, 4163
DNA325985, 4165
DNA325986, 4167
DNA325987, 4168
DNA325988, 4172
DNA325989, 4174
DNA325990, 4176
DNA325991, 4178
DNA325992, 4180
DNA325993, 4184
DNA325994, 4186
DNA325995, 4187
DNA325996, 4189
DNA325997, 4191
DNA325998, 4193
DNA325999, 4195
DNA326000, 4197
DNA326001, 4199
DNA326002, 4200
DNA326003, 4202
DNA326004, 4203
DNA326005, 4205
DNA326006, 4207
DNA326007, 4210
DNA326008, 4211
DNA326009, 4213
DNA326010, 4216
DNA326011, 4218
DNA326012, 4220
DNA326013, 4221
DNA326014, 4222
DNA326015, 4226
DNA326016, 4228
DNA326017, 4230
DNA326018, 4232
DNA326019, 4234
DNA326020, 4236
DNA326021, 4237

DNA326022, 4239
DNA326023, 4241
DNA326024, 4244
DNA326025, 4245
DNA326026, 4246
DNA326027, 4248
DNA326028, 4250
DNA326029, 4251
DNA326030, 4252
DNA326031, 4254
DNA326032, 4256
DNA326033, 4257
DNA326034, 4259
DNA326035, 4261
DNA326036, 4263
DNA326037, 4269
DNA326038, 4270
DNA326039, 4272
DNA326040, 4273
DNA326041, 4275
DNA326042, 4277
DNA326043, 4278
DNA326044, 4279
DNA326045, 4281
DNA326046, 4282
DNA326047, 4283
DNA326048, 4285
DNA326049, 4286
DNA326050, 4287
DNA326051, 4289
DNA326052, 4290
DNA326053, 4292
DNA326054, 4293
DNA326055, 4295
DNA326056, 4296
DNA326057, 4298
DNA326058, 4302
DNA326059, 4304
DNA326060, 4307
DNA326061, 4309
DNA326062, 4310
DNA326063, 4311
DNA326064, 4312
DNA326065, 4314
DNA326066, 4315
DNA326067, 4317
DNA326068, 4319
DNA326069, 4322
DNA326070, 4323
DNA326071, 4325
DNA326072, 4326
DNA326073, 4327
DNA326074, 4329
DNA326075, 4331
DNA326076, 4333
DNA326077, 4334

DNA326078, 4335
DNA326079, 4337
DNA326080, 4338
DNA326081, 4340
DNA326082, 4342
DNA326083, 4344
DNA326084, 4346
DNA326085, 4348
DNA326086, 4350
DNA326087, 4352
DNA326088, 4353
DNA326089, 4354
DNA326090, 4356
DNA326091, 4358
DNA326092, 4364
DNA326093, 4366
DNA326094, 4368
DNA326095, 4372
DNA326096, 4376
DNA326097, 4378
DNA326098, 4380
DNA326099, 4382
DNA326100, 4384
DNA326101, 4386
DNA326102, 4388
DNA326103, 4390
DNA326104, 4392
DNA326105, 4394
DNA326106, 4396
DNA326107, 4398
DNA326108, 4400
DNA326109, 4402
DNA326110, 4404
DNA326111, 4406
DNA326112, 4408
DNA326113, 4410
DNA326114, 4411
DNA326115, 4413
DNA326116, 4414
DNA326117, 4416
DNA326118, 4418
DNA326119, 4420
DNA326120, 4423
DNA326121, 4425
DNA326122, 4426
DNA326123, 4427
DNA326124, 4429
DNA326125, 4430
DNA326126, 4431
DNA326127, 4432
DNA326128, 4434
DNA326129, 4435
DNA326130, 4436
DNA326131, 4438
DNA326132, 4440
DNA326133, 4442

DNA326134, 4444
DNA326135, 4448
DNA326136, 4449
DNA326137, 4451
DNA326138, 4453
DNA326139, 4454
DNA326140, 4456
DNA326141, 4458
DNA326142, 4460
DNA326143, 4461
DNA326144, 4462
DNA326145, 4463
DNA326146, 4465
DNA326147, 4467
DNA326148, 4468
DNA326149, 4470
DNA326150, 4472
DNA326151, 4474
DNA326152, 4478
DNA326153, 4479
DNA326154, 4480
DNA326155, 4482
DNA326156, 4483
DNA326157, 4484
DNA326158, 4485
DNA326159, 4489
DNA326160, 4490
DNA326161, 4491
DNA326162, 4493
DNA326163, 4495
DNA326164, 4497
DNA326165, 4498
DNA326166, 4500
DNA326167, 4502
DNA326168, 4504
DNA326169, 4505
DNA326170, 4509
DNA326171, 4511
DNA326172, 4513
DNA326173, 4514
DNA326174, 4518
DNA326175, 4522
DNA326176, 4524
DNA326177, 4526
DNA326178, 4527
DNA326179, 4528
DNA326180, 4532
DNA326181, 4534
DNA326182, 4535
DNA326183, 4537
DNA326184, 4538
DNA326185, 4539
DNA326186, 4541
DNA326187, 4543
DNA326188, 4544
DNA326189, 4545

DNA326190, 4547
DNA326191, 4549
DNA326192, 4551
DNA326193, 4553
DNA326194, 4555
DNA326195, 4556
DNA326196, 4558
DNA326197, 4560
DNA326198, 4561
DNA326199, 4562
DNA326200, 4566
DNA326201, 4570
DNA326202, 4571
DNA326203, 4573
DNA326204, 4577
DNA326205, 4581
DNA326206, 4583
DNA326207, 4584
DNA326208, 4586
DNA326209, 4588
DNA326210, 4590
DNA326211, 4592
DNA326212, 4594
DNA326213, 4596
DNA326214, 4597
DNA326215, 4599
DNA326216, 4600
DNA326217, 4602
DNA326218, 4604
DNA326219, 4606
DNA326220, 4608
DNA326221, 4610
DNA326222, 4612
DNA326223, 4614
DNA326224, 4616
DNA326225, 4617
DNA326226, 4619
DNA326227, 4621
DNA326228, 4622
DNA326229, 4624
DNA326230, 4628
DNA326231, 4630
DNA326232, 4632
DNA326233, 4633
DNA326234, 4635
DNA326235, 4637
DNA326236, 4638
DNA326237, 4640
DNA326238, 4641
DNA326239, 4642
DNA326240, 4644
DNA326241, 4645
DNA326242, 4646
DNA326243, 4647
DNA326244, 4648
DNA326245, 4650

DNA326246, 4651
DNA326247, 4653
DNA326248, 4654
DNA326249, 4656
DNA326250, 4658
DNA326251, 4659
DNA326252, 4661
DNA326253, 4663
DNA326254, 4665
DNA326255, 4667
DNA326256, 4669
DNA326257, 4671
DNA326258, 4672
DNA326259, 4674
DNA326260, 4675
DNA326261, 4677
DNA326262, 4678
DNA326263, 4680
DNA326264, 4682
DNA326265, 4684
DNA326266, 4686
DNA326267, 4689
DNA326268, 4691
DNA326269, 4693
DNA326270, 4694
DNA326271, 4695
DNA326272, 4696
DNA326273, 4697
DNA326274, 4701
DNA326275, 4703
DNA326276, 4704
DNA326277, 4706
DNA326278, 4707
DNA326279, 4710
DNA326280, 4712
DNA326281, 4713
DNA326282, 4716
DNA326283, 4718
DNA326284, 4721
DNA326285, 4723
DNA326286, 4724
DNA326287, 4725
DNA326288, 4727
DNA326289, 4730
DNA326290, 4732
DNA326291, 4734
DNA326292, 4735
DNA326293, 4737
DNA326294, 4739
DNA326295, 4741
DNA326296, 4744
DNA326297, 4745
DNA326298, 4749
DNA326299, 4750
DNA326300, 4751
DNA326301, 4752

DNA326302, 4754	DNA326358, 4867
DNA326303, 4755	DNA326359, 4869
DNA326304, 4757	DNA326360, 4871
DNA326305, 4758	DNA326361, 4873
DNA326306, 4760	DNA326362, 4875
DNA326307, 4761	DNA326363, 4880
DNA326308, 4763	DNA326364, 4881
DNA326309, 4765	DNA326365, 4883
DNA326310, 4767	DNA326366, 4885
DNA326311, 4768	DNA326367, 4893
DNA326312, 4769	DNA326368, 4895
DNA326313, 4771	DNA326369, 4897
DNA326314, 4773	DNA326370, 4902
DNA326315, 4775	DNA326371, 4905
DNA326316, 4777	DNA326372, 4906
DNA326317, 4780	DNA326373, 4908
DNA326318, 4784	DNA326374, 4910
DNA326319, 4786	DNA326375, 4911
DNA326320, 4788	DNA326376, 4913
DNA326321, 4790	DNA326377, 4915
DNA326322, 4792	DNA326378, 4916
DNA326323, 4794	DNA326379, 4917
DNA326324, 4798	DNA326380, 4921
DNA326325, 4800	DNA326381, 4923
DNA326326, 4801	DNA326382, 4924
DNA326327, 4803	DNA326383, 4926
DNA326328, 4807	DNA326384, 4927
DNA326329, 4809	DNA326385, 4929
DNA326330, 4810	DNA326386, 4931
DNA326331, 4814	DNA326387, 4933
DNA326332, 4816	DNA326388, 4935
DNA326333, 4818	DNA326389, 4938
DNA326334, 4819	DNA326390, 4941
DNA326335, 4822	DNA326391, 4942
DNA326336, 4824	DNA326392, 4943
DNA326337, 4825	DNA326393, 4944
DNA326338, 4826	DNA326394, 4945
DNA326339, 4827	DNA326395, 4946
DNA326340, 4829	DNA326396, 4948
DNA326341, 4830	DNA326397, 4950
DNA326342, 4832	DNA326398, 4951
DNA326343, 4834	DNA326399, 4955
DNA326344, 4836	DNA326400, 4957
DNA326345, 4838	DNA326401, 4958
DNA326346, 4840	DNA326402, 4960
DNA326347, 4847	DNA326403, 4962
DNA326348, 4849	DNA326404, 4965
DNA326349, 4850	DNA326405, 4967
DNA326350, 4852	DNA326406, 4969
DNA326351, 4856	DNA326407, 4971
DNA326352, 4857	DNA326408, 4973
DNA326353, 4859	DNA326409, 4977
DNA326354, 4861	DNA326410, 4978
DNA326355, 4863	DNA326411, 4980
DNA326356, 4864	DNA326412, 4982
DNA326357, 4865	DNA326413, 4984

DNA326414, 4987
DNA326415, 4988
DNA326416, 4989
DNA326417, 4991
DNA326418, 4992
DNA326419, 4994
DNA326420, 4995
DNA326421, 4996
DNA326422, 4998
DNA326423, 4999
DNA326424, 5000
DNA326425, 5001
DNA326426, 5002
DNA326427, 5004
DNA326428, 5006
DNA326429, 5008
DNA326430, 5010
DNA326431, 5011
DNA326432, 5013
DNA326433, 5016
DNA326434, 5018
DNA326435, 5019
DNA326436, 5020
DNA326437, 5021
DNA326438, 5022
DNA326439, 5025
DNA326440, 5026
DNA326441, 5027
DNA326442, 5028
DNA326443, 5030
DNA326444, 5031
DNA326445, 5032
DNA326446, 5034
DNA326447, 5036
DNA326448, 5037
DNA326449, 5042
DNA326450, 5043
DNA326451, 5045
DNA326452, 5046
DNA326453, 5048
DNA326454, 5049
DNA326455, 5054
DNA326456, 5055
DNA326457, 5058
DNA326458, 5060
DNA326459, 5062
DNA326460, 5064
DNA326461, 5065
DNA326462, 5066
DNA326463, 5067
DNA326464, 5069
DNA326465, 5071
DNA326466, 5072
DNA326467, 5074
DNA326468, 5075
DNA326469, 5076

DNA326470, 5078
DNA326471, 5080
DNA326472, 5082
DNA326473, 5083
DNA326474, 5084
DNA326475, 5086
DNA326476, 5088
DNA326477, 5089
DNA326478, 5090
DNA326479, 5092
DNA326480, 5093
DNA326481, 5095
DNA326482, 5097
DNA326483, 5098
DNA326484, 5100
DNA326485, 5102
DNA326486, 5104
DNA326487, 5106
DNA326488, 5108
DNA326489, 5109
DNA326490, 5110
DNA326491, 5112
DNA326492, 5113
DNA326493, 5114
DNA326494, 5117
DNA326495, 5119
DNA326496, 5120
DNA326497, 5122
DNA326498, 5124
DNA326499, 5126
DNA326500, 5128
DNA326501, 5130
DNA326502, 5131
DNA326503, 5132
DNA326504, 5134
DNA326505, 5135
DNA326506, 5137
DNA326507, 5138
DNA326508, 5140
DNA326509, 5141
DNA326510, 5143
DNA326511, 5145
DNA326512, 5148
DNA326513, 5150
DNA326514, 5152
DNA326515, 5155
DNA326516, 5157
DNA326517, 5159
DNA326518, 5160
DNA326519, 5161
DNA326520, 5163
DNA326521, 5165
DNA326522, 5166
DNA326523, 5168
DNA326524, 5169
DNA326525, 5171

DNA326526, 5173	DNA326583, 5270
DNA326527, 5175	DNA326584, 5274
DNA326528, 5176	DNA326585, 5276
DNA326529, 5178	DNA326586, 5281
DNA326530, 5180	DNA326587, 5283
DNA326531, 5181	DNA326588, 5285
DNA326532, 5183	DNA326589, 5286
DNA326533, 5184	DNA326590, 5288
DNA326534, 5186	DNA326591, 5290
DNA326535, 5188	DNA326592, 5292
DNA326536, 5190	DNA326593, 5294
DNA326537, 5192	DNA326594, 5295
DNA326538, 5194	DNA326595, 5297
DNA326539, 5195	DNA326596, 5300
DNA326540, 5196	DNA326597, 5302
DNA326541, 5197	DNA326598, 5303
DNA326542, 5203	DNA326599, 5305
DNA326543, 5205	DNA326600, 5307
DNA326544, 5208	DNA326601, 5308
DNA326546, 5210	DNA326602, 5310
DNA326547, 5212	DNA326603, 5311
DNA326548, 5213	DNA326604, 5314
DNA326549, 5214	DNA326605, 5316
DNA326550, 5216	DNA326606, 5317
DNA326551, 5218	DNA326607, 5319
DNA326552, 5219	DNA326608, 5321
DNA326553, 5221	DNA326609, 5323
DNA326554, 5222	DNA326610, 5325
DNA326555, 5223	DNA326611, 5326
DNA326556, 5225	DNA326612, 5330
DNA326557, 5226	DNA326613, 5331
DNA326558, 5227	DNA326614, 5332
DNA326559, 5229	DNA326615, 5334
DNA326560, 5230	DNA326616, 5336
DNA326561, 5236	DNA326617, 5337
DNA326562, 5237	DNA326618, 5338
DNA326563, 5239	DNA326619, 5339
DNA326564, 5240	DNA326620, 5341
DNA326565, 5241	DNA326621, 5343
DNA326566, 5243	DNA326622, 5345
DNA326567, 5244	DNA326623, 5347
DNA326568, 5246	DNA326624, 5349
DNA326569, 5247	DNA326625, 5350
DNA326570, 5248	DNA326626, 5354
DNA326571, 5250	DNA326627, 5355
DNA326572, 5252	DNA326628, 5357
DNA326573, 5254	DNA326629, 5358
DNA326574, 5256	DNA326630, 5360
DNA326575, 5257	DNA326631, 5362
DNA326576, 5260	DNA326632, 5364
DNA326577, 5261	DNA326633, 5366
DNA326578, 5262	DNA326634, 5367
DNA326579, 5264	DNA326635, 5369
DNA326580, 5266	DNA326636, 5370
DNA326581, 5267	DNA326637, 5371
DNA326582, 5269	DNA326638, 5372

DNA326639, 5374	DNA326695, 5474
DNA326640, 5376	DNA326696, 5478
DNA326641, 5378	DNA326697, 5480
DNA326642, 5379	DNA326698, 5482
DNA326643, 5380	DNA326699, 5483
DNA326644, 5382	DNA326700, 5484
DNA326645, 5383	DNA326701, 5485
DNA326646, 5384	DNA326702, 5486
DNA326647, 5385	DNA326703, 5487
DNA326648, 5389	DNA326704, 5488
DNA326649, 5391	DNA326705, 5489
DNA326650, 5393	DNA326706, 5491
DNA326651, 5395	DNA326707, 5492
DNA326652, 5396	DNA326708, 5496
DNA326653, 5398	DNA326709, 5497
DNA326654, 5399	DNA326710, 5499
DNA326655, 5401	DNA326711, 5501
DNA326656, 5403	DNA326712, 5508
DNA326657, 5404	DNA326713, 5510
DNA326658, 5406	DNA326714, 5519
DNA326659, 5408	DNA326715, 5521
DNA326660, 5409	DNA326716, 5522
DNA326661, 5411	DNA326717, 5525
DNA326662, 5413	DNA326718, 5527
DNA326663, 5415	DNA326719, 5528
DNA326664, 5417	DNA326720, 5529
DNA326665, 5419	DNA326721, 5530
DNA326666, 5423	DNA326722, 5531
DNA326667, 5425	DNA326723, 5532
DNA326668, 5428	DNA326724, 5534
DNA326669, 5430	DNA326725, 5536
DNA326670, 5432	DNA326726, 5537
DNA326671, 5436	DNA326727, 5539
DNA326672, 5438	DNA326728, 5541
DNA326673, 5439	DNA326729, 5544
DNA326674, 5440	DNA326730, 5546
DNA326675, 5443	DNA326731, 5548
DNA326676, 5444	DNA326732, 5549
DNA326677, 5445	DNA326733, 5552
DNA326678, 5446	DNA326734, 5554
DNA326679, 5447	DNA326735, 5556
DNA326680, 5450	DNA326736, 5558
DNA326681, 5451	DNA326737, 5560
DNA326682, 5453	DNA326738, 5564
DNA326683, 5454	DNA326739, 5566
DNA326684, 5456	DNA326740, 5570
DNA326685, 5458	DNA326741, 5571
DNA326686, 5460	DNA326742, 5573
DNA326687, 5461	DNA326743, 5574
DNA326688, 5462	DNA326744, 5578
DNA326689, 5463	DNA326745, 5580
DNA326690, 5465	DNA326746, 5582
DNA326691, 5466	DNA326747, 5584
DNA326692, 5468	DNA326748, 5586
DNA326693, 5470	DNA326749, 5588
DNA326694, 5472	DNA326750, 5592

DNA326751, 5595	DNA326807, 5712
DNA326752, 5597	DNA326808, 5713
DNA326753, 5598	DNA326809, 5715
DNA326754, 5600	DNA326810, 5717
DNA326755, 5602	DNA326811, 5719
DNA326756, 5603	DNA326812, 5723
DNA326757, 5605	DNA326813, 5725
DNA326758, 5607	DNA326814, 5727
DNA326759, 5608	DNA326815, 5728
DNA326760, 5610	DNA326816, 5729
DNA326761, 5612	DNA326817, 5731
DNA326762, 5613	DNA326818, 5733
DNA326763, 5617	DNA326819, 5736
DNA326764, 5619	DNA326820, 5740
DNA326765, 5621	DNA326821, 5742
DNA326766, 5623	DNA326822, 5744
DNA326767, 5629	DNA326823, 5749
DNA326768, 5631	DNA326824, 5750
DNA326769, 5633	DNA326825, 5752
DNA326770, 5635	DNA326826, 5754
DNA326771, 5636	DNA326827, 5756
DNA326772, 5642	DNA326828, 5757
DNA326773, 5644	DNA326829, 5759
DNA326774, 5646	DNA326830, 5762
DNA326775, 5647	DNA326831, 5763
DNA326776, 5648	DNA326832, 5765
DNA326777, 5650	DNA326833, 5766
DNA326778, 5652	DNA326834, 5768
DNA326779, 5656	DNA326835, 5769
DNA326780, 5658	DNA326836, 5773
DNA326781, 5660	DNA326837, 5776
DNA326782, 5661	DNA326838, 5778
DNA326783, 5663	DNA326839, 5779
DNA326784, 5665	DNA326840, 5781
DNA326785, 5667	DNA326841, 5783
DNA326786, 5670	DNA326842, 5787
DNA326787, 5671	DNA326843, 5793
DNA326788, 5673	DNA326844, 5794
DNA326789, 5674	DNA326845, 5795
DNA326790, 5675	DNA326846, 5796
DNA326791, 5678	DNA326847, 5798
DNA326792, 5683	DNA326848, 5800
DNA326793, 5687	DNA326849, 5802
DNA326794, 5688	DNA326850, 5804
DNA326795, 5689	DNA326851, 5806
DNA326796, 5691	DNA326852, 5808
DNA326797, 5693	DNA326853, 5809
DNA326798, 5695	DNA326854, 5811
DNA326799, 5696	DNA326855, 5813
DNA326800, 5698	DNA326856, 5816
DNA326801, 5700	DNA326857, 5818
DNA326802, 5701	DNA326858, 5819
DNA326803, 5705	DNA326859, 5821
DNA326804, 5706	DNA326860, 5823
DNA326805, 5708	DNA326861, 5824
DNA326806, 5710	DNA326862, 5826

DNA326863, 5828
DNA326864, 5832
DNA326865, 5834
DNA326866, 5838
DNA326867, 5840
DNA326868, 5842
DNA326869, 5846
DNA326870, 5847
DNA326871, 5849
DNA326872, 5851
DNA326873, 5853
DNA326874, 5855
DNA326875, 5857
DNA326876, 5859
DNA326877, 5861
DNA326878, 5863
DNA326879, 5865
DNA326880, 5867
DNA326881, 5869
DNA326882, 5871
DNA326883, 5875
DNA326884, 5876
DNA326885, 5877
DNA326886, 5878
DNA326887, 5879
DNA326888, 5883
DNA326889, 5887
DNA326890, 5889
DNA326891, 5894
DNA326892, 5898
DNA326893, 5900
DNA326894, 5902
DNA326895, 5903
DNA326896, 5905
DNA326897, 5907
DNA326898, 5908
DNA326899, 5910
DNA326900, 5911
DNA326901, 5913
DNA326902, 5914
DNA326903, 5915
DNA326904, 5917
DNA326905, 5919
DNA326906, 5923
DNA326907, 5924
DNA326908, 5925
DNA326909, 5926
DNA326910, 5927
DNA326911, 5928
DNA326912, 5929
DNA326913, 5930
DNA326914, 5931
DNA326915, 5933
DNA326916, 5937
DNA326917, 5941
DNA326918, 5943

DNA326919, 5945
DNA326920, 5946
DNA326921, 5949
DNA326922, 5950
DNA326923, 5951
DNA326924, 5953
DNA326925, 5954
DNA326926, 5958
DNA326927, 5960
DNA326928, 5961
DNA326929, 5963
DNA326930, 5964
DNA326931, 5967
DNA326932, 5968
DNA326933, 5969
DNA326934, 5971
DNA326935, 5975
DNA326936, 5977
DNA326937, 5979
DNA326938, 5981
DNA326939, 5983
DNA326940, 5985
DNA326941, 5986
DNA326942, 5987
DNA326943, 5991
DNA326944, 5993
DNA326945, 5996
DNA326946, 5998
DNA326947, 5999
DNA326948, 6001
DNA326949, 6007
DNA326950, 6009
DNA326951, 6013
DNA326952, 6014
DNA326953, 6015
DNA326954, 6017
DNA326955, 6019
DNA326956, 6022
DNA326957, 6024
DNA326958, 6025
DNA326959, 6029
DNA326960, 6031
DNA326961, 6032
DNA326962, 6036
DNA326963, 6040
DNA326964, 6042
DNA326965, 6043
DNA326966, 6047
DNA326967, 6049
DNA326968, 6051
DNA326969, 6052
DNA326970, 6054
DNA326971, 6056
DNA326972, 6058
DNA326973, 6060
DNA326974, 6061

DNA326975, 6063
DNA326976, 6064
DNA326977, 6065
DNA326978, 6066
DNA326979, 6070
DNA326980, 6072
DNA326981, 6074
DNA326982, 6077
DNA326983, 6081
DNA326984, 6083
DNA326985, 6085
DNA326986, 6087
DNA326987, 6088
DNA326988, 6089
DNA326989, 6090
DNA326990, 6091
DNA326991, 6093
DNA326992, 6094
DNA326993, 6095
DNA326994, 6097
DNA326995, 6099
DNA326996, 6103
DNA326997, 6106
DNA326998, 6108
DNA326999, 6109
DNA327000, 6111
DNA327001, 6113
DNA327002, 6114
DNA327003, 6116
DNA327004, 6118
DNA327005, 6119
DNA327006, 6121
DNA327007, 6122
DNA327008, 6123
DNA327009, 6124
DNA327010, 6128
DNA327011, 6130
DNA327012, 6131
DNA327013, 6132
DNA327014, 6134
DNA327015, 6136
DNA327016, 6138
DNA327017, 6140
DNA327018, 6142
DNA327019, 6143
DNA327020, 6145
DNA327021, 6146
DNA327022, 6151
DNA327023, 6152
DNA327024, 6153
DNA327025, 6155
DNA327026, 6157
DNA327027, 6158
DNA327028, 6159
DNA327029, 6161
DNA327030, 6163

DNA327031, 6165
DNA327032, 6167
DNA327033, 6169
DNA327034, 6170
DNA327035, 6172
DNA327036, 6173
DNA327037, 6174
DNA327038, 6176
DNA327039, 6177
DNA327040, 6179
DNA327041, 6183
DNA327042, 6185
DNA327043, 6189
DNA327044, 6192
DNA327045, 6194
DNA327046, 6196
DNA327047, 6199
DNA327048, 6201
DNA327049, 6203
DNA327050, 6204
DNA327051, 6206
DNA327052, 6207
DNA327053, 6209
DNA327054, 6210
DNA327055, 6212
DNA327056, 6216
DNA327057, 6218
DNA327058, 6220
DNA327059, 6222
DNA327060, 6224
DNA327061, 6226
DNA327062, 6227
DNA327063, 6228
DNA327064, 6229
DNA327065, 6232
DNA327066, 6233
DNA327067, 6235
DNA327068, 6237
DNA327069, 6238
DNA327070, 6241
DNA327071, 6242
DNA327072, 6244
DNA327073, 6246
DNA327074, 6248
DNA327075, 6250
DNA327076, 6251
DNA327077, 6253
DNA327078, 6255
DNA327079, 6256
DNA327080, 6259
DNA327081, 6261
DNA327082, 6263
DNA327083, 6265
DNA327084, 6267
DNA327085, 6268
DNA327086, 6269

DNA327087, 6274	DNA88051, 898
DNA327088, 6275	DNA88084, 5511
DNA327089, 6276	DNA88100, 1089
DNA327090, 6278	DNA88114, 3452
DNA327091, 6280	DNA88176, 3333
DNA327092, 6281	DNA88239, 5791
DNA327093, 6282	DNA88261, 4579
DNA327094, 6284	DNA88281, 5050
DNA327095, 6289	DNA88350, 2796
DNA327096, 6291	DNA88378, 4845
DNA327097, 6293	DNA88430, 4963
DNA327098, 6295	DNA88457, 5040
DNA327099, 6297	DNA88547, 1223
DNA327100, 6299	DNA88554, 4903
DNA327101, 6300	DNA88562, 2961
DNA327102, 6302	DNA88569, 5789
DNA327103, 6304	DNA89239, 1327
DNA327104, 6306	DNA89242, 2695
DNA327105, 6308	DNA97285, 3175
DNA327106, 6310	DNA97290, 4887
DNA327107, 6311	DNA97293, 4421
DNA327108, 6313	DNA97298, 5734
DNA327109, 6315	DNA97300, 4687
DNA327110, 6316	
DNA327111, 6320	
DNA327112, 6323	
DNA327113, 6325	
DNA327114, 6326	
DNA327115, 6328	
DNA327116, 6329	
DNA327117, 6330	
DNA327118, 6336	
DNA327119, 6346	
DNA327120, 6348	
DNA327121, 6349	
DNA327122, 6350	
DNA327123, 6351	
DNA327124, 6352	
DNA327125, 6353	
DNA327126, 6354	
DNA327127, 6355	
DNA66475, 4796	
DNA75863, 3245	
DNA76504, 6270	
DNA79101, 3678	
DNA79129, 1352	
DNA79313, 3524	
DNA82328, 624	
DNA83020, 1671	
DNA83022, 2495	
DNA83046, 558	
DNA83085, 173	
DNA83141, 2361	
DNA83154, 5590	
DNA83170, 5679	
DNA83180, 3476	

PRO Index (to Figure number)

PRO, 1189	PRO12520, 1025
PRO10002, 487	PRO12565, 1146
PRO10194, 2441	PRO12573, 3527
PRO10297, 1479	PRO12618, 45
PRO10360, 1923	PRO12683, 4399
PRO10400, 4928	PRO12774, 4306
PRO10404, 3952	PRO12779, 1154
PRO10485, 5127	PRO12792, 807
PRO10498, 967	PRO12797, 2035
PRO10602, 1207	PRO12800, 5503
PRO10685, 1633	PRO12806, 4954
PRO10692, 644	PRO12813, 3014
PRO10723, 6245	PRO12822, 5429
PRO10760, 211	PRO12838, 2547
PRO1077, 5094	PRO12839, 3758
PRO10824, 2652	PRO12841, 1067
PRO10838, 3657	PRO12845, 6023
PRO10849, 1709	PRO1285, 1665
PRO10935, 6279	PRO12851, 2905
PRO11048, 1285	PRO12878, 3250
PRO11077, 1571	PRO12886, 6021
PRO1108, 2532	PRO12892, 5477
PRO1112, 2003	PRO12902, 3467
PRO11139, 2981	PRO12916, 4080
PRO11197, 833	PRO1314, 1239
PRO11213, 3655	PRO1555, 2457
PRO11262, 3172	PRO1707, 625
PRO11265, 2589	PRO1720, 5782
PRO11403, 902, 4970	PRO1869, 3909
PRO11582, 556	PRO188, 530
PRO11601, 3521	PRO1910, 2835
PRO11691, 3186	PRO1927, 1847
PRO1182, 646	PRO19615, 1822
PRO119, 2229	PRO19933, 2109
PRO11982, 3915	PRO201, 5209
PRO1204, 4797	PRO20117, 3257, 3259
PRO12077, 1420	PRO20136, 49
PRO12130, 5315	PRO2018, 3246
PRO12134, 6006	PRO2042, 2496
PRO12135, 5897	PRO2054, 4066
PRO12187, 3412	PRO2065, 5780
PRO12198, 4142	PRO2066, 4049
PRO12199, 682	PRO2077, 1217
PRO12224, 3205	PRO2109, 5591
PRO12265, 4937	PRO2146, 899
PRO12324, 5704	PRO21481, 2669
PRO124, 3121	PRO2172, 1090
PRO12416, 1733	PRO21728, 5837
PRO12448, 3385	PRO21773, 3666
PRO12460, 5722	PRO21887, 4783
PRO12468, 2185	PRO21924, 3481
PRO1248, 565	PRO2198, 4639
PRO12490, 6055	PRO22196, 94

PRO22262, 168
PRO22304, 147
PRO224, 5217
PRO22481, 6028
PRO22613, 5284
PRO22637, 4569
PRO2267, 5051
PRO2269, 61
PRO22771, 1625
PRO22897, 2339
PRO22907, 2634, 2636
PRO231, 329
PRO23123, 999
PRO23124, 949, 951
PRO23201, 2615
PRO23231, 6059
PRO23238, 5589
PRO23248, 2568
PRO23300, 586
PRO23362, 2194
PRO23364, 2948
PRO2355, 4512
PRO2373, 6125
PRO23746, 13
PRO23794, 5251
PRO23797, 2024, 2151
PRO23845, 5394
PRO23942, 429
PRO24002, 5748
PRO24021, 6317
PRO24028, 855
PRO24075, 4531
PRO24077, 5761
PRO24091, 978
PRO2420, 5790
PRO24831, 3307
PRO24851, 577
PRO24856, 125
PRO25115, 4878
PRO25245, 6312
PRO25302, 5882
PRO2537, 6271
PRO2549, 3679
PRO2551, 1353
PRO2555, 3525
PRO2560, 5096
PRO2561, 1672
PRO2569, 559
PRO2570, 2477
PRO2583, 174
PRO25845, 3298
PRO25849, 1853
PRO25881, 5498
PRO25985, 3156
PRO2604, 2362
PRO2610, 981

PRO2615, 5680
PRO26194, 82
PRO2622, 3477
PRO26228, 983
PRO2644, 5512
PRO2660, 3453
PRO2665, 922
PRO2672, 4550
PRO2685, 3334
PRO2711, 5792
PRO2718, 5282
PRO2719, 4580
PRO2720, 4219
PRO2732, 4175
PRO2733, 2443
PRO2758, 2797
PRO2769, 4846
PRO2788, 4964
PRO2799, 5041
PRO283, 3664
PRO2837, 1224
PRO2839, 4904
PRO2841, 3741, 3743
PRO2842, 2962
PRO2846, 3661
PRO2851, 177
PRO28687, 5880
PRO287, 1277
PRO2871, 3995
PRO2875, 2974
PRO2906, 1328
PRO2907, 2696
PRO292, 3134
PRO29371, 5329
PRO302, 4918
PRO303, 4409
PRO329, 504
PRO3344, 2484
PRO33679, 368
PRO33717, 3963
PRO33818, 2773
PRO34043, 6205
PRO34073, 3052
PRO34151, 5479
PRO34323, 5259
PRO34473, 2783
PRO3449, 3601
PRO34531, 6076
PRO34544, 1676
PRO34557, 4183
PRO34584, 6186
PRO36020, 1741
PRO36047, 1490
PRO36055, 1331
PRO36058, 1735
PRO36093, 2768

PRO36094, 2175
PRO36095, 3474
PRO36112, 4043
PRO36118, 6339
PRO36134, 2507
PRO36184, 6215
PRO36215, 3377
PRO36263, 6335
PRO36272, 357
PRO3629, 4355, 4357
PRO36305, 1960
PRO36316, 1958
PRO3632, 3176
PRO36328, 3977
PRO3637, 4888
PRO36372, 1829
PRO36373, 1129
PRO36382, 1447
PRO36383, 1512
PRO36384, 1516
PRO3640, 4422
PRO36417, 5948
PRO3645, 5735
PRO36468, 554
PRO3647, 4688
PRO36474, 5518
PRO36477, 3730
PRO36491, 3490
PRO36543, 3207
PRO36568, 3993
PRO36588, 410
PRO36680, 3005
PRO36693, 2656
PRO36723, 272
PRO36725, 106
PRO36735, 1096
PRO36787, 4096
PRO36800, 2459
PRO36808, 2671
PRO36841, 1919
PRO36852, 4821
PRO36872, 5922
PRO36879, 2263
PRO36881, 1792
PRO36891, 742
PRO36959, 2566
PRO36963, 5490
PRO36970, 3456
PRO37010, 1109
PRO37012, 5976
PRO37023, 2394
PRO37024, 5957
PRO37073, 2987
PRO37080, 5936
PRO37082, 475
PRO37083, 6160

PRO37091, 1765
PRO37109, 4225
PRO37221, 5746
PRO37234, 3499
PRO37256, 437
PRO37316, 3867
PRO37335, 1690
PRO37476, 6333
PRO37518, 4940
PRO37534, 4890
PRO37535, 385
PRO37540, 4990
PRO37547, 4743
PRO37551, 3221
PRO37555, 3594
PRO37557, 3629
PRO37628, 685
PRO37634, 3725
PRO37635, 2965
PRO37636, 1574
PRO37644, 6273
PRO37653, 815
PRO37654, 3589
PRO37667, 1887
PRO37669, 4171
PRO37675, 924
PRO37676, 158
PRO37697, 4627
PRO37709, 551
PRO37712, 5353
PRO37730, 2513
PRO37731, 2243
PRO37743, 5233
PRO37764, 4934
PRO37770, 1166
PRO37783, 1813
PRO37784, 3985
PRO37791, 4793
PRO37806, 498
PRO37811, 5682
PRO37905, 1943
PRO37935, 5772
PRO37937, 3721
PRO37938, 2461
PRO37951, 5164
PRO37954, 2692
PRO37961, 4343
PRO37967, 595
PRO37972, 3077
PRO37991, 804
PRO37992, 347
PRO38008, 699
PRO38010, 3459
PRO38021, 6217
PRO38022, 4162
PRO38028, 2667

PRO38038, 1509	PRO4813, 5845
PRO38040, 375	PRO4814, 4582
PRO38066, 5810	PRO4832, 1150
PRO38070, 1962	PRO4833, 2991
PRO38101, 5565	PRO48357, 1082
PRO38119, 6286	PRO4836, 4111
PRO38152, 6148	PRO4841, 3479
PRO38227, 4892	PRO4852, 5775
PRO38258, 793	PRO4870, 3312
PRO38284, 37	PRO4872, 6082
PRO38311, 4359	PRO4873, 3684
PRO38336, 4842	PRO4884, 1950
PRO38380, 6322	PRO4885, 6345
PRO38387, 2100	PRO4900, 3050
PRO38392, 2207	PRO4904, 4064, 5495
PRO38406, 6198	PRO4908, 1780
PRO38464, 4336	PRO4912, 2275
PRO38480, 4373	PRO4914, 617
PRO38496, 5133	PRO4917, 712
PRO38730, 6343	PRO4918, 765
PRO38852, 4215	PRO49182, 4705
PRO39030, 6105	PRO49209, 1371
PRO39127, 6182	PRO49256, 6004
PRO39201, 4983	PRO49262, 1628
PRO39530, 4643	PRO49278, 6069
PRO39648, 3009	PRO49298, 3330
PRO39773, 2399	PRO49310, 4720
PRO4, 2535	PRO49316, 995
PRO41882, 2366	PRO49352, 6046
PRO42022, 6225	PRO49409, 500
PRO42208, 4519	PRO49457, 604
PRO4348, 3577	PRO49639, 4488
PRO4379, 4179	PRO49642, 343
PRO4426, 3632	PRO49648, 2741
PRO44999, 579	PRO49653, 5628
PRO45014, 2183	PRO49675, 5886
PRO4544, 219	PRO49685, 1156
PRO4547, 650	PRO49722, 1317
PRO4569, 5577	PRO49726, 3469
PRO4583, 189	PRO4984, 1909
PRO4586, 6071	PRO49869, 2694
PRO4605, 1450	PRO49875, 3778
PRO4650, 5273	PRO49879, 4375
PRO4666, 3682	PRO49881, 6319
PRO4676, 1599	PRO49883, 6258
PRO4710, 1678	PRO49888, 4899
PRO4729, 4709	PRO49967, 4578
PRO47354, 5516	PRO50083, 5891
PRO4738, 4799	PRO50095, 1133
PRO4749, 2983	PRO50134, 5940
PRO4756, 5377	PRO50165, 3114
PRO4763, 458	PRO50409, 4209
PRO4789, 5995	PRO50438, 4266
PRO4793, 3848	PRO50481, 4748
PRO4798, 2071	PRO50582, 1927
PRO4801, 3314	PRO50596, 860

PRO50658, 4613	PRO58642, 3897
PRO50756, 3110	PRO58702, 5207
PRO51109, 1273	PRO58784, 1100
PRO51119, 6102	PRO58837, 3592
PRO51121, 3512	PRO58875, 6240
PRO51389, 2055	PRO58939, 2877
PRO51539, 200	PRO58974, 471
PRO51565, 5514	PRO58984, 1893
PRO51586, 5147	PRO58986, 1387
PRO51744, 5057	PRO58991, 5235
PRO51767, 5388	PRO58993, 1804
PRO51771, 5435	PRO59001, 3817
PRO51775, 4363	PRO59022, 6243
PRO51815, 4371	PRO59040, 1851
PRO51836, 546	PRO59042, 3824
PRO51851, 1643	PRO59043, 3056
PRO51901, 2747	PRO59061, 6012
PRO52010, 4855	PRO59074, 2372
PRO52083, 1438	PRO59084, 3296
PRO52101, 5507	PRO59099, 128
PRO52119, 5966	PRO59136, 795
PRO52449, 403	PRO59142, 5649, 5651
PRO52492, 3416	PRO59168, 6154
PRO52537, 2924	PRO59220, 5361
PRO54594, 4204	PRO59230, 2551
PRO57307, 3327	PRO59262, 3440
PRO57854, 3102	PRO59264, 5505
PRO57901, 5594	PRO59285, 6080
PRO57917, 4060	PRO59305, 4844
PRO57942, 5815	PRO59309, 4806
PRO58006, 1855	PRO59313, 959
PRO58042, 5313	PRO59321, 2663
PRO58046, 5123	PRO59328, 4912
PRO58092, 3899	PRO59332, 289
PRO58118, 268	PRO59339, 5677
PRO58140, 1196	PRO59351, 2856
PRO58155, 5874	PRO59365, 1998
PRO58177, 1257	PRO59380, 2397
PRO58198, 6127	PRO59384, 752
PRO58207, 3285	PRO59441, 6139
PRO58213, 1688	PRO59491, 4508
PRO58219, 1647	PRO59504, 1094
PRO58232, 5990	PRO59544, 762
PRO58259, 1271	PRO59546, 230
PRO58263, 2553	PRO59558, 704
PRO58292, 5299	PRO59579, 2674
PRO58308, 1063	PRO59629, 3381
PRO58328, 1098	PRO59647, 3551
PRO58348, 3094	PRO59669, 5904
PRO58410, 3865	PRO59717, 2105
PRO58437, 2370	PRO59721, 3272
PRO58440, 3688	PRO59725, 462
PRO58446, 5268	PRO59785, 3728
PRO58523, 3209	PRO59868, 6188
PRO58543, 747	PRO59895, 935
PRO58606, 3300	PRO59913, 1722

PRO60006, 2752
PRO60008, 3282
PRO60070, 4102
PRO60115, 2807
PRO60121, 5053
PRO60123, 3393
PRO60127, 2661
PRO6018, 395
PRO60207, 1698
PRO60261, 520
PRO60298, 203
PRO60311, 3345
PRO60321, 2601
PRO60325, 4450
PRO60333, 5626
PRO60360, 2349
PRO60397, 882
PRO60438, 1867
PRO60475, 2735
PRO60499, 4262
PRO60542, 1397
PRO60575, 4087
PRO60579, 2181
PRO60603, 5427
PRO60634, 3556
PRO60666, 3391
PRO60674, 5202
PRO60741, 1336
PRO60753, 872
PRO60781, 2715
PRO60800, 5073
PRO60815, 84
PRO60847, 3216
PRO60860, 236
PRO60924, 3575
PRO60945, 5743
PRO60956, 1495
PRO60979, 4813
PRO60991, 3087
PRO61085, 4268
PRO61113, 5070
PRO61125, 195
PRO61129, 5569
PRO61146, 397
PRO61219, 4260
PRO61238, 3323
PRO61246, 5003
PRO61250, 90
PRO61271, 6231
PRO61308, 5575
PRO61325, 781
PRO61327, 5786
PRO61349, 5616
PRO61458, 5422
PRO61470, 6288
PRO61498, 5739

PRO61502, 3067
PRO61575, 5449
PRO61638, 349
PRO61661, 5024
PRO61679, 43
PRO61688, 2250
PRO61721, 2900
PRO61744, 6141
PRO61761, 689
PRO61799, 4361
PRO61812, 2237
PRO61824, 2247
PRO61870, 1183
PRO61897, 2795
PRO61938, 6191
PRO61948, 4477
PRO61977, 5278
PRO61999, 3913
PRO62039, 5116
PRO62065, 5893
PRO62069, 2865
PRO62075, 5442
PRO62077, 516
PRO62099, 4070
PRO62108, 2492
PRO62110, 4517
PRO62112, 5242
PRO62135, 1831
PRO62153, 1171
PRO62212, 5524
PRO62225, 5179
PRO62236, 2781
PRO62239, 750
PRO62244, 2177
PRO62273, 3764
PRO62302, 5162
PRO62328, 6000
PRO62389, 181
PRO62466, 6327
PRO62500, 5407
PRO62518, 193
PRO62529, 341
PRO62531, 5200
PRO62574, 453
PRO62582, 5543
PRO62588, 6150
PRO62607, 637
PRO62617, 2882
PRO62760, 931
PRO62770, 663
PRO62780, 4666
PRO62786, 745
PRO62849, 293
PRO62852, 4301
PRO62882, 4321
PRO62893, 652

PRO62899, 5103
PRO62927, 865
PRO62981, 4717
PRO63000, 2724
PRO63009, 2233
PRO63052, 1972
PRO63068, 4565
PRO63082, 1680
PRO63226, 5238
PRO63253, 1905
PRO63299, 6341
PRO6360, 1077
PRO6373, 2213
PRO65, 848
PRO66265, 4670
PRO66275, 3901
PRO66279, 2127
PRO66282, 2129
PRO69461, 3302
PRO69463, 32
PRO69471, 3840
PRO69473, 3027, 3760
PRO69475, 2266
PRO69486, 5906
PRO69496, 2702
PRO69506, 1953
PRO69513, 5015
PRO69518, 5280
PRO69521, 1901
PRO69523, 3011
PRO69528, 3237
PRO69531, 906
PRO69533, 5669
PRO69541, 5655
PRO69542, 2764
PRO69549, 3461
PRO69554, 1583
PRO69560, 5686
PRO69561, 4920
PRO69568, 3254
PRO69584, 1970
PRO69595, 4243
PRO69617, 4521
PRO69635, 3138
PRO69674, 3219
PRO69681, 1301
PRO69682, 4901
PRO69684, 4779
PRO70011, 2704
PRO70138, 1968
PRO70258, 656
PRO70276, 4447
PRO70290, 2762
PRO703, 380
PRO70327, 1637, 1639
PRO70331, 6030

PRO70333, 541
PRO70383, 6035
PRO70385, 5551
PRO70393, 2008
PRO70433, 351
PRO70449, 4729
PRO70453, 3621
PRO70536, 1460
PRO70544, 2033
PRO70595, 2681
PRO70675, 991
PRO70694, 3786
PRO70703, 4976
PRO70754, 439
PRO70810, 5639
PRO70812, 4700
PRO70989, 3828, 3830
PRO70993, 1719
PRO71031, 3433, 3435
PRO71057, 2997
PRO71085, 5563
PRO71088, 1947
PRO71089, 5641
PRO71091, 2591
PRO71093, 370
PRO71095, 1964
PRO71096, 3888
PRO71097, 5831
PRO71103, 1148
PRO71106, 1875
PRO71111, 2436
PRO71112, 221
PRO71120, 3718
PRO71125, 1985, 1987
PRO71130, 4576
PRO71133, 2255
PRO71136, 2309
PRO71141, 4715
PRO71142, 1913
PRO71145, 6039
PRO71146, 372
PRO71211, 2343
PRO71242, 5974
PRO7143, 4986
PRO730, 4274
PRO7427, 2239
PRO7445, 2594
PRO80480, 5
PRO80481, 7
PRO80482, 9
PRO80483, 11
PRO80484, 16
PRO80485, 18
PRO80487, 21
PRO80488, 23
PRO80489, 25

PRO80490, 27	PRO80587, 240
PRO80492, 30	PRO80588, 242
PRO80493, 35	PRO80591, 246
PRO80494, 39	PRO80592, 248
PRO80497, 47	PRO80593, 252
PRO80498, 51	PRO80595, 255
PRO80499, 53	PRO80597, 258
PRO80501, 56	PRO80599, 261
PRO80505, 63	PRO80600, 263
PRO80506, 65	PRO80602, 266
PRO80510, 70	PRO80603, 270
PRO80511, 72	PRO80604, 274
PRO80512, 74	PRO80607, 278
PRO80517, 80	PRO80611, 283
PRO80518, 86	PRO80612, 285
PRO80519, 88	PRO80613, 287
PRO80520, 92	PRO80614, 291
PRO80521, 96	PRO80617, 297
PRO80524, 100	PRO80618, 299
PRO80527, 104	PRO80619, 301
PRO80528, 108	PRO80620, 303
PRO80530, 111	PRO80621, 305
PRO80533, 115	PRO80622, 307
PRO80534, 117	PRO80623, 309
PRO80535, 119	PRO80624, 311
PRO80536, 121	PRO80625, 313
PRO80537, 123	PRO80627, 316
PRO80542, 132	PRO80630, 320
PRO80547, 138	PRO80631, 322
PRO80550, 143	PRO80633, 325
PRO80553, 149	PRO80638, 333
PRO80554, 151	PRO80639, 335
PRO80555, 153	PRO80640, 337
PRO80557, 156	PRO80641, 339
PRO80558, 160	PRO80642, 345
PRO80559, 162	PRO80644, 355
PRO80560, 164	PRO80645, 359
PRO80561, 166	PRO80646, 362
PRO80562, 170	PRO80648, 365
PRO80563, 172	PRO80651, 378
PRO80565, 179	PRO80652, 382
PRO80567, 184	PRO80654, 387
PRO80568, 186	PRO80656, 390
PRO80570, 191	PRO80657, 393
PRO80571, 197	PRO80658, 399
PRO80574, 205	PRO80659, 401
PRO80575, 207	PRO80660, 405
PRO80576, 209	PRO80661, 407
PRO80579, 215	PRO80664, 413
PRO80580, 217	PRO80665, 415
PRO80581, 223	PRO80666, 417
PRO80582, 225	PRO80667, 419
PRO80583, 227	PRO80668, 421
PRO80584, 232	PRO80669, 423
PRO80585, 234	PRO80670, 425
PRO80586, 238	PRO80671, 427

PRO80672, 431
PRO80675, 435
PRO80676, 441
PRO80677, 443
PRO80678, 445
PRO80679, 447
PRO80680, 449
PRO80684, 456
PRO80685, 460
PRO80686, 464
PRO80688, 467
PRO80689, 469
PRO80693, 478
PRO80694, 480
PRO80695, 482
PRO80699, 489
PRO80700, 491
PRO80704, 496
PRO80705, 502
PRO80706, 506
PRO80707, 508
PRO80708, 510
PRO80709, 512
PRO80710, 514
PRO80711, 518
PRO80714, 526
PRO80715, 528
PRO80717, 533
PRO80719, 536
PRO80720, 539
PRO80725, 549
PRO80730, 563
PRO80734, 570
PRO80735, 572
PRO80736, 574
PRO80740, 584
PRO80741, 588
PRO80742, 590
PRO80745, 597
PRO80752, 607
PRO80753, 609
PRO80754, 611
PRO80755, 613
PRO80756, 615
PRO80759, 621
PRO80760, 623
PRO80761, 627
PRO80762, 629
PRO80763, 631
PRO80764, 633
PRO80765, 635
PRO80767, 640
PRO80770, 648
PRO80771, 654
PRO80772, 658
PRO80773, 660

PRO80775, 666
PRO80776, 668
PRO80778, 671
PRO80779, 673
PRO80780, 675
PRO80781, 677
PRO80782, 679
PRO80785, 687
PRO80786, 691
PRO80787, 693
PRO80788, 695
PRO80789, 697
PRO80790, 702
PRO80791, 708
PRO80792, 710
PRO80793, 714
PRO80796, 718
PRO80797, 720
PRO80798, 722
PRO80799, 724
PRO80802, 728
PRO80803, 730
PRO80804, 732
PRO80806, 735
PRO80807, 737
PRO80808, 739
PRO80811, 754
PRO80812, 756
PRO80813, 758
PRO80814, 760
PRO80816, 767
PRO80817, 769
PRO80820, 774
PRO80823, 778
PRO80827, 786
PRO80830, 790
PRO80832, 797
PRO80833, 799
PRO80835, 802
PRO80837, 809
PRO80838, 811
PRO80839, 813
PRO80842, 819
PRO80843, 821
PRO80846, 826
PRO80847, 828
PRO80848, 830
PRO80850, 835
PRO80851, 837
PRO80853, 840
PRO80856, 844
PRO80857, 846
PRO80860, 852
PRO80866, 863
PRO80868, 868
PRO80869, 870

PRO80870, 874
PRO80871, 876
PRO80873, 879
PRO80875, 884
PRO80876, 886
PRO80877, 888
PRO80878, 890
PRO80879, 892
PRO80881, 895
PRO80882, 897
PRO80883, 904
PRO80884, 908
PRO80888, 913
PRO80889, 915
PRO80890, 917
PRO80891, 919
PRO80900, 937
PRO80901, 939
PRO80903, 943
PRO80904, 945
PRO80905, 947
PRO80906, 953
PRO80908, 956
PRO80910, 961
PRO80911, 963
PRO80915, 972
PRO80916, 974
PRO80917, 976
PRO80920, 987
PRO80921, 989
PRO80924, 997
PRO80925, 1001
PRO80926, 1003
PRO80927, 1005
PRO80929, 1008
PRO80930, 1010
PRO80932, 1013
PRO80933, 1015
PRO80934, 1017
PRO80935, 1019
PRO80936, 1021
PRO80937, 1023
PRO80938, 1027
PRO80941, 1031
PRO80942, 1033
PRO80943, 1035
PRO80945, 1038
PRO80949, 1044
PRO80950, 1046
PRO80951, 1048
PRO80952, 1050
PRO80953, 1052
PRO80954, 1054
PRO80955, 1056
PRO80956, 1058
PRO80958, 1061

PRO80959, 1065
PRO80960, 1069
PRO80961, 1071
PRO80962, 1073
PRO80966, 1080
PRO80967, 1084
PRO80969, 1087
PRO80970, 1092
PRO80971, 1102
PRO80972, 1104
PRO80974, 1107
PRO80975, 1111
PRO80977, 1114
PRO80978, 1116
PRO80979, 1118
PRO80983, 1124
PRO80984, 1126
PRO80988, 1135
PRO80990, 1138
PRO80993, 1142
PRO80994, 1144
PRO80995, 1152
PRO80996, 1158
PRO80997, 1160
PRO80999, 1164
PRO81000, 1168
PRO81002, 1173
PRO81003, 1175
PRO81004, 1177
PRO81005, 1179
PRO81006, 1181
PRO81007, 1185
PRO81010, 1191
PRO81012, 1194
PRO81015, 1200
PRO81022, 1210
PRO81023, 1212
PRO81025, 1215
PRO81026, 1219
PRO81028, 1222
PRO81029, 1226
PRO81030, 1228
PRO81031, 1230
PRO81033, 1233
PRO81034, 1236
PRO81036, 1241
PRO81040, 1247
PRO81041, 1249
PRO81042, 1251
PRO81043, 1253
PRO81046, 1259
PRO81047, 1261
PRO81053, 1269
PRO81056, 1279
PRO81057, 1281
PRO81058, 1283

PRO81059, 1287
PRO81064, 1293
PRO81068, 1298
PRO81070, 1303
PRO81071, 1305
PRO81072, 1307
PRO81073, 1309
PRO81074, 1311
PRO81079, 1319
PRO81080, 1321
PRO81082, 1324
PRO81083, 1326
PRO81086, 1334
PRO81088, 1339
PRO81090, 1342
PRO81093, 1346
PRO81095, 1349
PRO81096, 1351
PRO81097, 1355
PRO81098, 1357
PRO81102, 1362
PRO81106, 1367
PRO81107, 1373
PRO81108, 1375
PRO81109, 1377
PRO81110, 1379
PRO81111, 1381
PRO81112, 1383
PRO81113, 1385
PRO81114, 1389
PRO81115, 1391
PRO81116, 1393
PRO81117, 1395
PRO81118, 1399
PRO81119, 1401
PRO81120, 1403
PRO81121, 1405
PRO81122, 1407
PRO81123, 1409
PRO81124, 1411
PRO81127, 1415
PRO81131, 1422
PRO81134, 1426
PRO81135, 1428
PRO81137, 1431
PRO81141, 1436
PRO81146, 1444
PRO81148, 1454
PRO81150, 1458
PRO81151, 1462
PRO81156, 1467
PRO81163, 1475
PRO81166, 1481
PRO81169, 1486
PRO81170, 1488
PRO81171, 1492

PRO81174, 1498
PRO81176, 1501
PRO81177, 1503
PRO81178, 1505
PRO81179, 1507
PRO81181, 1514
PRO81182, 1518
PRO81184, 1521
PRO81185, 1523
PRO81188, 1527
PRO81189, 1529
PRO81195, 1536
PRO81196, 1538
PRO81199, 1542
PRO81202, 1546
PRO81213, 1558
PRO81214, 1560
PRO81216, 1563
PRO81219, 1566
PRO81221, 1569
PRO81223, 1576
PRO81224, 1578
PRO81225, 1580
PRO81227, 1585
PRO81230, 1589
PRO81234, 1594
PRO81238, 1601
PRO81239, 1603
PRO81240, 1605
PRO81241, 1607
PRO81246, 1613
PRO81248, 1616
PRO81249, 1618
PRO81250, 1620
PRO81254, 1630
PRO81256, 1635
PRO81259, 1645
PRO81260, 1649
PRO81261, 1651
PRO81262, 1653
PRO81264, 1657
PRO81265, 1659
PRO81266, 1661
PRO81269, 1667
PRO81272, 1674
PRO81273, 1682
PRO81274, 1684
PRO81275, 1686
PRO81276, 1692
PRO81277, 1694
PRO81278, 1696
PRO81280, 1703
PRO81281, 1705
PRO81282, 1707
PRO81286, 1715
PRO81287, 1717

PRO81289, 1725
PRO81290, 1727
PRO81291, 1729
PRO81292, 1731
PRO81293, 1737
PRO81294, 1739
PRO81295, 1743
PRO81296, 1745
PRO81297, 1747
PRO81298, 1749
PRO81299, 1751
PRO81300, 1753
PRO81301, 1755
PRO81302, 1757
PRO81303, 1759
PRO81304, 1761
PRO81305, 1763
PRO81306, 1767
PRO81307, 1769
PRO81308, 1771
PRO81309, 1773
PRO81310, 1775
PRO81311, 1777
PRO81313, 1782
PRO81314, 1784
PRO81315, 1786
PRO81316, 1788
PRO81317, 1790
PRO81318, 1794
PRO81319, 1796
PRO81323, 1801
PRO81325, 1806
PRO81327, 1809
PRO81330, 1815
PRO81336, 1825
PRO81337, 1827
PRO81338, 1833
PRO81339, 1835
PRO81340, 1837
PRO81341, 1839
PRO81345, 1844
PRO81347, 1849
PRO81354, 1864
PRO81355, 1869
PRO81356, 1873
PRO81359, 1881
PRO81362, 1885
PRO81363, 1889
PRO81364, 1891
PRO81365, 1895
PRO81366, 1897
PRO81367, 1899
PRO81368, 1903
PRO81369, 1907
PRO81370, 1911
PRO81371, 1915

PRO81372, 1917
PRO81375, 1925
PRO81377, 1930
PRO81379, 1933
PRO81380, 1935
PRO81387, 1945
PRO81394, 1966
PRO81395, 1974
PRO81396, 1976
PRO81397, 1978
PRO81398, 1980
PRO81399, 1982
PRO81400, 1989
PRO81401, 1991
PRO81402, 1993
PRO81404, 1996
PRO81406, 2001
PRO81407, 2005
PRO81409, 2010
PRO81410, 2012
PRO81411, 2014
PRO81414, 2018
PRO81415, 2020
PRO81416, 2022
PRO81417, 2026
PRO81418, 2028
PRO81419, 2030
PRO81421, 2038
PRO81422, 2040
PRO81424, 2043
PRO81426, 2046
PRO81427, 2048
PRO81429, 2051
PRO81430, 2053
PRO81435, 2061
PRO81436, 2063
PRO81439, 2067
PRO81441, 2073
PRO81443, 2076
PRO81444, 2078
PRO81446, 2082
PRO81447, 2084
PRO81448, 2086
PRO81449, 2088
PRO81453, 2093
PRO81454, 2095
PRO81455, 2097
PRO81457, 2102
PRO81462, 2112
PRO81464, 2115
PRO81465, 2117
PRO81467, 2120
PRO81471, 2125
PRO81474, 2133
PRO81476, 2136
PRO81477, 2138

PRO81481, 2143
PRO81486, 2149
PRO81487, 2153
PRO81490, 2156
PRO81491, 2158
PRO81494, 2162
PRO81495, 2164
PRO81496, 2166
PRO81498, 2169
PRO81499, 2171
PRO81500, 2173
PRO81501, 2179
PRO81502, 2187
PRO81503, 2189
PRO81505, 2192
PRO81506, 2196
PRO81508, 2199
PRO81509, 2201
PRO81514, 2209
PRO81515, 2211
PRO81516, 2215
PRO81517, 2217
PRO81520, 2221
PRO81521, 2223
PRO81523, 2227
PRO81524, 2231
PRO81525, 2235
PRO81526, 2241
PRO81529, 2252
PRO81531, 2257
PRO81534, 2261
PRO81536, 2268
PRO81537, 2270
PRO81538, 2272
PRO81540, 2277
PRO81541, 2279
PRO81544, 2283
PRO81545, 2285
PRO81546, 2287
PRO81547, 2289
PRO81548, 2291
PRO81550, 2294
PRO81551, 2296
PRO81552, 2298
PRO81556, 2303
PRO81557, 2305
PRO81558, 2307
PRO81561, 2314
PRO81566, 2320
PRO81569, 2324
PRO81571, 2327
PRO81572, 2330
PRO81573, 2332
PRO81574, 2334
PRO81575, 2336
PRO81578, 2341

PRO81579, 2345
PRO81580, 2347
PRO81584, 2354
PRO81585, 2356
PRO81586, 2358
PRO81587, 2360
PRO81588, 2364
PRO81589, 2368
PRO81590, 2374
PRO81591, 2377
PRO81592, 2379
PRO81594, 2382
PRO81595, 2384
PRO81598, 2388
PRO81599, 2390
PRO81600, 2392
PRO81602, 2401
PRO81605, 2405
PRO81607, 2408
PRO81608, 2410
PRO81609, 2412
PRO81611, 2415
PRO81614, 2419
PRO81615, 2421
PRO81617, 2424
PRO81618, 2426
PRO81619, 2428
PRO81621, 2431
PRO81625, 2438
PRO81627, 2445
PRO81629, 2448
PRO81630, 2450
PRO81631, 2452
PRO81634, 2463
PRO81635, 2465
PRO81637, 2468
PRO81641, 2474
PRO81643, 2481
PRO81645, 2486
PRO81647, 2489
PRO81649, 2494
PRO81650, 2498
PRO81651, 2500
PRO81652, 2502
PRO81653, 2504
PRO81654, 2509
PRO81655, 2511
PRO81657, 2516
PRO81658, 2518
PRO81659, 2520
PRO81660, 2522
PRO81661, 2524
PRO81664, 2528
PRO81668, 2537
PRO81669, 2539
PRO81671, 2542

PRO81673, 2545
PRO81674, 2549
PRO81675, 2555
PRO81685, 2570
PRO81687, 2573
PRO81689, 2576
PRO81690, 2578
PRO81691, 2580
PRO81695, 2585
PRO81696, 2587
PRO81699, 2597
PRO81700, 2599
PRO81701, 2603
PRO81704, 2607
PRO81705, 2610
PRO81708, 2617
PRO81711, 2621
PRO81714, 2624
PRO81719, 2630
PRO81720, 2632
PRO81722, 2639
PRO81725, 2643
PRO81729, 2648
PRO81730, 2650
PRO81731, 2654
PRO81732, 2658
PRO81734, 2665
PRO81736, 2678
PRO81738, 2683
PRO81739, 2685
PRO81740, 2687
PRO81742, 2690
PRO81743, 2698
PRO81746, 2706
PRO81748, 2709
PRO81751, 2713
PRO81752, 2717
PRO81753, 2719
PRO81754, 2721
PRO81759, 2729
PRO81760, 2731
PRO81761, 2733
PRO81762, 2737
PRO81763, 2739
PRO81764, 2743
PRO81765, 2745
PRO81766, 2749
PRO81768, 2754
PRO81771, 2758
PRO81775, 2770
PRO81778, 2776
PRO81780, 2779
PRO81781, 2785
PRO81783, 2788
PRO81785, 2791
PRO81786, 2793

PRO81792, 2805
PRO81794, 2810
PRO81795, 2812
PRO81796, 2814
PRO81797, 2816
PRO81800, 2821
PRO81801, 2823
PRO81804, 2827
PRO81805, 2829
PRO81806, 2831
PRO81809, 2837
PRO81811, 2840
PRO81812, 2842
PRO81813, 2844
PRO81815, 2848
PRO81816, 2850
PRO81817, 2853
PRO81819, 2858
PRO81821, 2861
PRO81822, 2863
PRO81823, 2867
PRO81824, 2869
PRO81826, 2872
PRO81831, 2880
PRO81832, 2884
PRO81833, 2886
PRO81834, 2888
PRO81835, 2890
PRO81836, 2892
PRO81837, 2894
PRO81838, 2896
PRO81841, 2903
PRO81842, 2907
PRO81846, 2912
PRO81848, 2915
PRO81849, 2917
PRO81851, 2920
PRO81855, 2928
PRO81858, 2932
PRO81861, 2936
PRO81862, 2938
PRO81863, 2940
PRO81865, 2943
PRO81867, 2946
PRO81868, 2950
PRO81869, 2954
PRO81870, 2956
PRO81871, 2958
PRO81872, 2960
PRO81874, 2967
PRO81875, 2969
PRO81877, 2972
PRO81881, 2979
PRO81882, 2985
PRO81883, 2989
PRO81884, 2993

PRO81885, 2995
PRO81887, 3001
PRO81888, 3003
PRO81889, 3007
PRO81893, 3018
PRO81895, 3021
PRO81896, 3023
PRO81897, 3025
PRO81899, 3030
PRO81900, 3032
PRO81901, 3034
PRO81902, 3036
PRO81903, 3038
PRO81904, 3040
PRO81905, 3043
PRO81907, 3046
PRO81908, 3048
PRO81909, 3054
PRO81912, 3060
PRO81913, 3062
PRO81914, 3064
PRO81916, 3069
PRO81917, 3071
PRO81922, 3079
PRO81923, 3081
PRO81924, 3083
PRO81925, 3085
PRO81926, 3090
PRO81927, 3092
PRO81928, 3096
PRO81929, 3098
PRO81930, 3100
PRO81932, 3105
PRO81934, 3108
PRO81935, 3112
PRO81936, 3116
PRO81937, 3118
PRO81939, 3123
PRO81941, 3126
PRO81942, 3128
PRO81943, 3130
PRO81944, 3132
PRO81945, 3140
PRO81946, 3143
PRO81947, 3145
PRO81948, 3147
PRO81950, 3150
PRO81953, 3154
PRO81954, 3158
PRO81955, 3160
PRO81956, 3162
PRO81957, 3164
PRO81958, 3166
PRO81959, 3168
PRO81962, 3174
PRO81964, 3179

PRO81965, 3181
PRO81970, 3189
PRO81971, 3191
PRO81977, 3198
PRO81978, 3200
PRO81980, 3203
PRO81981, 3211
PRO81982, 3213
PRO81988, 3226
PRO81990, 3229
PRO81991, 3231
PRO81992, 3233
PRO81993, 3235
PRO81994, 3239
PRO81995, 3241
PRO81996, 3243
PRO81999, 3252
PRO82002, 3262
PRO82004, 3265
PRO82005, 3267
PRO82009, 3274
PRO82011, 3277
PRO82013, 3280
PRO82018, 3290
PRO82019, 3292
PRO82023, 3305
PRO82024, 3309
PRO82027, 3317
PRO82028, 3319
PRO82029, 3321
PRO82032, 3332
PRO82034, 3338
PRO82035, 3340
PRO82037, 3343
PRO82038, 3347
PRO82040, 3351
PRO82042, 3354
PRO82043, 3356
PRO82045, 3360
PRO82046, 3362
PRO82050, 3368
PRO82051, 3370
PRO82052, 3372
PRO82054, 3375
PRO82055, 3379
PRO82056, 3383
PRO82057, 3387
PRO82058, 3389
PRO82060, 3396
PRO82064, 3402
PRO82066, 3405
PRO82068, 3408
PRO82069, 3410
PRO82072, 3419
PRO82073, 3421
PRO82074, 3423

PRO82075, 3425
PRO82078, 3431
PRO82080, 3438
PRO82082, 3443
PRO82083, 3445
PRO82084, 3447
PRO82085, 3449
PRO82091, 3464
PRO82093, 3471
PRO82097, 3484
PRO82099, 3487
PRO82101, 3492
PRO82104, 3497
PRO82106, 3502
PRO82107, 3505
PRO82109, 3508
PRO82110, 3510
PRO82111, 3514
PRO82112, 3516
PRO82113, 3518
PRO82115, 3523
PRO82117, 3530
PRO82120, 3534
PRO82122, 3537
PRO82125, 3541
PRO82127, 3544
PRO82129, 3547
PRO82130, 3549
PRO82131, 3553
PRO82133, 3558
PRO82137, 3563
PRO82138, 3565
PRO82139, 3567
PRO82140, 3569
PRO82143, 3573
PRO82152, 3587
PRO82155, 3597
PRO82158, 3603
PRO82159, 3605
PRO82160, 3607
PRO82161, 3609
PRO82162, 3611
PRO82163, 3613
PRO82164, 3615
PRO82165, 3617
PRO82166, 3619
PRO82167, 3623
PRO82168, 3625
PRO82169, 3627
PRO82174, 3637
PRO82175, 3639
PRO82179, 3644
PRO82181, 3647
PRO82182, 3649
PRO82183, 3651
PRO82184, 3653

PRO82188, 3670
PRO82190, 3673
PRO82191, 3675
PRO82192, 3677
PRO82194, 3686
PRO82195, 3690
PRO82196, 3692
PRO82197, 3694
PRO82198, 3696
PRO82199, 3698
PRO82201, 3701
PRO82202, 3703
PRO82204, 3706
PRO82206, 3709
PRO82207, 3711
PRO82208, 3713
PRO82210, 3716
PRO82212, 3723
PRO82213, 3733
PRO82214, 3735
PRO82215, 3738
PRO82218, 3745
PRO82219, 3747
PRO82220, 3749
PRO82221, 3751
PRO82223, 3756
PRO82224, 3762
PRO82227, 3768
PRO82228, 3770
PRO82232, 3776
PRO82233, 3780
PRO82234, 3782
PRO82235, 3784
PRO82237, 3789
PRO82238, 3791
PRO82239, 3793
PRO82240, 3795
PRO82243, 3799
PRO82244, 3801
PRO82245, 3803
PRO82247, 3806
PRO82248, 3808
PRO82250, 3811
PRO82252, 3813
PRO82253, 3815
PRO82255, 3820
PRO82256, 3822
PRO82259, 3832
PRO82263, 3838
PRO82264, 3842
PRO82265, 3844
PRO82266, 3846
PRO82267, 3850
PRO82268, 3852
PRO82269, 3854
PRO82272, 3858

PRO82273, 3860
PRO82275, 3863
PRO82278, 3871
PRO82279, 3873
PRO82280, 3875
PRO82283, 3879
PRO82285, 3882
PRO82287, 3885
PRO82289, 3890
PRO82290, 3892
PRO82291, 3894
PRO82295, 3905
PRO82296, 3907
PRO82297, 3911
PRO82300, 3919
PRO82302, 3922
PRO82305, 3927
PRO82306, 3929
PRO82311, 3934
PRO82312, 3936
PRO82314, 3939
PRO82315, 3941
PRO82316, 3943
PRO82317, 3945
PRO82318, 3947
PRO82321, 3954
PRO82322, 3956
PRO82325, 3961
PRO82326, 3965
PRO82329, 3970
PRO82330, 3972
PRO82331, 3974
PRO82333, 3979
PRO82334, 3982
PRO82338, 3989
PRO82342, 3998
PRO82343, 4000
PRO82344, 4002
PRO82345, 4004
PRO82347, 4007
PRO82348, 4009
PRO82349, 4011
PRO82350, 4013
PRO82351, 4015
PRO82352, 4017
PRO82355, 4021
PRO82356, 4023
PRO82357, 4026
PRO82358, 4028
PRO82359, 4030
PRO82364, 4036
PRO82365, 4038
PRO82367, 4041
PRO82369, 4047
PRO82370, 4051
PRO82371, 4053

PRO82373, 4056
PRO82374, 4058
PRO82375, 4062
PRO82381, 4076
PRO82382, 4078
PRO82383, 4083
PRO82384, 4085
PRO82385, 4089
PRO82388, 4093
PRO82391, 4099
PRO82393, 4104
PRO82395, 4107
PRO82396, 4109
PRO82397, 4113
PRO82400, 4117
PRO82408, 4126
PRO82409, 4128
PRO82411, 4131
PRO82415, 4137
PRO82417, 4140
PRO82418, 4144
PRO82419, 4146
PRO82421, 4149
PRO82422, 4151
PRO82423, 4153
PRO82424, 4155
PRO82425, 4158
PRO82428, 4164
PRO82429, 4166
PRO82431, 4169
PRO82432, 4173
PRO82433, 4177
PRO82434, 4181
PRO82435, 4185
PRO82437, 4188
PRO82438, 4190
PRO82439, 4192
PRO82440, 4194
PRO82441, 4196
PRO82442, 4198
PRO82444, 4201
PRO82446, 4206
PRO82448, 4212
PRO82450, 4217
PRO82453, 4223
PRO82454, 4227
PRO82455, 4229
PRO82456, 4231
PRO82457, 4233
PRO82458, 4235
PRO82460, 4238
PRO82461, 4240
PRO82465, 4247
PRO82466, 4249
PRO82469, 4253
PRO82470, 4255

PRO82472, 4258
PRO82473, 4264
PRO82475, 4271
PRO82477, 4276
PRO82479, 4280
PRO82482, 4284
PRO82485, 4288
PRO82487, 4291
PRO82489, 4294
PRO82491, 4297
PRO82492, 4299
PRO82493, 4303
PRO82495, 4308
PRO82499, 4313
PRO82501, 4316
PRO82502, 4318
PRO82505, 4324
PRO82508, 4328
PRO82509, 4330
PRO82510, 4332
PRO82513, 4339
PRO82514, 4341
PRO82515, 4345
PRO82516, 4347
PRO82517, 4349
PRO82518, 4351
PRO82521, 4365
PRO82522, 4367
PRO82523, 4369
PRO82524, 4377
PRO82525, 4379
PRO82526, 4381
PRO82527, 4383
PRO82528, 4385
PRO82529, 4387
PRO82530, 4389
PRO82531, 4391
PRO82532, 4393
PRO82533, 4395
PRO82534, 4397
PRO82535, 4401
PRO82536, 4403
PRO82537, 4405
PRO82538, 4407
PRO82540, 4412
PRO82542, 4415
PRO82543, 4417
PRO82544, 4419
PRO82546, 4424
PRO82548, 4428
PRO82551, 4433
PRO82554, 4437
PRO82555, 4439
PRO82556, 4441
PRO82557, 4443
PRO82558, 4445

PRO82560, 4452
PRO82562, 4455
PRO82563, 4457
PRO82564, 4459
PRO82567, 4464
PRO82568, 4466
PRO82570, 4469
PRO82571, 4471
PRO82572, 4473
PRO82573, 4475
PRO82576, 4481
PRO82579, 4486
PRO82582, 4492
PRO82583, 4494
PRO82584, 4496
PRO82585, 4499
PRO82586, 4501
PRO82587, 4503
PRO82589, 4506
PRO82590, 4510
PRO82592, 4515
PRO82593, 4523
PRO82594, 4525
PRO82597, 4529
PRO82598, 4533
PRO82599, 4536
PRO82602, 4540
PRO82603, 4542
PRO82606, 4546
PRO82607, 4548
PRO82608, 4552
PRO82609, 4554
PRO82611, 4557
PRO82612, 4559
PRO82615, 4563
PRO82616, 4567
PRO82618, 4572
PRO82619, 4574
PRO82621, 4585
PRO82622, 4587
PRO82623, 4589
PRO82624, 4591
PRO82625, 4593
PRO82626, 4595
PRO82627, 4598
PRO82629, 4601
PRO82630, 4603
PRO82631, 4605
PRO82632, 4607
PRO82633, 4609
PRO82634, 4611
PRO82635, 4615
PRO82637, 4618
PRO82638, 4620
PRO82640, 4623
PRO82641, 4625

PRO82642, 4629
PRO82643, 4631
PRO82645, 4634
PRO82646, 4636
PRO82654, 4649
PRO82656, 4652
PRO82658, 4655
PRO82659, 4657
PRO82661, 4660
PRO82662, 4662
PRO82663, 4664
PRO82664, 4668
PRO82665, 4673
PRO82667, 4676
PRO82669, 4679
PRO82670, 4681
PRO82671, 4683
PRO82672, 4685
PRO82674, 4690
PRO82675, 4692
PRO82678, 4698
PRO82679, 4702
PRO82683, 4711
PRO82687, 4722
PRO82689, 4726
PRO82691, 4731
PRO82692, 4733
PRO82694, 4736
PRO82695, 4738
PRO82696, 4740
PRO82699, 4746
PRO82702, 4753
PRO82704, 4756
PRO82706, 4759
PRO82707, 4762
PRO82708, 4764
PRO82709, 4766
PRO82712, 4770
PRO82713, 4772
PRO82714, 4774
PRO82715, 4776
PRO82717, 4781
PRO82718, 4785
PRO82719, 4787
PRO82720, 4789
PRO82721, 4791
PRO82722, 4795
PRO82724, 4802
PRO82725, 4804
PRO82726, 4808
PRO82728, 4811
PRO82729, 4815
PRO82730, 4817
PRO82732, 4823
PRO82736, 4828
PRO82737, 4831

PRO82738, 4833
PRO82739, 4835
PRO82740, 4837
PRO82741, 4839
PRO82743, 4848
PRO82745, 4851
PRO82746, 4853
PRO82748, 4858
PRO82749, 4860
PRO82750, 4862
PRO82753, 4866
PRO82754, 4868
PRO82755, 4870
PRO82756, 4872
PRO82757, 4874
PRO82758, 4876
PRO82760, 4882
PRO82761, 4884
PRO82762, 4886
PRO82763, 4894
PRO82764, 4896
PRO82768, 4907
PRO82769, 4909
PRO82771, 4914
PRO82774, 4922
PRO82776, 4925
PRO82778, 4930
PRO82779, 4932
PRO82787, 4947
PRO82788, 4949
PRO82790, 4952
PRO82791, 4956
PRO82792, 4959
PRO82793, 4961
PRO82794, 4966
PRO82795, 4968
PRO82796, 4972
PRO82797, 4974
PRO82799, 4979
PRO82800, 4981
PRO82805, 4993
PRO82807, 4997
PRO82812, 5005
PRO82813, 5007
PRO82814, 5009
PRO82816, 5012
PRO82818, 5017
PRO82825, 5029
PRO82828, 5033
PRO82829, 5035
PRO82831, 5038
PRO82833, 5044
PRO82835, 5047
PRO82840, 5059
PRO82841, 5061
PRO82842, 5063

PRO82846, 5068
PRO82850, 5077
PRO82851, 5079
PRO82852, 5081
PRO82855, 5085
PRO82856, 5087
PRO82859, 5091
PRO82861, 5099
PRO82862, 5101
PRO82863, 5105
PRO82864, 5107
PRO82867, 5111
PRO82871, 5118
PRO82872, 5121
PRO82873, 5125
PRO82874, 5129
PRO82877, 5136
PRO82879, 5139
PRO82881, 5142
PRO82882, 5144
PRO82884, 5149
PRO82885, 5151
PRO82886, 5153
PRO82887, 5156
PRO82888, 5158
PRO82892, 5167
PRO82893, 5170
PRO82894, 5172
PRO82895, 5174
PRO82897, 5177
PRO82899, 5182
PRO82901, 5185
PRO82902, 5187
PRO82903, 5189
PRO82904, 5191
PRO82905, 5193
PRO82909, 5198
PRO82910, 5204
PRO82912, 5211
PRO82915, 5215
PRO82917, 5220
PRO82920, 5224
PRO82923, 5228
PRO82925, 5231
PRO82930, 5245
PRO82933, 5249
PRO82934, 5253
PRO82935, 5255
PRO82939, 5263
PRO82940, 5265
PRO82943, 5271
PRO82944, 5275
PRO82947, 5287
PRO82948, 5289
PRO82949, 5291
PRO82950, 5293

PRO82952, 5296
PRO82954, 5301
PRO82956, 5304
PRO82957, 5306
PRO82958, 5309
PRO82962, 5318
PRO82963, 5320
PRO82964, 5322
PRO82965, 5324
PRO82967, 5327
PRO82970, 5333
PRO82971, 5335
PRO82975, 5340
PRO82976, 5342
PRO82977, 5344
PRO82978, 5346
PRO82979, 5348
PRO82980, 5351
PRO82982, 5356
PRO82983, 5359
PRO82984, 5363
PRO82985, 5365
PRO82987, 5368
PRO82991, 5373
PRO82992, 5375
PRO82995, 5381
PRO82998, 5386
PRO82999, 5390
PRO83000, 5392
PRO83002, 5397
PRO83004, 5400
PRO83005, 5402
PRO83007, 5405
PRO83008, 5410
PRO83009, 5412
PRO83010, 5414
PRO83011, 5416
PRO83012, 5418
PRO83013, 5420
PRO83014, 5424
PRO83016, 5431
PRO83017, 5433
PRO83018, 5437
PRO83027, 5452
PRO83029, 5455
PRO83030, 5457
PRO83031, 5459
PRO83035, 5464
PRO83037, 5467
PRO83038, 5469
PRO83039, 5471
PRO83040, 5473
PRO83041, 5475
PRO83042, 5481
PRO83050, 5493
PRO83052, 5500

PRO83054, 5509
PRO83056, 5520
PRO83059, 5526
PRO83065, 5533
PRO83066, 5535
PRO83068, 5538
PRO83069, 5540
PRO83071, 5545
PRO83072, 5547
PRO83073, 5553
PRO83074, 5555
PRO83075, 5557
PRO83076, 5559
PRO83077, 5561
PRO83078, 5567
PRO83080, 5572
PRO83082, 5579
PRO83083, 5581
PRO83084, 5583
PRO83085, 5585
PRO83086, 5587
PRO83087, 5596
PRO83089, 5599
PRO83090, 5601
PRO83092, 5604
PRO83093, 5606
PRO83095, 5609
PRO83096, 5611
PRO83098, 5614
PRO83099, 5618
PRO83100, 5620
PRO83101, 5622
PRO83102, 5624
PRO83103, 5630
PRO83104, 5632
PRO83105, 5634
PRO83107, 5637
PRO83108, 5643
PRO83109, 5645
PRO83112, 5653
PRO83113, 5657
PRO83114, 5659
PRO83116, 5662
PRO83117, 5664
PRO83118, 5666
PRO83121, 5672
PRO83125, 5684
PRO83128, 5690
PRO83129, 5692
PRO83130, 5694
PRO83132, 5697
PRO83133, 5699
PRO83135, 5702
PRO83137, 5707
PRO83138, 5709
PRO83139, 5711

PRO83141, 5714
PRO83142, 5716
PRO83143, 5718
PRO83144, 5720
PRO83145, 5724
PRO83146, 5726
PRO83149, 5730
PRO83150, 5732
PRO83152, 5737
PRO83153, 5741
PRO83155, 5751
PRO83156, 5753
PRO83157, 5755
PRO83159, 5758
PRO83161, 5764
PRO83163, 5767
PRO83165, 5770
PRO83167, 5777
PRO83169, 5784
PRO83170, 5788
PRO83174, 5797
PRO83175, 5799
PRO83176, 5801
PRO83177, 5803
PRO83178, 5805
PRO83179, 5807
PRO83180, 5812
PRO83182, 5817
PRO83183, 5820
PRO83184, 5822
PRO83185, 5827
PRO83186, 5829
PRO83187, 5833
PRO83188, 5835
PRO83189, 5839
PRO83190, 5841
PRO83191, 5843
PRO83193, 5848
PRO83194, 5850
PRO83195, 5852
PRO83196, 5854
PRO83197, 5856
PRO83198, 5858
PRO83199, 5860
PRO83200, 5862
PRO83201, 5864
PRO83202, 5866
PRO83203, 5868
PRO83204, 5870
PRO83205, 5872
PRO83210, 5884
PRO83211, 5888
PRO83212, 5895
PRO83213, 5899
PRO83214, 5901
PRO83217, 5909

PRO83219, 5912	PRO83323, 6144
PRO83222, 5916	PRO83328, 6156
PRO83223, 5918	PRO83331, 6162
PRO83224, 5920	PRO83332, 6164
PRO83233, 5932	PRO83333, 6166
PRO83234, 5934	PRO83334, 6168
PRO83235, 5938	PRO83335, 6171
PRO83236, 5942	PRO83337, 6175
PRO83237, 5944	PRO83339, 6178
PRO83242, 5952	PRO83340, 6180
PRO83244, 5955	PRO83341, 6184
PRO83245, 5959	PRO83343, 6193
PRO83247, 5962	PRO83344, 6195
PRO83252, 5970	PRO83345, 6200
PRO83253, 5972	PRO83346, 6202
PRO83254, 5978	PRO83349, 6208
PRO83255, 5980	PRO83351, 6211
PRO83256, 5982	PRO83352, 6213
PRO83257, 5984	PRO83353, 6219
PRO83260, 5988	PRO83354, 6221
PRO83261, 5992	PRO83355, 6223
PRO83263, 5997	PRO83360, 6234
PRO83265, 6002	PRO83361, 6236
PRO83266, 6008	PRO83365, 6247
PRO83267, 6010	PRO83366, 6249
PRO83270, 6016	PRO83368, 6252
PRO83271, 6018	PRO83369, 6254
PRO83273, 6026	PRO83372, 6260
PRO83274, 6033	PRO83373, 6262
PRO83275, 6037	PRO83374, 6264
PRO83276, 6041	PRO83375, 6266
PRO83278, 6044	PRO83381, 6277
PRO83279, 6048	PRO83383, 6283
PRO83280, 6050	PRO83385, 6290
PRO83282, 6053	PRO83386, 6292
PRO83283, 6057	PRO83387, 6294
PRO83285, 6062	PRO83388, 6296
PRO83288, 6067	PRO83389, 6298
PRO83289, 6073	PRO83391, 6301
PRO83291, 6078	PRO83392, 6303
PRO83292, 6084	PRO83393, 6305
PRO83293, 6086	PRO83394, 6307
PRO83297, 6092	PRO83395, 6309
PRO83300, 6096	PRO83397, 6314
PRO83301, 6098	PRO83400, 6324
PRO83302, 6100	PRO83403, 6331
PRO83304, 6107	PRO83404, 6337
PRO83306, 6110	PRO83405, 6347
PRO83307, 6112	PRO868, 1871
PRO83309, 6115	PRO9112, 3668
PRO83310, 6117	PRO9785, 1369
PRO83312, 6120	PRO9819, 2676
PRO83316, 6129	PRO983, 5825
PRO83319, 6133	PRO9886, 706
PRO83320, 6135	PRO9902, 2952
PRO83321, 6137	PRO9980, 2479

PRO9984, 969
PRO9987, 3753

Accession Index (to Figure number)

NM_000018, 4669	NM_000484, 5882
NM_000026, 6068	NM_000505, 1828
NM_000029, 624	NM_000508, 1511
NM_000033, 6342	NM_000509, 1515
NM_000034, 4520	NM_000516, 5830
NM_000039, 3376	NM_000517, 4354
NM_000041, 5511	NM_000521, 1627
NM_000070, 4161	NM_000526, 4816
NM_000075, 3683	NM_000532, 1260
NM_000077, 2655	NM_000554, 5480
NM_000079, 898	NM_000558, 4356
NM_000090, 921	NM_000559, 3142
NM_000107, 3208	NM_000569, 505
NM_000114, 5836	NM_000574, 558
NM_000121, 5258	NM_000576, 847
NM_000126, 4267	NM_000582, 1459
NM_000137, 4300	NM_000592, 1957
NM_000143, 636	NM_000598, 2228
NM_000146, 5562	NM_000602, 2361
NM_000154, 4967	NM_000612, 3120
NM_000156, 5122	NM_000638, 4763
NM_000165, 2099	NM_000661, 1425
NM_000177, 2796	NM_000666, 1172
NM_000178, 5738	NM_000687, 5736
NM_000179, 744	NM_000688, 1167
NM_000182, 713	NM_000700, 2695
NM_000183, 711	NM_000701, 312
NM_000184, 3144	NM_000743, 4259
NM_000196, 4547	NM_000754, 5956
NM_000213, 4963	NM_000760, 173
NM_000221, 701	NM_000785, 3687
NM_000224, 3593	NM_000787, 2830
NM_000227, 5040	NM_000795, 3384
NM_000228, 553	NM_000801, 5648
NM_000239, 3729	NM_000852, 3297
NM_000250, 4903	NM_000858, 612
NM_000251, 741	NM_000893, 1327
NM_000268, 5994	NM_000895, 3763
NM_000269, 4889	NM_000930, 2534
NM_000274, 3076	NM_000931, 2536
NM_000284, 6138	NM_000942, 4218
NM_000291, 6230	NM_000954, 2868
NM_000358, 1671	NM_000964, 4820
NM_000365, 3460	NM_000967, 6061
NM_000368, 2806	NM_000969, 284
NM_000385, 2262	NM_000970, 3781
NM_000386, 4843	NM_000971, 2569
NM_000396, 356	NM_000972, 2826
NM_000404, 1089	NM_000973, 2633
NM_000407, 5947	NM_000975, 87
NM_000422, 4807	NM_000976, 2780
NM_000425, 6334	NM_000977, 4633
NM_000447, 594	NM_000978, 4801

NM_000979, 5571
NM_000980, 5334
NM_000981, 4798
NM_000982, 3091
NM_000983, 34
NM_000985, 5067
NM_000986, 1206
NM_000987, 4714
NM_000989, 2588
NM_000990, 3155
NM_000991, 5613
NM_000992, 1170
NM_000993, 832
NM_000994, 1064
NM_000997, 1570
NM_000998, 966
NM_001000, 6278
NM_001002, 3827
NM_001003, 4228
NM_001005, 3331
NM_001006, 1506
NM_001007, 6224
NM_001009, 5633
NM_001010, 2651
NM_001011, 643
NM_001012, 210
NM_001016, 2111
NM_001017, 3171
NM_001018, 5126
NM_001020, 5426
NM_001021, 4283
NM_001022, 5468
NM_001023, 2552
NM_001024, 5847
NM_001025, 1632
NM_001026, 2980
NM_001028, 3361
NM_001029, 3656
NM_001030, 440
NM_001034, 651
NM_001038, 3478
NM_001043, 4487
NM_001050, 4841
NM_001064, 1159
NM_001065, 3480
NM_001068, 1079
NM_001069, 2050
NM_001084, 2369
NM_001087, 994
NM_001098, 6079
NM_001101, 2174
NM_001102, 4040
NM_001122, 2649
NM_001134, 1446
NM_001154, 1489
NM_001157, 2990

NM_001168, 4985
NM_001190, 5568
NM_001199, 2495
NM_001207, 1624
NM_001211, 4139
NM_001218, 4203
NM_001235, 3333
NM_001238, 5374
NM_001247, 5703
NM_001255, 194
NM_001262, 229
NM_001273, 3468
NM_001274, 3411
NM_001275, 4065
NM_001283, 2365
NM_001287, 4372
NM_001288, 1969
NM_001293, 3337
NM_001294, 5508
NM_001313, 1396
NM_001319, 5141
NM_001320, 1971
NM_001324, 5814
NM_001325, 6239
NM_001333, 2736
NM_001344, 3984
NM_001350, 1942
NM_001363, 6318
NM_001407, 1132
NM_001415, 6143
NM_001416, 4687
NM_001418, 3163
NM_001428, 31
NM_001436, 5436
NM_001444, 2575
NM_001450, 836
NM_001463, 916
NM_001465, 1573
NM_001467, 3359
NM_001469, 6081
NM_001494, 2891
NM_001500, 2052
NM_001517, 1997
NM_001521, 689
NM_001530, 4016
NM_001536, 5539
NM_001539, 2660
NM_001540, 2308
NM_001553, 1435
NM_001554, 269
NM_001560, 6270
NM_001567, 3322
NM_001568, 2596
NM_001569, 6332
NM_001571, 5542
NM_001605, 4564

NM_001607, 1097
NM_001610, 3206
NM_001613, 3008
NM_001622, 1330
NM_001628, 2423
NM_001641, 3997
NM_001644, 3511
NM_001647, 1352
NM_001648, 5590
NM_001659, 3550
NM_001662, 2398
NM_001667, 3284
NM_001673, 2355
NM_001687, 5115
NM_001688, 308
NM_001696, 5941
NM_001697, 5892
NM_001710, 1959
NM_001734, 3452
NM_001743, 5494
NM_001747, 806
NM_001751, 3137
NM_001753, 2391
NM_001757, 5894
NM_001760, 1898
NM_001762, 2274
NM_001780, 3663
NM_001791, 81
NM_001816, 5478
NM_001819, 5679
NM_001827, 2714
NM_001831, 2506
NM_001833, 2689
NM_001842, 2668
NM_001853, 5853
NM_001861, 4614
NM_001862, 827
NM_001878, 392
NM_001907, 4579
NM_001909, 3133
NM_001920, 3740
NM_001930, 5267
NM_001935, 894
NM_001944, 5050
NM_001959, 950
NM_001961, 5178
NM_001964, 1689
NM_001969, 4098
NM_001970, 4697
NM_001975, 3458
NM_001983, 5502
NM_001985, 5593
NM_002003, 2834
NM_002004, 422
NM_002011, 1836
NM_002014, 3439

NM_002015, 3896
NM_002018, 4719
NM_002028, 4010
NM_002046, 3473
NM_002047, 2265
NM_002075, 3463
NM_002079, 3066
NM_002083, 4012
NM_002084, 1704
NM_002085, 5112
NM_002086, 4953
NM_002087, 4845
NM_002106, 1478
NM_002109, 1779
NM_002128, 3887
NM_002129, 1522
NM_002130, 1582
NM_002133, 6020
NM_002137, 2210
NM_002157, 930
NM_002161, 2716
NM_002168, 4293
NM_002178, 3600
NM_002211, 2919
NM_002212, 5742
NM_002229, 5272
NM_002265, 4834
NM_002273, 3591
NM_002274, 4814
NM_002275, 4812
NM_002276, 4810
NM_002295, 1108
NM_002305, 6038
NM_002306, 4022
NM_002339, 3115
NM_002340, 5931
NM_002342, 3476
NM_002345, 3752
NM_002355, 3489
NM_002358, 1485
NM_002364, 6147
NM_002385, 5086
NM_002386, 4626
NM_002388, 1866
NM_002396, 5069
NM_002397, 1646
NM_002401, 4933
NM_002411, 3245
NM_002413, 1494
NM_002414, 6124
NM_002415, 5979
NM_002453, 751
NM_002466, 5774
NM_002468, 1095
NM_002473, 6025
NM_002477, 1368

NM_002484, 4416
NM_002486, 2734
NM_002489, 2193
NM_002492, 1297
NM_002512, 4887
NM_002520, 1803
NM_002537, 4210
NM_002539, 659
NM_002567, 3816
NM_002568, 2593
NM_002574, 220
NM_002588, 1728
NM_002606, 5900
NM_002615, 4647
NM_002617, 12
NM_002632, 4052
NM_002634, 4939
NM_002638, 5779
NM_002654, 4242
NM_002660, 5771
NM_002668, 6185
NM_002689, 3289
NM_002691, 5580
NM_002707, 681
NM_002712, 1030
NM_002720, 4518
NM_002727, 2961
NM_002730, 5298
NM_002733, 3555
NM_002766, 4975
NM_002787, 2254
NM_002789, 4261
NM_002792, 5838
NM_002793, 2137
NM_002796, 346
NM_002802, 4059
NM_002803, 2378
NM_002809, 4805
NM_002810, 348
NM_002812, 5401
NM_002813, 3837
NM_002815, 4778
NM_002819, 5102
NM_002827, 5809
NM_002846, 980
NM_002854, 1188
NM_002856, 5515
NM_002857, 481
NM_002863, 4029
NM_002870, 438
NM_002878, 4784
NM_002883, 6075
NM_002887, 1800
NM_002913, 1427
NM_002915, 3891
NM_002921, 3002

NM_002923, 540
NM_002934, 3992
NM_002938, 1386
NM_002946, 127
NM_002947, 2188
NM_002948, 1076
NM_002952, 4382
NM_002954, 749
NM_002961, 369
NM_002965, 364
NM_002979, 235
NM_003002, 3390
NM_003021, 5161
NM_003025, 5188
NM_003055, 2947
NM_003064, 5781
NM_003072, 5254
NM_003076, 3568
NM_003088, 2176
NM_003090, 4320
NM_003091, 5654
NM_003092, 5683
NM_003104, 4187
NM_003107, 2032
NM_003123, 4511
NM_003124, 789
NM_003128, 746
NM_003132, 50
NM_003137, 1916
NM_003143, 2435
NM_003145, 409
NM_003146, 3215
NM_003149, 1099
NM_003169, 5428
NM_003181, 2135
NM_003216, 6077
NM_003283, 5608
NM_003287, 2104
NM_003289, 2680
NM_003290, 5312
NM_003295, 3900
NM_003310, 649
NM_003316, 5896
NM_003334, 6167
NM_003349, 5804
NM_003350, 2546
NM_003365, 1134
NM_003366, 4421
NM_003370, 5499
NM_003374, 1677
NM_003375, 2982
NM_003378, 2367
NM_003389, 2728
NM_003400, 761
NM_003401, 1636
NM_003406, 2590

NM.003418, 1250	NM.004053, 1900
NM.003453, 3864	NM.004060, 1791
NM.003461, 2440	NM.004074, 3264
NM.003472, 2034	NM.004084, 2476
NM.003516, 459	NM.004085, 6242
NM.003564, 474	NM.004092, 3099
NM.003598, 5556	NM.004111, 3253
NM.003617, 497	NM.004117, 1918
NM.003624, 5214	NM.004127, 5008
NM.003626, 3316	NM.004134, 1693
NM.003646, 3197	NM.004135, 6340
NM.003662, 6149	NM.004147, 6011
NM.003680, 157	NM.004152, 5154
NM.003681, 5905	NM.004159, 1952
NM.003685, 5203	NM.004175, 5983
NM.003687, 1673	NM.004176, 4742
NM.003689, 71	NM.004178, 3614
NM.003712, 5093	NM.004181, 1430
NM.003714, 1812	NM.004182, 6174
NM.003720, 5898	NM.004193, 3045
NM.003721, 5360	NM.004203, 4402
NM.003722, 1335	NM.004208, 6285
NM.003729, 288	NM.004217, 4699
NM.003735, 1730	NM.004219, 1795
NM.003736, 1732	NM.004240, 5206
NM.003739, 2883	NM.004247, 4879
NM.003752, 4449	NM.004261, 273
NM.003753, 6027	NM.004265, 3249
NM.003755, 5234	NM.004309, 5002
NM.003756, 2598	NM.004322, 3256
NM.003757, 148	NM.004323, 2662
NM.003765, 5288	NM.004324, 5564
NM.003766, 4865	NM.004335, 5328
NM.003779, 468	NM.004339, 5921
NM.003780, 199	NM.004341, 692
NM.003787, 5052	NM.004345, 1128
NM.003815, 457	NM.004360, 4549
NM.003824, 3313	NM.004398, 3392
NM.003836, 4088	NM.004401, 48
NM.003837, 2723	NM.004404, 1034
NM.003859, 5811	NM.004435, 2761
NM.003876, 4708	NM.004448, 4796
NM.003877, 3757	NM.004461, 5279
NM.003906, 5933	NM.004483, 4602
NM.003908, 5734	NM.004493, 6190
NM.003915, 5747	NM.004509, 1012
NM.003932, 6070	NM.004510, 1014
NM.003937, 881	NM.004524, 4960
NM.003938, 5148	NM.004539, 5072
NM.003971, 4891	NM.004547, 1218
NM.003973, 1110	NM.004550, 470
NM.003979, 3498	NM.004551, 3199
NM.004000, 306	NM.004555, 4586
NM.004004, 3866	NM.004573, 4141
NM.004044, 955	NM.004595, 6140
NM.004048, 4178	NM.004596, 5448

NM_004599, 6085	NM_005015, 3981
NM_004618, 4716	NM_005016, 3620
NM_004632, 414	NM_005022, 4665
NM_004635, 1155	NM_005030, 4442
NM_004636, 1149	NM_005036, 6104
NM_004637, 1246	NM_005042, 3524
NM_004638, 1979	NM_005053, 5283
NM_004639, 1973	NM_005072, 4581
NM_004640, 1986	NM_005080, 5987
NM_004673, 529	NM_005109, 1093
NM_004691, 4545	NM_005110, 1854
NM_004697, 2751	NM_005112, 1421
NM_004699, 6323	NM_005115, 4500
NM_004701, 4197	NM_005132, 3962
NM_004704, 1182	NM_005141, 1508
NM_004706, 5470	NM_005163, 4110
NM_004714, 5434	NM_005171, 3574
NM_004725, 3093	NM_005174, 2895
NM_004728, 2959	NM_005194, 5808
NM_004735, 1026	NM_005217, 2478
NM_004738, 5824	NM_005220, 4946
NM_004739, 3230	NM_005224, 5104
NM_004766, 1270	NM_005243, 5989
NM_004767, 576	NM_005269, 3667
NM_004772, 1650	NM_005271, 3004
NM_004781, 44	NM_005291, 854
NM_004794, 6287	NM_005300, 6159
NM_004813, 3190	NM_005313, 4174
NM_004821, 1787	NM_005324, 4969
NM_004844, 1066	NM_005330, 3146
NM_004846, 998	NM_005333, 6126
NM_004859, 4921	NM_005345, 1963
NM_004870, 4689	NM_005346, 1961
NM_004889, 2342	NM_005347, 2790
NM_004893, 1685	NM_005348, 4092
NM_004905, 511	NM_005362, 6316
NM_004911, 2442	NM_005364, 6308
NM_004928, 5915	NM_005370, 5314
NM_004930, 69	NM_005371, 3689
NM_004933, 4638	NM_005378, 657
NM_004939, 662	NM_005389, 2126
NM_004957, 2775	NM_005432, 4101
NM_004960, 4465	NM_005439, 3466
NM_004964, 150	NM_005440, 4877
NM_004973, 2039	NM_005452, 1944
NM_004982, 3526	NM_005474, 4850
NM_004990, 3669	NM_005490, 5208
NM_004992, 6330	NM_005498, 5241
NM_004994, 5791	NM_005514, 2155
NM_004995, 3976	NM_005517, 110
NM_005000, 2396	NM_005520, 1850
NM_005002, 3448	NM_005548, 4568
NM_005003, 4446	NM_005563, 105
NM_005004, 3063	NM_005566, 3175
NM_005005, 2606	NM_005572, 404
NM_005008, 6083	NM_005573, 1718

NM.005581, 5517
NM.005594, 3628
NM.005614, 2460
NM.005617, 1708
NM.005620, 340
NM.005623, 4782
NM.005632, 4362
NM.005657, 4170
NM.005663, 1382
NM.005676, 6165
NM.005686, 550
NM.005692, 2458
NM.005693, 3204
NM.005698, 424
NM.005710, 6181
NM.005713, 1602
NM.005717, 517
NM.005718, 1055
NM.005720, 2348
NM.005724, 4273
NM.005726, 3695
NM.005729, 2986
NM.005731, 996
NM.005745, 6344
NM.005754, 1697
NM.005762, 5627
NM.005770, 4176
NM.005775, 2491
NM.005783, 829
NM.005787, 1316
NM.005796, 4575
NM.005806, 5887
NM.005826, 83
NM.005830, 3898
NM.005831, 4911
NM.005833, 2792
NM.005837, 2326
NM.005850, 461
NM.005851, 3301
NM.005855, 1024
NM.005866, 2670
NM.005877, 5999
NM.005884, 5421
NM.005889, 3509
NM.005911, 808
NM.005915, 864
NM.005917, 764
NM.005918, 2306
NM.005973, 389
NM.005981, 3681
NM.005983, 1579
NM.005985, 5802
NM.005997, 350
NM.006000, 982
NM.006012, 5201
NM.006013, 6326

NM.006019, 3304
NM.006023, 2899
NM.006039, 4936
NM.006053, 3306
NM.006058, 1702
NM.006066, 218
NM.006067, 4612
NM.006098, 1852
NM.006101, 5023
NM.006109, 3973
NM.006110, 4423
NM.006112, 159
NM.006114, 5513
NM.006115, 5975
NM.006128, 2497
NM.006131, 2499
NM.006132, 2501
NM.006136, 2393
NM.006169, 3380
NM.006184, 5566
NM.006227, 5789
NM.006230, 2246
NM.006245, 1892
NM.006247, 5497
NM.006250, 3522
NM.006253, 3831
NM.006262, 3546
NM.006265, 2600
NM.006271, 374
NM.006272, 5935
NM.006280, 6338
NM.006289, 2682
NM.006295, 1967
NM.006303, 2178
NM.006330, 2550
NM.006335, 571
NM.006339, 5171
NM.006342, 1374
NM.006349, 2371
NM.006354, 1049
NM.006362, 3242
NM.006365, 396
NM.006373, 4875
NM.006384, 4305
NM.006387, 5319
NM.006395, 1062
NM.006397, 5277
NM.006401, 2732
NM.006427, 4106
NM.006428, 4360
NM.006429, 792
NM.006430, 759
NM.006432, 4048
NM.006435, 3113
NM.006439, 1504
NM.006440, 5954

NM_006453, 4384
NM_006455, 4822
NM_006470, 4725
NM_006478, 5991
NM_006488, 703
NM_006494, 5476
NM_006503, 5441
NM_006513, 298
NM_006516, 188
NM_006523, 3055
NM_006530, 3727
NM_006556, 452
NM_006559, 146
NM_006576, 3697
NM_006585, 5885
NM_006586, 1894
NM_006589, 428
NM_006600, 118
NM_006601, 3636
NM_006621, 300
NM_006625, 93
NM_006636, 794
NM_006646, 3881
NM_006659, 3101
NM_006666, 5558
NM_006667, 6272
NM_006670, 2070
NM_006693, 2344
NM_006694, 436
NM_006698, 5760
NM_006708, 1904
NM_006711, 4392
NM_006746, 6134
NM_006761, 4642
NM_006763, 548
NM_006764, 1151
NM_006769, 271
NM_006787, 6197
NM_006791, 4279
NM_006799, 4408
NM_006801, 5576
NM_006805, 1687
NM_006808, 2740
NM_006810, 1223
NM_006812, 3678
NM_006815, 3847
NM_006816, 1830
NM_006817, 3785
NM_006821, 4046
NM_006824, 192
NM_006825, 3807
NM_006826, 655
NM_006833, 2338
NM_006835, 1449
NM_006837, 2565
NM_006839, 814

NM_006842, 3295
NM_006844, 5308
NM_006854, 2184
NM_006862, 344
NM_006888, 4063
NM_006899, 5661
NM_006908, 2182
NM_006924, 4908
NM_006928, 3660
NM_006932, 6007
NM_006938, 5039
NM_006941, 6049
NM_006942, 4691
NM_006990, 124
NM_007002, 5844
NM_007019, 5785
NM_007032, 6040
NM_007034, 267
NM_007046, 705
NM_007047, 2029
NM_007062, 3805
NM_007065, 5237
NM_007074, 4516
NM_007085, 1216
NM_007096, 2691
NM_007100, 1366
NM_007103, 3299
NM_007104, 1922
NM_007158, 302
NM_007165, 5152
NM_007173, 3348
NM_007178, 3501
NM_007184, 1165
NM_007186, 5744
NM_007190, 3089
NM_007209, 2794
NM_007242, 4566
NM_007244, 3520
NM_007260, 89
NM_007262, 42
NM_007263, 5352
NM_007268, 6204
NM_007273, 3455
NM_007275, 1153
NM_007276, 2214
NM_007279, 5619
NM_007310, 5958
NM_007311, 6095
NM_007317, 4507
NM_007355, 1874
NM_007364, 4277
NM_007372, 4931
NM_012068, 5525
NM_012098, 2782
NM_012099, 5504
NM_012100, 977

NM_012101, 3420
NM_012111, 4055
NM_012112, 5715
NM_012116, 5519
NM_012138, 4838
NM_012170, 4265
NM_012179, 6017
NM_012181, 5350
NM_012203, 2693
NM_012207, 2955
NM_012237, 5409
NM_012248, 4451
NM_012255, 5698
NM_012264, 6054
NM_012286, 6246
NM_012296, 3344
NM_012323, 6052
NM_012391, 1929
NM_012412, 2236
NM_012423, 5550
NM_012437, 381
NM_012458, 5155
NM_012469, 5873
NM_012486, 596
NM_013237, 1834
NM_013247, 801
NM_013265, 3279
NM_013274, 3037
NM_013277, 3566
NM_013296, 292
NM_013333, 5617
NM_013336, 1238
NM_013341, 903
NM_013363, 1276
NM_013365, 6032
NM_013369, 5911
NM_013375, 2027
NM_013393, 2165
NM_013402, 3251
NM_013403, 5492
NM_013406, 5269
NM_013407, 5270
NM_013417, 2718
NM_013442, 2675
NM_013451, 3013
NM_014003, 4592
NM_014008, 6187
NM_014033, 3576
NM_014035, 1664
NM_014042, 3320
NM_014062, 4556
NM_014063, 2251
NM_014107, 2077
NM_014138, 6163
NM_014166, 3906
NM_014172, 2862

NM_014173, 5326
NM_014176, 578
NM_014184, 585
NM_014188, 17
NM_014189, 1390
NM_014190, 1388
NM_014203, 5536
NM_014214, 5032
NM_014226, 4095
NM_014236, 626
NM_014248, 6072
NM_014255, 3631
NM_014267, 3173
NM_014275, 1846
NM_014285, 2820
NM_014294, 2567
NM_014303, 6003
NM_014306, 6015
NM_014311, 3606
NM_014320, 2116
NM_014321, 4476
NM_014325, 3777
NM_014335, 4182
NM_014341, 1906
NM_014353, 4386
NM_014408, 167
NM_014413, 2180
NM_014426, 5685
NM_014444, 4168
NM_014445, 1284
NM_014452, 1870
NM_014453, 5625
NM_014481, 6199
NM_014501, 5615
NM_014502, 3220
NM_014515, 3724
NM_014556, 1394
NM_014571, 142
NM_014585, 923
NM_014587, 4370
NM_014610, 3232
NM_014624, 367
NM_014649, 5199
NM_014663, 202
NM_014670, 934
NM_014685, 4530
NM_014713, 667
NM_014736, 4214
NM_014737, 5676
NM_014742, 5721
NM_014747, 180
NM_014748, 684
NM_014752, 3329
NM_014773, 1721
NM_014776, 3792
NM_014778, 3878

NM_014800, 2259
NM_014814, 1195
NM_014829, 1681
NM_014837, 519
NM_014847, 446
NM_014849, 463
NM_014851, 36
NM_014868, 3823
NM_014887, 3889
NM_014919, 1378
NM_014931, 5610
NM_014933, 1457
NM_014941, 6005
NM_014972, 4628
NM_015043, 1843
NM_015062, 3042
NM_015064, 3430
NM_015068, 2319
NM_015129, 6276
NM_015140, 6097
NM_015179, 3024
NM_015322, 4226
NM_015324, 3149
NM_015373, 6056
NM_015388, 1886
NM_015438, 3470
NM_015449, 444
NM_015453, 1043
NM_015472, 1282
NM_015484, 99
NM_015511, 5752
NM_015533, 3225
NM_015544, 4780
NM_015584, 4761
NM_015629, 5600
NM_015636, 686
NM_015640, 260
NM_015644, 1057
NM_015646, 3720
NM_015665, 3604
NM_015702, 885
NM_015714, 555
NM_015853, 3238
NM_015920, 4205
NM_015932, 3884
NM_015934, 941
NM_015937, 5783
NM_015953, 5546
NM_015965, 5362
NM_015966, 5745
NM_016003, 2172
NM_016016, 4847
NM_016022, 334
NM_016026, 4037
NM_016030, 647
NM_016059, 1908

NM_016085, 694
NM_016091, 6045
NM_016095, 4610
NM_016111, 4374
NM_016119, 3912
NM_016143, 5652
NM_016169, 3051
NM_016174, 2767
NM_016176, 26
NM_016183, 73
NM_016202, 5621
NM_016223, 3210
NM_016249, 6300
NM_016263, 5169
NM_016267, 6293
NM_016286, 5006
NM_016292, 4414
NM_016304, 4193
NM_016328, 2293
NM_016357, 3572
NM_016359, 4152
NM_016361, 328
NM_016410, 2664
NM_016440, 5523
NM_016445, 4035
NM_016456, 564
NM_016498, 6001
NM_016526, 3107
NM_016539, 5181
NM_016558, 5750
NM_016567, 3097
NM_016579, 5216
NM_016587, 2216
NM_016592, 5826
NM_016638, 3843
NM_016639, 4398
NM_016641, 4335
NM_016645, 4302
NM_016647, 2614
NM_016732, 5733
NM_016838, 887
NM_016839, 889
NM_016930, 1400
NM_016940, 5883
NM_016941, 5432
NM_017443, 2753
NM_017458, 4498
NM_017491, 1419
NM_017546, 834
NM_017566, 4617
NM_017572, 5146
NM_017595, 4871
NM_017601, 1902
NM_017610, 4195
NM_017613, 5890
NM_017647, 4929

NM.017668, 4327	NM.018209, 5861
NM.017670, 3266	NM.018212, 587
NM.017684, 4208	NM.018217, 5740
NM.017722, 5286	NM.018238, 2437
NM.017751, 859	NM.018242, 4747
NM.017760, 2467	NM.018250, 2510
NM.017761, 91	NM.018253, 418
NM.017768, 262	NM.018255, 5056
NM.017777, 4906	NM.018270, 5849
NM.017789, 825	NM.018310, 2527
NM.017797, 5143	NM.018346, 4898
NM.017801, 1081	NM.018357, 4232
NM.017803, 4584	NM.018410, 1018
NM.017807, 4003	NM.018454, 4154
NM.017815, 3971	NM.018457, 3610
NM.017822, 3552	NM.018463, 3442
NM.017825, 165	NM.018464, 2951
NM.017827, 5413	NM.018468, 5387
NM.017829, 5939	NM.018486, 6222
NM.017847, 513	NM.018509, 4900
NM.017853, 4594	NM.018607, 721
NM.017868, 3386	NM.018660, 2512
NM.017874, 5668	NM.018668, 4312
NM.017876, 5098	NM.018674, 973
NM.017882, 4224	NM.018686, 3513
NM.017883, 6179	NM.018912, 1734
NM.017891, 8	NM.018913, 1736
NM.017895, 5798	NM.018914, 1738
NM.017900, 22	NM.018915, 1740
NM.017901, 3810	NM.018916, 1742
NM.017910, 674	NM.018917, 1744
NM.017916, 5554	NM.018918, 1746
NM.017952, 812	NM.018919, 1748
NM.017955, 4112	NM.018920, 1750
NM.017974, 1020	NM.018921, 1752
NM.018019, 4737	NM.018922, 1754
NM.018023, 1306	NM.018923, 1756
NM.018032, 4358	NM.018924, 1758
NM.018034, 1575	NM.018925, 1760
NM.018035, 5458	NM.018926, 1762
NM.018047, 1706	NM.018927, 1764
NM.018048, 3517	NM.018928, 1766
NM.018054, 4436	NM.018929, 1768
NM.018066, 116	NM.018947, 2208
NM.018070, 239	NM.018948, 41
NM.018085, 569	NM.018950, 2017
NM.018096, 4792	NM.018955, 4728
NM.018110, 4535	NM.018957, 6034
NM.018113, 3548	NM.018977, 6214
NM.018116, 420	NM.019013, 4682
NM.018122, 535	NM.019058, 2971
NM.018124, 4588	NM.019059, 2206
NM.018135, 1880	NM.019082, 2242
NM.018154, 5300	NM.019095, 5681
NM.018174, 5332	NM.019099, 310
NM.018188, 10	NM.019554, 371

NM.019606, 2333	NM.021932, 3109
NM.019609, 5663	NM.021934, 3588
NM.019619, 2916	NM.021948, 394
NM.019848, 6321	NM.021953, 3444
NM.019852, 3988	NM.021966, 4079
NM.019887, 3839	NM.021999, 3908
NM.020037, 4895	NM.022003, 3369
NM.020038, 4893	NM.022039, 3039
NM.020132, 5908	NM.022044, 5973
NM.020134, 709	NM.022048, 4216
NM.020149, 4136	NM.022105, 5857
NM.020158, 5454	NM.022137, 4042
NM.020188, 4604	NM.022141, 6101
NM.020230, 5232	NM.022158, 5016
NM.020243, 6058	NM.022170, 2288
NM.020299, 2425	NM.022171, 1145
NM.020315, 6036	NM.022362, 3029
NM.020320, 2075	NM.022369, 4246
NM.020347, 1113	NM.022371, 527
NM.020401, 3717	NM.022442, 5806
NM.020414, 4069	NM.022453, 988
NM.020418, 1180	NM.022458, 2464
NM.020548, 871	NM.022461, 1086
NM.020675, 896	NM.022485, 1045
NM.020677, 4340	NM.022550, 1638
NM.020701, 1248	NM.022551, 1946
NM.020990, 4172	NM.022552, 717
NM.020992, 3017	NM.022566, 4296
NM.021019, 3646	NM.022727, 5961
NM.021029, 6244	NM.022744, 4468
NM.021079, 4883	NM.022747, 4084
NM.021095, 698	NM.022748, 2226
NM.021103, 803	NM.022752, 5474
NM.021104, 3654	NM.022758, 1926
NM.021107, 5415	NM.022770, 4539
NM.021121, 948	NM.022778, 107
NM.021126, 6029	NM.022839, 4290
NM.021129, 2964	NM.022963, 1838
NM.021130, 2238	NM.023009, 152
NM.021141, 958	NM.023011, 3940
NM.021154, 2701	NM.023032, 3691
NM.021158, 5638	NM.023033, 3693
NM.021177, 1965	NM.023078, 2620
NM.021178, 4006	NM.023936, 4378
NM.021195, 4400	NM.023942, 2449
NM.021213, 4919	NM.024003, 6336
NM.021219, 5879	NM.024026, 3872
NM.021226, 2945	NM.024027, 645
NM.021626, 4917	NM.024029, 5250
NM.021709, 4108	NM.024031, 4458
NM.021728, 4020	NM.024033, 2427
NM.021826, 5665	NM.024040, 3047
NM.021830, 3033	NM.024045, 2957
NM.021831, 707	NM.024048, 4470
NM.021870, 1517	NM.024067, 2186
NM.021871, 1513	NM.024068, 3643

NM.024070, 2335
NM.024089, 3935
NM.024098, 3218
NM.024099, 3236
NM.024104, 5323
NM.024111, 4148
NM.024294, 1924
NM.024297, 4672
NM.024299, 5865
NM.024319, 614
NM.024321, 5389
NM.024329, 62
NM.024330, 379
NM.024333, 5186
NM.024339, 4396
NM.024407, 5120
NM.024507, 4406
NM.024516, 4502
NM.024537, 3938
NM.024567, 2508
NM.024571, 4350
NM.024572, 719
NM.024586, 247
NM.024589, 4346
NM.024602, 206
NM.024603, 241
NM.024613, 2584
NM.024627, 5951
NM.024640, 137
NM.024653, 2373
NM.024658, 3960
NM.024664, 183
NM.024668, 1724
NM.024671, 4454
NM.024691, 5636
NM.024709, 603
NM.024748, 1526
NM.024824, 4057
NM.024844, 4955
NM.024854, 3529
NM.024855, 5769
NM.024863, 6248
NM.024881, 5321
NM.024900, 1491
NM.024918, 5757
NM.024942, 3095
NM.025070, 2541
NM.025072, 2772
NM.025108, 4411
NM.025129, 5534
NM.025150, 358
NM.025164, 3374
NM.025168, 1863
NM.025197, 4830
NM.025202, 1000
NM.025203, 678

NM.025204, 6109
NM.025205, 1414
NM.025207, 455
NM.025226, 499
NM.025232, 2503
NM.025233, 4859
NM.025234, 4270
NM.025241, 5190
NM.025263, 2007
NM.030567, 1826
NM.030573, 5965
NM.030579, 4553
NM.030587, 196
NM.030593, 5411
NM.030775, 3432
NM.030782, 1545
NM.030815, 5719
NM.030819, 4573
NM.030877, 5763
NM.030900, 2232
NM.030920, 332
NM.030921, 1272
NM.030925, 3910
NM.030926, 1009
NM.030935, 2331
NM.030973, 5532
NM.031157, 3612
NM.031206, 6210
NM.031213, 5138
NM.031228, 5642
NM.031229, 5640
NM.031243, 2212
NM.031263, 2708
NM.031289, 3496
NM.031300, 1832
NM.031417, 5506
NM.031434, 2456
NM.031443, 2234
NM.031453, 2902
NM.031459, 131
NM.031465, 3446
NM.031472, 3261
NM.031478, 4522
NM.031479, 3665
NM.031482, 1629
NM.031484, 3070
NM.031485, 5574
NM.031901, 336
NM.031925, 2304
NM.031942, 905
NM.031966, 1598
NM.031968, 5014
NM.031989, 3622
NM.031990, 5100
NM.031992, 2290
NM.032023, 2923

NM.032038, 4495
NM.032088, 1770
NM.032092, 1772
NM.032112, 3031
NM.032140, 4571
NM.032162, 4310
NM.032164, 2340
NM.032196, 4150
NM.032204, 5996
NM.032207, 5317
NM.032211, 3068
NM.032212, 843
NM.032219, 1370
NM.032227, 6257
NM.032271, 4388
NM.032280, 1642
NM.032288, 1354
NM.032292, 412
NM.032299, 3395
NM.032313, 1437
NM.032322, 4771
NM.032323, 402
NM.032324, 630
NM.032330, 4485
NM.032331, 1318
NM.032333, 2996
NM.032338, 3712
NM.032342, 2746
NM.032343, 1235
NM.032350, 2163
NM.032361, 1814
NM.032376, 4854
NM.032377, 5262
NM.032379, 3346
NM.032383, 1280
NM.032390, 875
NM.032402, 1776
NM.032403, 1774
NM.032486, 4444
NM.032527, 5869
NM.032565, 3914
NM.032626, 4440
NM.032627, 5345
NM.032635, 5393
NM.032636, 296
NM.032637, 1577
NM.032642, 3434
NM.032656, 3851
NM.032667, 3240
NM.032712, 5588
NM.032726, 990
NM.032737, 5157
NM.032738, 503
NM.032747, 3061
NM.032750, 1174
NM.032753, 5173

NM.032756, 222
NM.032792, 5631
NM.032799, 2763
NM.032814, 3812
NM.032822, 785
NM.032827, 810
NM.032864, 245
NM.032871, 3326
NM.032872, 122
NM.032873, 3415
NM.032890, 606
NM.032904, 3794
NM.032905, 2893
NM.032907, 4248
NM.032928, 2860
NM.032929, 2081
NM.032933, 5037
NM.032951, 2284
NM.032953, 2286
NM.032958, 2376
NM.032989, 3258
NM.032997, 2949
NM.032999, 2295
NM.033008, 1176
NM.033010, 1178
NM.033011, 2538
NM.033022, 2978
NM.033046, 796
NM.033070, 5937
NM.033161, 2828
NM.033197, 5729
NM.033219, 2730
NM.033251, 4635
NM.033296, 1404
NM.033301, 2635
NM.033316, 1348
NM.033363, 5417
NM.033410, 4456
NM.033415, 5355
NM.033416, 878
NM.033421, 5787
NM.033440, 60
NM.033534, 15
NM.033544, 4315
NM.033551, 1785
NM.052837, 426
NM.052848, 5451
NM.052859, 1157
NM.052862, 488
NM.052881, 5656
NM.052886, 2602
NM.052936, 6251
NM.052963, 2616
NM.052984, 3685
NM.053043, 2462
NM.053056, 3311

NM_053275, 3829
NM_054012, 2822
NM_054013, 1848
NM_054014, 5650
NM_054016, 95
NM_057089, 2363
NM_057161, 1890
NM_057169, 3790
NM_057174, 3188
NM_057182, 5376
NM_058164, 5230
NM_058179, 2703
NM_058192, 4366
NM_058193, 3422
NM_058195, 2653
NM_058196, 2657
NM_058199, 2836
NM_078467, 1912
NM_079423, 3648
NM_079425, 3650
NM_080424, 1016
NM_080425, 5828
NM_080426, 5832
NM_080491, 3342
NM_080592, 696
NM_080594, 4394
NM_080598, 1984
NM_080648, 3999
NM_080649, 4001
NM_080670, 1726
NM_080686, 1981
NM_080687, 3942
NM_080702, 1977
NM_080703, 1975
NM_080796, 5855
NM_080797, 5859
NM_080820, 5693
NM_080822, 4654
NM_106552, 670
NM_130398, 639
NM_130442, 2260
NM_130468, 4143
NM_130898, 434
NM_133330, 1376
NM_133332, 1380
NM_133373, 4885
NM_133375, 4222
NM_133436, 2357
NM_133480, 1051
NM_133481, 1053
NM_133483, 3676
NM_133503, 3742
NM_133504, 3744
NM_133505, 3746
NM_133506, 3750
NM_133507, 3748

NM_133627, 4786
NM_133629, 4790
NM_133630, 4788
NM_133637, 798
NM_133645, 2066
NM_134269, 6009
NM_134323, 3616
NM_134324, 3618
NM_134440, 5358
NM_138385, 1372
NM_138391, 545
NM_138427, 4739
NM_138434, 2451
NM_138443, 5060
NM_138483, 1037
NM_138578, 5713
NM_138614, 1125
NM_138699, 1406
NM_138801, 727
NM_138924, 5124

XM_001289, 524
XM_001299, 33
XM_001389, 1453
XM_001468, 342
XM_001472, 250
XM_001482, 3658
XM_001589, 24
XM_001616, 101
XM_001640, 126
XM_001807, 135
XM_001812, 134
XM_001826, 78
XM_001897, 486
XM_001914, 567
XM_001916, 568
XM_001958, 599
XM_002068, 523
XM_002105, 141
XM_002114, 113
XM_002217, 845
XM_002255, 1361
XM_002435, 700
XM_002447, 877
XM_002480, 680
XM_002540, 1006
XM_002611, 823
XM_002636, 964
XM_002647, 770
XM_002669, 946
XM_002674, 776
XM_002704, 853
XM_002727, 788
XM_002739, 779
XM_002742, 1036
XM_002828, 1143
XM_002854, 1187

XM_002855, 1186
XM_002859, 1274
XM_002899, 1127
XM_003213, 1162
XM_003222, 1119
XM_003245, 1136
XM_003305, 1451
XM_003435, 1432
XM_003477, 1530
XM_003511, 1448
XM_003555, 1500
XM_003611, 2083
XM_003716, 1811
XM_003771, 1644
XM_003789, 1712
XM_003825, 1540
XM_003830, 1666
XM_003841, 1699
XM_003869, 1572
XM_003896, 1581
XM_003937, 1710
XM_004009, 1565
XM_004098, 3704
XM_004151, 2065
XM_004256, 2114
XM_004297, 2113
XM_004330, 3194
XM_004379, 2122
XM_004383, 2130
XM_004526, 2110
XM_004627, 2402
XM_004901, 2292
XM_005060, 2605
XM_005086, 1042
XM_005100, 2908
XM_005180, 1332
XM_005305, 2485
XM_005348, 2755
XM_005365, 2760
XM_005490, 2707
XM_005525, 2727
XM_005543, 2666
XM_005675, 3103
XM_005698, 3053
XM_005724, 2878
XM_005938, 3058
XM_005969, 3088
XM_006139, 3127
XM_006170, 3201
XM_006212, 3167
XM_006290, 98
XM_006297, 3196
XM_006424, 3151
XM_006432, 3371
XM_006464, 3355
XM_006467, 3399

XM_006475, 3135
XM_006483, 3136
XM_006529, 3281
XM_006533, 3270
XM_006566, 3849
XM_006578, 3736
XM_006589, 3766
XM_006595, 3835
XM_006694, 3535
XM_006710, 3626
XM_006748, 3536
XM_006826, 3559
XM_006887, 3765
XM_006925, 3485
XM_006936, 3483
XM_006937, 5074
XM_006947, 3482
XM_006958, 3475
XM_007002, 3797
XM_007003, 3796
XM_007199, 3923
XM_007254, 4097
XM_007272, 4081
XM_007288, 3968
XM_007293, 3967
XM_007315, 3958
XM_007316, 3957
XM_007324, 4027
XM_007328, 4024
XM_007441, 4045
XM_007483, 4072
XM_007488, 4005
XM_007491, 3996
XM_007531, 4167
XM_007545, 4156
XM_007623, 4221
XM_007651, 4189
XM_007751, 4129
XM_007963, 4474
XM_007988, 4430
XM_008064, 4509
XM_008065, 4497
XM_008106, 4463
XM_008126, 4353
XM_008150, 4800
XM_008231, 4694
XM_008253, 4926
XM_008323, 4750
XM_008334, 4671
XM_008351, 4856
XM_008401, 4867
XM_008402, 4869
XM_008432, 4902
XM_008441, 4686
XM_008459, 4915
XM_008462, 4777

XM_008486, 4760	XM_010272, 6132
XM_008509, 4658	XM_010362, 6274
XM_008538, 4684	XM_010378, 6169
XM_008557, 4650	XM_010436, 6280
XM_008579, 4809	XM_010494, 3429
XM_008679, 4693	XM_010615, 253
XM_008695, 5089	XM_010636, 451
XM_008723, 5054	XM_010664, 133
XM_008812, 5083	XM_010682, 581
XM_008830, 5597	XM_010712, 182
XM_008851, 5522	XM_010732, 593
XM_008854, 5325	XM_010778, 925
XM_008860, 5485	XM_010852, 938
XM_008878, 5472	XM_010858, 1004
XM_008887, 5243	XM_010866, 992
XM_008912, 5453	XM_010881, 771
XM_008985, 5531	XM_010886, 755
XM_009010, 5205	XM_010938, 4641
XM_009036, 5486	XM_010941, 1433
XM_009063, 5274	XM_010953, 1130
XM_009082, 5256	XM_010978, 1290
XM_009125, 5484	XM_011074, 1320
XM_009126, 5496	XM_011089, 5076
XM_009149, 5406	XM_011117, 2059
XM_009180, 5378	XM_011118, 4941
XM_009203, 5443	XM_011129, 1423
XM_009222, 5165	XM_011160, 1365
XM_009277, 5113	XM_011548, 2411
XM_009279, 5110	XM_011618, 2400
XM_009293, 5338	XM_011629, 2533
XM_009303, 5310	XM_011642, 2586
XM_009330, 5357	XM_011650, 66
XM_009338, 5384	XM_011657, 2592
XM_009436, 5705	XM_011749, 2798
XM_009450, 5728	XM_011752, 2786
XM_009501, 5754	XM_011769, 2562
XM_009549, 5816	XM_011778, 2832
XM_009622, 5647	XM_011988, 3260
XM_009642, 5759	XM_012124, 3836
XM_009671, 5823	XM_012145, 3761
XM_009672, 5821	XM_012159, 3494
XM_009686, 5762	XM_012162, 3598
XM_009805, 5919	XM_012179, 5337
XM_009947, 6022	XM_012182, 3638
XM_009967, 6031	XM_012184, 3861
XM_009973, 6042	XM_012219, 3759
XM_010000, 6063	XM_012272, 3543
XM_010002, 6064	XM_012284, 2395
XM_010024, 6087	XM_012376, 3990
XM_010029, 6094	XM_012377, 3983
XM_010040, 6103	XM_012398, 4133
XM_010055, 6108	XM_012418, 4199
XM_010117, 6269	XM_012462, 4322
XM_010141, 6216	XM_012487, 4555
XM_010156, 5266	XM_012549, 4734
XM_010178, 6310	XM_012569, 4461

XM.012609, 4945
XM.012615, 4744
XM.012634, 4950
XM.012638, 3874
XM.012642, 4849
XM.012651, 4916
XM.012676, 4675
XM.012741, 5031
XM.012798, 5212
XM.012812, 5370
XM.012860, 5439
XM.012862, 5195
XM.012913, 5114
XM.012931, 5768
XM.012970, 5700
XM.013010, 6066
XM.013015, 6089
XM.013029, 6118
XM.013042, 6207
XM.013060, 6196
XM.013086, 6145
XM.013112, 2530
XM.013127, 2577
XM.015234, 75
XM.015241, 5088
XM.015243, 3148
XM.015258, 2244
XM.015366, 4239
XM.015434, 547
XM.015462, 1208
XM.015468, 3596
XM.015476, 3585
XM.015481, 3580
XM.015516, 6206
XM.015563, 1525
XM.015652, 2937
XM.015697, 5264
XM.015700, 4478
XM.015705, 3214
XM.015717, 257
XM.015755, 5046
XM.015769, 5369
XM.015835, 4311
XM.015840, 3921
XM.015842, 3932
XM.015920, 909
XM.015922, 911
XM.016047, 2604
XM.016076, 4237
XM.016093, 2992
XM.016113, 2712
XM.016125, 6275
XM.016139, 3170
XM.016164, 276
XM.016170, 1554
XM.016199, 600

XM.016288, 880
XM.016308, 2726
XM.016334, 1294
XM.016345, 1799
XM.016351, 3924
XM.016378, 5364
XM.016382, 5036
XM.016410, 5438
XM.016480, 326
XM.016486, 4071
XM.016487, 4068
XM.016605, 3708
XM.016625, 773
XM.016640, 3538
XM.016674, 1652
XM.016700, 2433
XM.016713, 4165
XM.016733, 2256
XM.016843, 766
XM.016857, 1941
XM.016871, 5180
XM.016985, 4213
XM.017080, 3436
XM.017096, 4644
XM.017204, 5240
XM.017234, 4712
XM.017240, 4135
XM.017315, 67
XM.017356, 1291
XM.017364, 1105
XM.017369, 3394
XM.017432, 3895
XM.017442, 2313
XM.017474, 1679
XM.017483, 2280
XM.017508, 3710
XM.017517, 2080
XM.017578, 4980
XM.017591, 1701
XM.017641, 1544
XM.017698, 861
XM.017816, 2581
XM.017831, 2119
XM.017846, 109
XM.017857, 1640
XM.017914, 3953
XM.017925, 1476
XM.017930, 6284
XM.017931, 2659
XM.017971, 4319
XM.017984, 4338
XM.017996, 2711
XM.018006, 2710
XM.018019, 6157
XM.018039, 784
XM.018041, 642

XM.018054, 4123	XM.028347, 4074
XM.018088, 4472	XM.028358, 4073
XM.018108, 6313	XM.028398, 4667
XM.018109, 6315	XM.028417, 4678
XM.018136, 161	XM.028643, 3624
XM.018142, 6232	XM.028662, 3561
XM.018149, 1264	XM.028666, 5383
XM.018167, 3015	XM.028672, 5382
XM.018182, 2098	XM.028744, 5025
XM.018205, 64	XM.028760, 3554
XM.018241, 6161	XM.028783, 5851
XM.018279, 3057	XM.028806, 5765
XM.018287, 2595	XM.028810, 5766
XM.018301, 763	XM.028834, 5863
XM.018332, 314	XM.028848, 4390
XM.018359, 2281	XM.028918, 5867
XM.018399, 3918	XM.028966, 5871
XM.018432, 4331	XM.029031, 169
XM.018473, 1658	XM.029096, 1539
XM.018515, 5354	XM.029104, 1314
XM.018523, 1359	XM.029132, 1313
XM.018534, 4840	XM.029136, 1310
XM.018539, 6014	XM.029168, 2841
XM.018540, 841	XM.029187, 6194
XM.026944, 2787	XM.029228, 2069
XM.026951, 2771	XM.029288, 4067
XM.026968, 2769	XM.029369, 1198
XM.026985, 2766	XM.029438, 4656
XM.026987, 2765	XM.029450, 5404
XM.027102, 3802	XM.029455, 5403
XM.027143, 6106	XM.029461, 6282
XM.027161, 1220	XM.029567, 2609
XM.027214, 2385	XM.029631, 3602
XM.027309, 4329	XM.029728, 3595
XM.027313, 226	XM.029746, 2128
XM.027365, 4334	XM.029805, 3507
XM.027412, 4368	XM.029810, 5776
XM.027440, 2505	XM.029822, 5778
XM.027558, 4352	XM.029842, 176
XM.027651, 2490	XM.029844, 145
XM.027679, 2488	XM.030044, 5796
XM.027825, 4661	XM.030203, 1028
XM.027904, 5548	XM.030268, 2543
XM.027916, 76	XM.030274, 2544
XM.027952, 6353	XM.030326, 3187
XM.027963, 936	XM.030373, 6233
XM.027964, 1619	XM.030417, 1112
XM.027983, 213	XM.030423, 154
XM.028034, 940	XM.030447, 3065
XM.028064, 5119	XM.030470, 68
XM.028067, 5117	XM.030485, 5159
XM.028151, 4562	XM.030529, 862
XM.028192, 3117	XM.030582, 883
XM.028263, 5488	XM.030621, 5818
XM.028267, 5491	XM.030699, 5834
XM.028322, 4075	XM.030714, 5145

XM_030720, 5137	XM_032588, 3457
XM_030721, 5135	XM_032614, 3462
XM_030771, 1821	XM_032710, 5247
XM_030777, 1823	XM_032719, 5248
XM_030782, 1824	XM_032724, 5252
XM_030812, 1256	XM_032759, 1700
XM_030834, 952	XM_032766, 4864
XM_030895, 5465	XM_032774, 5257
XM_030901, 5456	XM_032782, 5261
XM_030914, 5450	XM_032813, 4863
XM_030920, 40	XM_032817, 4861
XM_031025, 4032	XM_032852, 4857
XM_031074, 4039	XM_032895, 1590
XM_031251, 5307	XM_032902, 1588
XM_031263, 5305	XM_032930, 6189
XM_031273, 5303	XM_032944, 2470
XM_031276, 5302	XM_032996, 5943
XM_031292, 4295	XM_033015, 5902
XM_031320, 1445	XM_033016, 5903
XM_031345, 5292	XM_033090, 5946
XM_031354, 4292	XM_033147, 6241
XM_031404, 4285	XM_033227, 3450
XM_031415, 4767	XM_033232, 6351
XM_031427, 4769	XM_033251, 3959
XM_031466, 4765	XM_033263, 3472
XM_031515, 4147	XM_033294, 1123
XM_031519, 731	XM_033337, 3964
XM_031527, 733	XM_033355, 2819
XM_031536, 4758	XM_033359, 2818
XM_031554, 4145	XM_033360, 2817
XM_031585, 782	XM_033361, 2815
XM_031586, 783	XM_033362, 2811
XM_031596, 780	XM_033380, 2809
XM_031617, 4138	XM_033385, 2808
XM_031626, 738	XM_033391, 3969
XM_031718, 4159	XM_033424, 2774
XM_031807, 3491	XM_033435, 3975
XM_031857, 5184	XM_033445, 3980
XM_031866, 3041	XM_033457, 2777
XM_031890, 3044	XM_033460, 2778
XM_031917, 5176	XM_033553, 3991
XM_031944, 5066	XM_033595, 3994
XM_031949, 3049	XM_033654, 79
XM_031992, 3059	XM_033683, 77
XM_032020, 5281	XM_033689, 4646
XM_032121, 2455	XM_033714, 4645
XM_032201, 4836	XM_033813, 5960
XM_032216, 2454	XM_033862, 6173
XM_032269, 1221	XM_033876, 2383
XM_032285, 5399	XM_033878, 6172
XM_032391, 216	XM_033884, 6170
XM_032403, 4180	XM_033910, 2134
XM_032443, 3930	XM_033912, 2132
XM_032476, 2976	XM_033922, 4606
XM_032520, 2970	XM_034000, 501
XM_032553, 1626	XM_034082, 454

XM_034321, 1502
XM_034375, 4460
XM_034377, 5623
XM_034431, 3185
XM_034586, 4376
XM_034590, 4380
XM_034640, 2638
XM_034662, 319
XM_034671, 318
XM_034710, 1466
XM_034713, 1468
XM_034744, 1655
XM_034862, 1675
XM_034890, 4184
XM_034897, 4256
XM_034935, 6201
XM_034952, 857
XM_034953, 4116
XM_035014, 4119
XM_035103, 2824
XM_035107, 2439
XM_035109, 2825
XM_035220, 800
XM_035368, 2626
XM_035370, 2631
XM_035373, 2629
XM_035465, 6123
XM_035485, 3571
XM_035490, 3564
XM_035497, 3562
XM_035572, 1392
XM_035625, 5197
XM_035627, 5196
XM_035636, 5194
XM_035638, 5192
XM_035640, 5034
XM_035662, 2483
XM_035680, 2482
XM_035824, 1402
XM_035919, 5612
XM_035986, 1456
XM_035999, 5907
XM_036002, 1440
XM_036011, 5910
XM_036042, 5913
XM_036087, 5917
XM_036104, 4965
XM_036107, 5923
XM_036115, 4971
XM_036118, 1262
XM_036175, 5924
XM_036299, 155
XM_036339, 3178
XM_036413, 2469
XM_036450, 664
XM_036462, 4827

XM_036465, 4825
XM_036500, 573
XM_036507, 575
XM_036528, 4410
XM_036556, 566
XM_036593, 2939
XM_036659, 4707
XM_036680, 4342
XM_036727, 4134
XM_036744, 433
XM_036755, 5927
XM_036785, 4982
XM_036829, 442
XM_036845, 450
XM_036934, 448
XM_036937, 5969
XM_036938, 1197
XM_037002, 1668
XM_037056, 2107
XM_037101, 873
XM_037108, 831
XM_037147, 3212
XM_037173, 3202
XM_037195, 4988
XM_037196, 4987
XM_037202, 5840
XM_037206, 5842
XM_037217, 5846
XM_037260, 1608
XM_037329, 591
XM_037377, 1300
XM_037381, 1299
XM_037423, 1163
XM_037468, 6114
XM_037474, 6116
XM_037565, 5106
XM_037572, 5109
XM_037600, 1304
XM_037657, 2608
XM_037662, 5372
XM_037682, 5977
XM_037741, 2276
XM_037778, 4244
XM_037797, 5981
XM_037808, 3263
XM_037875, 2045
XM_037945, 5993
XM_037971, 4897
XM_038030, 2855
XM_038049, 2864
XM_038063, 2866
XM_038098, 5343
XM_038146, 5339
XM_038221, 1695
XM_038243, 1341
XM_038308, 3737

XM_038371, 3902
XM_038391, 2757
XM_038424, 5018
XM_038536, 2909
XM_038576, 734
XM_038584, 6019
XM_038659, 3533
XM_038791, 3841
XM_038852, 244
XM_038872, 5062
XM_038911, 237
XM_038946, 1840
XM_039165, 1413
XM_039173, 1416
XM_039176, 1417
XM_039225, 4125
XM_039236, 6047
XM_039248, 6051
XM_039306, 4551
XM_039339, 6060
XM_039372, 6065
XM_039395, 3732
XM_039474, 4794
XM_039654, 2646
XM_039702, 4200
XM_039712, 716
XM_039721, 321
XM_039723, 5140
XM_039796, 1292
XM_039805, 1258
XM_039908, 5598
XM_039910, 4721
XM_039921, 4732
XM_039952, 1213
XM_039975, 1783
XM_040009, 377
XM_040066, 6088
XM_040095, 6091
XM_040221, 3707
XM_040267, 2879
XM_040272, 2876
XM_040321, 1524
XM_040498, 2417
XM_040623, 2074
XM_040644, 3734
XM_040709, 315
XM_040752, 1493
XM_040853, 2218
XM_040898, 4100
XM_040942, 4094
XM_040952, 4090
XM_041014, 4086
XM_041020, 2697
XM_041059, 1670
XM_041100, 3503
XM_041209, 3925

XM_041211, 1161
XM_041221, 1410
XM_041235, 4008
XM_041248, 6111
XM_041473, 3928
XM_041484, 3944
XM_041507, 1147
XM_041583, 4957
XM_041678, 5027
XM_041694, 1614
XM_041712, 1592
XM_041872, 5090
XM_041879, 353
XM_041884, 354
XM_041921, 6304
XM_041964, 4680
XM_042018, 5095
XM_042025, 1600
XM_042153, 6348
XM_042155, 6346
XM_042168, 1286
XM_042301, 1474
XM_042326, 1032
XM_042422, 2145
XM_042473, 2148
XM_042618, 1229
XM_042621, 4596
XM_042658, 2561
XM_042695, 1364
XM_042698, 4710
XM_042765, 5701
XM_042781, 2434
XM_042788, 2744
XM_042841, 1072
XM_042852, 3339
XM_042860, 1070
XM_042963, 6295
XM_042967, 537
XM_042968, 6297
XM_043047, 4577
XM_043173, 866
XM_043220, 3111
XM_043340, 1805
XM_043388, 1808
XM_043589, 2998
XM_043605, 2999
XM_043614, 6099
XM_043643, 6250
XM_043771, 1568
XM_044075, 416
XM_044077, 391
XM_044127, 398
XM_044128, 408
XM_044166, 406
XM_044172, 411
XM_044334, 3859

XM_044354, 2968	XM_046160, 5708
XM_044367, 4938	XM_046179, 5710
XM_044372, 4943	XM_046313, 5544
XM_044376, 4935	XM_046349, 187
XM_044394, 4927	XM_046401, 1085
XM_044426, 4924	XM_046419, 5578
XM_044523, 4304	XM_046450, 201
XM_044533, 4307	XM_046464, 522
XM_044565, 4269	XM_046472, 5004
XM_044569, 4272	XM_046481, 4999
XM_044593, 4278	XM_046520, 5689
XM_044608, 5213	XM_046551, 212
XM_044619, 5210	XM_046557, 208
XM_044627, 2563	XM_046565, 204
XM_044866, 2139	XM_046642, 3951
XM_044914, 5658	XM_046648, 3950
XM_044915, 5660	XM_046651, 3949
XM_044932, 3129	XM_046743, 3035
XM_044957, 3131	XM_046765, 5020
XM_045010, 3821	XM_046767, 5022
XM_045044, 4749	XM_046769, 5021
XM_045104, 4989	XM_046822, 5150
XM_045140, 2973	XM_046836, 2722
XM_045151, 5226	XM_046863, 2720
XM_045170, 928	XM_046918, 112
XM_045183, 4651	XM_046932, 4958
XM_045187, 3833	XM_046934, 5160
XM_045283, 757	XM_047007, 5723
XM_045290, 1214	XM_047011, 5725
XM_045296, 2759	XM_047018, 5727
XM_045401, 2403	XM_047024, 6177
XM_045418, 5667	XM_047032, 6176
XM_045451, 5671	XM_047083, 2521
XM_045460, 5674	XM_047175, 690
XM_045499, 3276	XM_047374, 5446
XM_045525, 3278	XM_047376, 5445
XM_045535, 4751	XM_047409, 5444
XM_045551, 4752	XM_047436, 4624
XM_045581, 4996	XM_047477, 1429
XM_045602, 3856	XM_047479, 495
XM_045612, 3273	XM_047499, 610
XM_045613, 3271	XM_047525, 4632
XM_045642, 3269	XM_047545, 616
XM_045667, 3074	XM_047561, 1137
XM_045681, 4287	XM_047584, 5131
XM_045750, 3157	XM_047600, 5132
XM_045802, 3826	XM_047964, 1798
XM_045856, 2407	XM_048088, 753
XM_045901, 4852	XM_048119, 4344
XM_045952, 2413	XM_048258, 5385
XM_045963, 3834	XM_048286, 3255
XM_046001, 2414	XM_048351, 5218
XM_046035, 4453	XM_048364, 5219
XM_046041, 3726	XM_048404, 6329
XM_046057, 1443	XM_048410, 6328
XM_046090, 5423	XM_048420, 6325

XM_048471, 5082
XM_048479, 2679
XM_048518, 2684
XM_048539, 2686
XM_048603, 3674
XM_048654, 4829
XM_048690, 1007
XM_048780, 57
XM_048859, 2881
XM_048905, 6306
XM_048943, 3640
XM_048957, 3931
XM_048991, 3642
XM_049048, 3652
XM_049108, 820
XM_049113, 822
XM_049116, 818
XM_049141, 3586
XM_049148, 3581
XM_049150, 3659
XM_049197, 3161
XM_049201, 3772
XM_049211, 3771
XM_049226, 2623
XM_049237, 5391
XM_049247, 2618
XM_049282, 5223
XM_049310, 139
XM_049337, 6320
XM_049354, 4275
XM_049372, 4317
XM_049421, 2637
XM_049502, 5236
XM_049561, 5239
XM_049663, 3493
XM_049680, 476
XM_049690, 483
XM_049742, 14
XM_049795, 3082
XM_049899, 2121
XM_049904, 3937
XM_049920, 5482
XM_049931, 4995
XM_049934, 4994
XM_049937, 4818
XM_050074, 3528
XM_050101, 4773
XM_050159, 4880
XM_050194, 4462
XM_050200, 1487
XM_050215, 2525
XM_050236, 5602
XM_050265, 2278
XM_050278, 4103
XM_050293, 2487
XM_050403, 6192

XM_050430, 2389
XM_050435, 5227
XM_050506, 2583
XM_050534, 4348
XM_050552, 1234
XM_050589, 5603
XM_050638, 979
XM_050660, 5330
XM_050731, 2571
XM_050891, 984
XM_050962, 975
XM_050964, 4220
XM_051219, 4479
XM_051264, 1237
XM_051298, 2612
XM_051364, 5290
XM_051430, 3398
XM_051435, 3358
XM_051463, 4230
XM_051471, 6238
XM_051476, 6237
XM_051489, 3367
XM_051518, 1131
XM_051556, 6
XM_051586, 5092
XM_051712, 4025
XM_051716, 3373
XM_051763, 4727
XM_051778, 4600
XM_051860, 4298
XM_051877, 515
XM_052113, 3378
XM_052310, 1060
XM_052313, 1535
XM_052336, 1477
XM_052460, 3714
XM_052474, 3719
XM_052530, 1424
XM_052542, 3755
XM_052626, 1398
XM_052635, 5166
XM_052641, 3769
XM_052661, 5168
XM_052721, 2056
XM_052725, 2784
XM_052786, 3153
XM_052862, 3404
XM_052893, 3825
XM_052974, 608
XM_052989, 817
XM_053074, 5430
XM_053122, 1363
XM_053164, 3641
XM_053183, 58
XM_053206, 2875
XM_053245, 400

XM_053323, 1078
XM_053585, 4252
XM_053633, 544
XM_053712, 1074
XM_053717, 4663
XM_053787, 3283
XM_053796, 3288
XM_053952, 3722
XM_053955, 1859
XM_054038, 4832
XM_054098, 6183
XM_054221, 6155
XM_054344, 4973
XM_054474, 2933
XM_054475, 2935
XM_054520, 1047
XM_054566, 5926
XM_054706, 2146
XM_054752, 2849
XM_054763, 2852
XM_054856, 3193
XM_054868, 228
XM_054900, 4309
XM_054978, 295
XM_055013, 3853
XM_055061, 4826
XM_055132, 4514
XM_055195, 4427
XM_055199, 4942
XM_055230, 5336
XM_055254, 954
XM_055369, 3397
XM_055481, 251
XM_055551, 1461
XM_055573, 3086
XM_055641, 2064
XM_055658, 5592
XM_055686, 5163
XM_055771, 4505
XM_055859, 5483
XM_055880, 583
XM_055993, 5646
XM_056035, 5678
XM_056082, 4648
XM_056260, 4438
XM_056286, 5582
XM_056315, 1723
XM_056317, 4077
XM_056346, 3645
XM_056353, 3662
XM_056421, 5175
XM_056481, 3545
XM_056602, 5408
XM_056681, 3700
XM_056730, 4775
XM_056884, 618

XM_056923, 521
XM_056957, 1471
XM_056963, 1793
XM_056970, 628
XM_056996, 3798
XM_057020, 4257
XM_057074, 5260
XM_057150, 4619
XM_057236, 5756
XM_057374, 5793
XM_057492, 1548
XM_057664, 740
XM_057780, 2557
XM_057994, 1541
XM_058039, 1934
XM_058098, 986
XM_058116, 4526
XM_058125, 5635
XM_058210, 4018
XM_058232, 5225
XM_058240, 102
XM_058247, 466
XM_058266, 2144
XM_058267, 1278
XM_058343, 3020
XM_058361, 3078
XM_058405, 552
XM_058406, 3084
XM_058414, 3159
XM_058450, 3352
XM_058505, 3125
XM_058528, 3671
XM_058556, 3773
XM_058567, 3504
XM_058574, 3454
XM_058602, 3022
XM_058611, 3926
XM_058618, 4091
XM_058636, 4118
XM_058646, 3986
XM_058647, 3978
XM_058677, 4061
XM_058684, 4186
XM_058699, 4250
XM_058702, 294
XM_058739, 4621
XM_058745, 4543
XM_058784, 4404
XM_058796, 4337
XM_058830, 4803
XM_058867, 4755
XM_058900, 4730
XM_058918, 5949
XM_058927, 1441
XM_058949, 5463
XM_058967, 5295

XM.058968, 2619
XM.058977, 3920
XM.058987, 5570
XM.058990, 5584
XM.058991, 5552
XM.059045, 5419
XM.059052, 5447
XM.059066, 114
XM.059067, 120
XM.059088, 130
XM.059094, 465
XM.059117, 103
XM.059120, 562
XM.059133, 224
XM.059171, 171
XM.059180, 256
XM.059191, 492
XM.059201, 1
XM.059210, 330
XM.059214, 185
XM.059230, 55
XM.059268, 5675
XM.059321, 5607
XM.059335, 6013
XM.059351, 920
XM.059368, 653
XM.059372, 1029
XM.059422, 968
XM.059461, 971
XM.059465, 907
XM.059516, 1266
XM.059557, 1068
XM.059561, 1059
XM.059583, 1252
XM.059593, 1434
XM.059623, 1519
XM.059628, 1442
XM.059633, 1469
XM.059637, 2804
XM.059653, 1596
XM.059669, 1617
XM.059709, 1604
XM.059720, 2914
XM.059741, 2118
XM.059745, 2131
XM.059773, 2141
XM.059776, 2062
XM.059801, 1939
XM.059839, 2430
XM.059876, 2282
XM.059933, 2531
XM.059945, 2838
XM.059961, 2859
XM.059966, 2871
XM.059979, 2644
XM.059986, 2813

XM.059998, 2673
XM.060006, 2647
XM.060012, 4115
XM.060030, 6146
XM.060042, 4281
XM.060067, 1499
XM.060331, 509
XM.060517, 531
XM.060976, 2885
XM.061125, 2931
XM.061126, 2930
XM.062437, 3775
XM.063639, 4234
XM.064091, 4597
XM.065884, 777
XM.066291, 5998
XM.066900, 6261
XM.067264, 1240
XM.067325, 5030
XM.067715, 1169
XM.068164, 1497
XM.068395, 1789
XM.068853, 1714
XM.068919, 2085
XM.068963, 2072
XM.070188, 2480
XM.070203, 2473
XM.070873, 2742
XM.071178, 2705
XM.071580, 1557
XM.071605, 2381
XM.071623, 1439
XM.071801, 4122
XM.071873, 4630
XM.071937, 2152
XM.072173, 5876
XM.072430, 2387
XM.072526, 2857
XM.076414, 1199
XM.083842, 3026
XM.083852, 3141
XM.083864, 3774
XM.083866, 3715
XM.083868, 3590
XM.083892, 3787
XM.083939, 4364
XM.083966, 4923
XM.083983, 4881
XM.084007, 5055
XM.084014, 5246
XM.084023, 5528
XM.084026, 5549
XM.084055, 580
XM.084084, 6090
XM.084110, 1340
XM.084111, 1243

XM_084120, 1315	XM_084884, 3583
XM_084123, 1263	XM_084885, 3582
XM_084129, 1231	XM_084889, 3814
XM_084141, 1041	XM_084901, 3488
XM_084158, 1465	XM_084909, 3702
XM_084168, 1547	XM_084912, 3705
XM_084179, 1591	XM_084918, 3500
XM_084180, 1781	XM_084922, 3495
XM_084204, 2079	XM_084941, 3788
XM_084238, 2453	XM_084946, 3800
XM_084241, 2337	XM_084948, 3804
XM_084270, 2851	XM_084982, 3870
XM_084283, 6229	XM_084997, 3933
XM_084287, 6203	XM_084998, 2142
XM_084288, 6153	XM_085017, 3893
XM_084296, 6227	XM_085044, 3916
XM_084311, 6350	XM_085065, 4044
XM_084359, 3073	XM_085066, 4033
XM_084372, 3016	XM_085068, 1480
XM_084385, 2944	XM_085106, 3987
XM_084413, 3028	XM_085125, 4031
XM_084420, 2910	XM_085127, 4014
XM_084429, 2911	XM_085141, 4019
XM_084450, 2942	XM_085151, 4050
XM_084451, 2953	XM_085162, 4054
XM_084467, 2994	XM_085166, 3955
XM_084477, 3010	XM_085203, 4130
XM_084480, 3012	XM_085204, 4132
XM_084505, 3080	XM_085215, 4282
XM_084514, 3180	XM_085239, 4254
XM_084515, 3183	XM_085249, 4236
XM_084516, 3182	XM_085262, 4314
XM_084517, 3184	XM_085280, 4289
XM_084522, 3424	XM_085283, 4211
XM_084525, 3428	XM_085307, 4160
XM_084527, 3169	XM_085327, 4622
XM_084570, 3357	XM_085340, 4448
XM_084601, 3353	XM_085393, 4480
XM_084610, 3350	XM_085395, 4482
XM_084632, 3072	XM_085408, 4637
XM_084645, 3731	XM_085434, 4524
XM_084654, 3388	XM_085442, 4513
XM_084658, 3382	XM_085445, 4425
XM_084681, 3195	XM_085452, 4435
XM_084702, 3287	XM_085471, 4558
XM_084739, 3124	XM_085475, 4561
XM_084742, 3122	XM_085483, 4616
XM_084770, 3515	XM_085525, 4323
XM_084789, 3599	XM_085531, 4977
XM_084800, 3783	XM_085545, 4741
XM_084801, 3672	XM_085548, 4735
XM_084807, 3531	XM_085563, 4991
XM_084808, 3818	XM_085581, 472
XM_084824, 3630	XM_085589, 4948
XM_084841, 3540	XM_085613, 4724
XM_084866, 3557	XM_085627, 4951

XM_085636, 4873	XM_086328, 542
XM_085672, 4757	XM_086343, 265
XM_085687, 4659	XM_086357, 85
XM_085691, 4677	XM_086360, 29
XM_085716, 4992	XM_086375, 97
XM_085722, 4745	XM_086378, 485
XM_085735, 5019	XM_086381, 479
XM_085743, 4718	XM_086384, 178
XM_085775, 5058	XM_086389, 243
XM_085779, 5075	XM_086391, 231
XM_085788, 5049	XM_086397, 323
XM_085789, 5043	XM_086400, 366
XM_085790, 5045	XM_086428, 2161
XM_085791, 5042	XM_086431, 589
XM_085856, 5501	XM_086432, 592
XM_085862, 5244	XM_086444, 136
XM_085874, 5460	XM_086481, 490
XM_085875, 5461	XM_086484, 494
XM_085876, 5462	XM_086485, 493
XM_085909, 5297	XM_086494, 538
XM_085916, 5285	XM_086515, 324
XM_085917, 5276	XM_086518, 317
XM_085927, 5527	XM_086543, 190
XM_085928, 5489	XM_086552, 432
XM_085934, 5537	XM_086564, 388
XM_085935, 5573	XM_086567, 430
XM_085950, 5487	XM_086586, 52
XM_085971, 5371	XM_086587, 54
XM_085972, 5629	XM_086648, 5819
XM_085981, 4599	XM_086701, 5687
XM_085986, 5398	XM_086710, 5670
XM_086004, 5425	XM_086715, 5695
XM_086074, 5311	XM_086736, 5717
XM_086101, 5128	XM_086745, 5712
XM_086102, 5130	XM_086759, 5877
XM_086116, 5331	XM_086760, 5878
XM_086132, 304	XM_086770, 5914
XM_086138, 282	XM_086773, 5928
XM_086142, 557	XM_086777, 5930
XM_086151, 46	XM_086779, 5064
XM_086164, 277	XM_086805, 5963
XM_086165, 279	XM_086809, 5953
XM_086166, 281	XM_086821, 5985
XM_086167, 280	XM_086830, 6043
XM_086178, 4	XM_086844, 6074
XM_086180, 19	XM_086873, 5964
XM_086204, 38	XM_086875, 6093
XM_086228, 1356	XM_086920, 805
XM_086244, 601	XM_086923, 849
XM_086245, 602	XM_086925, 850
XM_086257, 632	XM_086944, 933
XM_086271, 383	XM_086950, 858
XM_086278, 4434	XM_086961, 926
XM_086282, 543	XM_086980, 791
XM_086296, 331	XM_087028, 942
XM_086324, 214	XM_087038, 2803

XM_087040, 842
XM_087041, 2800
XM_087045, 932
XM_087051, 748
XM_087061, 912
XM_087062, 914
XM_087068, 775
XM_087069, 772
XM_087118, 891
XM_087122, 839
XM_087151, 683
XM_087162, 985
XM_087166, 993
XM_087181, 965
XM_087193, 726
XM_087195, 725
XM_087206, 669
XM_087211, 743
XM_087218, 1011
XM_087240, 901
XM_087254, 1302
XM_087268, 1203
XM_087278, 1358
XM_087284, 1075
XM_087289, 1323
XM_087295, 1322
XM_087297, 1360
XM_087322, 1312
XM_087331, 1211
XM_087341, 1267
XM_087342, 1265
XM_087346, 1115
XM_087349, 1106
XM_087359, 1343
XM_087370, 1101
XM_087392, 1333
XM_087410, 1347
XM_087448, 1184
XM_087480, 3000
XM_087498, 1463
XM_087514, 1483
XM_087527, 1455
XM_087583, 1418
XM_087588, 1120
XM_087597, 1549
XM_087599, 1551
XM_087600, 1553
XM_087601, 1550
XM_087610, 1597
XM_087611, 1595
XM_087614, 1564
XM_087621, 1711
XM_087635, 1660
XM_087637, 1662
XM_087652, 1713
XM_087659, 1537

XM_087686, 1543
XM_087710, 3247
XM_087713, 1559
XM_087745, 1656
XM_087773, 1816
XM_087790, 1631
XM_087823, 1858
XM_087834, 2123
XM_087836, 2124
XM_087853, 2090
XM_087855, 2089
XM_087939, 2000
XM_087945, 1990
XM_087955, 3857
XM_087960, 1883
XM_087990, 1936
XM_087991, 2154
XM_088009, 3106
XM_088020, 1621
XM_088073, 2386
XM_088099, 2416
XM_088103, 2418
XM_088105, 2409
XM_088107, 605
XM_088119, 2422
XM_088122, 2420
XM_088135, 2446
XM_088180, 2352
XM_088239, 2297
XM_088264, 2195
XM_088294, 2529
XM_088316, 2611
XM_088321, 2628
XM_088323, 2574
XM_088325, 2572
XM_088336, 2519
XM_088338, 2515
XM_088370, 2613
XM_088399, 2559
XM_088401, 2560
XM_088422, 2839
XM_088426, 2833
XM_088459, 2847
XM_088461, 2870
XM_088472, 1472
XM_088550, 2640
XM_088552, 2641
XM_088553, 2642
XM_088563, 2672
XM_088569, 2748
XM_088571, 2750
XM_088587, 4120
XM_088588, 4114
XM_088589, 4121
XM_088592, 6311
XM_088619, 6151

XM_088622, 6152
XM_088630, 6209
XM_088637, 2700
XM_088638, 768
XM_088665, 6158
XM_088688, 6220
XM_088689, 6218
XM_088710, 6253
XM_088736, 6265
XM_088738, 6267
XM_088739, 6268
XM_088745, 6289
XM_088747, 6128
XM_088788, 338
XM_088863, 286
XM_088945, 507
XM_089030, 622
XM_089138, 254
XM_089514, 3019
XM_089551, 3006
XM_090218, 3542
XM_090413, 3779
XM_090458, 3767
XM_090833, 638
XM_090914, 4082
XM_090991, 4191
XM_091076, 1091
XM_091100, 4263
XM_091108, 4124
XM_091159, 4157
XM_091270, 4483
XM_091399, 4590
XM_091420, 4544
XM_091786, 3426
XM_091886, 5595
XM_091938, 5221
XM_091981, 5586
XM_091984, 5396
XM_092042, 5108
XM_092046, 5341
XM_092049, 5380
XM_092135, 672
XM_092158, 918
XM_092346, 944
XM_092489, 867
XM_092517, 676
XM_092545, 970
XM_092760, 5696
XM_092888, 5986
XM_092966, 6113
XM_093050, 6212
XM_093130, 6226
XM_093219, 6299
XM_093241, 6228
XM_093423, 1308
XM_093487, 1255

XM_093546, 1201
XM_093624, 1083
XM_094243, 1797
XM_094440, 1561
XM_094741, 1862
XM_094855, 2060
XM_095146, 2432
XM_095371, 2475
XM_095545, 2514
XM_095667, 2554
XM_096038, 3699
XM_096060, 4241
XM_096146, 3539
XM_096149, 661
XM_096155, 5967
XM_096156, 5968
XM_096169, 1022
XM_096172, 787
XM_096195, 1190
XM_096198, 1117
XM_096203, 1464
XM_096303, 6256
XM_096486, 3315
XM_096520, 3165
XM_096544, 3119
XM_096566, 3680
XM_096572, 3819
XM_096597, 3739
XM_096606, 3608
XM_096620, 3578
XM_096630, 3486
XM_096661, 3441
XM_096744, 4034
XM_096772, 3966
XM_096842, 4245
XM_096844, 4286
XM_097043, 4984
XM_097193, 5001
XM_097195, 5000
XM_097204, 4754
XM_097232, 5048
XM_097274, 5510
XM_097275, 5521
XM_097300, 5222
XM_097365, 5440
XM_097420, 5134
XM_097453, 2068
XM_097519, 561
XM_097565, 249
XM_097639, 352
XM_097649, 198
XM_097713, 5800
XM_097727, 5773
XM_097731, 5795
XM_097749, 5644
XM_097772, 5731

XM_097807, 5929	XM_113330, 5011
XM_097817, 5925	XM_113334, 4819
XM_097833, 5950	XM_113343, 5028
XM_097886, 5971	XM_113348, 5316
XM_097976, 715	XM_113352, 5294
XM_098004, 729	XM_113360, 386
XM_098047, 962	XM_113361, 598
XM_098048, 960	XM_113369, 361
XM_098109, 1345	XM_113374, 140
XM_098111, 1245	XM_113379, 473
XM_098154, 1232	XM_113380, 5749
XM_098158, 1103	XM_113390, 929
XM_098173, 1227	XM_113395, 1193
XM_098248, 1384	XM_113397, 1244
XM_098351, 1609	XM_113405, 1140
XM_098352, 1611	XM_113408, 1296
XM_098354, 1610	XM_113409, 1202
XM_098362, 1634	XM_113410, 1088
XM_098387, 1778	XM_113417, 1254
XM_098405, 1534	XM_113422, 1329
XM_098468, 2108	XM_113425, 1452
XM_098599, 619	XM_113452, 1556
XM_098654, 2447	XM_113454, 1841
XM_098669, 2466	XM_113463, 1654
XM_098747, 2582	XM_113467, 1720
XM_098761, 2564	XM_113468, 1845
XM_098913, 2843	XM_113476, 1860
XM_098943, 2725	XM_113531, 2526
XM_098995, 6302	XM_113532, 2627
XM_099467, 363	XM_113540, 2548
XM_102377, 4432	XM_113557, 2493
XM_103946, 665	XM_113564, 2846
XM_104983, 6263	XM_113585, 6122
XM_105236, 1289	XM_113615, 2927
XM_105658, 1325	XM_113702, 3862
XM_106246, 1520	XM_113712, 3635
XM_106739, 1562	XM_113719, 3560
XM_107825, 2225	XM_113726, 3584
XM_109162, 3075	XM_113730, 3519
XM_113223, 3268	XM_113737, 3855
XM_113224, 3275	XM_113739, 3437
XM_113226, 3400	XM_113752, 3946
XM_113229, 3366	XM_113759, 4105
XM_113230, 3363	XM_113823, 4163
XM_113238, 3152	XM_113836, 4326
XM_113266, 4202	XM_113840, 4608
XM_113268, 4207	XM_113843, 4420
XM_113291, 4429	XM_113845, 4418
XM_113293, 4467	XM_113853, 4570
XM_113299, 4504	XM_113855, 4560
XM_113303, 5013	XM_113874, 4431
XM_113310, 4723	XM_113876, 4426
XM_113315, 4944	XM_113882, 4640
XM_113324, 4674	XM_113892, 4978
XM_113325, 4703	XM_113901, 4653
XM_113328, 4695	XM_113919, 4905

XM_113929, 4696
XM_113931, 4706
XM_113938, 4824
XM_113943, 5010
XM_113945, 4998
XM_113951, 4962
XM_113988, 5229
XM_114004, 5349
XM_114018, 5097
XM_114024, 5560
XM_114025, 5530
XM_114027, 5366
XM_114030, 560
XM_114044, 129
XM_114055, 384
XM_114062, 3
XM_114097, 376
XM_114098, 360
XM_114109, 525
XM_114125, 259
XM_114137, 634
XM_114153, 484
XM_114154, 5875
XM_114163, 5794
XM_114165, 5813
XM_114174, 5673
XM_114178, 5706
XM_114185, 5889
XM_114209, 6024
XM_114215, 816
XM_114229, 838
XM_114247, 824
XM_114266, 851
XM_114267, 856
XM_114298, 957
XM_114301, 1225
XM_114309, 1242
XM_114323, 1141
XM_114328, 1344
XM_114356, 1288
XM_114364, 1122
XM_114368, 1510
XM_114401, 1496
XM_114424, 1473
XM_114426, 1470
XM_114434, 1555
XM_114435, 1552
XM_114437, 1567
XM_114439, 1586
XM_114440, 1587
XM_114442, 1584
XM_114453, 1819
XM_114457, 1817
XM_114469, 1623
XM_114482, 1683
XM_114492, 2106

XM_114497, 2058
XM_114555, 2429
XM_114578, 2444
XM_114602, 2404
XM_114613, 2625
XM_114617, 2517
XM_114618, 2523
XM_114640, 2556
XM_114646, 2756
XM_114649, 2873
XM_114655, 2854
XM_114661, 2677
XM_114662, 2688
XM_114669, 2845
XM_114677, 2802
XM_114678, 2801
XM_114679, 2799
XM_114686, 2699
XM_114692, 6354
XM_114708, 6291
XM_114720, 6130
XM_114724, 6119
XM_114798, 233
XM_114862, 3104
XM_114894, 2977
XM_114981, 3139
XM_115031, 3286
XM_115062, 3364
XM_115063, 3365
XM_115081, 3177
XM_115117, 3570
XM_115140, 3634
XM_115197, 3809
XM_115215, 3948
XM_115352, 4333
XM_115480, 4910
XM_115603, 5466
XM_115615, 5395
XM_115672, 869
XM_115706, 1039
XM_115722, 1040
XM_115825, 1002
XM_115846, 5691
XM_115874, 6281
XM_115886, 6131
XM_115890, 6136
XM_115923, 6259
XM_115924, 6121
XM_116034, 1338
XM_116058, 1295
XM_116071, 1204
XM_116072, 1205
XM_116204, 1532
XM_116205, 1533
XM_116247, 1484
XM_116285, 1408

XM_116307, 1691
XM_116340, 1807
XM_116365, 1856
XM_116427, 1648
XM_116439, 1593
XM_116447, 1606
XM_116465, 1716
XM_116511, 1857
XM_116514, 1861
XM_116524, 2140
XM_116806, 2789
XM_116818, 2738
XM_116853, 1139
XM_116856, 1810
XM_116863, 2975
XM_116913, 3845
XM_116926, 3451
XM_117061, 4913
XM_117066, 4768
XM_117096, 5084
XM_117118, 5379
XM_117122, 5183
XM_117128, 5605
XM_117159, 2
XM_117181, 534
XM_117184, 163
XM_117185, 582
XM_117196, 641
XM_117209, 5688
XM_117264, 736
XM_117311, 1337
XM_117351, 1412
XM_117387, 1622
XM_117398, 1641
XM_117444, 2471
XM_117449, 2160
XM_117452, 2472
XM_117481, 2406
XM_117487, 2622
XM_117519, 2874
XM_117539, 6352
XM_117555, 6349
XM_117692, 28
XM_118637, 4251
XM_165390, 3427
XM_165410, 4583
XM_165411, 4413
XM_165418, 4713
XM_165421, 4701
XM_165422, 4704
XM_165432, 5541
XM_165438, 144
XM_165439, 620
XM_165442, 59
XM_165443, 477
XM_165448, 723

XM_165451, 1268
XM_165465, 1531
XM_165470, 1528
XM_165473, 1482
XM_165483, 1818
XM_165484, 1820
XM_165488, 1615
XM_165499, 2057
XM_165514, 2579
XM_165530, 6355
XM_165533, 6235
XM_165551, 2913
XM_165555, 2889
XM_165557, 2897
XM_165560, 2925
XM_165563, 2926
XM_165567, 2921
XM_165571, 3407
XM_165584, 3414
XM_165586, 3413
XM_165592, 3401
XM_165598, 3303
XM_165600, 3310
XM_165610, 3222
XM_165611, 3217
XM_165612, 3223
XM_165616, 3325
XM_165627, 3335
XM_165628, 3341
XM_165631, 3328
XM_165636, 3903
XM_165639, 3917
XM_165645, 4534
XM_165647, 4528
XM_165648, 4537
XM_165649, 4527
XM_165656, 4484
XM_165657, 4493
XM_165658, 4489
XM_165669, 2091
XM_165692, 2159
XM_165698, 1949
XM_165717, 1954
XM_165728, 2036
XM_165738, 1999
XM_165740, 1865
XM_165743, 1937
XM_165747, 1948
XM_165749, 2037
XM_165758, 2013
XM_165764, 2011
XM_165765, 1988
XM_165770, 1951
XM_165771, 1983
XM_165772, 1876
XM_165777, 2044

XM.165794, 1921	XM.166177, 3406
XM.165799, 2006	XM.166181, 3403
XM.165801, 1956	XM.166196, 3308
XM.165809, 2016	XM.166232, 3227
XM.165836, 2350	XM.166234, 3224
XM.165839, 2346	XM.166235, 3293
XM.165841, 2197	XM.166236, 3294
XM.165860, 2167	XM.166239, 3349
XM.165867, 2249	XM.166253, 3336
XM.165870, 2245	XM.166266, 3904
XM.165872, 2253	XM.166273, 3886
XM.165876, 2258	XM.166277, 4532
XM.165877, 2240	XM.166282, 4491
XM.165882, 2248	XM.166285, 4490
XM.165888, 2934	XM.166288, 5071
XM.165890, 2929	XM.166303, 2092
XM.165891, 2941	XM.166310, 2101
XM.165903, 3633	XM.166327, 2157
XM.165905, 3579	XM.166333, 1932
XM.165906, 3532	XM.166336, 2021
XM.165910, 3465	XM.166340, 1882
XM.165921, 4127	XM.166349, 1872
XM.165923, 4325	XM.166353, 2002
XM.165954, 5026	XM.166357, 2049
XM.165960, 5347	XM.166360, 1938
XM.165963, 5367	XM.166361, 2009
XM.165975, 327	XM.166362, 1884
XM.165976, 373	XM.166363, 1940
XM.165977, 264	XM.166376, 2004
XM.165978, 532	XM.166381, 1992
XM.165981, 290	XM.166392, 2019
XM.165983, 275	XM.166401, 1995
XM.165984, 175	XM.166402, 1896
XM.165994, 927	XM.166406, 2015
XM.165998, 893	XM.166412, 1910
XM.166007, 910	XM.166417, 1914
XM.166008, 900	XM.166419, 1920
XM.166011, 1121	XM.166425, 1888
XM.166014, 1275	XM.166446, 2042
XM.166015, 1192	XM.166457, 1878
XM.166017, 1350	XM.166459, 1931
XM.166026, 1669	XM.166469, 1879
XM.166027, 1663	XM.166480, 1955
XM.166028, 1842	XM.166482, 2351
XM.166029, 1802	XM.166485, 2353
XM.166037, 1612	XM.166494, 2224
XM.166042, 2054	XM.166504, 2222
XM.166049, 2147	XM.166505, 2202
XM.166063, 2540	XM.166506, 2200
XM.166064, 2558	XM.166509, 2219
XM.166078, 6142	XM.166512, 2205
XM.166081, 6255	XM.166513, 2220
XM.166093, 2984	XM.166514, 2203
XM.166125, 2966	XM.166515, 2204
XM.166157, 2922	XM.166521, 2198
XM.166174, 3409	XM.166523, 2170

XM_166531, 2190
XM_166540, 2191,
XM_166541, 2168
XM_166594, 2230
XM_166599, 20
XM_166605, 3506
XM_166629, 2988
XM_166665, 2918
XM_166717, 2906
XM_166743, 3418
XM_167008, 5080
XM_167016, 2087
XM_167027, 2094
XM_167037, 2096
XM_167046, 2150
XM_167128, 2023
XM_167161, 2025
XM_167169, 1868
XM_167179, 2031
XM_167196, 2041
XM_167225, 2047
XM_167339, 2264
XM_167363, 5065
XM_167366, 1209
XM_167374, 2898
XM_167395, 2963
XM_167411, 2901
XM_167414, 2904
XM_167433, 3324
XM_167437, 3192
XM_167439, 3876
XM_167453, 4538
XM_167456, 4541
XM_167476, 2321
XM_167477, 2325
XM_167483, 2328
XM_167484, 2329
XM_167494, 2273
XM_167498, 2301
XM_167500, 2299
XM_167502, 2312
XM_167504, 2300
XM_167518, 3754
XM_167530, 5529
XM_167538, 5945
XM_167558, 2645
XM_167626, 2887
XM_167716, 3244
XM_167726, 3248
XM_167747, 3234
XM_167748, 3228
XM_167780, 3417
XM_167804, 3291
XM_167853, 3318
XM_167892, 3883
XM_167906, 3877

XM_167911, 3868
XM_167918, 3869
XM_168054, 2103
XM_168070, 1928
XM_168104, 1994
XM_168123, 1877
XM_168181, 2322
XM_168251, 2323
XM_168354, 2271
XM_168378, 2269
XM_168435, 2316
XM_168450, 2315
XM_168454, 2302
XM_168461, 2311
XM_168464, 2317
XM_168470, 2310
XM_168548, 2375
XM_168572, 2380
XM_168586, 2360
XM_169414, 3880
XM_169540, 5078
XM_170195, 2267
XM_170427, 2318

Source Index (to Figure number)

gen.NM_000018,4669	gen.NM_000484,5882
gen.NM_000026,6068	gen.NM_000505,1828
gen.NM_000029,624	gen.NM_000508,1511
gen.NM_000033,6342	gen.NM_000509,1515
gen.NM_000034,4520	gen.NM_000516,5830
gen.NM_000039,3376	gen.NM_000517,4354
gen.NM_000041,5511	gen.NM_000521,1627
gen.NM_000070,4161	gen.NM_000526,4816
gen.NM_000075,3683	gen.NM_000532,1260
gen.NM_000077,2655	gen.NM_000554,5480
gen.NM_000079,898	gen.NM_000558,4356
gen.NM_000090,921	gen.NM_000559,3142
gen.NM_000107,3208	gen.NM_000569,505
gen.NM_000114,5836	gen.NM_000574,558
gen.NM_000121,5258	gen.NM_000576,847
gen.NM_000126,4267	gen.NM_000582,1459
gen.NM_000137,4300	gen.NM_000592,1957
gen.NM_000143,636	gen.NM_000598,2228
gen.NM_000146,5562	gen.NM_000602,2361
gen.NM_000154,4967	gen.NM_000612,3120
gen.NM_000156,5122	gen.NM_000638,4763
gen.NM_000165,2099	gen.NM_000661,1425
gen.NM_000177,2796	gen.NM_000666,1172
gen.NM_000178,5738	gen.NM_000687,5736
gen.NM_000179,744	gen.NM_000688,1167
gen.NM_000182,713	gen.NM_000700,2695
gen.NM_000183,711	gen.NM_000701,312
gen.NM_000184,3144	gen.NM_000743,4259
gen.NM_000196,4547	gen.NM_000754,5956
gen.NM_000213,4963	gen.NM_000760,173
gen.NM_000221,701	gen.NM_000785,3687
gen.NM_000224,3593	gen.NM_000787,2830
gen.NM_000227,5040	gen.NM_000795,3384
gen.NM_000228,553	gen.NM_000801,5648
gen.NM_000239,3729	gen.NM_000852,3297
gen.NM_000250,4903	gen.NM_000858,612
gen.NM_000251,741	gen.NM_000893,1327
gen.NM_000268,5994	gen.NM_000895,3763
gen.NM_000269,4889	gen.NM_000930,2534
gen.NM_000274,3076	gen.NM_000931,2536
gen.NM_000284,6138	gen.NM_000942,4218
gen.NM_000291,6230	gen.NM_000954,2868
gen.NM_000358,1671	gen.NM_000964,4820
gen.NM_000365,3460	gen.NM_000967,6061
gen.NM_000368,2806	gen.NM_000969,284
gen.NM_000385,2262	gen.NM_000970,3781
gen.NM_000386,4843	gen.NM_000971,2569
gen.NM_000396,356	gen.NM_000972,2826
gen.NM_000404,1089	gen.NM_000973,2633
gen.NM_000407,5947	gen.NM_000975,87
gen.NM_000422,4807	gen.NM_000976,2780
gen.NM_000425,6334	gen.NM_000977,4633
gen.NM_000447,594	gen.NM_000978,4801

gen.NM_000979, 5571
gen.NM_000980, 5334
gen.NM_000981, 4798
gen.NM_000982, 3091
gen.NM_000983, 34
gen.NM_000985, 5067
gen.NM_000986, 1206
gen.NM_000987, 4714
gen.NM_000989, 2588
gen.NM_000990, 3155
gen.NM_000991, 5613
gen.NM_000992, 1170
gen.NM_000993, 832
gen.NM_000994, 1064
gen.NM_000997, 1570
gen.NM_000998, 966
gen.NM_001000, 6278
gen.NM_001002, 3827
gen.NM_001003, 4228
gen.NM_001005, 3331
gen.NM_001006, 1506
gen.NM_001007, 6224
gen.NM_001009, 5633
gen.NM_001010, 2651
gen.NM_001011, 643
gen.NM_001012, 210
gen.NM_001016, 2111
gen.NM_001017, 3171
gen.NM_001018, 5126
gen.NM_001020, 5426
gen.NM_001021, 4283
gen.NM_001022, 5468
gen.NM_001023, 2552
gen.NM_001024, 5847
gen.NM_001025, 1632
gen.NM_001026, 2980
gen.NM_001028, 3361
gen.NM_001029, 3656
gen.NM_001030, 440
gen.NM_001034, 651
gen.NM_001038, 3478
gen.NM_001043, 4487
gen.NM_001050, 4841
gen.NM_001064, 1159
gen.NM_001065, 3480
gen.NM_001068, 1079
gen.NM_001069, 2050
gen.NM_001084, 2369
gen.NM_001087, 994
gen.NM_001098, 6079
gen.NM_001101, 2174
gen.NM_001102, 4040
gen.NM_001122, 2649
gen.NM_001134, 1446
gen.NM_001154, 1489
gen.NM_001157, 2990

gen.NM_001168, 4985
gen.NM_001190, 5568
gen.NM_001199, 2495
gen.NM_001207, 1624
gen.NM_001211, 4139
gen.NM_001218, 4203
gen.NM_001235, 3333
gen.NM_001238, 5374
gen.NM_001247, 5703
gen.NM_001255, 194
gen.NM_001262, 229
gen.NM_001273, 3468
gen.NM_001274, 3411
gen.NM_001275, 4065
gen.NM_001283, 2365
gen.NM_001287, 4372
gen.NM_001288, 1969
gen.NM_001293, 3337
gen.NM_001294, 5508
gen.NM_001313, 1396
gen.NM_001319, 5141
gen.NM_001320, 1971
gen.NM_001324, 5814
gen.NM_001325, 6239
gen.NM_001333, 2736
gen.NM_001344, 3984
gen.NM_001350, 1942
gen.NM_001363, 6318
gen.NM_001407, 1132
gen.NM_001415, 6143
gen.NM_001416, 4687
gen.NM_001418, 3163
gen.NM_001428, 31
gen.NM_001436, 5436
gen.NM_001444, 2575
gen.NM_001450, 836
gen.NM_001463, 916
gen.NM_001465, 1573
gen.NM_001467, 3359
gen.NM_001469, 6081
gen.NM_001494, 2891
gen.NM_001500, 2052
gen.NM_001517, 1997
gen.NM_001521, 689
gen.NM_001530, 4016
gen.NM_001536, 5539
gen.NM_001539, 2660
gen.NM_001540, 2308
gen.NM_001553, 1435
gen.NM_001554, 269
gen.NM_001560, 6270
gen.NM_001567, 3322
gen.NM_001568, 2596
gen.NM_001569, 6332
gen.NM_001571, 5542
gen.NM_001605, 4564

gen.NM_001607, 1097
gen.NM_001610, 3206
gen.NM_001613, 3008
gen.NM_001622, 1330
gen.NM_001628, 2423
gen.NM_001641, 3997
gen.NM_001644, 3511
gen.NM_001647, 1352
gen.NM_001648, 5590
gen.NM_001659, 3550
gen.NM_001662, 2398
gen.NM_001667, 3284
gen.NM_001673, 2355
gen.NM_001687, 5115
gen.NM_001688, 308
gen.NM_001696, 5941
gen.NM_001697, 5892
gen.NM_001710, 1959
gen.NM_001734, 3452
gen.NM_001743, 5494
gen.NM_001747, 806
gen.NM_001751, 3137
gen.NM_001753, 2391
gen.NM_001757, 5894
gen.NM_001760, 1898
gen.NM_001762, 2274
gen.NM_001780, 3663
gen.NM_001791, 81
gen.NM_001816, 5478
gen.NM_001819, 5679
gen.NM_001827, 2714
gen.NM_001831, 2506
gen.NM_001833, 2689
gen.NM_001842, 2668
gen.NM_001853, 5853
gen.NM_001861, 4614
gen.NM_001862, 827
gen.NM_001878, 392
gen.NM_001907, 4579
gen.NM_001909, 3133
gen.NM_001920, 3740
gen.NM_001930, 5267
gen.NM_001935, 894
gen.NM_001944, 5050
gen.NM_001959, 950
gen.NM_001961, 5178
gen.NM_001964, 1689
gen.NM_001969, 4098
gen.NM_001970, 4697
gen.NM_001975, 3458
gen.NM_001983, 5502
gen.NM_001985, 5593
gen.NM_002003, 2834
gen.NM_002004, 422
gen.NM_002011, 1836
gen.NM_002014, 3439

gen.NM_002015, 3896
gen.NM_002018, 4719
gen.NM_002028, 4010
gen.NM_002046, 3473
gen.NM_002047, 2265
gen.NM_002075, 3463
gen.NM_002079, 3066
gen.NM_002083, 4012
gen.NM_002084, 1704
gen.NM_002085, 5112
gen.NM_002086, 4953
gen.NM_002087, 4845
gen.NM_002106, 1478
gen.NM_002109, 1779
gen.NM_002128, 3887
gen.NM_002129, 1522
gen.NM_002130, 1582
gen.NM_002133, 6020
gen.NM_002137, 2210
gen.NM_002157, 930
gen.NM_002161, 2716
gen.NM_002168, 4293
gen.NM_002178, 3600
gen.NM_002211, 2919
gen.NM_002212, 5742
gen.NM_002229, 5272
gen.NM_002265, 4834
gen.NM_002273, 3591
gen.NM_002274, 4814
gen.NM_002275, 4812
gen.NM_002276, 4810
gen.NM_002295, 1108
gen.NM_002305, 6038
gen.NM_002306, 4022
gen.NM_002339, 3115
gen.NM_002340, 5931
gen.NM_002342, 3476
gen.NM_002345, 3752
gen.NM_002355, 3489
gen.NM_002358, 1485
gen.NM_002364, 6147
gen.NM_002385, 5086
gen.NM_002386, 4626
gen.NM_002388, 1866
gen.NM_002396, 5069
gen.NM_002397, 1646
gen.NM_002401, 4933
gen.NM_002411, 3245
gen.NM_002413, 1494
gen.NM_002414, 6124
gen.NM_002415, 5979
gen.NM_002453, 751
gen.NM_002466, 5774
gen.NM_002468, 1095
gen.NM_002473, 6025
gen.NM_002477, 1368

gen.NM_002484,4416
gen.NM_002486,2734
gen.NM_002489,2193
gen.NM_002492,1297
gen.NM_002512,4887
gen.NM_002520,1803
gen.NM_002537,4210
gen.NM_002539,659
gen.NM_002567,3816
gen.NM_002568,2593
gen.NM_002574,220
gen.NM_002588,1728
gen.NM_002606,5900
gen.NM_002615,4647
gen.NM_002617,12
gen.NM_002632,4052
gen.NM_002634,4939
gen.NM_002638,5779
gen.NM_002654,4242
gen.NM_002660,5771
gen.NM_002668,6185
gen.NM_002689,3289
gen.NM_002691,5580
gen.NM_002707,681
gen.NM_002712,1030
gen.NM_002720,4518
gen.NM_002727,2961
gen.NM_002730,5298
gen.NM_002733,3555
gen.NM_002766,4975
gen.NM_002787,2254
gen.NM_002789,4261
gen.NM_002792,5838
gen.NM_002793,2137
gen.NM_002796,346
gen.NM_002802,4059
gen.NM_002803,2378
gen.NM_002809,4805
gen.NM_002810,348
gen.NM_002812,5401
gen.NM_002813,3837
gen.NM_002815,4778
gen.NM_002819,5102
gen.NM_002827,5809
gen.NM_002846,980
gen.NM_002854,1188
gen.NM_002856,5515
gen.NM_002857,481
gen.NM_002863,4029
gen.NM_002870,438
gen.NM_002878,4784
gen.NM_002883,6075
gen.NM_002887,1800
gen.NM_002913,1427
gen.NM_002915,3891
gen.NM_002921,3002

gen.NM_002923,540
gen.NM_002934,3992
gen.NM_002938,1386
gen.NM_002946,127
gen.NM_002947,2188
gen.NM_002948,1076
gen.NM_002952,4382
gen.NM_002954,749
gen.NM_002961,369
gen.NM_002965,364
gen.NM_002979,235
gen.NM_003002,3390
gen.NM_003021,5161
gen.NM_003025,5188
gen.NM_003055,2947
gen.NM_003064,5781
gen.NM_003072,5254
gen.NM_003076,3568
gen.NM_003088,2176
gen.NM_003090,4320
gen.NM_003091,5654
gen.NM_003092,5683
gen.NM_003104,4187
gen.NM_003107,2032
gen.NM_003123,4511
gen.NM_003124,789
gen.NM_003128,746
gen.NM_003132,50
gen.NM_003137,1916
gen.NM_003143,2435
gen.NM_003145,409
gen.NM_003146,3215
gen.NM_003149,1099
gen.NM_003169,5428
gen.NM_003181,2135
gen.NM_003216,6077
gen.NM_003283,5608
gen.NM_003287,2104
gen.NM_003289,2680
gen.NM_003290,5312
gen.NM_003295,3900
gen.NM_003310,649
gen.NM_003316,5896
gen.NM_003334,6167
gen.NM_003349,5804
gen.NM_003350,2546
gen.NM_003365,1134
gen.NM_003366,4421
gen.NM_003370,5499
gen.NM_003374,1677
gen.NM_003375,2982
gen.NM_003378,2367
gen.NM_003389,2728
gen.NM_003400,761
gen.NM_003401,1636
gen.NM_003406,2590

gen.NM_003418, 1250
gen.NM_003453, 3864
gen.NM_003461, 2440
gen.NM_003472, 2034
gen.NM_003516, 459
gen.NM_003564, 474
gen.NM_003598, 5556
gen.NM_003617, 497
gen.NM_003624, 5214
gen.NM_003626, 3316
gen.NM_003646, 3197
gen.NM_003662, 6149
gen.NM_003680, 157
gen.NM_003681, 5905
gen.NM_003685, 5203
gen.NM_003687, 1673
gen.NM_003689, 71
gen.NM_003712, 5093
gen.NM_003714, 1812
gen.NM_003720, 5898
gen.NM_003721, 5360
gen.NM_003722, 1335
gen.NM_003729, 288
gen.NM_003735, 1730
gen.NM_003736, 1732
gen.NM_003739, 2883
gen.NM_003752, 4449
gen.NM_003753, 6027
gen.NM_003755, 5234
gen.NM_003756, 2598
gen.NM_003757, 148
gen.NM_003765, 5288
gen.NM_003766, 4865
gen.NM_003779, 468
gen.NM_003780, 199
gen.NM_003787, 5052
gen.NM_003815, 457
gen.NM_003824, 3313
gen.NM_003836, 4088
gen.NM_003837, 2723
gen.NM_003859, 5811
gen.NM_003876, 4708
gen.NM_003877, 3757
gen.NM_003906, 5933
gen.NM_003908, 5734
gen.NM_003915, 5747
gen.NM_003932, 6070
gen.NM_003937, 881
gen.NM_003938, 5148
gen.NM_003971, 4891
gen.NM_003973, 1110
gen.NM_003979, 3498
gen.NM_004000, 306
gen.NM_004004, 3866
gen.NM_004044, 955
gen.NM_004048, 4178

gen.NM_004053, 1900
gen.NM_004060, 1791
gen.NM_004074, 3264
gen.NM_004084, 2476
gen.NM_004085, 6242
gen.NM_004092, 3099
gen.NM_004111, 3253
gen.NM_004117, 1918
gen.NM_004127, 5008
gen.NM_004134, 1693
gen.NM_004135, 6340
gen.NM_004147, 6011
gen.NM_004152, 5154
gen.NM_004159, 1952
gen.NM_004175, 5983
gen.NM_004176, 4742
gen.NM_004178, 3614
gen.NM_004181, 1430
gen.NM_004182, 6174
gen.NM_004193, 3045
gen.NM_004203, 4402
gen.NM_004208, 6285
gen.NM_004217, 4699
gen.NM_004219, 1795
gen.NM_004240, 5206
gen.NM_004247, 4879
gen.NM_004261, 273
gen.NM_004265, 3249
gen.NM_004309, 5002
gen.NM_004322, 3256
gen.NM_004323, 2662
gen.NM_004324, 5564
gen.NM_004335, 5328
gen.NM_004339, 5921
gen.NM_004341, 692
gen.NM_004345, 1128
gen.NM_004360, 4549
gen.NM_004398, 3392
gen.NM_004401, 48
gen.NM_004404, 1034
gen.NM_004435, 2761
gen.NM_004448, 4796
gen.NM_004461, 5279
gen.NM_004483, 4602
gen.NM_004493, 6190
gen.NM_004509, 1012
gen.NM_004510, 1014
gen.NM_004524, 4960
gen.NM_004539, 5072
gen.NM_004547, 1218
gen.NM_004550, 470
gen.NM_004551, 3199
gen.NM_004555, 4586
gen.NM_004573, 4141
gen.NM_004595, 6140
gen.NM_004596, 5448

gen.NM_004599,6085
gen.NM_004618,4716
gen.NM_004632,414
gen.NM_004635,1155
gen.NM_004636,1149
gen.NM_004637,1246
gen.NM_004638,1979
gen.NM_004639,1973
gen.NM_004640,1986
gen.NM_004673,529
gen.NM_004691,4545
gen.NM_004697,2751
gen.NM_004699,6323
gen.NM_004701,4197
gen.NM_004704,1182
gen.NM_004706,5470
gen.NM_004714,5434
gen.NM_004725,3093
gen.NM_004728,2959
gen.NM_004735,1026
gen.NM_004738,5824
gen.NM_004739,3230
gen.NM_004766,1270
gen.NM_004767,576
gen.NM_004772,1650
gen.NM_004781,44
gen.NM_004794,6287
gen.NM_004813,3190
gen.NM_004821,1787
gen.NM_004844,1066
gen.NM_004846,998
gen.NM_004859,4921
gen.NM_004870,4689
gen.NM_004889,2342
gen.NM_004893,1685
gen.NM_004905,511
gen.NM_004911,2442
gen.NM_004928,5915
gen.NM_004930,69
gen.NM_004933,4638
gen.NM_004939,662
gen.NM_004957,2775
gen.NM_004960,4465
gen.NM_004964,150
gen.NM_004973,2039
gen.NM_004982,3526
gen.NM_004990,3669
gen.NM_004992,6330
gen.NM_004994,5791
gen.NM_004995,3976
gen.NM_005000,2396
gen.NM_005002,3448
gen.NM_005003,4446
gen.NM_005004,3063
gen.NM_005005,2606
gen.NM_005008,6083

gen.NM_005015,3981
gen.NM_005016,3620
gen.NM_005022,4665
gen.NM_005030,4442
gen.NM_005036,6104
gen.NM_005042,3524
gen.NM_005053,5283
gen.NM_005072,4581
gen.NM_005080,5987
gen.NM_005109,1093
gen.NM_005110,1854
gen.NM_005112,1421
gen.NM_005115,4500
gen.NM_005132,3962
gen.NM_005141,1508
gen.NM_005163,4110
gen.NM_005171,3574
gen.NM_005174,2895
gen.NM_005194,5808
gen.NM_005217,2478
gen.NM_005220,4946
gen.NM_005224,5104
gen.NM_005243,5989
gen.NM_005269,3667
gen.NM_005271,3004
gen.NM_005291,854
gen.NM_005300,6159
gen.NM_005313,4174
gen.NM_005324,4969
gen.NM_005330,3146
gen.NM_005333,6126
gen.NM_005345,1963
gen.NM_005346,1961
gen.NM_005347,2790
gen.NM_005348,4092
gen.NM_005362,6316
gen.NM_005364,6308
gen.NM_005370,5314
gen.NM_005371,3689
gen.NM_005378,657
gen.NM_005389,2126
gen.NM_005432,4101
gen.NM_005439,3466
gen.NM_005440,4877
gen.NM_005452,1944
gen.NM_005474,4850
gen.NM_005490,5208
gen.NM_005498,5241
gen.NM_005514,2155
gen.NM_005517,110
gen.NM_005520,1850
gen.NM_005548,4568
gen.NM_005563,105
gen.NM_005566,3175
gen.NM_005572,404
gen.NM_005573,1718

gen.NM_005581,5517
gen.NM_005594,3628
gen.NM_005614,2460
gen.NM_005617,1708
gen.NM_005620,340
gen.NM_005623,4782
gen.NM_005632,4362
gen.NM_005657,4170
gen.NM_005663,1382
gen.NM_005676,6165
gen.NM_005686,550
gen.NM_005692,2458
gen.NM_005693,3204
gen.NM_005698,424
gen.NM_005710,6181
gen.NM_005713,1602
gen.NM_005717,517
gen.NM_005718,1055
gen.NM_005720,2348
gen.NM_005724,4273
gen.NM_005726,3695
gen.NM_005729,2986
gen.NM_005731,996
gen.NM_005745,6344
gen.NM_005754,1697
gen.NM_005762,5627
gen.NM_005770,4176
gen.NM_005775,2491
gen.NM_005783,829
gen.NM_005787,1316
gen.NM_005796,4575
gen.NM_005806,5887
gen.NM_005826,83
gen.NM_005830,3898
gen.NM_005831,4911
gen.NM_005833,2792
gen.NM_005837,2326
gen.NM_005850,461
gen.NM_005851,3301
gen.NM_005855,1024
gen.NM_005866,2670
gen.NM_005877,5999
gen.NM_005884,5421
gen.NM_005889,3509
gen.NM_005911,808
gen.NM_005915,864
gen.NM_005917,764
gen.NM_005918,2306
gen.NM_005973,389
gen.NM_005981,3681
gen.NM_005983,1579
gen.NM_005985,5802
gen.NM_005997,350
gen.NM_006000,982
gen.NM_006012,5201
gen.NM_006013,6326

gen.NM_006019,3304
gen.NM_006023,2899
gen.NM_006039,4936
gen.NM_006053,3306
gen.NM_006058,1702
gen.NM_006066,218
gen.NM_006067,4612
gen.NM_006098,1852
gen.NM_006101,5023
gen.NM_006109,3973
gen.NM_006110,4423
gen.NM_006112,159
gen.NM_006114,5513
gen.NM_006115,5975
gen.NM_006128,2497
gen.NM_006131,2499
gen.NM_006132,2501
gen.NM_006136,2393
gen.NM_006169,3380
gen.NM_006184,5566
gen.NM_006227,5789
gen.NM_006230,2246
gen.NM_006245,1892
gen.NM_006247,5497
gen.NM_006250,3522
gen.NM_006253,3831
gen.NM_006262,3546
gen.NM_006265,2600
gen.NM_006271,374
gen.NM_006272,5935
gen.NM_006280,6338
gen.NM_006289,2682
gen.NM_006295,1967
gen.NM_006303,2178
gen.NM_006330,2550
gen.NM_006335,571
gen.NM_006339,5171
gen.NM_006342,1374
gen.NM_006349,2371
gen.NM_006354,1049
gen.NM_006362,3242
gen.NM_006365,396
gen.NM_006373,4875
gen.NM_006384,4305
gen.NM_006387,5319
gen.NM_006395,1062
gen.NM_006397,5277
gen.NM_006401,2732
gen.NM_006427,4106
gen.NM_006428,4360
gen.NM_006429,792
gen.NM_006430,759
gen.NM_006432,4048
gen.NM_006435,3113
gen.NM_006439,1504
gen.NM_006440,5954

gen.NM_006453,4384
gen.NM_006455,4822
gen.NM_006470,4725
gen.NM_006478,5991
gen.NM_006488,703
gen.NM_006494,5476
gen.NM_006503,5441
gen.NM_006513,298
gen.NM_006516,188
gen.NM_006523,3055
gen.NM_006530,3727
gen.NM_006556,452
gen.NM_006559,146
gen.NM_006576,3697
gen.NM_006585,5885
gen.NM_006586,1894
gen.NM_006589,428
gen.NM_006600,118
gen.NM_006601,3636
gen.NM_006621,300
gen.NM_006625,93
gen.NM_006636,794
gen.NM_006646,3881
gen.NM_006659,3101
gen.NM_006666,5558
gen.NM_006667,6272
gen.NM_006670,2070
gen.NM_006693,2344
gen.NM_006694,436
gen.NM_006698,5760
gen.NM_006708,1904
gen.NM_006711,4392
gen.NM_006746,6134
gen.NM_006761,4642
gen.NM_006763,548
gen.NM_006764,1151
gen.NM_006769,271
gen.NM_006787,6197
gen.NM_006791,4279
gen.NM_006799,4408
gen.NM_006801,5576
gen.NM_006805,1687
gen.NM_006808,2740
gen.NM_006810,1223
gen.NM_006812,3678
gen.NM_006815,3847
gen.NM_006816,1830
gen.NM_006817,3785
gen.NM_006821,4046
gen.NM_006824,192
gen.NM_006825,3807
gen.NM_006826,655
gen.NM_006833,2338
gen.NM_006835,1449
gen.NM_006837,2565
gen.NM_006839,814

gen.NM_006842,3295
gen.NM_006844,5308
gen.NM_006854,2184
gen.NM_006862,344
gen.NM_006888,4063
gen.NM_006899,5661
gen.NM_006908,2182
gen.NM_006924,4908
gen.NM_006928,3660
gen.NM_006932,6007
gen.NM_006938,5039
gen.NM_006941,6049
gen.NM_006942,4691
gen.NM_006990,124
gen.NM_007002,5844
gen.NM_007019,5785
gen.NM_007032,6040
gen.NM_007034,267
gen.NM_007046,705
gen.NM_007047,2029
gen.NM_007062,3805
gen.NM_007065,5237
gen.NM_007074,4516
gen.NM_007085,1216
gen.NM_007096,2691
gen.NM_007100,1366
gen.NM_007103,3299
gen.NM_007104,1922
gen.NM_007158,302
gen.NM_007165,5152
gen.NM_007173,3348
gen.NM_007178,3501
gen.NM_007184,1165
gen.NM_007186,5744
gen.NM_007190,3089
gen.NM_007209,2794
gen.NM_007242,4566
gen.NM_007244,3520
gen.NM_007260,89
gen.NM_007262,42
gen.NM_007263,5352
gen.NM_007268,6204
gen.NM_007273,3455
gen.NM_007275,1153
gen.NM_007276,2214
gen.NM_007279,5619
gen.NM_007310,5958
gen.NM_007311,6095
gen.NM_007317,4507
gen.NM_007355,1874
gen.NM_007364,4277
gen.NM_007372,4931
gen.NM_012068,5525
gen.NM_012098,2782
gen.NM_012099,5504
gen.NM_012100,977

gen.NM_012101,3420
gen.NM_012111,4055
gen.NM_012112,5715
gen.NM_012116,5519
gen.NM_012138,4838
gen.NM_012170,4265
gen.NM_012179,6017
gen.NM_012181,5350
gen.NM_012203,2693
gen.NM_012207,2955
gen.NM_012237,5409
gen.NM_012248,4451
gen.NM_012255,5698
gen.NM_012264,6054
gen.NM_012286,6246
gen.NM_012296,3344
gen.NM_012323,6052
gen.NM_012391,1929
gen.NM_012412,2236
gen.NM_012423,5550
gen.NM_012437,381
gen.NM_012458,5155
gen.NM_012469,5873
gen.NM_012486,596
gen.NM_013237,1834
gen.NM_013247,801
gen.NM_013265,3279
gen.NM_013274,3037
gen.NM_013277,3566
gen.NM_013296,292
gen.NM_013333,5617
gen.NM_013336,1238
gen.NM_013341,903
gen.NM_013363,1276
gen.NM_013365,6032
gen.NM_013369,5911
gen.NM_013375,2027
gen.NM_013393,2165
gen.NM_013402,3251
gen.NM_013403,5492
gen.NM_013406,5269
gen.NM_013407,5270
gen.NM_013417,2718
gen.NM_013442,2675
gen.NM_013451,3013
gen.NM_014003,4592
gen.NM_014008,6187
gen.NM_014033,3576
gen.NM_014035,1664
gen.NM_014042,3320
gen.NM_014062,4556
gen.NM_014063,2251
gen.NM_014107,2077
gen.NM_014138,6163
gen.NM_014166,3906
gen.NM_014172,2862

gen.NM_014173,5326
gen.NM_014176,578
gen.NM_014184,585
gen.NM_014188,17
gen.NM_014189,1390
gen.NM_014190,1388
gen.NM_014203,5536
gen.NM_014214,5032
gen.NM_014226,4095
gen.NM_014236,626
gen.NM_014248,6072
gen.NM_014255,3631
gen.NM_014267,3173
gen.NM_014275,1846
gen.NM_014285,2820
gen.NM_014294,2567
gen.NM_014303,6003
gen.NM_014306,6015
gen.NM_014311,3606
gen.NM_014320,2116
gen.NM_014321,4476
gen.NM_014325,3777
gen.NM_014335,4182
gen.NM_014341,1906
gen.NM_014353,4386
gen.NM_014408,167
gen.NM_014413,2180
gen.NM_014426,5685
gen.NM_014444,4168
gen.NM_014445,1284
gen.NM_014452,1870
gen.NM_014453,5625
gen.NM_014481,6199
gen.NM_014501,5615
gen.NM_014502,3220
gen.NM_014515,3724
gen.NM_014556,1394
gen.NM_014571,142
gen.NM_014585,923
gen.NM_014587,4370
gen.NM_014610,3232
gen.NM_014624,367
gen.NM_014649,5199
gen.NM_014663,202
gen.NM_014670,934
gen.NM_014685,4530
gen.NM_014713,667
gen.NM_014736,4214
gen.NM_014737,5676
gen.NM_014742,5721
gen.NM_014747,180
gen.NM_014748,684
gen.NM_014752,3329
gen.NM_014773,1721
gen.NM_014776,3792
gen.NM_014778,3878

gen.NM_014800,2259
gen.NM_014814,1195
gen.NM_014829,1681
gen.NM_014837,519
gen.NM_014847,446
gen.NM_014849,463
gen.NM_014851,36
gen.NM_014868,3823
gen.NM_014887,3889
gen.NM_014919,1378
gen.NM_014931,5610
gen.NM_014933,1457
gen.NM_014941,6005
gen.NM_014972,4628
gen.NM_015043,1843
gen.NM_015062,3042
gen.NM_015064,3430
gen.NM_015068,2319
gen.NM_015129,6276
gen.NM_015140,6097
gen.NM_015179,3024
gen.NM_015322,4226
gen.NM_015324,3149
gen.NM_015373,6056
gen.NM_015388,1886
gen.NM_015438,3470
gen.NM_015449,444
gen.NM_015453,1043
gen.NM_015472,1282
gen.NM_015484,99
gen.NM_015511,5752
gen.NM_015533,3225
gen.NM_015544,4780
gen.NM_015584,4761
gen.NM_015629,5600
gen.NM_015636,686
gen.NM_015640,260
gen.NM_015644,1057
gen.NM_015646,3720
gen.NM_015665,3604
gen.NM_015702,885
gen.NM_015714,555
gen.NM_015853,3238
gen.NM_015920,4205
gen.NM_015932,3884
gen.NM_015934,941
gen.NM_015937,5783
gen.NM_015953,5546
gen.NM_015965,5362
gen.NM_015966,5745
gen.NM_016003,2172
gen.NM_016016,4847
gen.NM_016022,334
gen.NM_016026,4037
gen.NM_016030,647
gen.NM_016059,1908

gen.NM_016085,694
gen.NM_016091,6045
gen.NM_016095,4610
gen.NM_016111,4374
gen.NM_016119,3912
gen.NM_016143,5652
gen.NM_016169,3051
gen.NM_016174,2767
gen.NM_016176,26
gen.NM_016183,73
gen.NM_016202,5621
gen.NM_016223,3210
gen.NM_016249,6300
gen.NM_016263,5169
gen.NM_016267,6293
gen.NM_016286,5006
gen.NM_016292,4414
gen.NM_016304,4193
gen.NM_016328,2293
gen.NM_016357,3572
gen.NM_016359,4152
gen.NM_016361,328
gen.NM_016410,2664
gen.NM_016440,5523
gen.NM_016445,4035
gen.NM_016456,564
gen.NM_016498,6001
gen.NM_016526,3107
gen.NM_016539,5181
gen.NM_016558,5750
gen.NM_016567,3097
gen.NM_016579,5216
gen.NM_016587,2216
gen.NM_016592,5826
gen.NM_016638,3843
gen.NM_016639,4398
gen.NM_016641,4335
gen.NM_016645,4302
gen.NM_016647,2614
gen.NM_016732,5733
gen.NM_016838,887
gen.NM_016839,889
gen.NM_016930,1400
gen.NM_016940,5883
gen.NM_016941,5432
gen.NM_017443,2753
gen.NM_017458,4498
gen.NM_017491,1419
gen.NM_017546,834
gen.NM_017566,4617
gen.NM_017572,5146
gen.NM_017595,4871
gen.NM_017601,1902
gen.NM_017610,4195
gen.NM_017613,5890
gen.NM_017647,4929

gen.NM_017668,4327
gen.NM_017670,3266
gen.NM_017684,4208
gen.NM_017722,5286
gen.NM_017751,859
gen.NM_017760,2467
gen.NM_017761,91
gen.NM_017768,262
gen.NM_017777,4906
gen.NM_017789,825
gen.NM_017797,5143
gen.NM_017801,1081
gen.NM_017803,4584
gen.NM_017807,4003
gen.NM_017815,3971
gen.NM_017822,3552
gen.NM_017825,165
gen.NM_017827,5413
gen.NM_017829,5939
gen.NM_017847,513
gen.NM_017853,4594
gen.NM_017868,3386
gen.NM_017874,5668
gen.NM_017876,5098
gen.NM_017882,4224
gen.NM_017883,6179
gen.NM_017891,8
gen.NM_017895,5798
gen.NM_017900,22
gen.NM_017901,3810
gen.NM_017910,674
gen.NM_017916,5554
gen.NM_017952,812
gen.NM_017955,4112
gen.NM_017974,1020
gen.NM_018019,4737
gen.NM_018023,1306
gen.NM_018032,4358
gen.NM_018034,1575
gen.NM_018035,5458
gen.NM_018047,1706
gen.NM_018048,3517
gen.NM_018054,4436
gen.NM_018066,116
gen.NM_018070,239
gen.NM_018085,569
gen.NM_018096,4792
gen.NM_018110,4535
gen.NM_018113,3548
gen.NM_018116,420
gen.NM_018122,535
gen.NM_018124,4588
gen.NM_018135,1880
gen.NM_018154,5300
gen.NM_018174,5332
gen.NM_018188,10

gen.NM_018209,5861
gen.NM_018212,587
gen.NM_018217,5740
gen.NM_018238,2437
gen.NM_018242,4747
gen.NM_018250,2510
gen.NM_018253,418
gen.NM_018255,5056
gen.NM_018270,5849
gen.NM_018310,2527
gen.NM_018346,4898
gen.NM_018357,4232
gen.NM_018410,1018
gen.NM_018454,4154
gen.NM_018457,3610
gen.NM_018463,3442
gen.NM_018464,2951
gen.NM_018468,5387
gen.NM_018486,6222
gen.NM_018509,4900
gen.NM_018607,721
gen.NM_018660,2512
gen.NM_018668,4312
gen.NM_018674,973
gen.NM_018686,3513
gen.NM_018912,1734
gen.NM_018913,1736
gen.NM_018914,1738
gen.NM_018915,1740
gen.NM_018916,1742
gen.NM_018917,1744
gen.NM_018918,1746
gen.NM_018919,1748
gen.NM_018920,1750
gen.NM_018921,1752
gen.NM_018922,1754
gen.NM_018923,1756
gen.NM_018924,1758
gen.NM_018925,1760
gen.NM_018926,1762
gen.NM_018927,1764
gen.NM_018928,1766
gen.NM_018929,1768
gen.NM_018947,2208
gen.NM_018948,41
gen.NM_018950,2017
gen.NM_018955,4728
gen.NM_018957,6034
gen.NM_018977,6214
gen.NM_019013,4682
gen.NM_019058,2971
gen.NM_019059,2206
gen.NM_019082,2242
gen.NM_019095,5681
gen.NM_019099,310
gen.NM_019554,371

gen.NM_019606,2333
gen.NM_019609,5663
gen.NM_019619,2916
gen.NM_019848,6321
gen.NM_019852,3988
gen.NM_019887,3839
gen.NM_020037,4895
gen.NM_020038,4893
gen.NM_020132,5908
gen.NM_020134,709
gen.NM_020149,4136
gen.NM_020158,5454
gen.NM_020188,4604
gen.NM_020230,5232
gen.NM_020243,6058
gen.NM_020299,2425
gen.NM_020315,6036
gen.NM_020320,2075
gen.NM_020347,1113
gen.NM_020401,3717
gen.NM_020414,4069
gen.NM_020418,1180
gen.NM_020548,871
gen.NM_020675,896
gen.NM_020677,4340
gen.NM_020701,1248
gen.NM_020990,4172
gen.NM_020992,3017
gen.NM_021019,3646
gen.NM_021029,6244
gen.NM_021079,4883
gen.NM_021095,698
gen.NM_021103,803
gen.NM_021104,3654
gen.NM_021107,5415
gen.NM_021121,948
gen.NM_021126,6029
gen.NM_021129,2964
gen.NM_021130,2238
gen.NM_021141,958
gen.NM_021154,2701
gen.NM_021158,5638
gen.NM_021177,1965
gen.NM_021178,4006
gen.NM_021195,4400
gen.NM_021213,4919
gen.NM_021219,5879
gen.NM_021226,2945
gen.NM_021626,4917
gen.NM_021709,4108
gen.NM_021728,4020
gen.NM_021826,5665
gen.NM_021830,3033
gen.NM_021831,707
gen.NM_021870,1517
gen.NM_021871,1513

gen.NM_021932,3109
gen.NM_021934,3588
gen.NM_021948,394
gen.NM_021953,3444
gen.NM_021966,4079
gen.NM_021999,3908
gen.NM_022003,3369
gen.NM_022039,3039
gen.NM_022044,5973
gen.NM_022048,4216
gen.NM_022105,5857
gen.NM_022137,4042
gen.NM_022141,6101
gen.NM_022158,5016
gen.NM_022170,2288
gen.NM_022171,1145
gen.NM_022362,3029
gen.NM_022369,4246
gen.NM_022371,527
gen.NM_022442,5806
gen.NM_022453,988
gen.NM_022458,2464
gen.NM_022461,1086
gen.NM_022485,1045
gen.NM_022550,1638
gen.NM_022551,1946
gen.NM_022552,717
gen.NM_022566,4296
gen.NM_022727,5961
gen.NM_022744,4468
gen.NM_022747,4084
gen.NM_022748,2226
gen.NM_022752,5474
gen.NM_022758,1926
gen.NM_022770,4539
gen.NM_022778,107
gen.NM_022839,4290
gen.NM_022963,1838
gen.NM_023009,152
gen.NM_023011,3940
gen.NM_023032,3691
gen.NM_023033,3693
gen.NM_023078,2620
gen.NM_023936,4378
gen.NM_023942,2449
gen.NM_024003,6336
gen.NM_024026,3872
gen.NM_024027,645
gen.NM_024029,5250
gen.NM_024031,4458
gen.NM_024033,2427
gen.NM_024040,3047
gen.NM_024045,2957
gen.NM_024048,4470
gen.NM_024067,2186
gen.NM_024068,3643

gen.NM_024070,2335
gen.NM_024089,3935
gen.NM_024098,3218
gen.NM_024099,3236
gen.NM_024104,5323
gen.NM_024111,4148
gen.NM_024294,1924
gen.NM_024297,4672
gen.NM_024299,5865
gen.NM_024319,614
gen.NM_024321,5389
gen.NM_024329,62
gen.NM_024330,379
gen.NM_024333,5186
gen.NM_024339,4396
gen.NM_024407,5120
gen.NM_024507,4406
gen.NM_024516,4502
gen.NM_024537,3938
gen.NM_024567,2508
gen.NM_024571,4350
gen.NM_024572,719
gen.NM_024586,247
gen.NM_024589,4346
gen.NM_024602,206
gen.NM_024603,241
gen.NM_024613,2584
gen.NM_024627,5951
gen.NM_024640,137
gen.NM_024653,2373
gen.NM_024658,3960
gen.NM_024664,183
gen.NM_024668,1724
gen.NM_024671,4454
gen.NM_024691,5636
gen.NM_024709,603
gen.NM_024748,1526
gen.NM_024824,4057
gen.NM_024844,4955
gen.NM_024854,3529
gen.NM_024855,5769
gen.NM_024863,6248
gen.NM_024881,5321
gen.NM_024900,1491
gen.NM_024918,5757
gen.NM_024942,3095
gen.NM_025070,2541
gen.NM_025072,2772
gen.NM_025108,4411
gen.NM_025129,5534
gen.NM_025150,358
gen.NM_025164,3374
gen.NM_025168,1863
gen.NM_025197,4830
gen.NM_025202,1000
gen.NM_025203,678

gen.NM_025204,6109
gen.NM_025205,1414
gen.NM_025207,455
gen.NM_025226,499
gen.NM_025232,2503
gen.NM_025233,4859
gen.NM_025234,4270
gen.NM_025241,5190
gen.NM_025263,2007
gen.NM_030567,1826
gen.NM_030573,5965
gen.NM_030579,4553
gen.NM_030587,196
gen.NM_030593,5411
gen.NM_030775,3432
gen.NM_030782,1545
gen.NM_030815,5719
gen.NM_030819,4573
gen.NM_030877,5763
gen.NM_030900,2232
gen.NM_030920,332
gen.NM_030921,1272
gen.NM_030925,3910
gen.NM_030926,1009
gen.NM_030935,2331
gen.NM_030973,5532
gen.NM_031157,3612
gen.NM_031206,6210
gen.NM_031213,5138
gen.NM_031228,5642
gen.NM_031229,5640
gen.NM_031243,2212
gen.NM_031263,2708
gen.NM_031289,3496
gen.NM_031300,1832
gen.NM_031417,5506
gen.NM_031434,2456
gen.NM_031443,2234
gen.NM_031453,2902
gen.NM_031459,131
gen.NM_031465,3446
gen.NM_031472,3261
gen.NM_031478,4522
gen.NM_031479,3665
gen.NM_031482,1629
gen.NM_031484,3070
gen.NM_031485,5574
gen.NM_031901,336
gen.NM_031925,2304
gen.NM_031942,905
gen.NM_031966,1598
gen.NM_031968,5014
gen.NM_031989,3622
gen.NM_031990,5100
gen.NM_031992,2290
gen.NM_032023,2923

gen.NM_032038,4495
gen.NM_032088,1770
gen.NM_032092,1772
gen.NM_032112,3031
gen.NM_032140,4571
gen.NM_032162,4310
gen.NM_032164,2340
gen.NM_032196,4150
gen.NM_032204,5996
gen.NM_032207,5317
gen.NM_032211,3068
gen.NM_032212,843
gen.NM_032219,1370
gen.NM_032227,6257
gen.NM_032271,4388
gen.NM_032280,1642
gen.NM_032288,1354
gen.NM_032292,412
gen.NM_032299,3395
gen.NM_032313,1437
gen.NM_032322,4771
gen.NM_032323,402
gen.NM_032324,630
gen.NM_032330,4485
gen.NM_032331,1318
gen.NM_032333,2996
gen.NM_032338,3712
gen.NM_032342,2746
gen.NM_032343,1235
gen.NM_032350,2163
gen.NM_032361,1814
gen.NM_032376,4854
gen.NM_032377,5262
gen.NM_032379,3346
gen.NM_032383,1280
gen.NM_032390,875
gen.NM_032402,1776
gen.NM_032403,1774
gen.NM_032486,4444
gen.NM_032527,5869
gen.NM_032565,3914
gen.NM_032626,4440
gen.NM_032627,5345
gen.NM_032635,5393
gen.NM_032636,296
gen.NM_032637,1577
gen.NM_032642,3434
gen.NM_032656,3851
gen.NM_032667,3240
gen.NM_032712,5588
gen.NM_032726,990
gen.NM_032737,5157
gen.NM_032738,503
gen.NM_032747,3061
gen.NM_032750,1174
gen.NM_032753,5173

gen.NM_032756,222
gen.NM_032792,5631
gen.NM_032799,2763
gen.NM_032814,3812
gen.NM_032822,785
gen.NM_032827,810
gen.NM_032864,245
gen.NM_032871,3326
gen.NM_032872,122
gen.NM_032873,3415
gen.NM_032890,606
gen.NM_032904,3794
gen.NM_032905,2893
gen.NM_032907,4248
gen.NM_032928,2860
gen.NM_032929,2081
gen.NM_032933,5037
gen.NM_032951,2284
gen.NM_032953,2286
gen.NM_032958,2376
gen.NM_032989,3258
gen.NM_032997,2949
gen.NM_032999,2295
gen.NM_033008,1176
gen.NM_033010,1178
gen.NM_033011,2538
gen.NM_033022,2978
gen.NM_033046,796
gen.NM_033070,5937
gen.NM_033161,2828
gen.NM_033197,5729
gen.NM_033219,2730
gen.NM_033251,4635
gen.NM_033296,1404
gen.NM_033301,2635
gen.NM_033316,1348
gen.NM_033363,5417
gen.NM_033410,4456
gen.NM_033415,5355
gen.NM_033416,878
gen.NM_033421,5787
gen.NM_033440,60
gen.NM_033534,15
gen.NM_033544,4315
gen.NM_033551,1785
gen.NM_052837,426
gen.NM_052848,5451
gen.NM_052859,1157
gen.NM_052862,488
gen.NM_052881,5656
gen.NM_052886,2602
gen.NM_052936,6251
gen.NM_052963,2616
gen.NM_052984,3685
gen.NM_053043,2462
gen.NM_053056,3311

gen.NM_053275,3829
gen.NM_054012,2822
gen.NM_054013,1848
gen.NM_054014,5650
gen.NM_054016,95
gen.NM_057089,2363
gen.NM_057161,1890
gen.NM_057169,3790
gen.NM_057174,3188
gen.NM_057182,5376
gen.NM_058164,5230
gen.NM_058179,2703
gen.NM_058192,4366
gen.NM_058193,3422
gen.NM_058195,2653
gen.NM_058196,2657
gen.NM_058199,2836
gen.NM_078467,1912
gen.NM_079423,3648
gen.NM_079425,3650
gen.NM_080424,1016
gen.NM_080425,5828
gen.NM_080426,5832
gen.NM_080491,3342
gen.NM_080592,696
gen.NM_080594,4394
gen.NM_080598,1984
gen.NM_080648,3999
gen.NM_080649,4001
gen.NM_080670,1726
gen.NM_080686,1981
gen.NM_080687,3942
gen.NM_080702,1977
gen.NM_080703,1975
gen.NM_080796,5855
gen.NM_080797,5859
gen.NM_080820,5693
gen.NM_080822,4654
gen.NM_106552,670
gen.NM_130398,639
gen.NM_130442,2260
gen.NM_130468,4143
gen.NM_130898,434
gen.NM_133330,1376
gen.NM_133332,1380
gen.NM_133373,4885
gen.NM_133375,4222
gen.NM_133436,2357
gen.NM_133480,1051
gen.NM_133481,1053
gen.NM_133483,3676
gen.NM_133503,3742
gen.NM_133504,3744
gen.NM_133505,3746
gen.NM_133506,3750
gen.NM_133507,3748

gen.NM_133627,4786
gen.NM_133629,4790
gen.NM_133630,4788
gen.NM_133637,798
gen.NM_133645,2066
gen.NM_134269,6009
gen.NM_134323,3616
gen.NM_134324,3618
gen.NM_134440,5358
gen.NM_138385,1372
gen.NM_138391,545
gen.NM_138427,4739
gen.NM_138434,2451
gen.NM_138443,5060
gen.NM_138483,1037
gen.NM_138578,5713
gen.NM_138614,1125
gen.NM_138699,1406
gen.NM_138801,727
gen.NM_138924,5124
gen.XM_001289,524
gen.XM_001299,33
gen.XM_001389,1453
gen.XM_001468,342
gen.XM_001472,250
gen.XM_001482,3658
gen.XM_001589,24
gen.XM_001616,101
gen.XM_001640,126
gen.XM_001807,135
gen.XM_001812,134
gen.XM_001826,78
gen.XM_001897,486
gen.XM_001914,567
gen.XM_001916,568
gen.XM_001958,599
gen.XM_002068,523
gen.XM_002105,141
gen.XM_002114,113
gen.XM_002217,845
gen.XM_002255,1361
gen.XM_002435,700
gen.XM_002447,877
gen.XM_002480,680
gen.XM_002540,1006
gen.XM_002611,823
gen.XM_002636,964
gen.XM_002647,770
gen.XM_002669,946
gen.XM_002674,776
gen.XM_002704,853
gen.XM_002727,788
gen.XM_002739,779
gen.XM_002742,1036
gen.XM_002828,1143
gen.XM_002854,1187

gen.XM_002855,1186
gen.XM_002859,1274
gen.XM_002899,1127
gen.XM_003213,1162
gen.XM_003222,1119
gen.XM_003245,1136
gen.XM_003305,1451
gen.XM_003435,1432
gen.XM_003477,1530
gen.XM_003511,1448
gen.XM_003555,1500
gen.XM_003611,2083
gen.XM_003716,1811
gen.XM_003771,1644
gen.XM_003789,1712
gen.XM_003825,1540
gen.XM_003830,1666
gen.XM_003841,1699
gen.XM_003869,1572
gen.XM_003896,1581
gen.XM_003937,1710
gen.XM_004009,1565
gen.XM_004098,3704
gen.XM_004151,2065
gen.XM_004256,2114
gen.XM_004297,2113
gen.XM_004330,3194
gen.XM_004379,2122
gen.XM_004383,2130
gen.XM_004526,2110
gen.XM_004627,2402
gen.XM_004901,2292
gen.XM_005060,2605
gen.XM_005086,1042
gen.XM_005100,2908
gen.XM_005180,1332
gen.XM_005305,2485
gen.XM_005348,2755
gen.XM_005365,2760
gen.XM_005490,2707
gen.XM_005525,2727
gen.XM_005543,2666
gen.XM_005675,3103
gen.XM_005698,3053
gen.XM_005724,2878
gen.XM_005938,3058
gen.XM_005969,3088
gen.XM_006139,3127
gen.XM_006170,3201
gen.XM_006212,3167
gen.XM_006290,98
gen.XM_006297,3196
gen.XM_006424,3151
gen.XM_006432,3371
gen.XM_006464,3355
gen.XM_006467,3399

gen.XM_006475,3135
gen.XM_006483,3136
gen.XM_006529,3281
gen.XM_006533,3270
gen.XM_006566,3849
gen.XM_006578,3736
gen.XM_006589,3766
gen.XM_006595,3835
gen.XM_006694,3535
gen.XM_006710,3626
gen.XM_006748,3536
gen.XM_006826,3559
gen.XM_006887,3765
gen.XM_006925,3485
gen.XM_006936,3483
gen.XM_006937,5074
gen.XM_006947,3482
gen.XM_006958,3475
gen.XM_007002,3797
gen.XM_007003,3796
gen.XM_007199,3923
gen.XM_007254,4097
gen.XM_007272,4081
gen.XM_007288,3968
gen.XM_007293,3967
gen.XM_007315,3958
gen.XM_007316,3957
gen.XM_007324,4027
gen.XM_007328,4024
gen.XM_007441,4045
gen.XM_007483,4072
gen.XM_007488,4005
gen.XM_007491,3996
gen.XM_007531,4167
gen.XM_007545,4156
gen.XM_007623,4221
gen.XM_007651,4189
gen.XM_007751,4129
gen.XM_007963,4474
gen.XM_007988,4430
gen.XM_008064,4509
gen.XM_008065,4497
gen.XM_008106,4463
gen.XM_008126,4353
gen.XM_008150,4800
gen.XM_008231,4694
gen.XM_008253,4926
gen.XM_008323,4750
gen.XM_008334,4671
gen.XM_008351,4856
gen.XM_008401,4867
gen.XM_008402,4869
gen.XM_008432,4902
gen.XM_008441,4686
gen.XM_008459,4915
gen.XM_008462,4777

gen.XM_008486,4760
gen.XM_008509,4658
gen.XM_008538,4684
gen.XM_008557,4650
gen.XM_008579,4809
gen.XM_008679,4693
gen.XM_008695,5089
gen.XM_008723,5054
gen.XM_008812,5083
gen.XM_008830,5597
gen.XM_008851,5522
gen.XM_008854,5325
gen.XM_008860,5485
gen.XM_008878,5472
gen.XM_008887,5243
gen.XM_008912,5453
gen.XM_008985,5531
gen.XM_009010,5205
gen.XM_009036,5486
gen.XM_009063,5274
gen.XM_009082,5256
gen.XM_009125,5484
gen.XM_009126,5496
gen.XM_009149,5406
gen.XM_009180,5378
gen.XM_009203,5443
gen.XM_009222,5165
gen.XM_009277,5113
gen.XM_009279,5110
gen.XM_009293,5338
gen.XM_009303,5310
gen.XM_009330,5357
gen.XM_009338,5384
gen.XM_009436,5705
gen.XM_009450,5728
gen.XM_009501,5754
gen.XM_009549,5816
gen.XM_009622,5647
gen.XM_009642,5759
gen.XM_009671,5823
gen.XM_009672,5821
gen.XM_009686,5762
gen.XM_009805,5919
gen.XM_009947,6022
gen.XM_009967,6031
gen.XM_009973,6042
gen.XM_010000,6063
gen.XM_010002,6064
gen.XM_010024,6087
gen.XM_010029,6094
gen.XM_010040,6103
gen.XM_010055,6108
gen.XM_010117,6269
gen.XM_010141,6216
gen.XM_010156,5266
gen.XM_010178,6310

gen.XM_010272,6132
gen.XM_010362,6274
gen.XM_010378,6169
gen.XM_010436,6280
gen.XM_010494,3429
gen.XM_010615,253
gen.XM_010636,451
gen.XM_010664,133
gen.XM_010682,581
gen.XM_010712,182
gen.XM_010732,593
gen.XM_010778,925
gen.XM_010852,938
gen.XM_010858,1004
gen.XM_010866,992
gen.XM_010881,771
gen.XM_010886,755
gen.XM_010938,4641
gen.XM_010941,1433
gen.XM_010953,1130
gen.XM_010978,1290
gen.XM_011074,1320
gen.XM_011089,5076
gen.XM_011117,2059
gen.XM_011118,4941
gen.XM_011129,1423
gen.XM_011160,1365
gen.XM_011548,2411
gen.XM_011618,2400
gen.XM_011629,2533
gen.XM_011642,2586
gen.XM_011650,66
gen.XM_011657,2592
gen.XM_011749,2798
gen.XM_011752,2786
gen.XM_011769,2562
gen.XM_011778,2832
gen.XM_011988,3260
gen.XM_012124,3836
gen.XM_012145,3761
gen.XM_012159,3494
gen.XM_012162,3598
gen.XM_012179,5337
gen.XM_012182,3638
gen.XM_012184,3861
gen.XM_012219,3759
gen.XM_012272,3543
gen.XM_012284,2395
gen.XM_012376,3990
gen.XM_012377,3983
gen.XM_012398,4133
gen.XM_012418,4199
gen.XM_012462,4322
gen.XM_012487,4555
gen.XM_012549,4734
gen.XM_012569,4461

gen.XM_012609,4945
gen.XM_012615,4744
gen.XM_012634,4950
gen.XM_012638,3874
gen.XM_012642,4849
gen.XM_012651,4916
gen.XM_012676,4675
gen.XM_012741,5031
gen.XM_012798,5212
gen.XM_012812,5370
gen.XM_012860,5439
gen.XM_012862,5195
gen.XM_012913,5114
gen.XM_012931,5768
gen.XM_012970,5700
gen.XM_013010,6066
gen.XM_013015,6089
gen.XM_013029,6118
gen.XM_013042,6207
gen.XM_013060,6196
gen.XM_013086,6145
gen.XM_013112,2530
gen.XM_013127,2577
gen.XM_015234,75
gen.XM_015241,5088
gen.XM_015243,3148
gen.XM_015258,2244
gen.XM_015366,4239
gen.XM_015434,547
gen.XM_015462,1208
gen.XM_015468,3596
gen.XM_015476,3585
gen.XM_015481,3580
gen.XM_015516,6206
gen.XM_015563,1525
gen.XM_015652,2937
gen.XM_015697,5264
gen.XM_015700,4478
gen.XM_015705,3214
gen.XM_015717,257
gen.XM_015755,5046
gen.XM_015769,5369
gen.XM_015835,4311
gen.XM_015840,3921
gen.XM_015842,3932
gen.XM_015920,909
gen.XM_015922,911
gen.XM_016047,2604
gen.XM_016076,4237
gen.XM_016093,2992
gen.XM_016113,2712
gen.XM_016125,6275
gen.XM_016139,3170
gen.XM_016164,276
gen.XM_016170,1554
gen.XM_016199,600

gen.XM_016288,880
gen.XM_016308,2726
gen.XM_016334,1294
gen.XM_016345,1799
gen.XM_016351,3924
gen.XM_016378,5364
gen.XM_016382,5036
gen.XM_016410,5438
gen.XM_016480,326
gen.XM_016486,4071
gen.XM_016487,4068
gen.XM_016605,3708
gen.XM_016625,773
gen.XM_016640,3538
gen.XM_016674,1652
gen.XM_016700,2433
gen.XM_016713,4165
gen.XM_016733,2256
gen.XM_016843,766
gen.XM_016857,1941
gen.XM_016871,5180
gen.XM_016985,4213
gen.XM_017080,3436
gen.XM_017096,4644
gen.XM_017204,5240
gen.XM_017234,4712
gen.XM_017240,4135
gen.XM_017315,67
gen.XM_017356,1291
gen.XM_017364,1105
gen.XM_017369,3394
gen.XM_017432,3895
gen.XM_017442,2313
gen.XM_017474,1679
gen.XM_017483,2280
gen.XM_017508,3710
gen.XM_017517,2080
gen.XM_017578,4980
gen.XM_017591,1701
gen.XM_017641,1544
gen.XM_017698,861
gen.XM_017816,2581
gen.XM_017831,2119
gen.XM_017846,109
gen.XM_017857,1640
gen.XM_017914,3953
gen.XM_017925,1476
gen.XM_017930,6284
gen.XM_017931,2659
gen.XM_017971,4319
gen.XM_017984,4338
gen.XM_017996,2711
gen.XM_018006,2710
gen.XM_018019,6157
gen.XM_018039,784
gen.XM_018041,642

gen.XM_018054,4123
gen.XM_018088,4472
gen.XM_018108,6313
gen.XM_018109,6315
gen.XM_018136,161
gen.XM_018142,6232
gen.XM_018149,1264
gen.XM_018167,3015
gen.XM_018182,2098
gen.XM_018205,64
gen.XM_018241,6161
gen.XM_018279,3057
gen.XM_018287,2595
gen.XM_018301,763
gen.XM_018332,314
gen.XM_018359,2281
gen.XM_018399,3918
gen.XM_018432,4331
gen.XM_018473,1658
gen.XM_018515,5354
gen.XM_018523,1359
gen.XM_018534,4840
gen.XM_018539,6014
gen.XM_018540,841
gen.XM_026944,2787
gen.XM_026951,2771
gen.XM_026968,2769
gen.XM_026985,2766
gen.XM_026987,2765
gen.XM_027102,3802
gen.XM_027143,6106
gen.XM_027161,1220
gen.XM_027214,2385
gen.XM_027309,4329
gen.XM_027313,226
gen.XM_027365,4334
gen.XM_027412,4368
gen.XM_027440,2505
gen.XM_027558,4352
gen.XM_027651,2490
gen.XM_027679,2488
gen.XM_027825,4661
gen.XM_027904,5548
gen.XM_027916,76
gen.XM_027952,6353
gen.XM_027963,936
gen.XM_027964,1619
gen.XM_027983,213
gen.XM_028034,940
gen.XM_028064,5119
gen.XM_028067,5117
gen.XM_028151,4562
gen.XM_028192,3117
gen.XM_028263,5488
gen.XM_028267,5491
gen.XM_028322,4075

gen.XM_028347,4074
gen.XM_028358,4073
gen.XM_028398,4667
gen.XM_028417,4678
gen.XM_028643,3624
gen.XM_028662,3561
gen.XM_028666,5383
gen.XM_028672,5382
gen.XM_028744,5025
gen.XM_028760,3554
gen.XM_028783,5851
gen.XM_028806,5765
gen.XM_028810,5766
gen.XM_028834,5863
gen.XM_028848,4390
gen.XM_028918,5867
gen.XM_028966,5871
gen.XM_029031,169
gen.XM_029096,1539
gen.XM_029104,1314
gen.XM_029132,1313
gen.XM_029136,1310
gen.XM_029168,2841
gen.XM_029187,6194
gen.XM_029228,2069
gen.XM_029288,4067
gen.XM_029369,1198
gen.XM_029438,4656
gen.XM_029450,5404
gen.XM_029455,5403
gen.XM_029461,6282
gen.XM_029567,2609
gen.XM_029631,3602
gen.XM_029728,3595
gen.XM_029746,2128
gen.XM_029805,3507
gen.XM_029810,5776
gen.XM_029822,5778
gen.XM_029842,176
gen.XM_029844,145
gen.XM_030044,5796
gen.XM_030203,1028
gen.XM_030268,2543
gen.XM_030274,2544
gen.XM_030326,3187
gen.XM_030373,6233
gen.XM_030417,1112
gen.XM_030423,154
gen.XM_030447,3065
gen.XM_030470,68
gen.XM_030485,5159
gen.XM_030529,862
gen.XM_030582,883
gen.XM_030621,5818
gen.XM_030699,5834
gen.XM_030714,5145

gen.XM_030720, 5137
gen.XM_030721, 5135
gen.XM_030771, 1821
gen.XM_030777, 1823
gen.XM_030782, 1824
gen.XM_030812, 1256
gen.XM_030834, 952
gen.XM_030895, 5465
gen.XM_030901, 5456
gen.XM_030914, 5450
gen.XM_030920, 40
gen.XM_031025, 4032
gen.XM_031074, 4039
gen.XM_031251, 5307
gen.XM_031263, 5305
gen.XM_031273, 5303
gen.XM_031276, 5302
gen.XM_031292, 4295
gen.XM_031320, 1445
gen.XM_031345, 5292
gen.XM_031354, 4292
gen.XM_031404, 4285
gen.XM_031415, 4767
gen.XM_031427, 4769
gen.XM_031466, 4765
gen.XM_031515, 4147
gen.XM_031519, 731
gen.XM_031527, 733
gen.XM_031536, 4758
gen.XM_031554, 4145
gen.XM_031585, 782
gen.XM_031586, 783
gen.XM_031596, 780
gen.XM_031617, 4138
gen.XM_031626, 738
gen.XM_031718, 4159
gen.XM_031807, 3491
gen.XM_031857, 5184
gen.XM_031866, 3041
gen.XM_031890, 3044
gen.XM_031917, 5176
gen.XM_031944, 5066
gen.XM_031949, 3049
gen.XM_031992, 3059
gen.XM_032020, 5281
gen.XM_032121, 2455
gen.XM_032201, 4836
gen.XM_032216, 2454
gen.XM_032269, 1221
gen.XM_032285, 5399
gen.XM_032391, 216
gen.XM_032403, 4180
gen.XM_032443, 3930
gen.XM_032476, 2976
gen.XM_032520, 2970
gen.XM_032553, 1626

gen.XM_032588, 3457
gen.XM_032614, 3462
gen.XM_032710, 5247
gen.XM_032719, 5248
gen.XM_032724, 5252
gen.XM_032759, 1700
gen.XM_032766, 4864
gen.XM_032774, 5257
gen.XM_032782, 5261
gen.XM_032813, 4863
gen.XM_032817, 4861
gen.XM_032852, 4857
gen.XM_032895, 1590
gen.XM_032902, 1588
gen.XM_032930, 6189
gen.XM_032944, 2470
gen.XM_032996, 5943
gen.XM_033015, 5902
gen.XM_033016, 5903
gen.XM_033090, 5946
gen.XM_033147, 6241
gen.XM_033227, 3450
gen.XM_033232, 6351
gen.XM_033251, 3959
gen.XM_033263, 3472
gen.XM_033294, 1123
gen.XM_033337, 3964
gen.XM_033355, 2819
gen.XM_033359, 2818
gen.XM_033360, 2817
gen.XM_033361, 2815
gen.XM_033362, 2811
gen.XM_033380, 2809
gen.XM_033385, 2808
gen.XM_033391, 3969
gen.XM_033424, 2774
gen.XM_033435, 3975
gen.XM_033445, 3980
gen.XM_033457, 2777
gen.XM_033460, 2778
gen.XM_033553, 3991
gen.XM_033595, 3994
gen.XM_033654, 79
gen.XM_033683, 77
gen.XM_033689, 4646
gen.XM_033714, 4645
gen.XM_033813, 5960
gen.XM_033862, 6173
gen.XM_033876, 2383
gen.XM_033878, 6172
gen.XM_033884, 6170
gen.XM_033910, 2134
gen.XM_033912, 2132
gen.XM_033922, 4606
gen.XM_034000, 501
gen.XM_034082, 454

gen.XM_034321,1502
gen.XM_034375,4460
gen.XM_034377,5623
gen.XM_034431,3185
gen.XM_034586,4376
gen.XM_034590,4380
gen.XM_034640,2638
gen.XM_034662,319
gen.XM_034671,318
gen.XM_034710,1466
gen.XM_034713,1468
gen.XM_034744,1655
gen.XM_034862,1675
gen.XM_034890,4184
gen.XM_034897,4256
gen.XM_034935,6201
gen.XM_034952,857
gen.XM_034953,4116
gen.XM_035014,4119
gen.XM_035103,2824
gen.XM_035107,2439
gen.XM_035109,2825
gen.XM_035220,800
gen.XM_035368,2626
gen.XM_035370,2631
gen.XM_035373,2629
gen.XM_035465,6123
gen.XM_035485,3571
gen.XM_035490,3564
gen.XM_035497,3562
gen.XM_035572,1392
gen.XM_035625,5197
gen.XM_035627,5196
gen.XM_035636,5194
gen.XM_035638,5192
gen.XM_035640,5034
gen.XM_035662,2483
gen.XM_035680,2482
gen.XM_035824,1402
gen.XM_035919,5612
gen.XM_035986,1456
gen.XM_035999,5907
gen.XM_036002,1440
gen.XM_036011,5910
gen.XM_036042,5913
gen.XM_036087,5917
gen.XM_036104,4965
gen.XM_036107,5923
gen.XM_036115,4971
gen.XM_036118,1262
gen.XM_036175,5924
gen.XM_036299,155
gen.XM_036339,3178
gen.XM_036413,2469
gen.XM_036450,664
gen.XM_036462,4827

gen.XM_036465,4825
gen.XM_036500,573
gen.XM_036507,575
gen.XM_036528,4410
gen.XM_036556,566
gen.XM_036593,2939
gen.XM_036659,4707
gen.XM_036680,4342
gen.XM_036727,4134
gen.XM_036744,433
gen.XM_036755,5927
gen.XM_036785,4982
gen.XM_036829,442
gen.XM_036845,450
gen.XM_036934,448
gen.XM_036937,5969
gen.XM_036938,1197
gen.XM_037002,1668
gen.XM_037056,2107
gen.XM_037101,873
gen.XM_037108,831
gen.XM_037147,3212
gen.XM_037173,3202
gen.XM_037195,4988
gen.XM_037196,4987
gen.XM_037202,5840
gen.XM_037206,5842
gen.XM_037217,5846
gen.XM_037260,1608
gen.XM_037329,591
gen.XM_037377,1300
gen.XM_037381,1299
gen.XM_037423,1163
gen.XM_037468,6114
gen.XM_037474,6116
gen.XM_037565,5106
gen.XM_037572,5109
gen.XM_037600,1304
gen.XM_037657,2608
gen.XM_037662,5372
gen.XM_037682,5977
gen.XM_037741,2276
gen.XM_037778,4244
gen.XM_037797,5981
gen.XM_037808,3263
gen.XM_037875,2045
gen.XM_037945,5993
gen.XM_037971,4897
gen.XM_038030,2855
gen.XM_038049,2864
gen.XM_038063,2866
gen.XM_038098,5343
gen.XM_038146,5339
gen.XM_038221,1695
gen.XM_038243,1341
gen.XM_038308,3737

gen.XM_038371,3902
gen.XM_038391,2757
gen.XM_038424,5018
gen.XM_038536,2909
gen.XM_038576,734
gen.XM_038584,6019
gen.XM_038659,3533
gen.XM_038791,3841
gen.XM_038852,244
gen.XM_038872,5062
gen.XM_038911,237
gen.XM_038946,1840
gen.XM_039165,1413
gen.XM_039173,1416
gen.XM_039176,1417
gen.XM_039225,4125
gen.XM_039236,6047
gen.XM_039248,6051
gen.XM_039306,4551
gen.XM_039339,6060
gen.XM_039372,6065
gen.XM_039395,3732
gen.XM_039474,4794
gen.XM_039654,2646
gen.XM_039702,4200
gen.XM_039712,716
gen.XM_039721,321
gen.XM_039723,5140
gen.XM_039796,1292
gen.XM_039805,1258
gen.XM_039908,5598
gen.XM_039910,4721
gen.XM_039921,4732
gen.XM_039952,1213
gen.XM_039975,1783
gen.XM_040009,377
gen.XM_040066,6088
gen.XM_040095,6091
gen.XM_040221,3707
gen.XM_040267,2879
gen.XM_040272,2876
gen.XM_040321,1524
gen.XM_040498,2417
gen.XM_040623,2074
gen.XM_040644,3734
gen.XM_040709,315
gen.XM_040752,1493
gen.XM_040853,2218
gen.XM_040898,4100
gen.XM_040942,4094
gen.XM_040952,4090
gen.XM_041014,4086
gen.XM_041020,2697
gen.XM_041059,1670
gen.XM_041100,3503
gen.XM_041209,3925

gen.XM_041211,1161
gen.XM_041221,1410
gen.XM_041235,4008
gen.XM_041248,6111
gen.XM_041473,3928
gen.XM_041484,3944
gen.XM_041507,1147
gen.XM_041583,4957
gen.XM_041678,5027
gen.XM_041694,1614
gen.XM_041712,1592
gen.XM_041872,5090
gen.XM_041879,353
gen.XM_041884,354
gen.XM_041921,6304
gen.XM_041964,4680
gen.XM_042018,5095
gen.XM_042025,1600
gen.XM_042153,6348
gen.XM_042155,6346
gen.XM_042168,1286
gen.XM_042301,1474
gen.XM_042326,1032
gen.XM_042422,2145
gen.XM_042473,2148
gen.XM_042618,1229
gen.XM_042621,4596
gen.XM_042658,2561
gen.XM_042695,1364
gen.XM_042698,4710
gen.XM_042765,5701
gen.XM_042781,2434
gen.XM_042788,2744
gen.XM_042841,1072
gen.XM_042852,3339
gen.XM_042860,1070
gen.XM_042963,6295
gen.XM_042967,537
gen.XM_042968,6297
gen.XM_043047,4577
gen.XM_043173,866
gen.XM_043220,3111
gen.XM_043340,1805
gen.XM_043388,1808
gen.XM_043589,2998
gen.XM_043605,2999
gen.XM_043614,6099
gen.XM_043643,6250
gen.XM_043771,1568
gen.XM_044075,416
gen.XM_044077,391
gen.XM_044127,398
gen.XM_044128,408
gen.XM_044166,406
gen.XM_044172,411
gen.XM_044334,3859

gen.XM_044354,2968
gen.XM_044367,4938
gen.XM_044372,4943
gen.XM_044376,4935
gen.XM_044394,4927
gen.XM_044426,4924
gen.XM_044523,4304
gen.XM_044533,4307
gen.XM_044565,4269
gen.XM_044569,4272
gen.XM_044593,4278
gen.XM_044608,5213
gen.XM_044619,5210
gen.XM_044627,2563
gen.XM_044866,2139
gen.XM_044914,5658
gen.XM_044915,5660
gen.XM_044932,3129
gen.XM_044957,3131
gen.XM_045010,3821
gen.XM_045044,4749
gen.XM_045104,4989
gen.XM_045140,2973
gen.XM_045151,5226
gen.XM_045170,928
gen.XM_045183,4651
gen.XM_045187,3833
gen.XM_045283,757
gen.XM_045290,1214
gen.XM_045296,2759
gen.XM_045401,2403
gen.XM_045418,5667
gen.XM_045451,5671
gen.XM_045460,5674
gen.XM_045499,3276
gen.XM_045525,3278
gen.XM_045535,4751
gen.XM_045551,4752
gen.XM_045581,4996
gen.XM_045602,3856
gen.XM_045612,3273
gen.XM_045613,3271
gen.XM_045642,3269
gen.XM_045667,3074
gen.XM_045681,4287
gen.XM_045750,3157
gen.XM_045802,3826
gen.XM_045856,2407
gen.XM_045901,4852
gen.XM_045952,2413
gen.XM_045963,3834
gen.XM_046001,2414
gen.XM_046035,4453
gen.XM_046041,3726
gen.XM_046057,1443
gen.XM_046090,5423

gen.XM_046160,5708
gen.XM_046179,5710
gen.XM_046313,5544
gen.XM_046349,187
gen.XM_046401,1085
gen.XM_046419,5578
gen.XM_046450,201
gen.XM_046464,522
gen.XM_046472,5004
gen.XM_046481,4999
gen.XM_046520,5689
gen.XM_046551,212
gen.XM_046557,208
gen.XM_046565,204
gen.XM_046642,3951
gen.XM_046648,3950
gen.XM_046651,3949
gen.XM_046743,3035
gen.XM_046765,5020
gen.XM_046767,5022
gen.XM_046769,5021
gen.XM_046822,5150
gen.XM_046836,2722
gen.XM_046863,2720
gen.XM_046918,112
gen.XM_046932,4958
gen.XM_046934,5160
gen.XM_047007,5723
gen.XM_047011,5725
gen.XM_047018,5727
gen.XM_047024,6177
gen.XM_047032,6176
gen.XM_047083,2521
gen.XM_047175,690
gen.XM_047374,5446
gen.XM_047376,5445
gen.XM_047409,5444
gen.XM_047436,4624
gen.XM_047477,1429
gen.XM_047479,495
gen.XM_047499,610
gen.XM_047525,4632
gen.XM_047545,616
gen.XM_047561,1137
gen.XM_047584,5131
gen.XM_047600,5132
gen.XM_047964,1798
gen.XM_048088,753
gen.XM_048119,4344
gen.XM_048258,5385
gen.XM_048286,3255
gen.XM_048351,5218
gen.XM_048364,5219
gen.XM_048404,6329
gen.XM_048410,6328
gen.XM_048420,6325

gen.XM_048471,5082
gen.XM_048479,2679
gen.XM_048518,2684
gen.XM_048539,2686
gen.XM_048603,3674
gen.XM_048654,4829
gen.XM_048690,1007
gen.XM_048780,57
gen.XM_048859,2881
gen.XM_048905,6306
gen.XM_048943,3640
gen.XM_048957,3931
gen.XM_048991,3642
gen.XM_049048,3652
gen.XM_049108,820
gen.XM_049113,822
gen.XM_049116,818
gen.XM_049141,3586
gen.XM_049148,3581
gen.XM_049150,3659
gen.XM_049197,3161
gen.XM_049201,3772
gen.XM_049211,3771
gen.XM_049226,2623
gen.XM_049237,5391
gen.XM_049247,2618
gen.XM_049282,5223
gen.XM_049310,139
gen.XM_049337,6320
gen.XM_049354,4275
gen.XM_049372,4317
gen.XM_049421,2637
gen.XM_049502,5236
gen.XM_049561,5239
gen.XM_049663,3493
gen.XM_049680,476
gen.XM_049690,483
gen.XM_049742,14
gen.XM_049795,3082
gen.XM_049899,2121
gen.XM_049904,3937
gen.XM_049920,5482
gen.XM_049931,4995
gen.XM_049934,4994
gen.XM_049937,4818
gen.XM_050074,3528
gen.XM_050101,4773
gen.XM_050159,4880
gen.XM_050194,4462
gen.XM_050200,1487
gen.XM_050215,2525
gen.XM_050236,5602
gen.XM_050265,2278
gen.XM_050278,4103
gen.XM_050293,2487
gen.XM_050403,6192

gen.XM_050430,2389
gen.XM_050435,5227
gen.XM_050506,2583
gen.XM_050534,4348
gen.XM_050552,1234
gen.XM_050589,5603
gen.XM_050638,979
gen.XM_050660,5330
gen.XM_050731,2571
gen.XM_050891,984
gen.XM_050962,975
gen.XM_050964,4220
gen.XM_051219,4479
gen.XM_051264,1237
gen.XM_051298,2612
gen.XM_051364,5290
gen.XM_051430,3398
gen.XM_051435,3358
gen.XM_051463,4230
gen.XM_051471,6238
gen.XM_051476,6237
gen.XM_051489,3367
gen.XM_051518,1131
gen.XM_051556,6
gen.XM_051586,5092
gen.XM_051712,4025
gen.XM_051716,3373
gen.XM_051763,4727
gen.XM_051778,4600
gen.XM_051860,4298
gen.XM_051877,515
gen.XM_052113,3378
gen.XM_052310,1060
gen.XM_052313,1535
gen.XM_052336,1477
gen.XM_052460,3714
gen.XM_052474,3719
gen.XM_052530,1424
gen.XM_052542,3755
gen.XM_052626,1398
gen.XM_052635,5166
gen.XM_052641,3769
gen.XM_052661,5168
gen.XM_052721,2056
gen.XM_052725,2784
gen.XM_052786,3153
gen.XM_052862,3404
gen.XM_052893,3825
gen.XM_052974,608
gen.XM_052989,817
gen.XM_053074,5430
gen.XM_053122,1363
gen.XM_053164,3641
gen.XM_053183,58
gen.XM_053206,2875
gen.XM_053245,400

gen.XM_053323, 1078
gen.XM_053585, 4252
gen.XM_053633, 544
gen.XM_053712, 1074
gen.XM_053717, 4663
gen.XM_053787, 3283
gen.XM_053796, 3288
gen.XM_053952, 3722
gen.XM_053955, 1859
gen.XM_054038, 4832
gen.XM_054098, 6183
gen.XM_054221, 6155
gen.XM_054344, 4973
gen.XM_054474, 2933
gen.XM_054475, 2935
gen.XM_054520, 1047
gen.XM_054566, 5926
gen.XM_054706, 2146
gen.XM_054752, 2849
gen.XM_054763, 2852
gen.XM_054856, 3193
gen.XM_054868, 228
gen.XM_054900, 4309
gen.XM_054978, 295
gen.XM_055013, 3853
gen.XM_055061, 4826
gen.XM_055132, 4514
gen.XM_055195, 4427
gen.XM_055199, 4942
gen.XM_055230, 5336
gen.XM_055254, 954
gen.XM_055369, 3397
gen.XM_055481, 251
gen.XM_055551, 1461
gen.XM_055573, 3086
gen.XM_055641, 2064
gen.XM_055658, 5592
gen.XM_055686, 5163
gen.XM_055771, 4505
gen.XM_055859, 5483
gen.XM_055880, 583
gen.XM_055993, 5646
gen.XM_056035, 5678
gen.XM_056082, 4648
gen.XM_056260, 4438
gen.XM_056286, 5582
gen.XM_056315, 1723
gen.XM_056317, 4077
gen.XM_056346, 3645
gen.XM_056353, 3662
gen.XM_056421, 5175
gen.XM_056481, 3545
gen.XM_056602, 5408
gen.XM_056681, 3700
gen.XM_056730, 4775
gen.XM_056884, 618

gen.XM_056923, 521
gen.XM_056957, 1471
gen.XM_056963, 1793
gen.XM_056970, 628
gen.XM_056996, 3798
gen.XM_057020, 4257
gen.XM_057074, 5260
gen.XM_057150, 4619
gen.XM_057236, 5756
gen.XM_057374, 5793
gen.XM_057492, 1548
gen.XM_057664, 740
gen.XM_057780, 2557
gen.XM_057994, 1541
gen.XM_058039, 1934
gen.XM_058098, 986
gen.XM_058116, 4526
gen.XM_058125, 5635
gen.XM_058210, 4018
gen.XM_058232, 5225
gen.XM_058240, 102
gen.XM_058247, 466
gen.XM_058266, 2144
gen.XM_058267, 1278
gen.XM_058343, 3020
gen.XM_058361, 3078
gen.XM_058405, 552
gen.XM_058406, 3084
gen.XM_058414, 3159
gen.XM_058450, 3352
gen.XM_058505, 3125
gen.XM_058528, 3671
gen.XM_058556, 3773
gen.XM_058567, 3504
gen.XM_058574, 3454
gen.XM_058602, 3022
gen.XM_058611, 3926
gen.XM_058618, 4091
gen.XM_058636, 4118
gen.XM_058646, 3986
gen.XM_058647, 3978
gen.XM_058677, 4061
gen.XM_058684, 4186
gen.XM_058699, 4250
gen.XM_058702, 294
gen.XM_058739, 4621
gen.XM_058745, 4543
gen.XM_058784, 4404
gen.XM_058796, 4337
gen.XM_058830, 4803
gen.XM_058867, 4755
gen.XM_058900, 4730
gen.XM_058918, 5949
gen.XM_058927, 1441
gen.XM_058949, 5463
gen.XM_058967, 5295

gen.XM_058968,2619
gen.XM_058977,3920
gen.XM_058987,5570
gen.XM_058990,5584
gen.XM_058991,5552
gen.XM_059045,5419
gen.XM_059052,5447
gen.XM_059066,114
gen.XM_059067,120
gen.XM_059088,130
gen.XM_059094,465
gen.XM_059117,103
gen.XM_059120,562
gen.XM_059133,224
gen.XM_059171,171
gen.XM_059180,256
gen.XM_059191,492
gen.XM_059201,1
gen.XM_059210,330
gen.XM_059214,185
gen.XM_059230,55
gen.XM_059268,5675
gen.XM_059321,5607
gen.XM_059335,6013
gen.XM_059351,920
gen.XM_059368,653
gen.XM_059372,1029
gen.XM_059422,968
gen.XM_059461,971
gen.XM_059465,907
gen.XM_059516,1266
gen.XM_059557,1068
gen.XM_059561,1059
gen.XM_059583,1252
gen.XM_059593,1434
gen.XM_059623,1519
gen.XM_059628,1442
gen.XM_059633,1469
gen.XM_059637,2804
gen.XM_059653,1596
gen.XM_059669,1617
gen.XM_059709,1604
gen.XM_059720,2914
gen.XM_059741,2118
gen.XM_059745,2131
gen.XM_059773,2141
gen.XM_059776,2062
gen.XM_059801,1939
gen.XM_059839,2430
gen.XM_059876,2282
gen.XM_059933,2531
gen.XM_059945,2838
gen.XM_059961,2859
gen.XM_059966,2871
gen.XM_059979,2644
gen.XM_059986,2813

gen.XM_059998,2673
gen.XM_060006,2647
gen.XM_060012,4115
gen.XM_060030,6146
gen.XM_060042,4281
gen.XM_060067,1499
gen.XM_060331,509
gen.XM_060517,531
gen.XM_060976,2885
gen.XM_061125,2931
gen.XM_061126,2930
gen.XM_062437,3775
gen.XM_063639,4234
gen.XM_064091,4597
gen.XM_065884,777
gen.XM_066291,5998
gen.XM_066900,6261
gen.XM_067264,1240
gen.XM_067325,5030
gen.XM_067715,1169
gen.XM_068164,1497
gen.XM_068395,1789
gen.XM_068853,1714
gen.XM_068919,2085
gen.XM_068963,2072
gen.XM_070188,2480
gen.XM_070203,2473
gen.XM_070873,2742
gen.XM_071178,2705
gen.XM_071580,1557
gen.XM_071605,2381
gen.XM_071623,1439
gen.XM_071801,4122
gen.XM_071873,4630
gen.XM_071937,2152
gen.XM_072173,5876
gen.XM_072430,2387
gen.XM_072526,2857
gen.XM_076414,1199
gen.XM_083842,3026
gen.XM_083852,3141
gen.XM_083864,3774
gen.XM_083866,3715
gen.XM_083868,3590
gen.XM_083892,3787
gen.XM_083939,4364
gen.XM_083966,4923
gen.XM_083983,4881
gen.XM_084007,5055
gen.XM_084014,5246
gen.XM_084023,5528
gen.XM_084026,5549
gen.XM_084055,580
gen.XM_084084,6090
gen.XM_084110,1340
gen.XM_084111,1243

gen.XM_084120,1315
gen.XM_084123,1263
gen.XM_084129,1231
gen.XM_084141,1041
gen.XM_084158,1465
gen.XM_084168,1547
gen.XM_084179,1591
gen.XM_084180,1781
gen.XM_084204,2079
gen.XM_084238,2453
gen.XM_084241,2337
gen.XM_084270,2851
gen.XM_084283,6229
gen.XM_084287,6203
gen.XM_084288,6153
gen.XM_084296,6227
gen.XM_084311,6350
gen.XM_084359,3073
gen.XM_084372,3016
gen.XM_084385,2944
gen.XM_084413,3028
gen.XM_084420,2910
gen.XM_084429,2911
gen.XM_084450,2942
gen.XM_084451,2953
gen.XM_084467,2994
gen.XM_084477,3010
gen.XM_084480,3012
gen.XM_084505,3080
gen.XM_084514,3180
gen.XM_084515,3183
gen.XM_084516,3182
gen.XM_084517,3184
gen.XM_084522,3424
gen.XM_084525,3428
gen.XM_084527,3169
gen.XM_084570,3357
gen.XM_084601,3353
gen.XM_084610,3350
gen.XM_084632,3072
gen.XM_084645,3731
gen.XM_084654,3388
gen.XM_084658,3382
gen.XM_084681,3195
gen.XM_084702,3287
gen.XM_084739,3124
gen.XM_084742,3122
gen.XM_084770,3515
gen.XM_084789,3599
gen.XM_084800,3783
gen.XM_084801,3672
gen.XM_084807,3531
gen.XM_084808,3818
gen.XM_084824,3630
gen.XM_084841,3540
gen.XM_084866,3557

gen.XM_084884,3583
gen.XM_084885,3582
gen.XM_084889,3814
gen.XM_084901,3488
gen.XM_084909,3702
gen.XM_084912,3705
gen.XM_084918,3500
gen.XM_084922,3495
gen.XM_084941,3788
gen.XM_084946,3800
gen.XM_084948,3804
gen.XM_084982,3870
gen.XM_084997,3933
gen.XM_084998,2142
gen.XM_085017,3893
gen.XM_085044,3916
gen.XM_085065,4044
gen.XM_085066,4033
gen.XM_085068,1480
gen.XM_085106,3987
gen.XM_085125,4031
gen.XM_085127,4014
gen.XM_085141,4019
gen.XM_085151,4050
gen.XM_085162,4054
gen.XM_085166,3955
gen.XM_085203,4130
gen.XM_085204,4132
gen.XM_085215,4282
gen.XM_085239,4254
gen.XM_085249,4236
gen.XM_085262,4314
gen.XM_085280,4289
gen.XM_085283,4211
gen.XM_085307,4160
gen.XM_085327,4622
gen.XM_085340,4448
gen.XM_085393,4480
gen.XM_085395,4482
gen.XM_085408,4637
gen.XM_085434,4524
gen.XM_085442,4513
gen.XM_085445,4425
gen.XM_085452,4435
gen.XM_085471,4558
gen.XM_085475,4561
gen.XM_085483,4616
gen.XM_085525,4323
gen.XM_085531,4977
gen.XM_085545,4741
gen.XM_085548,4735
gen.XM_085563,4991
gen.XM_085581,472
gen.XM_085589,4948
gen.XM_085613,4724
gen.XM_085627,4951

gen.XM_085636,4873
gen.XM_085672,4757
gen.XM_085687,4659
gen.XM_085691,4677
gen.XM_085716,4992
gen.XM_085722,4745
gen.XM_085735,5019
gen.XM_085743,4718
gen.XM_085775,5058
gen.XM_085779,5075
gen.XM_085788,5049
gen.XM_085789,5043
gen.XM_085790,5045
gen.XM_085791,5042
gen.XM_085856,5501
gen.XM_085862,5244
gen.XM_085874,5460
gen.XM_085875,5461
gen.XM_085876,5462
gen.XM_085909,5297
gen.XM_085916,5285
gen.XM_085917,5276
gen.XM_085927,5527
gen.XM_085928,5489
gen.XM_085934,5537
gen.XM_085935,5573
gen.XM_085950,5487
gen.XM_085971,5371
gen.XM_085972,5629
gen.XM_085981,4599
gen.XM_085986,5398
gen.XM_086004,5425
gen.XM_086074,5311
gen.XM_086101,5128
gen.XM_086102,5130
gen.XM_086116,5331
gen.XM_086132,304
gen.XM_086138,282
gen.XM_086142,557
gen.XM_086151,46
gen.XM_086164,277
gen.XM_086165,279
gen.XM_086166,281
gen.XM_086167,280
gen.XM_086178,4
gen.XM_086180,19
gen.XM_086204,38
gen.XM_086228,1356
gen.XM_086244,601
gen.XM_086245,602
gen.XM_086257,632
gen.XM_086271,383
gen.XM_086278,4434
gen.XM_086282,543
gen.XM_086296,331
gen.XM_086324,214

gen.XM_086328,542
gen.XM_086343,265
gen.XM_086357,85
gen.XM_086360,29
gen.XM_086375,97
gen.XM_086378,485
gen.XM_086381,479
gen.XM_086384,178
gen.XM_086389,243
gen.XM_086391,231
gen.XM_086397,323
gen.XM_086400,366
gen.XM_086428,2161
gen.XM_086431,589
gen.XM_086432,592
gen.XM_086444,136
gen.XM_086481,490
gen.XM_086484,494
gen.XM_086485,493
gen.XM_086494,538
gen.XM_086515,324
gen.XM_086518,317
gen.XM_086543,190
gen.XM_086552,432
gen.XM_086564,388
gen.XM_086567,430
gen.XM_086586,52
gen.XM_086587,54
gen.XM_086648,5819
gen.XM_086701,5687
gen.XM_086710,5670
gen.XM_086715,5695
gen.XM_086736,5717
gen.XM_086745,5712
gen.XM_086759,5877
gen.XM_086760,5878
gen.XM_086770,5914
gen.XM_086773,5928
gen.XM_086777,5930
gen.XM_086779,5064
gen.XM_086805,5963
gen.XM_086809,5953
gen.XM_086821,5985
gen.XM_086830,6043
gen.XM_086844,6074
gen.XM_086873,5964
gen.XM_086875,6093
gen.XM_086920,805
gen.XM_086923,849
gen.XM_086925,850
gen.XM_086944,933
gen.XM_086950,858
gen.XM_086961,926
gen.XM_086980,791
gen.XM_087028,942
gen.XM_087038,2803

gen.XM_087040, 842
gen.XM_087041, 2800
gen.XM_087045, 932
gen.XM_087051, 748
gen.XM_087061, 912
gen.XM_087062, 914
gen.XM_087068, 775
gen.XM_087069, 772
gen.XM_087118, 891
gen.XM_087122, 839
gen.XM_087151, 683
gen.XM_087162, 985
gen.XM_087166, 993
gen.XM_087181, 965
gen.XM_087193, 726
gen.XM_087195, 725
gen.XM_087206, 669
gen.XM_087211, 743
gen.XM_087218, 1011
gen.XM_087240, 901
gen.XM_087254, 1302
gen.XM_087268, 1203
gen.XM_087278, 1358
gen.XM_087284, 1075
gen.XM_087289, 1323
gen.XM_087295, 1322
gen.XM_087297, 1360
gen.XM_087322, 1312
gen.XM_087331, 1211
gen.XM_087341, 1267
gen.XM_087342, 1265
gen.XM_087346, 1115
gen.XM_087349, 1106
gen.XM_087359, 1343
gen.XM_087370, 1101
gen.XM_087392, 1333
gen.XM_087410, 1347
gen.XM_087448, 1184
gen.XM_087480, 3000
gen.XM_087498, 1463
gen.XM_087514, 1483
gen.XM_087527, 1455
gen.XM_087583, 1418
gen.XM_087588, 1120
gen.XM_087597, 1549
gen.XM_087599, 1551
gen.XM_087600, 1553
gen.XM_087601, 1550
gen.XM_087610, 1597
gen.XM_087611, 1595
gen.XM_087614, 1564
gen.XM_087621, 1711
gen.XM_087635, 1660
gen.XM_087637, 1662
gen.XM_087652, 1713
gen.XM_087659, 1537

gen.XM_087686, 1543
gen.XM_087710, 3247
gen.XM_087713, 1559
gen.XM_087745, 1656
gen.XM_087773, 1816
gen.XM_087790, 1631
gen.XM_087823, 1858
gen.XM_087834, 2123
gen.XM_087836, 2124
gen.XM_087853, 2090
gen.XM_087855, 2089
gen.XM_087939, 2000
gen.XM_087945, 1990
gen.XM_087955, 3857
gen.XM_087960, 1883
gen.XM_087990, 1936
gen.XM_087991, 2154
gen.XM_088009, 3106
gen.XM_088020, 1621
gen.XM_088073, 2386
gen.XM_088099, 2416
gen.XM_088103, 2418
gen.XM_088105, 2409
gen.XM_088107, 605
gen.XM_088119, 2422
gen.XM_088122, 2420
gen.XM_088135, 2446
gen.XM_088180, 2352
gen.XM_088239, 2297
gen.XM_088264, 2195
gen.XM_088294, 2529
gen.XM_088316, 2611
gen.XM_088321, 2628
gen.XM_088323, 2574
gen.XM_088325, 2572
gen.XM_088336, 2519
gen.XM_088338, 2515
gen.XM_088370, 2613
gen.XM_088399, 2559
gen.XM_088401, 2560
gen.XM_088422, 2839
gen.XM_088426, 2833
gen.XM_088459, 2847
gen.XM_088461, 2870
gen.XM_088472, 1472
gen.XM_088550, 2640
gen.XM_088552, 2641
gen.XM_088553, 2642
gen.XM_088563, 2672
gen.XM_088569, 2748
gen.XM_088571, 2750
gen.XM_088587, 4120
gen.XM_088588, 4114
gen.XM_088589, 4121
gen.XM_088592, 6311
gen.XM_088619, 6151

gen.XM_088622,6152
gen.XM_088630,6209
gen.XM_088637,2700
gen.XM_088638,768
gen.XM_088665,6158
gen.XM_088688,6220
gen.XM_088689,6218
gen.XM_088710,6253
gen.XM_088736,6265
gen.XM_088738,6267
gen.XM_088739,6268
gen.XM_088745,6289
gen.XM_088747,6128
gen.XM_088788,338
gen.XM_088863,286
gen.XM_088945,507
gen.XM_089030,622
gen.XM_089138,254
gen.XM_089514,3019
gen.XM_089551,3006
gen.XM_090218,3542
gen.XM_090413,3779
gen.XM_090458,3767
gen.XM_090833,638
gen.XM_090914,4082
gen.XM_090991,4191
gen.XM_091076,1091
gen.XM_091100,4263
gen.XM_091108,4124
gen.XM_091159,4157
gen.XM_091270,4483
gen.XM_091399,4590
gen.XM_091420,4544
gen.XM_091786,3426
gen.XM_091886,5595
gen.XM_091938,5221
gen.XM_091981,5586
gen.XM_091984,5396
gen.XM_092042,5108
gen.XM_092046,5341
gen.XM_092049,5380
gen.XM_092135,672
gen.XM_092158,918
gen.XM_092346,944
gen.XM_092489,867
gen.XM_092517,676
gen.XM_092545,970
gen.XM_092760,5696
gen.XM_092888,5986
gen.XM_092966,6113
gen.XM_093050,6212
gen.XM_093130,6226
gen.XM_093219,6299
gen.XM_093241,6228
gen.XM_093423,1308
gen.XM_093487,1255

gen.XM_093546,1201
gen.XM_093624,1083
gen.XM_094243,1797
gen.XM_094440,1561
gen.XM_094741,1862
gen.XM_094855,2060
gen.XM_095146,2432
gen.XM_095371,2475
gen.XM_095545,2514
gen.XM_095667,2554
gen.XM_096038,3699
gen.XM_096060,4241
gen.XM_096146,3539
gen.XM_096149,661
gen.XM_096155,5967
gen.XM_096156,5968
gen.XM_096169,1022
gen.XM_096172,787
gen.XM_096195,1190
gen.XM_096198,1117
gen.XM_096203,1464
gen.XM_096303,6256
gen.XM_096486,3315
gen.XM_096520,3165
gen.XM_096544,3119
gen.XM_096566,3680
gen.XM_096572,3819
gen.XM_096597,3739
gen.XM_096606,3608
gen.XM_096620,3578
gen.XM_096630,3486
gen.XM_096661,3441
gen.XM_096744,4034
gen.XM_096772,3966
gen.XM_096842,4245
gen.XM_096844,4286
gen.XM_097043,4984
gen.XM_097193,5001
gen.XM_097195,5000
gen.XM_097204,4754
gen.XM_097232,5048
gen.XM_097274,5510
gen.XM_097275,5521
gen.XM_097300,5222
gen.XM_097365,5440
gen.XM_097420,5134
gen.XM_097453,2068
gen.XM_097519,561
gen.XM_097565,249
gen.XM_097639,352
gen.XM_097649,198
gen.XM_097713,5800
gen.XM_097727,5773
gen.XM_097731,5795
gen.XM_097749,5644
gen.XM_097772,5731

gen.XM_097807,5929
gen.XM_097817,5925
gen.XM_097833,5950
gen.XM_097886,5971
gen.XM_097976,715
gen.XM_098004,729
gen.XM_098047,962
gen.XM_098048,960
gen.XM_098109,1345
gen.XM_098111,1245
gen.XM_098154,1232
gen.XM_098158,1103
gen.XM_098173,1227
gen.XM_098248,1384
gen.XM_098351,1609
gen.XM_098352,1611
gen.XM_098354,1610
gen.XM_098362,1634
gen.XM_098387,1778
gen.XM_098405,1534
gen.XM_098468,2108
gen.XM_098599,619
gen.XM_098654,2447
gen.XM_098669,2466
gen.XM_098747,2582
gen.XM_098761,2564
gen.XM_098913,2843
gen.XM_098943,2725
gen.XM_098995,6302
gen.XM_099467,363
gen.XM_102377,4432
gen.XM_103946,665
gen.XM_104983,6263
gen.XM_105236,1289
gen.XM_105658,1325
gen.XM_106246,1520
gen.XM_106739,1562
gen.XM_107825,2225
gen.XM_109162,3075
gen.XM_113223,3268
gen.XM_113224,3275
gen.XM_113226,3400
gen.XM_113229,3366
gen.XM_113230,3363
gen.XM_113238,3152
gen.XM_113266,4202
gen.XM_113268,4207
gen.XM_113291,4429
gen.XM_113293,4467
gen.XM_113299,4504
gen.XM_113303,5013
gen.XM_113310,4723
gen.XM_113315,4944
gen.XM_113324,4674
gen.XM_113325,4703
gen.XM_113328,4695

gen.XM_113330,5011
gen.XM_113334,4819
gen.XM_113343,5028
gen.XM_113348,5316
gen.XM_113352,5294
gen.XM_113360,386
gen.XM_113361,598
gen.XM_113369,361
gen.XM_113374,140
gen.XM_113379,473
gen.XM_113380,5749
gen.XM_113390,929
gen.XM_113395,1193
gen.XM_113397,1244
gen.XM_113405,1140
gen.XM_113408,1296
gen.XM_113409,1202
gen.XM_113410,1088
gen.XM_113417,1254
gen.XM_113422,1329
gen.XM_113425,1452
gen.XM_113452,1556
gen.XM_113454,1841
gen.XM_113463,1654
gen.XM_113467,1720
gen.XM_113468,1845
gen.XM_113476,1860
gen.XM_113531,2526
gen.XM_113532,2627
gen.XM_113540,2548
gen.XM_113557,2493
gen.XM_113564,2846
gen.XM_113585,6122
gen.XM_113615,2927
gen.XM_113702,3862
gen.XM_113712,3635
gen.XM_113719,3560
gen.XM_113726,3584
gen.XM_113730,3519
gen.XM_113737,3855
gen.XM_113739,3437
gen.XM_113752,3946
gen.XM_113759,4105
gen.XM_113823,4163
gen.XM_113836,4326
gen.XM_113840,4608
gen.XM_113843,4420
gen.XM_113845,4418
gen.XM_113853,4570
gen.XM_113855,4560
gen.XM_113874,4431
gen.XM_113876,4426
gen.XM_113882,4640
gen.XM_113892,4978
gen.XM_113901,4653
gen.XM_113919,4905

gen.XM_113929,4696
gen.XM_113931,4706
gen.XM_113938,4824
gen.XM_113943,5010
gen.XM_113945,4998
gen.XM_113951,4962
gen.XM_113988,5229
gen.XM_114004,5349
gen.XM_114018,5097
gen.XM_114024,5560
gen.XM_114025,5530
gen.XM_114027,5366
gen.XM_114030,560
gen.XM_114044,129
gen.XM_114055,384
gen.XM_114062,3
gen.XM_114097,376
gen.XM_114098,360
gen.XM_114109,525
gen.XM_114125,259
gen.XM_114137,634
gen.XM_114153,484
gen.XM_114154,5875
gen.XM_114163,5794
gen.XM_114165,5813
gen.XM_114174,5673
gen.XM_114178,5706
gen.XM_114185,5889
gen.XM_114209,6024
gen.XM_114215,816
gen.XM_114229,838
gen.XM_114247,824
gen.XM_114266,851
gen.XM_114267,856
gen.XM_114298,957
gen.XM_114301,1225
gen.XM_114309,1242
gen.XM_114323,1141
gen.XM_114328,1344
gen.XM_114356,1288
gen.XM_114364,1122
gen.XM_114368,1510
gen.XM_114401,1496
gen.XM_114424,1473
gen.XM_114426,1470
gen.XM_114434,1555
gen.XM_114435,1552
gen.XM_114437,1567
gen.XM_114439,1586
gen.XM_114440,1587
gen.XM_114442,1584
gen.XM_114453,1819
gen.XM_114457,1817
gen.XM_114469,1623
gen.XM_114482,1683
gen.XM_114492,2106

gen.XM_114497,2058
gen.XM_114555,2429
gen.XM_114578,2444
gen.XM_114602,2404
gen.XM_114613,2625
gen.XM_114617,2517
gen.XM_114618,2523
gen.XM_114640,2556
gen.XM_114646,2756
gen.XM_114649,2873
gen.XM_114655,2854
gen.XM_114661,2677
gen.XM_114662,2688
gen.XM_114669,2845
gen.XM_114677,2802
gen.XM_114678,2801
gen.XM_114679,2799
gen.XM_114686,2699
gen.XM_114692,6354
gen.XM_114708,6291
gen.XM_114720,6130
gen.XM_114724,6119
gen.XM_114798,233
gen.XM_114862,3104
gen.XM_114894,2977
gen.XM_114981,3139
gen.XM_115031,3286
gen.XM_115062,3364
gen.XM_115063,3365
gen.XM_115081,3177
gen.XM_115117,3570
gen.XM_115140,3634
gen.XM_115197,3809
gen.XM_115215,3948
gen.XM_115352,4333
gen.XM_115480,4910
gen.XM_115603,5466
gen.XM_115615,5395
gen.XM_115672,869
gen.XM_115706,1039
gen.XM_115722,1040
gen.XM_115825,1002
gen.XM_115846,5691
gen.XM_115874,6281
gen.XM_115886,6131
gen.XM_115890,6136
gen.XM_115923,6259
gen.XM_115924,6121
gen.XM_116034,1338
gen.XM_116058,1295
gen.XM_116071,1204
gen.XM_116072,1205
gen.XM_116204,1532
gen.XM_116205,1533
gen.XM_116247,1484
gen.XM_116285,1408

gen.XM_116307,1691
gen.XM_116340,1807
gen.XM_116365,1856
gen.XM_116427,1648
gen.XM_116439,1593
gen.XM_116447,1606
gen.XM_116465,1716
gen.XM_116511,1857
gen.XM_116514,1861
gen.XM_116524,2140
gen.XM_116806,2789
gen.XM_116818,2738
gen.XM_116853,1139
gen.XM_116856,1810
gen.XM_116863,2975
gen.XM_116913,3845
gen.XM_116926,3451
gen.XM_117061,4913
gen.XM_117066,4768
gen.XM_117096,5084
gen.XM_117118,5379
gen.XM_117122,5183
gen.XM_117128,5605
gen.XM_117159,2
gen.XM_117181,534
gen.XM_117184,163
gen.XM_117185,582
gen.XM_117196,641
gen.XM_117209,5688
gen.XM_117264,736
gen.XM_117311,1337
gen.XM_117351,1412
gen.XM_117387,1622
gen.XM_117398,1641
gen.XM_117444,2471
gen.XM_117449,2160
gen.XM_117452,2472
gen.XM_117481,2406
gen.XM_117487,2622
gen.XM_117519,2874
gen.XM_117539,6352
gen.XM_117555,6349
gen.XM_117692,28
gen.XM_118637,4251
gen.XM_165390,3427
gen.XM_165410,4583
gen.XM_165411,4413
gen.XM_165418,4713
gen.XM_165421,4701
gen.XM_165422,4704
gen.XM_165432,5541
gen.XM_165438,144
gen.XM_165439,620
gen.XM_165442,59
gen.XM_165443,477
gen.XM_165448,723

gen.XM_165451,1268
gen.XM_165465,1531
gen.XM_165470,1528
gen.XM_165473,1482
gen.XM_165483,1818
gen.XM_165484,1820
gen.XM_165488,1615
gen.XM_165499,2057
gen.XM_165514,2579
gen.XM_165530,6355
gen.XM_165533,6235
gen.XM_165551,2913
gen.XM_165555,2889
gen.XM_165557,2897
gen.XM_165560,2925
gen.XM_165563,2926
gen.XM_165567,2921
gen.XM_165571,3407
gen.XM_165584,3414
gen.XM_165586,3413
gen.XM_165592,3401
gen.XM_165598,3303
gen.XM_165600,3310
gen.XM_165610,3222
gen.XM_165611,3217
gen.XM_165612,3223
gen.XM_165616,3325
gen.XM_165627,3335
gen.XM_165628,3341
gen.XM_165631,3328
gen.XM_165636,3903
gen.XM_165639,3917
gen.XM_165645,4534
gen.XM_165647,4528
gen.XM_165648,4537
gen.XM_165649,4527
gen.XM_165656,4484
gen.XM_165657,4493
gen.XM_165658,4489
gen.XM_165669,2091
gen.XM_165692,2159
gen.XM_165698,1949
gen.XM_165717,1954
gen.XM_165728,2036
gen.XM_165738,1999
gen.XM_165740,1865
gen.XM_165743,1937
gen.XM_165747,1948
gen.XM_165749,2037
gen.XM_165758,2013
gen.XM_165764,2011
gen.XM_165765,1988
gen.XM_165770,1951
gen.XM_165771,1983
gen.XM_165772,1876
gen.XM_165777,2044

gen.XM_165794,1921
gen.XM_165799,2006
gen.XM_165801,1956
gen.XM_165809,2016
gen.XM_165836,2350
gen.XM_165839,2346
gen.XM_165841,2197
gen.XM_165860,2167
gen.XM_165867,2249
gen.XM_165870,2245
gen.XM_165872,2253
gen.XM_165876,2258
gen.XM_165877,2240
gen.XM_165882,2248
gen.XM_165888,2934
gen.XM_165890,2929
gen.XM_165891,2941
gen.XM_165903,3633
gen.XM_165905,3579
gen.XM_165906,3532
gen.XM_165910,3465
gen.XM_165921,4127
gen.XM_165923,4325
gen.XM_165954,5026
gen.XM_165960,5347
gen.XM_165963,5367
gen.XM_165975,327
gen.XM_165976,373
gen.XM_165977,264
gen.XM_165978,532
gen.XM_165981,290
gen.XM_165983,275
gen.XM_165984,175
gen.XM_165994,927
gen.XM_165998,893
gen.XM_166007,910
gen.XM_166008,900
gen.XM_166011,1121
gen.XM_166014,1275
gen.XM_166015,1192
gen.XM_166017,1350
gen.XM_166026,1669
gen.XM_166027,1663
gen.XM_166028,1842
gen.XM_166029,1802
gen.XM_166037,1612
gen.XM_166042,2054
gen.XM_166049,2147
gen.XM_166063,2540
gen.XM_166064,2558
gen.XM_166078,6142
gen.XM_166081,6255
gen.XM_166093,2984
gen.XM_166125,2966
gen.XM_166157,2922
gen.XM_166174,3409

gen.XM_166177,3406
gen.XM_166181,3403
gen.XM_166196,3308
gen.XM_166232,3227
gen.XM_166234,3224
gen.XM_166235,3293
gen.XM_166236,3294
gen.XM_166239,3349
gen.XM_166253,3336
gen.XM_166266,3904
gen.XM_166273,3886
gen.XM_166277,4532
gen.XM_166282,4491
gen.XM_166285,4490
gen.XM_166288,5071
gen.XM_166303,2092
gen.XM_166310,2101
gen.XM_166327,2157
gen.XM_166333,1932
gen.XM_166336,2021
gen.XM_166340,1882
gen.XM_166349,1872
gen.XM_166353,2002
gen.XM_166357,2049
gen.XM_166360,1938
gen.XM_166361,2009
gen.XM_166362,1884
gen.XM_166363,1940
gen.XM_166376,2004
gen.XM_166381,1992
gen.XM_166392,2019
gen.XM_166401,1995
gen.XM_166402,1896
gen.XM_166406,2015
gen.XM_166412,1910
gen.XM_166417,1914
gen.XM_166419,1920
gen.XM_166425,1888
gen.XM_166446,2042
gen.XM_166457,1878
gen.XM_166459,1931
gen.XM_166469,1879
gen.XM_166480,1955
gen.XM_166482,2351
gen.XM_166485,2353
gen.XM_166494,2224
gen.XM_166504,2222
gen.XM_166505,2202
gen.XM_166506,2200
gen.XM_166509,2219
gen.XM_166512,2205
gen.XM_166513,2220
gen.XM_166514,2203
gen.XM_166515,2204
gen.XM_166521,2198
gen.XM_166523,2170

gen.XM_166531,2190
gen.XM_166540,2191
gen.XM_166541,2168
gen.XM_166594,2230
gen.XM_166599,20
gen.XM_166605,3506
gen.XM_166629,2988
gen.XM_166665,2918
gen.XM_166717,2906
gen.XM_166743,3418
gen.XM_167008,5080
gen.XM_167016,2087
gen.XM_167027,2094
gen.XM_167037,2096
gen.XM_167046,2150
gen.XM_167128,2023
gen.XM_167161,2025
gen.XM_167169,1868
gen.XM_167179,2031
gen.XM_167196,2041
gen.XM_167225,2047
gen.XM_167339,2264
gen.XM_167363,5065
gen.XM_167366,1209
gen.XM_167374,2898
gen.XM_167395,2963
gen.XM_167411,2901
gen.XM_167414,2904
gen.XM_167433,3324
gen.XM_167437,3192
gen.XM_167439,3876
gen.XM_167453,4538
gen.XM_167456,4541
gen.XM_167476,2321
gen.XM_167477,2325
gen.XM_167483,2328
gen.XM_167484,2329
gen.XM_167494,2273
gen.XM_167498,2301
gen.XM_167500,2299
gen.XM_167502,2312
gen.XM_167504,2300
gen.XM_167518,3754
gen.XM_167530,5529
gen.XM_167538,5945
gen.XM_167558,2645
gen.XM_167626,2887
gen.XM_167716,3244
gen.XM_167726,3248
gen.XM_167747,3234
gen.XM_167748,3228
gen.XM_167780,3417
gen.XM_167804,3291
gen.XM_167853,3318
gen.XM_167892,3883
gen.XM_167906,3877

gen.XM_167911,3868
gen.XM_167918,3869
gen.XM_168054,2103
gen.XM_168070,1928
gen.XM_168104,1994
gen.XM_168123,1877
gen.XM_168181,2322
gen.XM_168251,2323
gen.XM_168354,2271
gen.XM_168378,2269
gen.XM_168435,2316
gen.XM_168450,2315
gen.XM_168454,2302
gen.XM_168461,2311
gen.XM_168464,2317
gen.XM_168470,2310
gen.XM_168548,2375
gen.XM_168572,2380
gen.XM_168586,2360
gen.XM_169414,3880
gen.XM_169540,5078
gen.XM_170195,2267
gen.XM_170427,2318

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTSI. Definitions

The terms "TAT polypeptide" and "TAT" as used herein and when immediately followed by a numerical designation, refer to various polypeptides, wherein the complete designation (i.e., TAT/number) refers to specific polypeptide sequences as described herein. The terms "TAT/number polypeptide" and "TAT/number" wherein the term "number" is provided as an actual numerical designation as used herein encompass native sequence polypeptides, polypeptide variants and fragments of native sequence polypeptides and polypeptide variants (which are further defined herein). The TAT polypeptides described herein may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods. The term "TAT polypeptide" refers to each individual TAT/number polypeptide disclosed herein. All disclosures in this specification which refer to the "TAT polypeptide" refer to each of the polypeptides individually as well as jointly. For example, descriptions of the preparation of, purification of, derivation of, formation of antibodies to or against, formation of TAT binding oligopeptides to or against, formation of TAT binding organic molecules to or against, administration of, compositions containing, treatment of a disease with, etc., pertain to each polypeptide of the invention individually. The term "TAT polypeptide" also includes variants of the TAT/number polypeptides disclosed herein.

A "native sequence TAT polypeptide" comprises a polypeptide having the same amino acid sequence as the corresponding TAT polypeptide derived from nature. Such native sequence TAT polypeptides can be isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence TAT polypeptide" specifically encompasses naturally-occurring truncated or secreted forms of the specific TAT polypeptide (*e.g.*, an extracellular domain sequence), naturally-occurring variant forms (*e.g.*, alternatively spliced forms) and naturally-occurring allelic variants of the polypeptide. In certain embodiments of the invention, the native sequence TAT polypeptides disclosed herein are mature or full-length native sequence polypeptides comprising the full-length amino acids sequences shown in the accompanying figures. Start and stop codons (if indicated) are shown in bold font and underlined in the figures. Nucleic acid residues indicated as "N" in the accompanying figures are any nucleic acid residue. However, while the TAT polypeptides disclosed in the accompanying figures are shown to begin with methionine residues designated herein as amino acid position 1 in the figures, it is conceivable and possible that other methionine residues located either upstream or downstream from the amino acid position 1 in the figures may be employed as the starting amino acid residue for the TAT polypeptides.

The TAT polypeptide "extracellular domain" or "ECD" refers to a form of the TAT polypeptide which is essentially free of the transmembrane and cytoplasmic domains. Ordinarily, a TAT polypeptide ECD will have less than 1% of such transmembrane and/or cytoplasmic domains and preferably, will have less than 0.5% of such domains. It will be understood that any transmembrane domains identified for the TAT polypeptides of the present invention are identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary but most likely by no more than about 5 amino acids at either end of the domain as initially identified herein. Optionally, therefore, an

extracellular domain of a TAT polypeptide may contain from about 5 or fewer amino acids on either side of the transmembrane domain/extracellular domain boundary as identified in the Examples or specification and such polypeptides, with or without the associated signal peptide, and nucleic acid encoding them, are contemplated by the present invention.

The approximate location of the "signal peptides" of the various TAT polypeptides disclosed herein may be shown in the present specification and/or the accompanying figures. It is noted, however, that the C-terminal boundary of a signal peptide may vary, but most likely by no more than about 5 amino acids on either side of the signal peptide C-terminal boundary as initially identified herein, wherein the C-terminal boundary of the signal peptide may be identified pursuant to criteria routinely employed in the art for identifying that type of amino acid sequence element (e.g., Nielsen et al., Prot. Eng. 10:1-6 (1997) and von Heinje et al., Nucl. Acids. Res. 14:4683-4690 (1986)). Moreover, it is also recognized that, in some cases, cleavage of a signal sequence from a secreted polypeptide is not entirely uniform, resulting in more than one secreted species. These mature polypeptides, where the signal peptide is cleaved within no more than about 5 amino acids on either side of the C-terminal boundary of the signal peptide as identified herein, and the polynucleotides encoding them, are contemplated by the present invention.

"TAT polypeptide variant" means a TAT polypeptide, preferably an active TAT polypeptide, as defined herein having at least about 80% amino acid sequence identity with a full-length native sequence TAT polypeptide sequence as disclosed herein, a TAT polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a TAT polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length TAT polypeptide sequence as disclosed herein (such as those encoded by a nucleic acid that represents only a portion of the complete coding sequence for a full-length TAT polypeptide). Such TAT polypeptide variants include, for instance, TAT polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the full-length native amino acid sequence. Ordinarily, a TAT polypeptide variant will have at least about 80% amino acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% amino acid sequence identity, to a full-length native sequence TAT polypeptide sequence as disclosed herein, a TAT polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a TAT polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length TAT polypeptide sequence as disclosed herein. Ordinarily, TAT variant polypeptides are at least about 10 amino acids in length, alternatively at least about 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600 amino acids in length, or more. Optionally, TAT variant polypeptides will have no more than one conservative amino acid substitution as compared to the native TAT polypeptide sequence, alternatively no more than 2, 3, 4, 5, 6, 7, 8, 9, or 10 conservative amino acid substitution as compared to the native TAT polypeptide sequence.

"Percent (%) amino acid sequence identity" with respect to the TAT polypeptide sequences identified

herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific TAT polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

$$100 \text{ times the fraction } X/Y$$

where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. As examples of % amino acid sequence identity calculations using this method, Tables 2 and 3 demonstrate how to calculate the % amino acid sequence identity of the amino acid sequence designated "Comparison Protein" to the amino acid sequence designated "TAT", wherein "TAT" represents the amino acid sequence of a hypothetical TAT polypeptide of interest, "Comparison Protein" represents the amino acid sequence of a polypeptide against which the "TAT" polypeptide of interest is being compared, and "X", "Y" and "Z" each represent different hypothetical amino acid residues. Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program.

"TAT variant polynucleotide" or "TAT variant nucleic acid sequence" means a nucleic acid molecule

which encodes a TAT polypeptide, preferably an active TAT polypeptide, as defined herein and which has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native sequence TAT polypeptide sequence as disclosed herein, a full-length native sequence TAT polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a TAT polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length TAT polypeptide sequence as disclosed herein (such as those encoded by a nucleic acid that represents only a portion of the complete coding sequence for a full-length TAT polypeptide). Ordinarily, a TAT variant polynucleotide will have at least about 80% nucleic acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% nucleic acid sequence identity with a nucleic acid sequence encoding a full-length native sequence TAT polypeptide sequence as disclosed herein, a full-length native sequence TAT polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a TAT polypeptide, with or without the signal sequence, as disclosed herein or any other fragment of a full-length TAT polypeptide sequence as disclosed herein. Variants do not encompass the native nucleotide sequence.

Ordinarily, TAT variant polynucleotides are at least about 5 nucleotides in length, alternatively at least about 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800, 810, 820, 830, 840, 850, 860, 870, 880, 890, 900, 910, 920, 930, 940, 950, 960, 970, 980, 990, or 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length.

"Percent (%) nucleic acid sequence identity" with respect to TAT-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the TAT nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. For purposes herein, however, % nucleic acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison

parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for nucleic acid sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

$$100 \text{ times the fraction } W/Z$$

where W is the number of nucleotides scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C. As examples of % nucleic acid sequence identity calculations, Tables 4 and 5, demonstrate how to calculate the % nucleic acid sequence identity of the nucleic acid sequence designated "Comparison DNA" to the nucleic acid sequence designated "TAT-DNA", wherein "TAT-DNA" represents a hypothetical TAT-encoding nucleic acid sequence of interest, "Comparison DNA" represents the nucleotide sequence of a nucleic acid molecule against which the "TAT-DNA" nucleic acid molecule of interest is being compared, and "N", "L" and "V" each represent different hypothetical nucleotides. Unless specifically stated otherwise, all % nucleic acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program.

In other embodiments, TAT variant polynucleotides are nucleic acid molecules that encode a TAT polypeptide and which are capable of hybridizing, preferably under stringent hybridization and wash conditions, to nucleotide sequences encoding a full-length TAT polypeptide as disclosed herein. TAT variant polypeptides may be those that are encoded by a TAT variant polynucleotide.

The term "full-length coding region" when used in reference to a nucleic acid encoding a TAT polypeptide refers to the sequence of nucleotides which encode the full-length TAT polypeptide of the invention (which is often shown between start and stop codons, inclusive thereof, in the accompanying figures). The term "full-length coding region" when used in reference to an ATCC deposited nucleic acid refers to the TAT polypeptide-encoding portion of the cDNA that is inserted into the vector deposited with the ATCC (which is often shown between start and stop codons, inclusive thereof, in the accompanying figures).

"Isolated," when used to describe the various TAT polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or,

preferably, silver stain. Isolated polypeptide includes polypeptide *in situ* within recombinant cells, since at least one component of the TAT polypeptide natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

An "isolated" TAT polypeptide-encoding nucleic acid or other polypeptide-encoding nucleic acid is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the polypeptide-encoding nucleic acid. An isolated polypeptide-encoding nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated polypeptide-encoding nucleic acid molecules therefore are distinguished from the specific polypeptide-encoding nucleic acid molecule as it exists in natural cells. However, an isolated polypeptide-encoding nucleic acid molecule includes polypeptide-encoding nucleic acid molecules contained in cells that ordinarily express the polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).

"Stringent conditions" or "high stringency conditions", as defined herein, may be identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium

chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C; or (3) overnight hybridization in a solution that employs 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with a 10 minute wash at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) followed by a 10 minute high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

"Moderately stringent conditions" may be identified as described by Sambrook et al., Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent than those described above. An example of moderately stringent conditions is overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

The term "epitope tagged" when used herein refers to a chimeric polypeptide comprising a TAT polypeptide or anti-TAT antibody fused to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the polypeptide to which it is fused. The tag polypeptide preferably also is fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and 50 amino acid residues (preferably, between about 10 and 20 amino acid residues).

"Active" or "activity" for the purposes herein refers to form(s) of a TAT polypeptide which retain a biological and/or an immunological activity of native or naturally-occurring TAT, wherein "biological" activity refers to a biological function (either inhibitory or stimulatory) caused by a native or naturally-occurring TAT other than the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring TAT and an "immunological" activity refers to the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring TAT.

The term "antagonist" is used in the broadest sense, and includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of a native TAT polypeptide disclosed herein. In a similar manner, the term "agonist" is used in the broadest sense and includes any molecule that mimics a biological activity of a native TAT polypeptide disclosed herein. Suitable agonist or antagonist molecules specifically include agonist or antagonist antibodies or antibody fragments, fragments or amino acid sequence variants of native TAT polypeptides, peptides, antisense oligonucleotides, small organic molecules, etc. Methods for identifying agonists or antagonists of a TAT polypeptide may comprise contacting a TAT polypeptide with a candidate agonist or antagonist molecule and measuring a detectable change in one or more biological activities

normally associated with the TAT polypeptide.

"Treating" or "treatment" or "alleviation" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented. A subject or mammal is successfully "treated" for a TAT polypeptide-expressing cancer if, after receiving a therapeutic amount of an anti-TAT antibody, TAT binding oligopeptide or TAT binding organic molecule according to the methods of the present invention, the patient shows observable and/or measurable reduction in or absence of one or more of the following: reduction in the number of cancer cells or absence of the cancer cells; reduction in the tumor size; inhibition (i.e., slow to some extent and preferably stop) of cancer cell infiltration into peripheral organs including the spread of cancer into soft tissue and bone; inhibition (i.e., slow to some extent and preferably stop) of tumor metastasis; inhibition, to some extent, of tumor growth; and/or relief to some extent, one or more of the symptoms associated with the specific cancer; reduced morbidity and mortality, and improvement in quality of life issues. To the extent the anti-TAT antibody or TAT binding oligopeptide may prevent growth and/or kill existing cancer cells, it may be cytostatic and/or cytotoxic. Reduction of these signs or symptoms may also be felt by the patient.

The above parameters for assessing successful treatment and improvement in the disease are readily measurable by routine procedures familiar to a physician. For cancer therapy, efficacy can be measured, for example, by assessing the time to disease progression (TTP) and/or determining the response rate (RR). Metastasis can be determined by staging tests and by bone scan and tests for calcium level and other enzymes to determine spread to the bone. CT scans can also be done to look for spread to the pelvis and lymph nodes in the area. Chest X-rays and measurement of liver enzyme levels by known methods are used to look for metastasis to the lungs and liver, respectively. Other routine methods for monitoring the disease include transrectal ultrasonography (TRUS) and transrectal needle biopsy (TRNB).

For bladder cancer, which is a more localized cancer, methods to determine progress of disease include urinary cytologic evaluation by cystoscopy, monitoring for presence of blood in the urine, visualization of the urothelial tract by sonography or an intravenous pyelogram, computed tomography (CT) and magnetic resonance imaging (MRI). The presence of distant metastases can be assessed by CT of the abdomen, chest x-rays, or radionuclide imaging of the skeleton.

"Chronic" administration refers to administration of the agent(s) in a continuous mode as opposed to an acute mode, so as to maintain the initial therapeutic effect (activity) for an extended period of time. "Intermittent" administration is treatment that is not consecutively done without interruption, but rather is cyclic in nature.

"Mammal" for purposes of the treatment of, alleviating the symptoms of or diagnosis of a cancer refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, cats, cattle, horses, sheep, pigs, goats, rabbits, etc. Preferably, the mammal is human.

Administration "in combination with" one or more further therapeutic agents includes simultaneous

(concurrent) and consecutive administration in any order.

"Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers which are nontoxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN[®], polyethylene glycol (PEG), and PLURONICS[®].

By "solid phase" or "solid support" is meant a non-aqueous matrix to which an antibody, TAT binding oligopeptide or TAT binding organic molecule of the present invention can adhere or attach. Examples of solid phases encompassed herein include those formed partially or entirely of glass (e.g., controlled pore glass), polysaccharides (e.g., agarose), polyacrylamides, polystyrene, polyvinyl alcohol and silicones. In certain embodiments, depending on the context, the solid phase can comprise the well of an assay plate; in others it is a purification column (e.g., an affinity chromatography column). This term also includes a discontinuous solid phase of discrete particles, such as those described in U.S. Patent No. 4,275,149.

A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug (such as a TAT polypeptide, an antibody thereto or a TAT binding oligopeptide) to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes.

A "small" molecule or "small" organic molecule is defined herein to have a molecular weight below about 500 Daltons.

An "effective amount" of a polypeptide, antibody, TAT binding oligopeptide, TAT binding organic molecule or an agonist or antagonist thereof as disclosed herein is an amount sufficient to carry out a specifically stated purpose. An "effective amount" may be determined empirically and in a routine manner, in relation to the stated purpose.

The term "therapeutically effective amount" refers to an amount of an antibody, polypeptide, TAT binding oligopeptide, TAT binding organic molecule or other drug effective to "treat" a disease or disorder in a subject or mammal. In the case of cancer, the therapeutically effective amount of the drug may reduce the number of cancer cells; reduce the tumor size; inhibit (i.e., slow to some extent and preferably stop) cancer cell infiltration into peripheral organs; inhibit (i.e., slow to some extent and preferably stop) tumor metastasis; inhibit, to some extent, tumor growth; and/or relieve to some extent one or more of the symptoms associated with the cancer. See the definition herein of "treating". To the extent the drug may prevent growth and/or kill existing cancer cells, it may be cytostatic and/or cytotoxic.

A "growth inhibitory amount" of an anti-TAT antibody, TAT polypeptide, TAT binding oligopeptide

or TAT binding organic molecule is an amount capable of inhibiting the growth of a cell, especially tumor, e.g., cancer cell, either *in vitro* or *in vivo*. A "growth inhibitory amount" of an anti-TAT antibody, TAT polypeptide, TAT binding oligopeptide or TAT binding organic molecule for purposes of inhibiting neoplastic cell growth may be determined empirically and in a routine manner.

5 A "cytotoxic amount" of an anti-TAT antibody, TAT polypeptide, TAT binding oligopeptide or TAT binding organic molecule is an amount capable of causing the destruction of a cell, especially tumor, e.g., cancer cell, either *in vitro* or *in vivo*. A "cytotoxic amount" of an anti-TAT antibody, TAT polypeptide, TAT binding oligopeptide or TAT binding organic molecule for purposes of inhibiting neoplastic cell growth may be determined empirically and in a routine manner.

10 The term "antibody" is used in the broadest sense and specifically covers, for example, single anti-TAT monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies), anti-TAT antibody compositions with polypeptopic specificity, polyclonal antibodies, single chain anti-TAT antibodies, and fragments of anti-TAT antibodies (see below) as long as they exhibit the desired biological or immunological activity. The term "immunoglobulin" (Ig) is used interchangeable with antibody herein.

15 An "isolated antibody" is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid
20 sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody *in situ* within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

25 The basic 4-chain antibody unit is a heterotetrameric glycoprotein composed of two identical light (L) chains and two identical heavy (H) chains (an IgM antibody consists of 5 of the basic heterotetramer unit along with an additional polypeptide called J chain, and therefore contain 10 antigen binding sites, while secreted IgA antibodies can polymerize to form polyvalent assemblages comprising 2-5 of the basic 4-chain units along with J chain). In the case of IgGs, the 4-chain unit is generally about 150,000 daltons. Each L chain is linked to a H chain by one covalent disulfide bond, while the two H chains are linked to each other by one or more
30 disulfide bonds depending on the H chain isotype. Each H and L chain also has regularly spaced intrachain disulfide bridges. Each H chain has at the N-terminus, a variable domain (V_H) followed by three constant domains (C_H) for each of the α and γ chains and four C_H domains for μ and ϵ isotypes. Each L chain has at the N-terminus, a variable domain (V_L) followed by a constant domain (C_L) at its other end. The V_L is aligned with the V_H and the C_L is aligned with the first constant domain of the heavy chain (C_{H1}). Particular amino acid
35 residues are believed to form an interface between the light chain and heavy chain variable domains. The pairing of a V_H and V_L together forms a single antigen-binding site. For the structure and properties of the

different classes of antibodies, see, e.g., Basic and Clinical Immunology, 8th edition, Daniel P. Stites, Abba I. Terr and Tristram G. Parslow (eds.), Appleton & Lange, Norwalk, CT, 1994, page 71 and Chapter 6.

The L chain from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains. Depending on the amino acid sequence of the constant domain of their heavy chains (C_H), immunoglobulins can be assigned to different classes or isotypes. There are five classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, having heavy chains designated α , δ , ϵ , γ , and μ , respectively. The γ and α classes are further divided into subclasses on the basis of relatively minor differences in C_H sequence and function, e.g., humans express the following subclasses: IgG1, IgG2, IgG3, IgG4, IgA1, and IgA2.

The term "variable" refers to the fact that certain segments of the variable domains differ extensively in sequence among antibodies. The V domain mediates antigen binding and define specificity of a particular antibody for its particular antigen. However, the variability is not evenly distributed across the 110-amino acid span of the variable domains. Instead, the V regions consist of relatively invariant stretches called framework regions (FRs) of 15-30 amino acids separated by shorter regions of extreme variability called "hypervariable regions" that are each 9-12 amino acids long. The variable domains of native heavy and light chains each comprise four FRs, largely adopting a β -sheet configuration, connected by three hypervariable regions, which form loops connecting, and in some cases forming part of, the β -sheet structure. The hypervariable regions in each chain are held together in close proximity by the FRs and, with the hypervariable regions from the other chain, contribute to the formation of the antigen-binding site of antibodies (see Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991)). The constant domains are not involved directly in binding an antibody to an antigen, but exhibit various effector functions, such as participation of the antibody in antibody dependent cellular cytotoxicity (ADCC).

The term "hypervariable region" when used herein refers to the amino acid residues of an antibody which are responsible for antigen-binding. The hypervariable region generally comprises amino acid residues from a "complementarity determining region" or "CDR" (e.g. around about residues 24-34 (L1), 50-56 (L2) and 89-97 (L3) in the V_L , and around about 1-35 (H1), 50-65 (H2) and 95-102 (H3) in the V_H ; Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991)) and/or those residues from a "hypervariable loop" (e.g. residues 26-32 (L1), 50-52 (L2) and 91-96 (L3) in the V_L , and 26-32 (H1), 53-55 (H2) and 96-101 (H3) in the V_H ; Chothia and Lesk J. Mol. Biol. 196:901-917 (1987)).

The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against a single antigenic site. Furthermore, in contrast to polyclonal antibody preparations which include different antibodies directed against different determinants (epitopes), each monoclonal antibody is directed against a single determinant on the antigen. In addition to their specificity, the monoclonal antibodies are advantageous in that they may be synthesized uncontaminated by other antibodies.

The modifier "monoclonal" is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies useful in the present invention may be prepared by the hybridoma methodology first described by Kohler et al., Nature, 256:495 (1975), or may be made using recombinant DNA methods in bacterial, eukaryotic animal or plant cells (see, e.g., U.S. Patent No. 4,816,567). The "monoclonal antibodies" may also be isolated from phage antibody libraries using the techniques described in Clackson et al., Nature, 352:624-628 (1991) and Marks et al., J. Mol. Biol., 222:581-597 (1991), for example.

The monoclonal antibodies herein include "chimeric" antibodies in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired biological activity (see U.S. Patent No. 4,816,567; and Morrison et al., Proc. Natl. Acad. Sci. USA, 81:6851-6855 (1984)). Chimeric antibodies of interest herein include "primatized" antibodies comprising variable domain antigen-binding sequences derived from a non-human primate (e.g. Old World Monkey, Ape etc), and human constant region sequences.

An "intact" antibody is one which comprises an antigen-binding site as well as a C_L and at least heavy chain constant domains, C_H1, C_H2 and C_H3. The constant domains may be native sequence constant domains (e.g. human native sequence constant domains) or amino acid sequence variant thereof. Preferably, the intact antibody has one or more effector functions.

"Antibody fragments" comprise a portion of an intact antibody, preferably the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', F(ab')₂, and Fv fragments; diabodies; linear antibodies (see U.S. Patent No. 5,641,870, Example 2; Zapata et al., Protein Eng. 8(10): 1057-1062 [1995]); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. The Fab fragment consists of an entire L chain along with the variable region domain of the H chain (V_H), and the first constant domain of one heavy chain (C_H1). Each Fab fragment is monovalent with respect to antigen binding, i.e., it has a single antigen-binding site. Pepsin treatment of an antibody yields a single large F(ab')₂ fragment which roughly corresponds to two disulfide linked Fab fragments having divalent antigen-binding activity and is still capable of cross-linking antigen. Fab' fragments differ from Fab fragments by having additional few residues at the carboxy terminus of the C_H1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. F(ab')₂ antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

The Fc fragment comprises the carboxy-terminal portions of both H chains held together by disulfides.

The effector functions of antibodies are determined by sequences in the Fc region, which region is also the part recognized by Fc receptors (FcR) found on certain types of cells.

"Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This fragment consists of a dimer of one heavy- and one light-chain variable region domain in tight, non-covalent association. From the folding of these two domains emanate six hypervariable loops (3 loops each from the H and L chain) that contribute the amino acid residues for antigen binding and confer antigen binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

"Single-chain Fv" also abbreviated as "sFv" or "scFv" are antibody fragments that comprise the V_H and V_L antibody domains connected into a single polypeptide chain. Preferably, the sFv polypeptide further comprises a polypeptide linker between the V_H and V_L domains which enables the sFv to form the desired structure for antigen binding. For a review of sFv, see Pluckthun in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenberg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994); Borrebaeck 1995, *infra*.

The term "diabodies" refers to small antibody fragments prepared by constructing sFv fragments (see preceding paragraph) with short linkers (about 5-10 residues) between the V_H and V_L domains such that inter-chain but not intra-chain pairing of the V domains is achieved, resulting in a bivalent fragment, i.e., fragment having two antigen-binding sites. Bispecific diabodies are heterodimers of two "crossover" sFv fragments in which the V_H and V_L domains of the two antibodies are present on different polypeptide chains. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., *Proc. Natl. Acad. Sci. USA*, 90:6444-6448 (1993).

"Humanized" forms of non-human (e.g., rodent) antibodies are chimeric antibodies that contain minimal sequence derived from the non-human antibody. For the most part, humanized antibodies are human immunoglobulins (recipient antibody) in which residues from a hypervariable region of the recipient are replaced by residues from a hypervariable region of a non-human species (donor antibody) such as mouse, rat, rabbit or non-human primate having the desired antibody specificity, affinity, and capability. In some instances, framework region (FR) residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, humanized antibodies may comprise residues that are not found in the recipient antibody or in the donor antibody. These modifications are made to further refine antibody performance. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the hypervariable loops correspond to those of a non-human immunoglobulin and all or substantially all of the FRs are those of a human immunoglobulin sequence. The humanized antibody optionally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For further details, see Jones et al., *Nature* 321:522-525 (1986); Riechmann et al., *Nature* 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.* 2:593-596 (1992).

A "species-dependent antibody," e.g., a mammalian anti-human IgE antibody, is an antibody which

has a stronger binding affinity for an antigen from a first mammalian species than it has for a homologue of that antigen from a second mammalian species. Normally, the species-dependent antibody "bind specifically" to a human antigen (i.e., has a binding affinity (Kd) value of no more than about 1×10^{-7} M, preferably no more than about 1×10^{-8} and most preferably no more than about 1×10^{-9} M) but has a binding affinity for a homologue of the antigen from a second non-human mammalian species which is at least about 50 fold, or at least about 500 fold, or at least about 1000 fold, weaker than its binding affinity for the human antigen. The species-dependent antibody can be of any of the various types of antibodies as defined above, but preferably is a humanized or human antibody.

A "TAT binding oligopeptide" is an oligopeptide that binds, preferably specifically, to a TAT polypeptide as described herein. TAT binding oligopeptides may be chemically synthesized using known oligopeptide synthesis methodology or may be prepared and purified using recombinant technology. TAT binding oligopeptides are usually at least about 5 amino acids in length, alternatively at least about 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100 amino acids in length or more, wherein such oligopeptides that are capable of binding, preferably specifically, to a TAT polypeptide as described herein. TAT binding oligopeptides may be identified without undue experimentation using well known techniques. In this regard, it is noted that techniques for screening oligopeptide libraries for oligopeptides that are capable of specifically binding to a polypeptide target are well known in the art (see, e.g., U.S. Patent Nos. 5,556,762, 5,750,373, 4,708,871, 4,833,092, 5,223,409, 5,403,484, 5,571,689, 5,663,143; PCT Publication Nos. WO 84/03506 and WO84/03564; Geysen et al., Proc. Natl. Acad. Sci. U.S.A., 81:3998-4002 (1984); Geysen et al., Proc. Natl. Acad. Sci. U.S.A., 82:178-182 (1985); Geysen et al., in *Synthetic Peptides as Antigens*, 130-149 (1986); Geysen et al., J. Immunol. Meth., 102:259-274 (1987); Schoofs et al., J. Immunol., 140:611-616 (1988), Cwirla, S. E. et al. (1990) Proc. Natl. Acad. Sci. USA, 87:6378; Lowman, H.B. et al. (1991) Biochemistry, 30:10832; Clackson, T. et al. (1991) Nature, 352: 624; Marks, J. D. et al. (1991), J. Mol. Biol., 222:581; Kang, A.S. et al. (1991) Proc. Natl. Acad. Sci. USA, 88:8363, and Smith, G. P. (1991) Current Opin. Biotechnol., 2:668).

A "TAT binding organic molecule" is an organic molecule other than an oligopeptide or antibody as defined herein that binds, preferably specifically, to a TAT polypeptide as described herein. TAT binding organic molecules may be identified and chemically synthesized using known methodology (see, e.g., PCT Publication Nos. WO00/00823 and WO00/39585). TAT binding organic molecules are usually less than about 2000 daltons in size, alternatively less than about 1500, 750, 500, 250 or 200 daltons in size, wherein such organic molecules that are capable of binding, preferably specifically, to a TAT polypeptide as described herein may be identified without undue experimentation using well known techniques. In this regard, it is noted that techniques for screening organic molecule libraries for molecules that are capable of binding to a polypeptide target are well known in the art (see, e.g., PCT Publication Nos. WO00/00823 and WO00/39585).

An antibody, oligopeptide or other organic molecule "which binds" an antigen of interest, e.g. a tumor-associated polypeptide antigen target, is one that binds the antigen with sufficient affinity such that the antibody, oligopeptide or other organic molecule is useful as a diagnostic and/or therapeutic agent in targeting a cell or tissue expressing the antigen, and does not significantly cross-react with other proteins. In such embodiments, the extent of binding of the antibody, oligopeptide or other organic molecule to a "non-target" protein will be less than about 10% of the binding of the antibody, oligopeptide or other organic molecule to its particular target protein as determined by fluorescence activated cell sorting (FACS) analysis or radioimmunoprecipitation (RIA). With regard to the binding of an antibody, oligopeptide or other organic molecule to a target molecule, the term "specific binding" or "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide target means binding that is measurably different from a non-specific interaction. Specific binding can be measured, for example, by determining binding of a molecule compared to binding of a control molecule, which generally is a molecule of similar structure that does not have binding activity. For example, specific binding can be determined by competition with a control molecule that is similar to the target, for example, an excess of non-labeled target. In this case, specific binding is indicated if the binding of the labeled target to a probe is competitively inhibited by excess unlabeled target. The term "specific binding" or "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide target as used herein can be exhibited, for example, by a molecule having a K_d for the target of at least about 10^{-4} M, alternatively at least about 10^{-5} M, alternatively at least about 10^{-6} M, alternatively at least about 10^{-7} M, alternatively at least about 10^{-8} M, alternatively at least about 10^{-9} M, alternatively at least about 10^{-10} M, alternatively at least about 10^{-11} M, alternatively at least about 10^{-12} M, or greater. In one embodiment, the term "specific binding" refers to binding where a molecule binds to a particular polypeptide or epitope on a particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope.

An antibody, oligopeptide or other organic molecule that "inhibits the growth of tumor cells expressing a TAT polypeptide" or a "growth inhibitory" antibody, oligopeptide or other organic molecule is one which results in measurable growth inhibition of cancer cells expressing or overexpressing the appropriate TAT polypeptide. The TAT polypeptide may be a transmembrane polypeptide expressed on the surface of a cancer cell or may be a polypeptide that is produced and secreted by a cancer cell. Preferred growth inhibitory anti-TAT antibodies, oligopeptides or organic molecules inhibit growth of TAT-expressing tumor cells by greater

than 20%, preferably from about 20% to about 50%, and even more preferably, by greater than 50% (e.g., from about 50% to about 100%) as compared to the appropriate control, the control typically being tumor cells not treated with the antibody, oligopeptide or other organic molecule being tested. In one embodiment, growth inhibition can be measured at an antibody concentration of about 0.1 to 30 µg/ml or about 0.5 nM to 200 nM in cell culture, where the growth inhibition is determined 1-10 days after exposure of the tumor cells to the antibody. Growth inhibition of tumor cells *in vivo* can be determined in various ways such as is described in the Experimental Examples section below. The antibody is growth inhibitory *in vivo* if administration of the anti-TAT antibody at about 1 µg/kg to about 100 mg/kg body weight results in reduction in tumor size or tumor cell proliferation within about 5 days to 3 months from the first administration of the antibody, preferably within about 5 to 30 days.

An antibody, oligopeptide or other organic molecule which "induces apoptosis" is one which induces programmed cell death as determined by binding of annexin V, fragmentation of DNA, cell shrinkage, dilation of endoplasmic reticulum, cell fragmentation, and/or formation of membrane vesicles (called apoptotic bodies). The cell is usually one which overexpresses a TAT polypeptide. Preferably the cell is a tumor cell, e.g., a prostate, breast, ovarian, stomach, endometrial, lung, kidney, colon, bladder cell. Various methods are available for evaluating the cellular events associated with apoptosis. For example, phosphatidyl serine (PS) translocation can be measured by annexin binding; DNA fragmentation can be evaluated through DNA laddering; and nuclear/chromatin condensation along with DNA fragmentation can be evaluated by any increase in hypodiploid cells. Preferably, the antibody, oligopeptide or other organic molecule which induces apoptosis is one which results in about 2 to 50 fold, preferably about 5 to 50 fold, and most preferably about 10 to 50 fold, induction of annexin binding relative to untreated cell in an annexin binding assay.

Antibody "effector functions" refer to those biological activities attributable to the Fc region (a native sequence Fc region or amino acid sequence variant Fc region) of an antibody, and vary with the antibody isotype. Examples of antibody effector functions include: C1q binding and complement dependent cytotoxicity; Fc receptor binding; antibody-dependent cell-mediated cytotoxicity (ADCC); phagocytosis; down regulation of cell surface receptors (e.g., B cell receptor); and B cell activation.

"Antibody-dependent cell-mediated cytotoxicity" or "ADCC" refers to a form of cytotoxicity in which secreted Ig bound onto Fc receptors (FcRs) present on certain cytotoxic cells (e.g., Natural Killer (NK) cells, neutrophils, and macrophages) enable these cytotoxic effector cells to bind specifically to an antigen-bearing target cell and subsequently kill the target cell with cytotoxins. The antibodies "arm" the cytotoxic cells and are absolutely required for such killing. The primary cells for mediating ADCC, NK cells, express FcγRIII only, whereas monocytes express FcγRI, FcγRII and FcγRIII. FcR expression on hematopoietic cells is summarized in Table 3 on page 464 of Ravetch and Kinet, Annu. Rev. Immunol. 9:457-92 (1991). To assess ADCC activity of a molecule of interest, an *in vitro* ADCC assay, such as that described in US Patent No. 5,500,362 or 5,821,337 may be performed. Useful effector cells for such assays include peripheral blood mononuclear cells (PBMC) and Natural Killer (NK) cells. Alternatively, or additionally, ADCC activity of the molecule of interest may be assessed *in vivo*, e.g., in a animal model such as that disclosed in Clynes et al.

(USA) 95:652-656 (1998).

"Fc receptor" or "FcR" describes a receptor that binds to the Fc region of an antibody. The preferred FcR is a native sequence human FcR. Moreover, a preferred FcR is one which binds an IgG antibody (a gamma receptor) and includes receptors of the Fc γ RI, Fc γ RII and Fc γ RIII subclasses, including allelic variants and alternatively spliced forms of these receptors. Fc γ RII receptors include Fc γ RIIA (an "activating receptor") and Fc γ RIIB (an "inhibiting receptor"), which have similar amino acid sequences that differ primarily in the cytoplasmic domains thereof. Activating receptor Fc γ RIIA contains an immunoreceptor tyrosine-based activation motif (ITAM) in its cytoplasmic domain. Inhibiting receptor Fc γ RIIB contains an immunoreceptor tyrosine-based inhibition motif (ITIM) in its cytoplasmic domain. (see review M. in Daëron, Annu. Rev. Immunol. 15:203-234 (1997)). FcRs are reviewed in Ravetch and Kinet, Annu. Rev. Immunol. 9:457-492 (1991); Capel et al., Immunomethods 4:25-34 (1994); and de Haas et al., J. Lab. Clin. Med. 126:330-41 (1995). Other FcRs, including those to be identified in the future, are encompassed by the term "FcR" herein. The term also includes the neonatal receptor, FcRn, which is responsible for the transfer of maternal IgGs to the fetus (Guyer et al., J. Immunol. 117:587 (1976) and Kim et al., J. Immunol. 24:249 (1994)).

"Human effector cells" are leukocytes which express one or more FcRs and perform effector functions. Preferably, the cells express at least Fc γ RIII and perform ADCC effector function. Examples of human leukocytes which mediate ADCC include peripheral blood mononuclear cells (PBMC), natural killer (NK) cells, monocytes, cytotoxic T cells and neutrophils; with PBMCs and NK cells being preferred. The effector cells may be isolated from a native source, e.g., from blood.

"Complement dependent cytotoxicity" or "CDC" refers to the lysis of a target cell in the presence of complement. Activation of the classical complement pathway is initiated by the binding of the first component of the complement system (C1q) to antibodies (of the appropriate subclass) which are bound to their cognate antigen. To assess complement activation, a CDC assay, e.g., as described in Gazzano-Santoro et al., J. Immunol. Methods 202:163 (1996), may be performed.

The terms "cancer" and "cancerous" refer to or describe the physiological condition in mammals that is typically characterized by unregulated cell growth. Examples of cancer include, but are not limited to, carcinoma, lymphoma, blastoma, sarcoma, and leukemia or lymphoid malignancies. More particular examples of such cancers include squamous cell cancer (e.g., epithelial squamous cell cancer), lung cancer including small-cell lung cancer, non-small cell lung cancer, adenocarcinoma of the lung and squamous carcinoma of the lung, cancer of the peritoneum, hepatocellular cancer, gastric or stomach cancer including gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, cancer of the urinary tract, hepatoma, breast cancer, colon cancer, rectal cancer, colorectal cancer, endometrial or uterine carcinoma, salivary gland carcinoma, kidney or renal cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma, anal carcinoma, penile carcinoma, melanoma, multiple myeloma and B-cell lymphoma, brain, as well as head and neck cancer, and associated metastases.

The terms "cell proliferative disorder" and "proliferative disorder" refer to disorders that are

associated with some degree of abnormal cell proliferation. In one embodiment, the cell proliferative disorder is cancer.

"Tumor", as used herein, refers to all neoplastic cell growth and proliferation, whether malignant or benign, and all pre-cancerous and cancerous cells and tissues.

5 An antibody, oligopeptide or other organic molecule which "induces cell death" is one which causes a viable cell to become nonviable. The cell is one which expresses a TAT polypeptide, preferably a cell that overexpresses a TAT polypeptide as compared to a normal cell of the same tissue type. The TAT polypeptide may be a transmembrane polypeptide expressed on the surface of a cancer cell or may be a polypeptide that is produced and secreted by a cancer cell. Preferably, the cell is a cancer cell, e.g., a breast, ovarian, stomach, endometrial, salivary gland, lung, kidney, colon, thyroid, pancreatic or bladder cell. Cell death *in vitro* may be determined in the absence of complement and immune effector cells to distinguish cell death induced by antibody-dependent cell-mediated cytotoxicity (ADCC) or complement dependent cytotoxicity (CDC). Thus, the assay for cell death may be performed using heat inactivated serum (i.e., in the absence of complement) and in the absence of immune effector cells. To determine whether the antibody, oligopeptide or other organic molecule is able to induce cell death, loss of membrane integrity as evaluated by uptake of propidium iodide (PI), trypan blue (see Moore et al. Cytotechnology 17:1-11 (1995)) or 7AAD can be assessed relative to untreated cells. Preferred cell death-inducing antibodies, oligopeptides or other organic molecules are those which induce PI uptake in the PI uptake assay in BT474 cells.

20 A "TAT-expressing cell" is a cell which expresses an endogenous or transfected TAT polypeptide either on the cell surface or in a secreted form. A "TAT-expressing cancer" is a cancer comprising cells that have a TAT polypeptide present on the cell surface or that produce and secrete a TAT polypeptide. A "TAT-expressing cancer" optionally produces sufficient levels of TAT polypeptide on the surface of cells thereof, such that an anti-TAT antibody, oligopeptide or other organic molecule can bind thereto and have a therapeutic effect with respect to the cancer. In another embodiment, a "TAT-expressing cancer" optionally produces and secretes sufficient levels of TAT polypeptide, such that an anti-TAT antibody, oligopeptide or other organic molecule antagonist can bind thereto and have a therapeutic effect with respect to the cancer. With regard to the latter, the antagonist may be an antisense oligonucleotide which reduces, inhibits or prevents production and secretion of the secreted TAT polypeptide by tumor cells. A cancer which "overexpresses" a TAT polypeptide is one which has significantly higher levels of TAT polypeptide at the cell surface thereof, or produces and secretes, compared to a noncancerous cell of the same tissue type. Such overexpression may be caused by gene amplification or by increased transcription or translation. TAT polypeptide overexpression may be determined in a diagnostic or prognostic assay by evaluating increased levels of the TAT protein present on the surface of a cell, or secreted by the cell (e.g., via an immunohistochemistry assay using anti-TAT antibodies prepared against an isolated TAT polypeptide which may be prepared using recombinant DNA technology from an isolated nucleic acid encoding the TAT polypeptide; FACS analysis, etc.). Alternatively, or additionally, one may measure levels of TAT polypeptide-encoding nucleic acid or mRNA in the cell, e.g., via fluorescent *in situ* hybridization using a nucleic acid based probe corresponding to a TAT-encoding nucleic acid or the complement

thereof; (FISH; see WO98/45479 published October, 1998), Southern blotting, Northern blotting, or polymerase chain reaction (PCR) techniques, such as real time quantitative PCR (RT-PCR). One may also study TAT polypeptide overexpression by measuring shed antigen in a biological fluid such as serum, e.g. using antibody-based assays (see also, e.g., U.S. Patent No. 4,933,294 issued June 12, 1990; WO91/05264 published April 18, 1991; U.S. Patent 5,401,638 issued March 28, 1995; and Sias et al., J. Immunol. Methods 132:73-80 (1990)).

5 Aside from the above assays, various *in vivo* assays are available to the skilled practitioner. For example, one may expose cells within the body of the patient to an antibody which is optionally labeled with a detectable label, e.g., a radioactive isotope, and binding of the antibody to cells in the patient can be evaluated, e.g., by external scanning for radioactivity or by analyzing a biopsy taken from a patient previously exposed to the antibody.

10 As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (i.e., is "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin

15 molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

20 The word "label" when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the antibody, oligopeptide or other organic molecule so as to generate a "labeled" antibody, oligopeptide or other organic molecule. The label may be detectable by itself (e.g. radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical alteration of a substrate compound or composition which is detectable.

25 The term "cytotoxic agent" as used herein refers to a substance that inhibits or prevents the function of cells and/or causes destruction of cells. The term is intended to include radioactive isotopes (e.g., ^{211}At , ^{131}I , ^{125}I , ^{90}Y , ^{186}Re , ^{188}Re , ^{153}Sm , ^{212}Bi , ^{32}P and radioactive isotopes of Lu), chemotherapeutic agents e.g. methotrexate, adriamycin, vinca alkaloids (vincristine, vinblastine, etoposide), doxorubicin, melphalan, mitomycin C, chlorambucil, daunorubicin or other intercalating agents, enzymes and fragments thereof such as nucleolytic enzymes, antibiotics, and toxins such as small molecule toxins or enzymatically active toxins of

30 bacterial, fungal, plant or animal origin, including fragments and/or variants thereof, and the various antitumor or anticancer agents disclosed below. Other cytotoxic agents are described below. A tumoricidal agent causes destruction of tumor cells.

A "growth inhibitory agent" when used herein refers to a compound or composition which inhibits growth of a cell, especially a TAT-expressing cancer cell, either *in vitro* or *in vivo*. Thus, the growth inhibitory

35 agent may be one which significantly reduces the percentage of TAT-expressing cells in S phase. Examples of growth inhibitory agents include agents that block cell cycle progression (at a place other than S phase), such

as agents that induce G1 arrest and M-phase arrest. Classical M-phase blockers include the vincas (vincristine and vinblastine), taxanes, and topoisomerase II inhibitors such as doxorubicin, epirubicin, daunorubicin, etoposide, and bleomycin. Those agents that arrest G1 also spill over into S-phase arrest, for example, DNA alkylating agents such as tamoxifen, prednisone, dacarbazine, mechlorethamine, cisplatin, methotrexate, 5-fluorouracil, and ara-C. Further information can be found in The Molecular Basis of Cancer, Mendelsohn and Israel, eds., Chapter 1, entitled "Cell cycle regulation, oncogenes, and antineoplastic drugs" by Murakami et al. (WB Saunders: Philadelphia, 1995), especially p. 13. The taxanes (paclitaxel and docetaxel) are anticancer drugs both derived from the yew tree. Docetaxel (TAXOTERE®, Rhone-Poulenc Rorer), derived from the European yew, is a semisynthetic analogue of paclitaxel (TAXOL®, Bristol-Myers Squibb). Paclitaxel and docetaxel promote the assembly of microtubules from tubulin dimers and stabilize microtubules by preventing depolymerization, which results in the inhibition of mitosis in cells.

"Doxorubicin" is an anthracycline antibiotic. The full chemical name of doxorubicin is (8S-cis)-10-[(3-amino-2,3,6-trideoxy- α -L-lyxo-hexapyranosyl)oxy]-7,8,9,10-tetrahydro-6,8,11-trihydroxy-8-(hydroxyacetyl)-1-methoxy-5,12-naphthacenedione.

The term "cytokine" is a generic term for proteins released by one cell population which act on another cell as intercellular mediators. Examples of such cytokines are lymphokines, monokines, and traditional polypeptide hormones. Included among the cytokines are growth hormone such as human growth hormone, N-methionyl human growth hormone, and bovine growth hormone; parathyroid hormone; thyroxine; insulin; proinsulin; relaxin; prorelaxin; glycoprotein hormones such as follicle stimulating hormone (FSH), thyroid stimulating hormone (TSH), and luteinizing hormone (LH); hepatic growth factor; fibroblast growth factor; prolactin; placental lactogen; tumor necrosis factor- α and - β ; mullerian-inhibiting substance; mouse gonadotropin-associated peptide; inhibin; activin; vascular endothelial growth factor; integrin; thrombopoietin (TPO); nerve growth factors such as NGF- β ; platelet-growth factor; transforming growth factors (TGFs) such as TGF- α and TGF- β ; insulin-like growth factor-I and -II; erythropoietin (EPO); osteoinductive factors; interferons such as interferon - α , - β , and - γ ; colony stimulating factors (CSFs) such as macrophage-CSF (M-CSF); granulocyte-macrophage-CSF (GM-CSF); and granulocyte-CSF (G-CSF); interleukins (ILs) such as IL-1, IL-1a, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-11, IL-12; a tumor necrosis factor such as TNF- α or TNF- β ; and other polypeptide factors including LIF and kit ligand (KL). As used herein, the term cytokine includes proteins from natural sources or from recombinant cell culture and biologically active equivalents of the native sequence cytokines.

The term “package insert” is used to refer to instructions customarily included in commercial packages of therapeutic products, that contain information about the indications, usage, dosage, administration, contraindications and/or warnings concerning the use of such therapeutic products.

Table 1

```

/*
*
* C-C increased from 12 to 15
* Z is average of EQ
5  * B is average of ND
* match with stop is _M; stop-stop = 0; J (joker) match = 0
*/
#define _M      -8      /* value of a match with a stop */

10 int  _day[26][26] = {
/*  A B C D E F G H I J K L M N O P Q R S T U V W X Y Z */
/* A */ { 2, 0, -2, 0, 0, -4, 1, -1, -1, 0, -1, -2, -1, 0, _M, 1, 0, -2, 1, 1, 0, 0, -6, 0, -3, 0},
/* B */ { 0, 3, -4, 3, 2, -5, 0, 1, -2, 0, 0, -3, -2, 2, _M, -1, 1, 0, 0, 0, 0, -2, -5, 0, -3, 1},
/* C */ {-2, -4, 15, -5, -5, -4, -3, -3, -2, 0, -5, -6, -5, -4, _M, -3, -5, -4, 0, -2, 0, -2, -8, 0, 0, -5},
15 /* D */ { 0, 3, -5, 4, 3, -6, 1, 1, -2, 0, 0, -4, -3, 2, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 2},
/* E */ { 0, 2, -5, 3, 4, -5, 0, 1, -2, 0, 0, -3, -2, 1, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 3},
/* F */ {-4, -5, -4, -6, -5, 9, -5, -2, 1, 0, -5, 2, 0, -4, _M, -5, -5, -4, -3, -3, 0, -1, 0, 0, 7, -5},
/* G */ { 1, 0, -3, 1, 0, -5, 5, -2, -3, 0, -2, -4, -3, 0, _M, -1, -1, -3, 1, 0, 0, -1, -7, 0, -5, 0},
/* H */ {-1, 1, -3, 1, 1, -2, -2, 6, -2, 0, 0, -2, -2, 2, _M, 0, 3, 2, -1, -1, 0, -2, -3, 0, 0, 2},
20 /* I */ {-1, -2, -2, -2, -2, 1, -3, -2, 5, 0, -2, 2, 2, -2, _M, -2, -2, -2, -1, 0, 0, 4, -5, 0, -1, -2},
/* J */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* K */ {-1, 0, -5, 0, 0, -5, -2, 0, -2, 0, 5, -3, 0, 1, _M, -1, 1, 3, 0, 0, 0, -2, -3, 0, -4, 0},
/* L */ {-2, -3, -6, -4, -3, 2, -4, -2, 2, 0, -3, 6, 4, -3, _M, -3, -2, -3, -3, -1, 0, 2, -2, 0, -1, -2},
/* M */ {-1, -2, -5, -3, -2, 0, -3, -2, 2, 0, 0, 4, 6, -2, _M, -2, -1, 0, -2, -1, 0, 2, -4, 0, -2, -1},
25 /* N */ { 0, 2, -4, 2, 1, -4, 0, 2, -2, 0, 1, -3, -2, 2, _M, -1, 1, 0, 1, 0, 0, -2, -4, 0, -2, 1},
/* O */ { _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M},
/* P */ { 1, -1, -3, -1, -1, -5, -1, 0, -2, 0, -1, -3, -2, -1, _M, 6, 0, 0, 1, 0, 0, -1, -6, 0, -5, 0},
/* Q */ { 0, 1, -5, 2, 2, -5, -1, 3, -2, 0, 1, -2, -1, 1, _M, 0, 4, 1, -1, -1, 0, -2, -5, 0, -4, 3},
/* R */ {-2, 0, -4, -1, -1, -4, -3, 2, -2, 0, 3, -3, 0, 0, _M, 0, 1, 6, 0, -1, 0, -2, 2, 0, -4, 0},
30 /* S */ { 1, 0, 0, 0, 0, -3, 1, -1, -1, 0, 0, -3, -2, 1, _M, 1, -1, 0, 2, 1, 0, -1, -2, 0, -3, 0},
/* T */ { 1, 0, -2, 0, 0, -3, 0, -1, 0, 0, 0, -1, -1, 0, _M, 0, -1, -1, 1, 3, 0, 0, -5, 0, -3, 0},
/* U */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* V */ { 0, -2, -2, -2, -2, -1, -1, -2, 4, 0, -2, 2, 2, -2, _M, -1, -2, -2, -1, 0, 0, 4, -6, 0, -2, -2},
/* W */ {-6, -5, -8, -7, -7, 0, -7, -3, -5, 0, -3, -2, -4, -4, _M, -6, -5, 2, -2, -5, 0, -6, 17, 0, 0, -6},
35 /* X */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* Y */ {-3, -3, 0, -4, -4, 7, -5, 0, -1, 0, -4, -1, -2, -2, _M, -5, -4, -4, -3, -3, 0, -2, 0, 0, 10, -4},
/* Z */ { 0, 1, -5, 2, 3, -5, 0, 2, -2, 0, 0, -2, -1, 1, _M, 0, 3, 0, 0, 0, 0, -2, -6, 0, -4, 4}
};

```

Table 1 (cont')

```

/*
*/
#include <stdio.h>
#include <ctype.h>

5
#define MAXJMP      16      /* max jumps in a diag */
#define MAXGAP      24      /* don't continue to penalize gaps larger than this */
#define JMPS        1024    /* max jmps in an path */
10
#define MX          4       /* save if there's at least MX-1 bases since last jmp */

#define DMAT        3       /* value of matching bases */
#define DMIS        0       /* penalty for mismatched bases */
#define DINS0       8       /* penalty for a gap */
15
#define DINS1       1       /* penalty per base */
#define PINS0       8       /* penalty for a gap */
#define PINS1       4       /* penalty per residue */

struct jmp {
20
    short           n[MAXJMP]; /* size of jmp (neg for dely) */
    unsigned short  x[MAXJMP]; /* base no. of jmp in seq x */
}; /* limits seq to 2^16 -1 */

struct diag {
25
    int             score;      /* score at last jmp */
    long            offset;     /* offset of prev block */
    short           ijmp;       /* current jmp index */
    struct jmp      jp;         /* list of jmps */
};

30
struct path {
    int             spc;        /* number of leading spaces */
    short           n[JMPS]; /* size of jmp (gap) */
    int             x[JMPS]; /* loc of jmp (last elem before gap) */
35
};

char             *ofile;      /* output file name */
char             *namex[2];   /* seq names: getseqs() */
char             *prog;       /* prog name for err msgs */
40
char             *seqx[2];     /* seqs: getseqs() */
int              dmax;        /* best diag: nw() */
int              dmax0;       /* final diag */
int              dna;         /* set if dna: main() */
int              endgaps;     /* set if penalizing end gaps */
45
int              gapx, gapy;   /* total gaps in seqs */
int              len0, len1;   /* seq lens */
int              ngapx, ngapy; /* total size of gaps */
int              smax;        /* max score: nw() */
int              *xbm;        /* bitmap for matching */
50
long            offset;       /* current offset in jmp file */
struct diag      *dx;         /* holds diagonals */
struct path      pp[2];       /* holds path for seqs */

char             *calloc(), *malloc(), *index(), *strcpy();
char             *getseq(), *g_calloc();

```

Table 1 (cont')

```

/* Needleman-Wunsch alignment program
*
* usage: progs file1 file2
* where file1 and file2 are two dna or two protein sequences.
5  * The sequences can be in upper- or lower-case an may contain ambiguity
* Any lines beginning with ';', '>' or '<' are ignored
* Max file length is 65535 (limited by unsigned short x in the jmp struct)
* A sequence with 1/3 or more of its elements ACGTU is assumed to be DNA
10 * Output is in the file "align.out"
*
* The program may create a tmp file in /tmp to hold info about traceback.
* Original version developed under BSD 4.3 on a vax 8650
*/
15 #include "nw.h"
#include "day.h"

static _dbval[26] = {
    1,14,2,13,0,0,4,11,0,0,12,0,3,15,0,0,0,5,6,8,8,7,9,0,10,0
};
20
static _pbval[26] = {
    1, 2|(1<<('D'-'A'))|(1<<('N'-'A')), 4, 8, 16, 32, 64,
    128, 256, 0xFFFFFFFF, 1<<10, 1<<11, 1<<12, 1<<13, 1<<14,
    1<<15, 1<<16, 1<<17, 1<<18, 1<<19, 1<<20, 1<<21, 1<<22,
25 1<<23, 1<<24, 1<<25|(1<<('E'-'A'))|(1<<('Q'-'A'))
};

main(ac, av)
30     int      ac;
     char      *av[];
{
    prog = av[0];
    if (ac != 3) {
35         fprintf(stderr, "usage: %s file1 file2\n", prog);
        fprintf(stderr, "where file1 and file2 are two dna or two protein sequences.\n");
        fprintf(stderr, "The sequences can be in upper- or lower-case\n");
        fprintf(stderr, "Any lines beginning with ';' or '<' are ignored\n");
        fprintf(stderr, "Output is in the file \"align.out\"\n");
        exit(1);
40     }
    namex[0] = av[1];
    namex[1] = av[2];
    seqx[0] = getseq(namex[0], &len0);
    seqx[1] = getseq(namex[1], &len1);
45     xbm = (dna)? _dbval : _pbval;

    endgaps = 0;                /* 1 to penalize endgaps */
    ofile = "align.out";        /* output file */

50     nw();                    /* fill in the matrix, get the possible jmps */
    readjmps();                /* get the actual jmps */
    print();                    /* print stats, alignment */

    cleanup(0);                /* unlink any tmp files */
}

```

main

Table 1 (cont')

```

/* do the alignment, return best score: main()
* dna: values in Fitch and Smith, PNAS, 80, 1382-1386, 1983
* pro: PAM 250 values
* When scores are equal, we prefer mismatches to any gap, prefer
* a new gap to extending an ongoing gap, and prefer a gap in seqx
* to a gap in seq y.
*/
nw()
{
    char      *px, *py;          /* seqs and ptrs */
    int        *ndely, *dely;     /* keep track of dely */
    int        ndelx, delx;       /* keep track of delx */
    int        *tmp;             /* for swapping row0, row1 */
    int        mis;              /* score for each type */
    int        ins0, ins1;       /* insertion penalties */
    register   id;               /* diagonal index */
    register   ij;              /* jmp index */
    register   *col0, *col1;     /* score for curr, last row */
    register   xx, yy;          /* index into seqs */

    dx = (struct diag *)g_calloc("to get diags", len0+len1+1, sizeof(struct diag));
    ndely = (int *)g_calloc("to get ndely", len1+1, sizeof(int));
    dely = (int *)g_calloc("to get dely", len1+1, sizeof(int));
    col0 = (int *)g_calloc("to get col0", len1+1, sizeof(int));
    col1 = (int *)g_calloc("to get col1", len1+1, sizeof(int));
    ins0 = (dna)? DINS0 : PINS0;
    ins1 = (dna)? DINS1 : PINS1;
    smax = -10000;
    if (endgaps) {
        for (col0[0] = dely[0] = -ins0, yy = 1; yy <= len1; yy++) {
            col0[yy] = dely[yy] = col0[yy-1] - ins1;
            ndely[yy] = yy;
        }
        col0[0] = 0;          /* Waterman Bull Math Biol 84 */
    }
    else
        for (yy = 1; yy <= len1; yy++)
            dely[yy] = -ins0;

    /* fill in match matrix
    */
    for (px = seqx[0], xx = 1; xx <= len0; px++, xx++) {
        /* initialize first entry in col
        */
        if (endgaps) {
            if (xx == 1)
                col1[0] = delx = -(ins0+ins1);
            else
                col1[0] = delx = col0[0] - ins1;
            ndelx = xx;
        }
        else {
            col1[0] = 0;
            delx = -ins0;
            ndelx = 0;
        }
    }
}

```

Table 1 (cont')**...nw**

```

5   for (py = seqx[1], yy = 1; yy <= len1; py++, yy++) {
        mis = col0[yy-1];
        if (dna)
            mis += (xbm[*px-'A']&xbm[*py-'A'])? DMAT : DMIS;
        else
            mis += _day[*px-'A'][*py-'A'];

10      /* update penalty for del in x seq;
        * favor new del over ongong del
        * ignore MAXGAP if weighting endgaps
        */
        if (endgaps || ndely[yy] < MAXGAP) {
            if (col0[yy] - ins0 >= dely[yy]) {
15                dely[yy] = col0[yy] - (ins0+ins1);
                ndely[yy] = 1;
            } else {
                dely[yy] -= ins1;
                ndely[yy]++;
20            }
        } else {
            if (col0[yy] - (ins0+ins1) >= dely[yy]) {
                dely[yy] = col0[yy] - (ins0+ins1);
                ndely[yy] = 1;
25            } else
                ndely[yy]++;
        }

        /* update penalty for del in y seq;
        * favor new del over ongong del
        */
        if (endgaps || ndelx < MAXGAP) {
            if (col1[yy-1] - ins0 >= delx) {
35                delx = col1[yy-1] - (ins0+ins1);
                ndelx = 1;
            } else {
                delx -= ins1;
                ndelx++;
40            }
        } else {
            if (col1[yy-1] - (ins0+ins1) >= delx) {
                delx = col1[yy-1] - (ins0+ins1);
                ndelx = 1;
45            } else
                ndelx++;
        }

        /* pick the maximum score; we're favoring
        * mis over any del and delx over dely
        */
50
        id = xx - yy + len1 - 1;
        if (mis >= delx && mis >= dely[yy])
55            col1[yy] = mis;

```

...nw

Table 1 (cont')

```

else if (delx >= dely[yy]) {
    col1[yy] = delx;
    ij = dx[id].ijmp;
    if (dx[id].jp.n[0] && (!dna || (ndelx >= MAXJMP
5      && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
        dx[id].ijmp++;
        if (++ij >= MAXJMP) {
            writejumps(id);
            ij = dx[id].ijmp = 0;
10          dx[id].offset = offset;
            offset += sizeof(struct jmp) + sizeof(offset);
        }
    }
    dx[id].jp.n[ij] = ndelx;
    dx[id].jp.x[ij] = xx;
    dx[id].score = delx;
15  }
    else {
        col1[yy] = dely[yy];
        ij = dx[id].ijmp;
        if (dx[id].jp.n[0] && (!dna || (ndely[yy] >= MAXJMP
20      && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
            dx[id].ijmp++;
            if (++ij >= MAXJMP) {
                writejumps(id);
                ij = dx[id].ijmp = 0;
25              dx[id].offset = offset;
                offset += sizeof(struct jmp) + sizeof(offset);
            }
        }
        dx[id].jp.n[ij] = -ndely[yy];
        dx[id].jp.x[ij] = xx;
        dx[id].score = dely[yy];
30    }
    if (xx == len0 && yy < len1) {
        /* last col
        */
        if (endgaps)
            col1[yy] -= ins0+ins1*(len1-yy);
        if (col1[yy] > smax) {
            smax = col1[yy];
            dmax = id;
40        }
    }
}
if (endgaps && xx < len0)
    col1[yy-1] -= ins0+ins1*(len0-xx);
if (col1[yy-1] > smax) {
    smax = col1[yy-1];
    dmax = id;
45  }
tmp = col0; col0 = col1; col1 = tmp;
(void) free((char *)ndely);
(void) free((char *)dely);
(void) free((char *)col0);
55 (void) free((char *)col1);
}

```

Table 1 (cont')

```

/*
*
* print() -- only routine visible outside this module
*
5  * static:
* getmat() -- trace back best path, count matches: print()
* pr_align() -- print alignment of described in array p[]: print()
* dumpblock() -- dump a block of lines with numbers, stars: pr_align()
10 * nums() -- put out a number line: dumpblock()
* putline() -- put out a line (name, [num], seq, [num]): dumpblock()
* stars() -- put a line of stars: dumpblock()
* stripname() -- strip any path and prefix from a seqname
*/

15 #include "nw.h"

#define SPC      3
#define P_LINE   256 /* maximum output line */
#define P_SPC    3    /* space between name or num and seq */

20 extern _day[26][26];
int olen; /* set output line length */
FILE *fx; /* output file */

25 print()
{
    int lx, ly, firstgap, lastgap; /* overlap */

    if ((fx = fopen(ofile, "w")) == 0) {
30         fprintf(stderr, "%s: can't write %s\n", prog, ofile);
        cleanup(1);
    }
    fprintf(fx, "<first sequence: %s (length = %d)\n", namex[0], len0);
    fprintf(fx, "<second sequence: %s (length = %d)\n", namex[1], len1);
35     olen = 60;
    lx = len0;
    ly = len1;
    firstgap = lastgap = 0;
    if (dmax < len1 - 1) { /* leading gap in x */
40         pp[0].spc = firstgap = len1 - dmax - 1;
        ly -= pp[0].spc;
    }
    else if (dmax > len1 - 1) { /* leading gap in y */
45         pp[1].spc = firstgap = dmax - (len1 - 1);
        lx -= pp[1].spc;
    }
    if (dmax0 < len0 - 1) { /* trailing gap in x */
50         lastgap = len0 - dmax0 - 1;
        lx -= lastgap;
    }
    else if (dmax0 > len0 - 1) { /* trailing gap in y */
55         lastgap = dmax0 - (len0 - 1);
        ly -= lastgap;
    }
    getmat(lx, ly, firstgap, lastgap);
    pr_align();
}

```

print

Table 1 (cont')

```

/*
 * trace back the best path, count matches
 */
static
5 getmat(lx, ly, firstgap, lastgap)                                getmat
    int      lx, ly;
    int      firstgap, lastgap;
    /* "core" (minus endgaps) */
    /* leading trailing overlap */
{
    int      nm, i0, i1, siz0, siz1;
10    char     outx[32];
    double    pct;
    register  n0, n1;
    register char *p0, *p1;
    /* get total matches, score
15    */
    i0 = i1 = siz0 = siz1 = 0;
    p0 = seqx[0] + pp[1].spc;
    p1 = seqx[1] + pp[0].spc;
    n0 = pp[1].spc + 1;
20    n1 = pp[0].spc + 1;
    nm = 0;
    while ( *p0 && *p1 ) {
        if (siz0) {
25            p1++;
            n1++;
            siz0--;
        }
        else if (siz1) {
30            p0++;
            n0++;
            siz1--;
        }
        else {
35            if (xbm[*p0-'A']&xbm[*p1-'A'])
                nm++;
            if (n0++ == pp[0].x[i0])
                siz0 = pp[0].n[i0++];
            if (n1++ == pp[1].x[i1])
                siz1 = pp[1].n[i1++];
40            p0++;
            p1++;
        }
    }

45    /* pct homology:
    * if penalizing endgaps, base is the shorter seq
    * else, knock off overhangs and take shorter core
    */
    if (endgaps)
50        lx = (len0 < len1)? len0 : len1;
    else
        lx = (lx < ly)? lx : ly;
    pct = 100.*(double)nm/(double)lx;
    fprintf(fx, "\n");
55    fprintf(fx, "< %d match%s in an overlap of %d: %.2f percent similarity\n",
        nm, (nm == 1)? "" : "es", lx, pct);

```

Table 1 (cont')

```

fprintf(fx, "<gaps in first sequence: %d", gapx);
if (gapx) {
    (void) sprintf(outx, "(%d %s%s)",
        ngapx, (dna)? "base":"residue", (ngapx == 1)? ":" : "s");
    fprintf(fx, "%s", outx);
    fprintf(fx, ", gaps in second sequence: %d", gapy);
    if (gapy) {
        (void) sprintf(outx, "(%d %s%s)",
            ngapy, (dna)? "base":"residue", (ngapy == 1)? ":" : "s");
        fprintf(fx, "%s", outx);
    }
    if (dna)
        fprintf(fx,
            "\n<score: %d (match = %d, mismatch = %d, gap penalty = %d + %d per base)\n",
            smax, DMAT, DMIS, DINS0, DINS1);
    else
        fprintf(fx,
            "\n<score: %d (Dayhoff PAM 250 matrix, gap penalty = %d + %d per residue)\n",
            smax, PINS0, PINS1);
    if (endgaps)
        fprintf(fx,
            "<endgaps penalized. left endgap: %d %s%s, right endgap: %d %s%s\n",
            firstgap, (dna)? "base" : "residue", (firstgap == 1)? ":" : "s",
            lastgap, (dna)? "base" : "residue", (lastgap == 1)? ":" : "s");
    else
        fprintf(fx, "<endgaps not penalized\n");
}
static nm; /* matches in core -- for checking */
static lmax; /* lengths of stripped file names */
static ij[2]; /* jmp index for a path */
static nc[2]; /* number at start of current line */
static ni[2]; /* current elem number -- for gapping */
static siz[2];
static char *ps[2]; /* ptr to current element */
static char *po[2]; /* ptr to next output char slot */
static char out[2][P_LINE]; /* output line */
static char star[P_LINE]; /* set by stars() */
/*
* print alignment of described in struct path pp[]
*/
static
pr_align()
{
    int nn; /* char count */
    int more;
    register i;

    for (i = 0, lmax = 0; i < 2; i++) {
        nn = stripname(namex[i]);
        if (nn > lmax)
            lmax = nn;
        nc[i] = 1;
        ni[i] = 1;
        siz[i] = ij[i] = 0;
        ps[i] = seqx[i];
        po[i] = out[i];
    }
}

```

...getmat

pr_align

Table 1 (cont')

	for (nn = nm = 0, more = 1; more;) {	...pr_align
	for (i = more = 0; i < 2; i++) {	
5	/*	
	* do we have more of this sequence?	
	*/	
	if (!*ps[i])	
	continue;	
10	more++;	
	if (pp[i].spc) { /* leading space */	
	*po[i]++ = ' ';	
	pp[i].spc--;	
	}	
15	else if (siz[i]) { /* in a gap */	
	*po[i]++ = '-';	
	siz[i]--;	
	}	
	else { /* we're putting a seq element	
20	*/	
	*po[i] = *ps[i];	
	if (islower(*ps[i]))	
	*ps[i] = toupper(*ps[i]);	
	po[i]++;	
25	ps[i]++;	
	/*	
	* are we at next gap for this seq?	
	*/	
	if (ni[i] == pp[i].x[ij[i]]) {	
30	/*	
	* we need to merge all gaps	
	* at this location	
	*/	
	siz[i] = pp[i].n[ij[i]++];	
35	while (ni[i] == pp[i].x[ij[i]])	
	siz[i] += pp[i].n[ij[i]++];	
	}	
	ni[i]++;	
	}	
40	} if (++nn == olen !more && nn) {	
	dumpblock();	
	for (i = 0; i < 2; i++)	
	po[i] = out[i];	
45	nn = 0;	
	}	
	}	
	/*	
50	* dump a block of lines, including numbers, stars: pr_align()	
	*/	
	static	
	dumpblock()	dumpblock
	{	
55	register i;	
	for (i = 0; i < 2; i++)	
	*po[i]-- = '\0';	

Table 1 (cont')**...dumpblock**

```

5      (void) putc('\n', fx);
      for (i = 0; i < 2; i++) {
          if (*out[i] && (*out[i] != ' ' || *(po[i]) != ' ')) {
              if (i == 0)
                  nums(i);
              if (i == 0 && *out[1])
                  stars();
              putline(i);
10         if (i == 0 && *out[1])
                  fprintf(fx, star);
              if (i == 1)
                  nums(i);
          }
      }
15  }
  }
  /*
  * put out a number line: dumpblock()
  */
20  static
  nums(ix)
      int    ix;      /* index in out[] holding seq line */
  {
      char    nline[P_LINE];
      register i, j;
      register char *pn, *px, *py;
      for (pn = nline, i = 0; i < lmax+P_SPC; i++, pn++)
          *pn = ' ';
      for (i = nc[ix], py = out[ix]; *py; py++, pn++) {
30         if (*py == ' ' || *py == '-')
              *pn = ' ';
          else {
              if (i%10 == 0 || (i == 1 && nc[ix] != 1)) {
                  j = (i < 0)? -i : i;
35                 for (px = pn; j /= 10, px--)
                      *px = j%10 + '0';
                  if (i < 0)
                      *px = '-';
              }
              else
40                 *pn = ' ';
              i++;
          }
      }
      *pn = '\0';
      nc[ix] = i;
      for (pn = nline; *pn; pn++)
          (void) putc(*pn, fx);
50  (void) putc('\n', fx);
  }
  /*
  * put out a line (name, [num], seq, [num]): dumpblock()
  */
  static
55  putline(ix)
      int    ix;
      {

```

nums**putline**

Table 1 (cont')**...putline**

```

5      int          i;
      register char *px;

      for (px = namex[ix], i = 0; *px && *px != ':'; px++, i++)
          (void) putc(*px, fx);
      for (; i < lmax+P_SPC; i++)
          (void) putc(' ', fx);

10     /* these count from 1:
       * ni[] is current element (from 1)
       * nc[] is number at start of current line
       */
15     for (px = out[ix]; *px; px++)
          (void) putc(*px&0x7F, fx);
      (void) putc('\n', fx);
  }

20  /*
   * put a line of stars (seqs always in out[0], out[1]): dumpblock()
   */
   static
25  stars()
  {
      int          i;
      register char *p0, *p1, cx, *px;

30     if (!*out[0] || (*out[0] == ' ' && *(po[0]) == ' ') ||
        !*out[1] || (*out[1] == ' ' && *(po[1]) == ' '))
          return;
      px = star;
      for (i = lmax+P_SPC; i--;)
35         *px++ = ' ';

      for (p0 = out[0], p1 = out[1]; *p0 && *p1; p0++, p1++) {
          if (isalpha(*p0) && isalpha(*p1)) {

40                 if (xbm[*p0-'A']&xbm[*p1-'A']) {
                        cx = '*';
                        nm++;
                    }
                    else if (!dna && _day[*p0-'A'][*p1-'A'] > 0)
45                         cx = '.';
                    else
                        cx = ' ';
                }
                else
50                 cx = ' ';
                *px++ = cx;
            }
            *px++ = '\n';
            *px = '\0';
55  }

```

stars

Table 1 (cont')

```

/*
 * strip path or prefix from pn, return len: pr_align()
 */
static
5 stripname(pn)                                stripname
    char    *pn;    /* file name (may be path) */
{
    register char    *px, *py;
10     py = 0;
    for (px = pn; *px; px++)
        if (*px == '/')
            py = px + 1;
15     if (py)
        (void) strcpy(pn, py);
    return(strlen(pn));
}
20

```

Table 1 (cont')

```

/*
 * cleanup() -- cleanup any tmp file
 * getseq() -- read in seq, set dna, len, maxlen
 * g_calloc() -- calloc() with error checkin
5  * readjumps() -- get the good jumps, from tmp file if necessary
 * writejumps() -- write a filled array of jumps to a tmp file: nw()
 */
#include "nw.h"
#include <sys/file.h>

10 char    *jname = "/tmp/homgXXXXXXX";          /* tmp file for jumps */
FILE      *fj;
int        cleanup();                          /* cleanup tmp file */
long       lseek();

15 /*
 * remove any tmp file if we blow
 */
cleanup(i)                                     cleanup
{
    int      i;
    if (fj)
        (void) unlink(jname);
    exit(i);
}
/*
 * read, return ptr to seq, set dna, len, maxlen
 * skip lines starting with ';', '<', or '>'
 * seq in upper or lower case
 */
30 char    *
getseq(file, len)                             getseq
{
    char    *file;    /* file name */
    int      *len;    /* seq len */

    {
        char    line[1024], *pseq;
        register char *px, *py;
        int      natgc, tlen;
        FILE      *fp;
        if ((fp = fopen(file, "r")) == 0) {
40             fprintf(stderr, "%s: can't read %s\n", prog, file);
             exit(1);
        }
        tlen = natgc = 0;
        while (fgets(line, 1024, fp)) {
45             if (*line == ';' || *line == '<' || *line == '>')
                 continue;
             for (px = line; *px != '\n'; px++)
                 if (isupper(*px) || islower(*px))
                     tlen++;
50         }
        if ((pseq = malloc((unsigned)(tlen+6))) == 0) {
             fprintf(stderr, "%s: malloc() failed to get %d bytes for %s\n", prog, tlen+6, file);
             exit(1);
        }
        pseq[0] = pseq[1] = pseq[2] = pseq[3] = '\0';
55

```

Table 1 (cont')

...getseq

```

py = pseq + 4;
*len = tlen;
rewind(fp);
5  while (fgets(line, 1024, fp)) {
    if (*line == ';' || *line == '<' || *line == '>')
        continue;
    for (px = line; *px != '\n'; px++) {
10         if (isupper(*px))
            *py++ = *px;
        else if (islower(*px))
            *py++ = toupper(*px);
        if (index("ATGCU", *(py-1)))
            natgc++;
15     }
    *py++ = '\0';
    *py = '\0';
    (void) fclose(fp);
20    dna = natgc > (tlen/3);
    return(pseq+4);
}
char *
g_alloc(msg, nx, sz)
25     char *msg;          /* program, calling routine */
    int nx, sz;          /* number and size of elements */
{
    char *px, *calloc();
30    if ((px = calloc((unsigned)nx, (unsigned)sz)) == 0) {
        if (*msg) {
            fprintf(stderr, "%s: g_alloc() failed %s (n=%d, sz=%d)\n", prog, msg, nx, sz);
            exit(1);
        }
    }
35    return(px);
}

/*
* get final jmps from dx[] or tmp file, set pp[], reset dmax: main()
*/
readjmps()
40 {
    int fd = -1;
    int siz, i0, i1;
45    register i, j, xx;
    if (fj) {
        (void) fclose(fj);
        if ((fd = open(jname, O_RDONLY, 0)) < 0) {
50             fprintf(stderr, "%s: can't open() %s\n", prog, jname);
            cleanup(1);
        }
    }
    for (i = i0 = i1 = 0, dmax0 = dmax, xx = len0; ; i++) {
55         while (1) {
            for (j = dx[dmax].ijmp; j >= 0 && dx[dmax].jp.x[j] >= xx; j--)
                ;

```

g_alloc

readjmps

Table 1 (cont')**...readjumps**

```

5         if (j < 0 && dx[dmax].offset && fj) {
            (void) lseek(fd, dx[dmax].offset, 0);
            (void) read(fd, (char *)&dx[dmax].jp, sizeof(struct jmp));
            (void) read(fd, (char *)&dx[dmax].offset, sizeof(dx[dmax].offset));
            dx[dmax].ijmp = MAXJMP-1;
        }
        else
            break;
    }
10    if (i >= JMPS) {
        fprintf(stderr, "%s: too many gaps in alignment\n", prog);
        cleanup(1);
    }
    if (j >= 0) {
15        siz = dx[dmax].jp.n[j];
        xx = dx[dmax].jp.x[j];
        dmax += siz;
        if (siz < 0) { /* gap in second seq */
20            pp[1].n[i1] = -siz;
            xx += siz;
            /* id = xx - yy + len1 - 1 */
            pp[1].x[i1] = xx - dmax + len1 - 1;
            gapy++;
            ngapy -= siz;
/* ignore MAXGAP when doing endgaps */
25        siz = (-siz < MAXGAP || endgaps)? -siz : MAXGAP;
            i1++;
        }
        else if (siz > 0) { /* gap in first seq */
30            pp[0].n[i0] = siz;
            pp[0].x[i0] = xx;
            gapx++;
            ngapx += siz;
/* ignore MAXGAP when doing endgaps */
35        siz = (siz < MAXGAP || endgaps)? siz : MAXGAP;
            i0++;
        }
    }
    else
        break;
40    }
    /* reverse the order of jumps */
    for (j = 0, i0--; j < i0; j++, i0--) {
        i = pp[0].n[j]; pp[0].n[j] = pp[0].n[i0]; pp[0].n[i0] = i;
        i = pp[0].x[j]; pp[0].x[j] = pp[0].x[i0]; pp[0].x[i0] = i;
45    }
    for (j = 0, i1--; j < i1; j++, i1--) {
        i = pp[1].n[j]; pp[1].n[j] = pp[1].n[i1]; pp[1].n[i1] = i;
        i = pp[1].x[j]; pp[1].x[j] = pp[1].x[i1]; pp[1].x[i1] = i;
50    }
    if (fd >= 0)
        (void) close(fd);
    if (fj) {
        (void) unlink(jname);
        fj = 0;
55        offset = 0;
    }
}

```

Table 1 (cont')

```

/*
 * write a filled jmp struct offset of the prev one (if any): nw()
 */
5  writejumps(ix)                                     writejumps
    int    ix;
    {
        char    *mktemp();
10         if (!fj) {
            if (mktemp(jname) < 0) {
                fprintf(stderr, "%s: can't mktemp() %s\n", prog, jname);
                cleanup(1);
            }
15         if ((fj = fopen(jname, "w")) == 0) {
            fprintf(stderr, "%s: can't write %s\n", prog, jname);
            exit(1);
        }
20         (void) fwrite((char *)&dx[ix].jp, sizeof(struct jmp), 1, fj);
        (void) fwrite((char *)&dx[ix].offset, sizeof(dx[ix].offset), 1, fj);
    }

```

Table 2

TAT	XXXXXXXXXXXXXXXXXX	(Length = 15 amino acids)
Comparison Protein	XXXXXXXXYYYYYYY	(Length = 12 amino acids)

5 % amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the TAT polypeptide) =

10 5 divided by 15 = 33.3%

Table 3

TAT	XXXXXXXXXXXX	(Length = 10 amino acids)
Comparison Protein	XXXXXXXXYYYYYYZZYZ	(Length = 15 amino acids)

15

% amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the TAT polypeptide) =

20

5 divided by 10 = 50%

Table 4

TAT-DNA	NNNNNNNNNNNNNN	(Length = 14 nucleotides)
Comparison DNA	NNNNNNLLLLLLLLLL	(Length = 16 nucleotides)

25

% nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the TAT-DNA nucleic acid sequence) =

30

6 divided by 14 = 42.9%

Table 5

TAT-DNA	NNNNNNNNNNNN	(Length = 12 nucleotides)
Comparison DNA	NNNNLLLVV	(Length = 9 nucleotides)

5 % nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the TAT-DNA nucleic acid sequence) =

10 4 divided by 12 = 33.3%

II. Compositions and Methods of the Invention

A. Anti-TAT Antibodies

15 In one embodiment, the present invention provides anti-TAT antibodies which may find use herein as therapeutic and/or diagnostic agents. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

1. Polyclonal Antibodies

20 Polyclonal antibodies are preferably raised in animals by multiple subcutaneous (sc) or intraperitoneal (ip) injections of the relevant antigen and an adjuvant. It may be useful to conjugate the relevant antigen (especially when synthetic peptides are used) to a protein that is immunogenic in the species to be immunized. For example, the antigen can be conjugated to keyhole limpet hemocyanin (KLH), serum albumin, bovine thyroglobulin, or soybean trypsin inhibitor, using a bifunctional or derivatizing agent, e.g., maleimidobenzoyl sulfosuccinimide ester (conjugation through cysteine residues), N-hydroxysuccinimide (through lysine residues), glutaraldehyde, succinic anhydride, SOCl₂, or R¹N=C=NR, where R and R¹ are different alkyl groups.

25 Animals are immunized against the antigen, immunogenic conjugates, or derivatives by combining, e.g., 100 µg or 5 µg of the protein or conjugate (for rabbits or mice, respectively) with 3 volumes of Freund's complete adjuvant and injecting the solution intradermally at multiple sites. One month later, the animals are boosted with 1/5 to 1/10 the original amount of peptide or conjugate in Freund's complete adjuvant by subcutaneous injection at multiple sites. Seven to 14 days later, the animals are bled and the serum is assayed
30 for antibody titer. Animals are boosted until the titer plateaus. Conjugates also can be made in recombinant cell culture as protein fusions. Also, aggregating agents such as alum are suitably used to enhance the immune response.

2. Monoclonal Antibodies

35 Monoclonal antibodies may be made using the hybridoma method first described by Kohler et al., Nature, 256:495 (1975), or may be made by recombinant DNA methods (U.S. Patent No. 4,816,567).

In the hybridoma method, a mouse or other appropriate host animal, such as a hamster, is immunized

as described above to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the protein used for immunization. Alternatively, lymphocytes may be immunized *in vitro*. After immunization, lymphocytes are isolated and then fused with a myeloma cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, pp.59-103 (Academic Press, 1986)).

5 The hybridoma cells thus prepared are seeded and grown in a suitable culture medium which medium preferably contains one or more substances that inhibit the growth or survival of the unfused, parental myeloma cells (also referred to as fusion partner). For example, if the parental myeloma cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the selective culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine (HAT medium), which substances
10 prevent the growth of HGPRT-deficient cells.

Preferred fusion partner myeloma cells are those that fuse efficiently, support stable high-level production of antibody by the selected antibody-producing cells, and are sensitive to a selective medium that selects against the unfused parental cells. Preferred myeloma cell lines are murine myeloma lines, such as those derived from MOPC-21 and MPC-11 mouse tumors available from the Salk Institute Cell Distribution Center,
15 San Diego, California USA, and SP-2 and derivatives e.g., X63-Ag8-653 cells available from the American Type Culture Collection, Manassas, Virginia, USA. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); and Brodeur et al., Monoclonal Antibody Production Techniques and Applications, pp. 51-63 (Marcel Dekker, Inc., New York, 1987)).

20 Culture medium in which hybridoma cells are growing is assayed for production of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunosorbent assay (ELISA).

The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis described in Munson et al., Anal. Biochem., 107:220 (1980).
25

Once hybridoma cells that produce antibodies of the desired specificity, affinity, and/or activity are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods (Goding, Monoclonal Antibodies: Principles and Practice, pp.59-103 (Academic Press, 1986)). Suitable culture media for this purpose include, for example, D-MEM or RPMI-1640 medium. In addition, the hybridoma cells may
30 be grown *in vivo* as ascites tumors in an animal e.g., by i.p. injection of the cells into mice.

The monoclonal antibodies secreted by the subclones are suitably separated from the culture medium, ascites fluid, or serum by conventional antibody purification procedures such as, for example, affinity chromatography (e.g., using protein A or protein G-Sepharose) or ion-exchange chromatography, hydroxylapatite chromatography, gel electrophoresis, dialysis, etc.

35 DNA encoding the monoclonal antibodies is readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the

heavy and light chains of murine antibodies). The hybridoma cells serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as *E. coli* cells, simian COS cells, Chinese Hamster Ovary (CHO) cells, or myeloma cells that do not otherwise produce antibody protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. Review articles on recombinant expression in bacteria of DNA encoding the antibody include Skerra et al., Curr. Opin. in Immunol., 5:256-262 (1993) and Plückthun, Immunol. Revs. 130:151-188 (1992).

In a further embodiment, monoclonal antibodies or antibody fragments can be isolated from antibody phage libraries generated using the techniques described in McCafferty et al., Nature, 348:552-554 (1990). Clackson et al., Nature, 352:624-628 (1991) and Marks et al., J. Mol. Biol., 222:581-597 (1991) describe the isolation of murine and human antibodies, respectively, using phage libraries. Subsequent publications describe the production of high affinity (nM range) human antibodies by chain shuffling (Marks et al., Bio/Technology, 10:779-783 (1992)), as well as combinatorial infection and *in vivo* recombination as a strategy for constructing very large phage libraries (Waterhouse et al., Nuc. Acids. Res. 21:2265-2266 (1993)). Thus, these techniques are viable alternatives to traditional monoclonal antibody hybridoma techniques for isolation of monoclonal antibodies.

The DNA that encodes the antibody may be modified to produce chimeric or fusion antibody polypeptides, for example, by substituting human heavy chain and light chain constant domain (C_H and C_L) sequences for the homologous murine sequences (U.S. Patent No. 4,816,567; and Morrison, et al., Proc. Natl. Acad. Sci. USA, 81:6851 (1984)), or by fusing the immunoglobulin coding sequence with all or part of the coding sequence for a non-immunoglobulin polypeptide (heterologous polypeptide). The non-immunoglobulin polypeptide sequences can substitute for the constant domains of an antibody, or they are substituted for the variable domains of one antigen-combining site of an antibody to create a chimeric bivalent antibody comprising one antigen-combining site having specificity for an antigen and another antigen-combining site having specificity for a different antigen.

3. Human and Humanized Antibodies

The anti-TAT antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are

those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)].

5 Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

15 The choice of human variable domains, both light and heavy, to be used in making the humanized antibodies is very important to reduce antigenicity and HAMA response (human anti-mouse antibody) when the antibody is intended for human therapeutic use. According to the so-called "best-fit" method, the sequence of the variable domain of a rodent antibody is screened against the entire library of known human variable domain sequences. The human V domain sequence which is closest to that of the rodent is identified and the human framework region (FR) within it accepted for the humanized antibody (Sims et al., J. Immunol. 151:2296 (1993); Chothia et al., J. Mol. Biol., 196:901 (1987)). Another method uses a particular framework region derived from the consensus sequence of all human antibodies of a particular subgroup of light or heavy chains. The same framework may be used for several different humanized antibodies (Carter et al., Proc. Natl. Acad. Sci. USA, 89:4285 (1992); Presta et al., J. Immunol. 151:2623 (1993)).

25 It is further important that antibodies be humanized with retention of high binding affinity for the antigen and other favorable biological properties. To achieve this goal, according to a preferred method, humanized antibodies are prepared by a process of analysis of the parental sequences and various conceptual humanized products using three-dimensional models of the parental and humanized sequences. Three-dimensional immunoglobulin models are commonly available and are familiar to those skilled in the art. Computer programs are available which illustrate and display probable three-dimensional conformational structures of selected candidate immunoglobulin sequences. Inspection of these displays permits analysis of the likely role of the residues in the functioning of the candidate immunoglobulin sequence, i.e., the analysis of residues that influence the ability of the candidate immunoglobulin to bind its antigen. In this way, FR residues can be selected and combined from the recipient and import sequences so that the desired antibody characteristic, such as increased affinity for the target antigen(s), is achieved. In general, the hypervariable region residues are directly and most substantially involved in influencing antigen binding.

30

35

Various forms of a humanized anti-TAT antibody are contemplated. For example, the humanized antibody may be an antibody fragment, such as a Fab, which is optionally conjugated with one or more cytotoxic agent(s) in order to generate an immunoconjugate. Alternatively, the humanized antibody may be an intact antibody, such as an intact IgG1 antibody.

As an alternative to humanization, human antibodies can be generated. For example, it is now possible to produce transgenic animals (e.g., mice) that are capable, upon immunization, of producing a full repertoire of human antibodies in the absence of endogenous immunoglobulin production. For example, it has been described that the homozygous deletion of the antibody heavy-chain joining region (J_H) gene in chimeric and germ-line mutant mice results in complete inhibition of endogenous antibody production. Transfer of the human germ-line immunoglobulin gene array into such germ-line mutant mice will result in the production of human antibodies upon antigen challenge. See, e.g., Jakobovits et al., Proc. Natl. Acad. Sci. USA, 90:2551 (1993); Jakobovits et al., Nature, 362:255-258 (1993); Bruggemann et al., Year in Immuno. 7:33 (1993); U.S. Patent Nos. 5,545,806, 5,569,825, 5,591,669 (all of GenPharm); 5,545,807; and WO 97/17852.

Alternatively, phage display technology (McCafferty et al., Nature 348:552-553 [1990]) can be used to produce human antibodies and antibody fragments *in vitro*, from immunoglobulin variable (V) domain gene repertoires from unimmunized donors. According to this technique, antibody V domain genes are cloned in-frame into either a major or minor coat protein gene of a filamentous bacteriophage, such as M13 or fd, and displayed as functional antibody fragments on the surface of the phage particle. Because the filamentous particle contains a single-stranded DNA copy of the phage genome, selections based on the functional properties of the antibody also result in selection of the gene encoding the antibody exhibiting those properties. Thus, the phage mimics some of the properties of the B-cell. Phage display can be performed in a variety of formats, reviewed in, e.g., Johnson, Kevin S. and Chiswell, David J., Current Opinion in Structural Biology 3:564-571 (1993). Several sources of V-gene segments can be used for phage display. Clackson et al. Nature, 352:624-628 (1991) isolated a diverse array of anti-oxazolone antibodies from a small random combinatorial library of V genes derived from the spleens of immunized mice. A repertoire of V genes from unimmunized human donors can be constructed and antibodies to a diverse array of antigens (including self-antigens) can be isolated essentially following the techniques described by Marks et al., J. Mol. Biol. 222:581-597 (1991), or Griffith et al., EMBO J. 12:725-734 (1993). See, also, U.S. Patent Nos. 5,565,332 and 5,573,905.

As discussed above, human antibodies may also be generated by *in vitro* activated B cells (see U.S. Patents 5,567,610 and 5,229,275).

4. Antibody fragments

In certain circumstances there are advantages of using antibody fragments, rather than whole antibodies. The smaller size of the fragments allows for rapid clearance, and may lead to improved access to solid tumors.

Various techniques have been developed for the production of antibody fragments. Traditionally, these fragments were derived via proteolytic digestion of intact antibodies (see, e.g., Morimoto et al., Journal of Biochemical and Biophysical Methods 24:107-117 (1992); and Brennan et al., Science, 229:81 (1985)).

However, these fragments can now be produced directly by recombinant host cells. Fab, Fv and ScFv antibody fragments can all be expressed in and secreted from *E. coli*, thus allowing the facile production of large amounts of these fragments. Antibody fragments can be isolated from the antibody phage libraries discussed above. Alternatively, Fab'-SH fragments can be directly recovered from *E. coli* and chemically coupled to form F(ab')₂ fragments (Carter et al., Bio/Technology 10:163-167 (1992)). According to another approach, F(ab')₂ fragments can be isolated directly from recombinant host cell culture. Fab and F(ab')₂ fragment with increased in vivo half-life comprising a salvage receptor binding epitope residues are described in U.S. Patent No. 5,869,046. Other techniques for the production of antibody fragments will be apparent to the skilled practitioner. In other embodiments, the antibody of choice is a single chain Fv fragment (scFv). See WO 93/16185; U.S. Patent No. 5,571,894; and U.S. Patent No. 5,587,458. Fv and sFv are the only species with intact combining sites that are devoid of constant regions; thus, they are suitable for reduced nonspecific binding during in vivo use. sFv fusion proteins may be constructed to yield fusion of an effector protein at either the amino or the carboxy terminus of an sFv. See Antibody Engineering, ed. Borrebaeck, supra. The antibody fragment may also be a "linear antibody", e.g., as described in U.S. Patent 5,641,870 for example. Such linear antibody fragments may be monospecific or bispecific.

5. Bispecific Antibodies

Bispecific antibodies are antibodies that have binding specificities for at least two different epitopes. Exemplary bispecific antibodies may bind to two different epitopes of a TAT protein as described herein. Other such antibodies may combine a TAT binding site with a binding site for another protein. Alternatively, an anti-TAT arm may be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD3), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16), so as to focus and localize cellular defense mechanisms to the TAT-expressing cell. Bispecific antibodies may also be used to localize cytotoxic agents to cells which express TAT. These antibodies possess a TAT-binding arm and an arm which binds the cytotoxic agent (e.g., saporin, anti-interferon-α, vinca alkaloid, ricin A chain, methotrexate or radioactive isotope hapten). Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g., F(ab')₂ bispecific antibodies).

WO 96/16673 describes a bispecific anti-ErbB2/anti-FcγRIII antibody and U.S. Patent No. 5,837,234 discloses a bispecific anti-ErbB2/anti-FcγRI antibody. A bispecific anti-ErbB2/Fc α antibody is shown in WO98/02463. U.S. Patent No. 5,821,337 teaches a bispecific anti-ErbB2/anti-CD3 antibody.

Methods for making bispecific antibodies are known in the art. Traditional production of full length bispecific antibodies is based on the co-expression of two immunoglobulin heavy chain-light chain pairs, where the two chains have different specificities (Millstein et al., Nature 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of 10 different antibody molecules, of which only one has the correct bispecific structure. Purification of the correct molecule, which is usually done by affinity chromatography steps, is rather cumbersome, and the product yields are low. Similar procedures are disclosed in WO 93/08829, and in Traunecker et al., EMBO J. 10:3655-3659 (1991).

According to a different approach, antibody variable domains with the desired binding specificities (antibody-antigen combining sites) are fused to immunoglobulin constant domain sequences. Preferably, the fusion is with an Ig heavy chain constant domain, comprising at least part of the hinge, C_H2, and C_H3 regions. It is preferred to have the first heavy-chain constant region (C_H1) containing the site necessary for light chain bonding, present in at least one of the fusions. DNAs encoding the immunoglobulin heavy chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host cell. This provides for greater flexibility in adjusting the mutual proportions of the three polypeptide fragments in embodiments when unequal ratios of the three polypeptide chains used in the construction provide the optimum yield of the desired bispecific antibody. It is, however, possible to insert the coding sequences for two or all three polypeptide chains into a single expression vector when the expression of at least two polypeptide chains in equal ratios results in high yields or when the ratios have no significant affect on the yield of the desired chain combination.

In a preferred embodiment of this approach, the bispecific antibodies are composed of a hybrid immunoglobulin heavy chain with a first binding specificity in one arm, and a hybrid immunoglobulin heavy chain-light chain pair (providing a second binding specificity) in the other arm. It was found that this asymmetric structure facilitates the separation of the desired bispecific compound from unwanted immunoglobulin chain combinations, as the presence of an immunoglobulin light chain in only one half of the bispecific molecule provides for a facile way of separation. This approach is disclosed in WO 94/04690. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology 121:210 (1986).

According to another approach described in U.S. Patent No. 5,731,168, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the C_H3 domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g., tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g., alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies include cross-linked or "heteroconjugate" antibodies. For example, one of the antibodies in the heteroconjugate can be coupled to avidin, the other to biotin. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360, WO 92/200373, and EP 03089). Heteroconjugate antibodies may be made using any convenient cross-linking methods. Suitable cross-linking agents are well known in the art, and are disclosed in U.S. Patent No. 4,676,980, along with a number of cross-linking techniques.

Techniques for generating bispecific antibodies from antibody fragments have also been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate

F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent, sodium arsenite, to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Recent progress has facilitated the direct recovery of Fab'-SH fragments from *E. coli*, which can be chemically coupled to form bispecific antibodies. Shalaby et al., *J. Exp. Med.* 175: 217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling *in vitro* to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., *J. Immunol.* 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., *Proc. Natl. Acad. Sci. USA* 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a V_H connected to a V_L by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See Gruber et al., *J. Immunol.*, 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., *J. Immunol.* 147:60 (1991).

6. Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Patent No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

7. Multivalent Antibodies

A multivalent antibody may be internalized (and/or catabolized) faster than a bivalent antibody by a cell expressing an antigen to which the antibodies bind. The antibodies of the present invention can be multivalent antibodies (which are other than of the IgM class) with three or more antigen binding sites (e.g. tetravalent antibodies), which can be readily produced by recombinant expression of nucleic acid encoding the polypeptide chains of the antibody. The multivalent antibody can comprise a dimerization domain and three or more antigen binding sites. The preferred dimerization domain comprises (or consists of) an Fc region or a hinge region. In this scenario, the antibody will comprise an Fc region and three or more antigen binding sites amino-terminal to the Fc region. The preferred multivalent antibody herein comprises (or consists of) three to about eight, but preferably four, antigen binding sites. The multivalent antibody comprises at least one polypeptide chain (and preferably two polypeptide chains), wherein the polypeptide chain(s) comprise two or more variable domains. For instance, the polypeptide chain(s) may comprise $VD1-(X1)_n-VD2-(X2)_n-Fc$, wherein VD1 is a first variable domain, VD2 is a second variable domain, Fc is one polypeptide chain of an Fc region, X1 and X2 represent an amino acid or polypeptide, and n is 0 or 1. For instance, the polypeptide chain(s) may comprise: VH-CH1-flexible linker-VH-CH1-Fc region chain; or VH-CH1-VH-CH1-Fc region chain. The multivalent antibody herein preferably further comprises at least two (and preferably four) light chain variable domain polypeptides. The multivalent antibody herein may, for instance, comprise from about two to about eight light chain variable domain polypeptides. The light chain variable domain polypeptides contemplated here comprise a light chain variable domain and, optionally, further comprise a CL domain.

8. Effector Function Engineering

It may be desirable to modify the antibody of the invention with respect to effector function, e.g., so as to enhance antigen-dependent cell-mediated cytotoxicity (ADCC) and/or complement dependent cytotoxicity (CDC) of the antibody. This may be achieved by introducing one or more amino acid substitutions in an Fc region of the antibody. Alternatively or additionally, cysteine residue(s) may be introduced in the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med. 176:1191-1195 (1992) and Shopes, B. J. Immunol. 148:2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity may also be prepared using heterobifunctional cross-linkers as described in Wolff et al., Cancer Research 53:2560-2565 (1993). Alternatively, an antibody can be engineered which has dual Fc regions and may thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design 3:219-230 (1989).

To increase the serum half life of the antibody, one may incorporate a salvage receptor binding epitope into the antibody (especially an antibody fragment) as described in U.S. Patent 5,739,277, for example. As used herein, the term "salvage receptor binding epitope" refers to an epitope of the Fc region of an IgG molecule (e.g., IgG₁, IgG₂, IgG₃, or IgG₄) that is responsible for increasing the *in vivo* serum half-life of the IgG molecule.

9. Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic

agent such as a chemotherapeutic agent, a growth inhibitory agent, a toxin (*e.g.*, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolacca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re . Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta *et al.*, Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

Conjugates of an antibody and one or more small molecule toxins, such as a calicheamicin, maytansinoids, a trichothene, and CC1065, and the derivatives of these toxins that have toxin activity, are also contemplated herein.

Maytansine and maytansinoids

In one preferred embodiment, an anti-TAT antibody (full length or fragments) of the invention is conjugated to one or more maytansinoid molecules.

Maytansinoids are mitototic inhibitors which act by inhibiting tubulin polymerization. Maytansine was first isolated from the east African shrub *Maytenus serrata* (U.S. Patent No. 3,896,111). Subsequently, it was discovered that certain microbes also produce maytansinoids, such as maytansinol and C-3 maytansinol esters (U.S. Patent No. 4,151,042). Synthetic maytansinol and derivatives and analogues thereof are disclosed, for example, in U.S. Patent Nos. 4,137,230; 4,248,870; 4,256,746; 4,260,608; 4,265,814; 4,294,757; 4,307,016; 4,308,268; 4,308,269; 4,309,428; 4,313,946; 4,315,929; 4,317,821; 4,322,348; 4,331,598; 4,361,650; 4,364,866; 4,424,219; 4,450,254; 4,362,663; and 4,371,533, the disclosures of which are hereby expressly incorporated by reference.

Maytansinoid-antibody conjugates

In an attempt to improve their therapeutic index, maytansine and maytansinoids have been conjugated to antibodies specifically binding to tumor cell antigens. Immunoconjugates containing maytansinoids and their therapeutic use are disclosed, for example, in U.S. Patent Nos. 5,208,020, 5,416,064 and European Patent EP

0 425 235 B1, the disclosures of which are hereby expressly incorporated by reference. Liu et al., Proc. Natl. Acad. Sci. USA 93:8618-8623 (1996) described immunoconjugates comprising a maytansinoid designated DM1 linked to the monoclonal antibody C242 directed against human colorectal cancer. The conjugate was found to be highly cytotoxic towards cultured colon cancer cells, and showed antitumor activity in an *in vivo* tumor growth assay. Chari et al., Cancer Research 52:127-131 (1992) describe immunoconjugates in which a
5 maytansinoid was conjugated via a disulfide linker to the murine antibody A7 binding to an antigen on human colon cancer cell lines, or to another murine monoclonal antibody TA.1 that binds the HER-2/*neu* oncogene. The cytotoxicity of the TA.1-maytansinoid conjugate was tested *in vitro* on the human breast cancer cell line SK-BR-3, which expresses 3×10^5 HER-2 surface antigens per cell. The drug conjugate achieved a degree of cytotoxicity similar to the free maytansinoid drug, which could be increased by increasing the number of
10 maytansinoid molecules per antibody molecule. The A7-maytansinoid conjugate showed low systemic cytotoxicity in mice.

Anti-TAT polypeptide antibody-maytansinoid conjugates (immunoconjugates)

Anti-TAT antibody-maytansinoid conjugates are prepared by chemically linking an anti-TAT antibody to a maytansinoid molecule without significantly diminishing the biological activity of either the antibody or the
15 maytansinoid molecule. An average of 3-4 maytansinoid molecules conjugated per antibody molecule has shown efficacy in enhancing cytotoxicity of target cells without negatively affecting the function or solubility of the antibody, although even one molecule of toxin/antibody would be expected to enhance cytotoxicity over the use of naked antibody. Maytansinoids are well known in the art and can be synthesized by known techniques or isolated from natural sources. Suitable maytansinoids are disclosed, for example, in U.S. Patent No.
20 5,208,020 and in the other patents and nonpatent publications referred to hereinabove. Preferred maytansinoids are maytansinol and maytansinol analogues modified in the aromatic ring or at other positions of the maytansinol molecule, such as various maytansinol esters.

There are many linking groups known in the art for making antibody-maytansinoid conjugates, including, for example, those disclosed in U.S. Patent No. 5,208,020 or EP Patent 0 425 235 B1, and Chari
25 et al., Cancer Research 52:127-131 (1992). The linking groups include disulfide groups, thioether groups, acid labile groups, photolabile groups, peptidase labile groups, or esterase labile groups, as disclosed in the above-identified patents, disulfide and thioether groups being preferred.

Conjugates of the antibody and maytansinoid may be made using a variety of bifunctional protein coupling agents such as N-succinimidyl-3-(2-pyridyldithio) propionate (SPDP), succinimidyl-4-(N-
30 maleimidomethyl) cyclohexane-1-carboxylate, iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as toluene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). Particularly preferred coupling agents
35 include N-succinimidyl-3-(2-pyridyldithio) propionate (SPDP) (Carlsson et al. Biochem. J. 173:723-737 [1978]) and N-succinimidyl-4-(2-pyridylthio)pentanoate (SPP) to provide for a disulfide linkage.

The linker may be attached to the maytansinoid molecule at various positions, depending on the type of the link. For example, an ester linkage may be formed by reaction with a hydroxyl group using conventional coupling techniques. The reaction may occur at the C-3 position having a hydroxyl group, the C-14 position modified with hydroxymethyl, the C-15 position modified with a hydroxyl group, and the C-20 position having a hydroxyl group. In a preferred embodiment, the linkage is formed at the C-3 position of maytansinol or a
5 maytansinol analogue.

Calicheamicin

Another immunoconjugate of interest comprises an anti-TAT antibody conjugated to one or more calicheamicin molecules. The calicheamicin family of antibiotics are capable of producing double-stranded DNA breaks at sub-picomolar concentrations. For the preparation of conjugates of the calicheamicin family, see U.S. patents 5,712,374, 5,714,586, 5,739,116, 5,767,285, 5,770,701, 5,770,710, 5,773,001, 5,877,296
10 (all to American Cyanamid Company). Structural analogues of calicheamicin which may be used include, but are not limited to, γ_1^I , α_2^I , α_3^I , N-acetyl- γ_1^I , PSAG and θ_1^I (Hinman et al., Cancer Research 53:3336-3342 (1993), Lode et al., Cancer Research 58:2925-2928 (1998) and the aforementioned U.S. patents to American Cyanamid). Another anti-tumor drug that the antibody can be conjugated is QFA which is an antifolate. Both
15 calicheamicin and QFA have intracellular sites of action and do not readily cross the plasma membrane. Therefore, cellular uptake of these agents through antibody mediated internalization greatly enhances their cytotoxic effects.

Other cytotoxic agents

Other antitumor agents that can be conjugated to the anti-TAT antibodies of the invention include
20 BCNU, streptozocin, vincristine and 5-fluorouracil, the family of agents known collectively LL-E33288 complex described in U.S. patents 5,053,394, 5,770,710, as well as esperamicins (U.S. patent 5,877,296).

Enzymatically active toxins and fragments thereof which can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A
25 chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcun, crocin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin and the tricothecenes. See, for example, WO 93/21232 published October 28, 1993.

The present invention further contemplates an immunoconjugate formed between an antibody and a
30 compound with nucleolytic activity (e.g., a ribonuclease or a DNA endonuclease such as a deoxyribonuclease; DNase).

For selective destruction of the tumor, the antibody may comprise a highly radioactive atom. A variety of radioactive isotopes are available for the production of radioconjugated anti-TAT antibodies. Examples include At^{211} , I^{131} , I^{125} , Y^{90} , Re^{186} , Re^{188} , Sm^{153} , Bi^{212} , P^{32} , Pb^{212} and radioactive isotopes of Lu. When the
35 conjugate is used for diagnosis, it may comprise a radioactive atom for scintigraphic studies, for example tc^{99m} or I^{123} , or a spin label for nuclear magnetic resonance (NMR) imaging (also known as magnetic resonance

imaging, mri), such as iodine-123 again, iodine-131, indium-111, fluorine-19, carbon-13, nitrogen-15, oxygen-17, gadolinium, manganese or iron.

The radio- or other labels may be incorporated in the conjugate in known ways. For example, the peptide may be biosynthesized or may be synthesized by chemical amino acid synthesis using suitable amino acid precursors involving, for example, fluorine-19 in place of hydrogen. Labels such as ^{99m}Tc or ^{123}I , ^{186}Re , ^{188}Re and ^{111}In can be attached via a cysteine residue in the peptide. Yttrium-90 can be attached via a lysine residue. The IODOGEN method (Fraker et al (1978) Biochem. Biophys. Res. Commun. 80: 49-57 can be used to incorporate iodine-123. "Monoclonal Antibodies in Immunoscintigraphy" (Chatal, CRC Press 1989) describes other methods in detail.

Conjugates of the antibody and cytotoxic agent may be made using a variety of bifunctional protein coupling agents such as N-succinimidyl-3-(2-pyridyldithio) propionate (SPDP), succinimidyl-4-(N-maleimidomethyl) cyclohexane-1-carboxylate, iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science 238:1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026. The linker may be a "cleavable linker" facilitating release of the cytotoxic drug in the cell. For example, an acid-labile linker, peptidase-sensitive linker, photolabile linker, dimethyl linker or disulfide-containing linker (Chari et al., Cancer Research 52:127-131 (1992); U.S. Patent No. 5,208,020) may be used.

Alternatively, a fusion protein comprising the anti-TAT antibody and cytotoxic agent may be made, e.g., by recombinant techniques or peptide synthesis. The length of DNA may comprise respective regions encoding the two portions of the conjugate either adjacent one another or separated by a region encoding a linker peptide which does not destroy the desired properties of the conjugate.

In yet another embodiment, the antibody may be conjugated to a "receptor" (such streptavidin) for utilization in tumor pre-targeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) which is conjugated to a cytotoxic agent (e.g., a radionucleotide).

10. Immunoliposomes

The anti-TAT antibodies disclosed herein may also be formulated as immunoliposomes. A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein et al., Proc. Natl. Acad. Sci. USA 82:3688 (1985); Hwang et al., Proc. Natl. Acad. Sci. USA 77:4030 (1980); U.S. Pat. Nos. 4,485,045 and 4,544,545;

and WO97/38731 published October 23, 1997. Liposomes with enhanced circulation time are disclosed in U.S. Patent No. 5,013,556.

Particularly useful liposomes can be generated by the reverse phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin et al., *J. Biol. Chem.* 257:286-288 (1982) via a disulfide interchange reaction. A chemotherapeutic agent is optionally contained within the liposome. See Gabizon et al., *J. National Cancer Inst.* 81(19):1484 (1989).

B. TAT Binding Oligopeptides

TAT binding oligopeptides of the present invention are oligopeptides that bind, preferably specifically, to a TAT polypeptide as described herein. TAT binding oligopeptides may be chemically synthesized using known oligopeptide synthesis methodology or may be prepared and purified using recombinant technology. TAT binding oligopeptides are usually at least about 5 amino acids in length, alternatively at least about 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100 amino acids in length or more, wherein such oligopeptides that are capable of binding, preferably specifically, to a TAT polypeptide as described herein. TAT binding oligopeptides may be identified without undue experimentation using well known techniques. In this regard, it is noted that techniques for screening oligopeptide libraries for oligopeptides that are capable of specifically binding to a polypeptide target are well known in the art (see, e.g., U.S. Patent Nos. 5,556,762, 5,750,373, 4,708,871, 4,833,092, 5,223,409, 5,403,484, 5,571,689, 5,663,143; PCT Publication Nos. WO 84/03506 and WO84/03564; Geysen et al., *Proc. Natl. Acad. Sci. U.S.A.*, 81:3998-4002 (1984); Geysen et al., *Proc. Natl. Acad. Sci. U.S.A.*, 82:178-182 (1985); Geysen et al., in *Synthetic Peptides as Antigens*, 130-149 (1986); Geysen et al., *J. Immunol. Meth.*, 102:259-274 (1987); Schoofs et al., *J. Immunol.*, 140:611-616 (1988), Cwirla, S. E. et al. (1990) *Proc. Natl. Acad. Sci. USA*, 87:6378; Lowman, H.B. et al. (1991) *Biochemistry*, 30:10832; Clackson, T. et al. (1991) *Nature*, 352: 624; Marks, J. D. et al. (1991), *J. Mol. Biol.*, 222:581; Kang, A.S. et al. (1991) *Proc. Natl. Acad. Sci. USA*, 88:8363, and Smith, G. P. (1991) *Current Opin. Biotechnol.*, 2:668).

In this regard, bacteriophage (phage) display is one well known technique which allows one to screen large oligopeptide libraries to identify member(s) of those libraries which are capable of specifically binding to a polypeptide target. Phage display is a technique by which variant polypeptides are displayed as fusion proteins to the coat protein on the surface of bacteriophage particles (Scott, J.K. and Smith, G. P. (1990) *Science* 249: 386). The utility of phage display lies in the fact that large libraries of selectively randomized protein variants (or randomly cloned cDNAs) can be rapidly and efficiently sorted for those sequences that bind to a target molecule with high affinity. Display of peptide (Cwirla, S. E. et al. (1990) *Proc. Natl. Acad. Sci.*

USA, 87:6378) or protein (Lowman, H.B. et al. (1991) Biochemistry, 30:10832; Clackson, T. et al. (1991) Nature, 352: 624; Marks, J. D. et al. (1991), J. Mol. Biol., 222:581; Kang, A.S. et al. (1991) Proc. Natl. Acad. Sci. USA, 88:8363) libraries on phage have been used for screening millions of polypeptides or oligopeptides for ones with specific binding properties (Smith, G. P. (1991) Current Opin. Biotechnol., 2:668). Sorting phage libraries of random mutants requires a strategy for constructing and propagating a large number of variants, a procedure for affinity purification using the target receptor, and a means of evaluating the results of binding enrichments. U.S. Patent Nos. 5,223,409, 5,403,484, 5,571,689, and 5,663,143.

Although most phage display methods have used filamentous phage, lambdoid phage display systems (WO 95/34683; U.S. 5,627,024), T4 phage display systems (Ren, Z-J. et al. (1998) Gene 215:439; Zhu, Z. (1997) CAN 33:534; Jiang, J. et al. (1997) can 128:44380; Ren, Z-J. et al. (1997) CAN 127:215644; Ren, Z-J. (1996) Protein Sci. 5:1833; Efimov, V. P. et al. (1995) Virus Genes 10:173) and T7 phage display systems (Smith, G. P. and Scott, J.K. (1993) Methods in Enzymology, 217, 228-257; U.S. 5,766,905) are also known.

Many other improvements and variations of the basic phage display concept have now been developed. These improvements enhance the ability of display systems to screen peptide libraries for binding to selected target molecules and to display functional proteins with the potential of screening these proteins for desired properties. Combinatorial reaction devices for phage display reactions have been developed (WO 98/14277) and phage display libraries have been used to analyze and control bimolecular interactions (WO 98/20169; WO 98/20159) and properties of constrained helical peptides (WO 98/20036). WO 97/35196 describes a method of isolating an affinity ligand in which a phage display library is contacted with one solution in which the ligand will bind to a target molecule and a second solution in which the affinity ligand will not bind to the target molecule, to selectively isolate binding ligands. WO 97/46251 describes a method of biopanning a random phage display library with an affinity purified antibody and then isolating binding phage, followed by a micropanning process using microplate wells to isolate high affinity binding phage. The use of *Staphylococcus aureus* protein A as an affinity tag has also been reported (Li et al. (1998) Mol Biotech., 9:187). WO 97/47314 describes the use of substrate subtraction libraries to distinguish enzyme specificities using a combinatorial library which may be a phage display library. A method for selecting enzymes suitable for use in detergents using phage display is described in WO 97/09446. Additional methods of selecting specific binding proteins are described in U.S. Patent Nos. 5,498,538, 5,432,018, and WO 98/15833.

Methods of generating peptide libraries and screening these libraries are also disclosed in U.S. Patent Nos. 5,723,286, 5,432,018, 5,580,717, 5,427,908, 5,498,530, 5,770,434, 5,734,018, 5,698,426, 5,763,192, and 5,723,323.

C. TAT Binding Organic Molecules

TAT binding organic molecules are organic molecules other than oligopeptides or antibodies as defined herein that bind, preferably specifically, to a TAT polypeptide as described herein. TAT binding organic molecules may be identified and chemically synthesized using known methodology (see, e.g., PCT Publication Nos. WO00/00823 and WO00/39585). TAT binding organic molecules are usually less than about 2000 daltons in size, alternatively less than about 1500, 750, 500, 250 or 200 daltons in size, wherein such organic molecules

that are capable of binding, preferably specifically, to a TAT polypeptide as described herein may be identified without undue experimentation using well known techniques. In this regard, it is noted that techniques for screening organic molecule libraries for molecules that are capable of binding to a polypeptide target are well known in the art (see, e.g., PCT Publication Nos. WO00/00823 and WO00/39585). TAT binding organic molecules may be, for example, aldehydes, ketones, oximes, hydrazones, semicarbazones, carbazides, primary amines, secondary amines, tertiary amines, N-substituted hydrazines, hydrazides, alcohols, ethers, thiols, thioethers, disulfides, carboxylic acids, esters, amides, ureas, carbamates, carbonates, ketals, thioketals, acetals, thioacetals, aryl halides, aryl sulfonates, alkyl halides, alkyl sulfonates, aromatic compounds, heterocyclic compounds, anilines, alkenes, alkynes, diols, amino alcohols, oxazolidines, oxazolines, thiazolidines, thiazolines, enamines, sulfonamides, epoxides, aziridines, isocyanates, sulfonyl chlorides, diazo compounds, acid chlorides, or the like.

D. Screening for Anti-TAT Antibodies, TAT Binding Oligopeptides and TAT Binding Organic Molecules With the Desired Properties

Techniques for generating antibodies, oligopeptides and organic molecules that bind to TAT polypeptides have been described above. One may further select antibodies, oligopeptides or other organic molecules with certain biological characteristics, as desired.

The growth inhibitory effects of an anti-TAT antibody, oligopeptide or other organic molecule of the invention may be assessed by methods known in the art, e.g., using cells which express a TAT polypeptide either endogenously or following transfection with the TAT gene. For example, appropriate tumor cell lines and TAT-transfected cells may be treated with an anti-TAT monoclonal antibody, oligopeptide or other organic molecule of the invention at various concentrations for a few days (e.g., 2-7) days and stained with crystal violet or MTT or analyzed by some other colorimetric assay. Another method of measuring proliferation would be by comparing ³H-thymidine uptake by the cells treated in the presence or absence of an anti-TAT antibody, TAT binding oligopeptide or TAT binding organic molecule of the invention. After treatment, the cells are harvested and the amount of radioactivity incorporated into the DNA quantitated in a scintillation counter. Appropriate positive controls include treatment of a selected cell line with a growth inhibitory antibody known to inhibit growth of that cell line. Growth inhibition of tumor cells *in vivo* can be determined in various ways known in the art. Preferably, the tumor cell is one that overexpresses a TAT polypeptide. Preferably, the anti-TAT antibody, TAT binding oligopeptide or TAT binding organic molecule will inhibit cell proliferation of a TAT-expressing tumor cell *in vitro* or *in vivo* by about 25-100% compared to the untreated tumor cell, more preferably, by about 30-100%, and even more preferably by about 50-100% or 70-100%, in one embodiment, at an antibody concentration of about 0.5 to 30 µg/ml. Growth inhibition can be measured at an antibody concentration of about 0.5 to 30 µg/ml or about 0.5 nM to 200 nM in cell culture, where the growth inhibition is determined 1-10 days after exposure of the tumor cells to the antibody. The antibody is growth inhibitory *in vivo* if administration of the anti-TAT antibody at about 1 µg/kg to about 100 mg/kg body weight results in reduction in tumor size or reduction of tumor cell proliferation within about 5 days to 3 months from the first administration of the antibody, preferably within about 5 to 30 days.

To select for an anti-TAT antibody, TAT binding oligopeptide or TAT binding organic molecule which induces cell death, loss of membrane integrity as indicated by, e.g., propidium iodide (PI), trypan blue or 7AAD uptake may be assessed relative to control. A PI uptake assay can be performed in the absence of complement and immune effector cells. TAT polypeptide-expressing tumor cells are incubated with medium alone or medium containing the appropriate anti-TAT antibody (e.g., at about 10 µg/ml), TAT binding oligopeptide or TAT binding organic molecule. The cells are incubated for a 3 day time period. Following each treatment, cells are washed and aliquoted into 35 mm strainer-capped 12 x 75 tubes (1ml per tube, 3 tubes per treatment group) for removal of cell clumps. Tubes then receive PI (10 µg/ml). Samples may be analyzed using a FACSCAN® flow cytometer and FACSCONVERT® CellQuest software (Becton Dickinson). Those anti-TAT antibodies, TAT binding oligopeptides or TAT binding organic molecules that induce statistically significant levels of cell death as determined by PI uptake may be selected as cell death-inducing anti-TAT antibodies, TAT binding oligopeptides or TAT binding organic molecules.

To screen for antibodies, oligopeptides or other organic molecules which bind to an epitope on a TAT polypeptide bound by an antibody of interest, a routine cross-blocking assay such as that described in Antibodies, A Laboratory Manual, Cold Spring Harbor Laboratory, Ed Harlow and David Lane (1988), can be performed. This assay can be used to determine if a test antibody, oligopeptide or other organic molecule binds the same site or epitope as a known anti-TAT antibody. Alternatively, or additionally, epitope mapping can be performed by methods known in the art. For example, the antibody sequence can be mutagenized such as by alanine scanning, to identify contact residues. The mutant antibody is initially tested for binding with polyclonal antibody to ensure proper folding. In a different method, peptides corresponding to different regions of a TAT polypeptide can be used in competition assays with the test antibodies or with a test antibody and an antibody with a characterized or known epitope.

E. Antibody Dependent Enzyme Mediated Prodrug Therapy (ADEPT)

The antibodies of the present invention may also be used in ADEPT by conjugating the antibody to a prodrug-activating enzyme which converts a prodrug (e.g., a peptidyl chemotherapeutic agent, see WO81/01145) to an active anti-cancer drug. See, for example, WO 88/07378 and U.S. Patent No. 4,975,278.

The enzyme component of the immunoconjugate useful for ADEPT includes any enzyme capable of acting on a prodrug in such a way so as to convert it into its more active, cytotoxic form.

Enzymes that are useful in the method of this invention include, but are not limited to, alkaline phosphatase useful for converting phosphate-containing prodrugs into free drugs; arylsulfatase useful for converting sulfate-containing prodrugs into free drugs; cytosine deaminase useful for converting non-toxic 5-fluorocytosine into the anti-cancer drug, 5-fluorouracil; proteases, such as serratio protease, thermolysin, subtilisin, carboxypeptidases and cathepsins (such as cathepsins B and L), that are useful for converting peptide-containing prodrugs into free drugs; D-alanylcarboxypeptidases, useful for converting prodrugs that contain D-amino acid substituents; carbohydrate-cleaving enzymes such as β-galactosidase and neuraminidase useful for converting glycosylated prodrugs into free drugs; β-lactamase useful for converting drugs derivatized with β-lactams into free drugs; and penicillin amidases, such as penicillin V amidase or penicillin G amidase, useful

for converting drugs derivatized at their amine nitrogens with phenoxyacetyl or phenylacetyl groups, respectively, into free drugs. Alternatively, antibodies with enzymatic activity, also known in the art as "abzymes", can be used to convert the prodrugs of the invention into free active drugs (see, e.g., Massey, Nature 328:457-458 (1987)). Antibody-abzyme conjugates can be prepared as described herein for delivery of the abzyme to a tumor cell population.

5 The enzymes of this invention can be covalently bound to the anti-TAT antibodies by techniques well known in the art such as the use of the heterobifunctional crosslinking reagents discussed above. Alternatively, fusion proteins comprising at least the antigen binding region of an antibody of the invention linked to at least a functionally active portion of an enzyme of the invention can be constructed using recombinant DNA techniques well known in the art (see, e.g., Neuberger et al., Nature 312:604-608 (1984)).

10 F. Full-Length TAT Polypeptides

The present invention also provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as TAT polypeptides. In particular, cDNAs (partial and full-length) encoding various TAT polypeptides have been identified and isolated, as disclosed in further detail in the Examples below.

15 As disclosed in the Examples below, various cDNA clones have been deposited with the ATCC. The actual nucleotide sequences of those clones can readily be determined by the skilled artisan by sequencing of the deposited clone using routine methods in the art. The predicted amino acid sequence can be determined from the nucleotide sequence using routine skill. For the TAT polypeptides and encoding nucleic acids described herein, in some cases, Applicants have identified what is believed to be the reading frame best identifiable with the sequence information available at the time.

20 G. Anti-TAT Antibody and TAT Polypeptide Variants

In addition to the anti-TAT antibodies and full-length native sequence TAT polypeptides described herein, it is contemplated that anti-TAT antibody and TAT polypeptide variants can be prepared. Anti-TAT antibody and TAT polypeptide variants can be prepared by introducing appropriate nucleotide changes into the encoding DNA, and/or by synthesis of the desired antibody or polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the anti-TAT antibody or TAT polypeptide, such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

25 Variations in the anti-TAT antibodies and TAT polypeptides described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative mutations set forth, for instance, in U.S. Patent No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more codons encoding the antibody or polypeptide that results in a change in the amino acid sequence as compared with the native sequence antibody or polypeptide. Optionally the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the anti-TAT antibody or TAT polypeptide. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by comparing the sequence of the anti-TAT antibody or

30
35

TAT polypeptide with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of about 1 to 5 amino acids. The variation allowed may be determined by systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity exhibited by the full-length or mature native sequence.

Anti-TAT antibody and TAT polypeptide fragments are provided herein. Such fragments may be truncated at the N-terminus or C-terminus, or may lack internal residues, for example, when compared with a full length native antibody or protein. Certain fragments lack amino acid residues that are not essential for a desired biological activity of the anti-TAT antibody or TAT polypeptide.

Anti-TAT antibody and TAT polypeptide fragments may be prepared by any of a number of conventional techniques. Desired peptide fragments may be chemically synthesized. An alternative approach involves generating antibody or polypeptide fragments by enzymatic digestion, e.g., by treating the protein with an enzyme known to cleave proteins at sites defined by particular amino acid residues, or by digesting the DNA with suitable restriction enzymes and isolating the desired fragment. Yet another suitable technique involves isolating and amplifying a DNA fragment encoding a desired antibody or polypeptide fragment, by polymerase chain reaction (PCR). Oligonucleotides that define the desired termini of the DNA fragment are employed at the 5' and 3' primers in the PCR. Preferably, anti-TAT antibody and TAT polypeptide fragments share at least one biological and/or immunological activity with the native anti-TAT antibody or TAT polypeptide disclosed herein.

In particular embodiments, conservative substitutions of interest are shown in Table 6 under the heading of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes, denominated exemplary substitutions in Table 6, or as further described below in reference to amino acid classes, are introduced and the products screened.

Table 6

	Original Residue	Exemplary Substitutions	Preferred Substitutions
5	Ala (A)	val; leu; ile	val
	Arg (R)	lys; gln; asn	lys
	Asn (N)	gln; his; lys; arg	gln
	Asp (D)	glu	glu
	Cys (C)	ser	ser
10	Gln (Q)	asn	asn
	Glu (E)	asp	asp
	Gly (G)	pro; ala	ala
	His (H)	asn; gln; lys; arg	arg
	Ile (I)	leu; val; met; ala; phe; norleucine	leu
15	Leu (L)	norleucine; ile; val; met; ala; phe	ile
	Lys (K)	arg; gln; asn	arg
	Met (M)	leu; phe; ile	leu
	Phe (F)	leu; val; ile; ala; tyr	leu
	Pro (P)	ala	ala
20	Ser (S)	thr	thr
	Thr (T)	ser	ser
	Trp (W)	tyr; phe	tyr
	Tyr (Y)	trp; phe; thr; ser	phe
	Val (V)	ile; leu; met; phe; ala; norleucine	leu

Substantial modifications in function or immunological identity of the anti-TAT antibody or TAT polypeptide are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

- (1) hydrophobic: norleucine, met, ala, val, leu, ile;
- (2) neutral hydrophilic: cys, ser, thr;
- (3) acidic: asp, glu;
- (4) basic: asn, gln, his, lys, arg;
- (5) residues that influence chain orientation: gly, pro; and
- (6) aromatic: trp, tyr, phe.

Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also may be introduced into the conservative substitution sites or, more preferably, into the remaining (non-conserved) sites.

The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter et al., Nucl. Acids Res., 13:4331 (1986); Zoller et al., Nucl. Acids Res., 10:6487 (1987)], cassette mutagenesis [Wells et al., Gene, 34:315 (1985)], restriction selection mutagenesis [Wells et al., Philos. Trans. R. Soc. London SerA, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the anti-TAT antibody or TAT polypeptide variant DNA.

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant [Cunningham and Wells, Science, 244:1081-1085 (1989)]. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, The Proteins, (W.H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

Any cysteine residue not involved in maintaining the proper conformation of the anti-TAT antibody or TAT polypeptide also may be substituted, generally with serine, to improve the oxidative stability of the molecule and prevent aberrant crosslinking. Conversely, cysteine bond(s) may be added to the anti-TAT antibody or TAT polypeptide to improve its stability (particularly where the antibody is an antibody fragment such as an Fv fragment).

A particularly preferred type of substitutional variant involves substituting one or more hypervariable region residues of a parent antibody (e.g., a humanized or human antibody). Generally, the resulting variant(s) selected for further development will have improved biological properties relative to the parent antibody from which they are generated. A convenient way for generating such substitutional variants involves affinity maturation using phage display. Briefly, several hypervariable region sites (e.g., 6-7 sites) are mutated to generate all possible amino substitutions at each site. The antibody variants thus generated are displayed in a monovalent fashion from filamentous phage particles as fusions to the gene III product of M13 packaged within each particle. The phage-displayed variants are then screened for their biological activity (e.g., binding affinity) as herein disclosed. In order to identify candidate hypervariable region sites for modification, alanine scanning mutagenesis can be performed to identify hypervariable region residues contributing significantly to antigen binding. Alternatively, or additionally, it may be beneficial to analyze a crystal structure of the antigen-antibody complex to identify contact points between the antibody and human TAT polypeptide. Such contact residues and neighboring residues are candidates for substitution according to the techniques elaborated herein. Once such variants are generated, the panel of variants is subjected to screening as described herein and antibodies with superior properties in one or more relevant assays may be selected for further development.

Nucleic acid molecules encoding amino acid sequence variants of the anti-TAT antibody are prepared by a variety of methods known in the art. These methods include, but are not limited to, isolation from a natural source (in the case of naturally occurring amino acid sequence variants) or preparation by oligonucleotide-

mediated (or site-directed) mutagenesis, PCR mutagenesis, and cassette mutagenesis of an earlier prepared variant or a non-variant version of the anti-TAT antibody.

H. Modifications of Anti-TAT Antibodies and TAT Polypeptides

Covalent modifications of anti-TAT antibodies and TAT polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of an anti-TAT antibody or TAT polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of the anti-TAT antibody or TAT polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking anti-TAT antibody or TAT polypeptide to a water-insoluble support matrix or surface for use in the method for purifying anti-TAT antibodies, and vice-versa. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimide.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the anti-TAT antibody or TAT polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the antibody or polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence anti-TAT antibody or TAT polypeptide (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that are not present in the native sequence anti-TAT antibody or TAT polypeptide. In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.

Glycosylation of antibodies and other polypeptides is typically either N-linked or O-linked. N-linked refers to the attachment of the carbohydrate moiety to the side chain of an asparagine residue. The tripeptide sequences asparagine-X-serine and asparagine-X-threonine, where X is any amino acid except proline, are the recognition sequences for enzymatic attachment of the carbohydrate moiety to the asparagine side chain. Thus, the presence of either of these tripeptide sequences in a polypeptide creates a potential glycosylation site. O-linked glycosylation refers to the attachment of one of the sugars N-acetylgalactosamine, galactose, or xylose to a hydroxyamino acid, most commonly serine or threonine, although 5-hydroxyproline or 5-hydroxylysine may also be used.

Addition of glycosylation sites to the anti-TAT antibody or TAT polypeptide is conveniently accomplished by altering the amino acid sequence such that it contains one or more of the above-described tripeptide sequences (for N-linked glycosylation sites). The alteration may also be made by the addition of, or substitution by, one or more serine or threonine residues to the sequence of the original anti-TAT antibody or TAT polypeptide (for O-linked glycosylation sites). The anti-TAT antibody or TAT polypeptide amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the anti-TAT antibody or TAT polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the anti-TAT antibody or TAT polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

Removal of carbohydrate moieties present on the anti-TAT antibody or TAT polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of anti-TAT antibody or TAT polypeptide comprises linking the antibody or polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337. The antibody or polypeptide also may be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization (for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively), in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nanoparticles and nanocapsules), or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, 16th edition, Oslo, A., Ed., (1980).

The anti-TAT antibody or TAT polypeptide of the present invention may also be modified in a way to form chimeric molecules comprising an anti-TAT antibody or TAT polypeptide fused to another, heterologous polypeptide or amino acid sequence.

In one embodiment, such a chimeric molecule comprises a fusion of the anti-TAT antibody or TAT polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl- terminus of the anti-TAT antibody or TAT polypeptide. The presence of such epitope-tagged forms of the anti-TAT antibody or TAT polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the anti-TAT

antibody or TAT polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; an α -tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

In an alternative embodiment, the chimeric molecule may comprise a fusion of the anti-TAT antibody or TAT polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. The Ig fusions preferably include the substitution of a soluble (transmembrane domain deleted or inactivated) form of an anti-TAT antibody or TAT polypeptide in place of at least one variable region within an Ig molecule. In a particularly preferred embodiment, the immunoglobulin fusion includes the hinge, CH₂ and CH₃, or the hinge, CH₁, CH₂ and CH₃ regions of an IgG1 molecule. For the production of immunoglobulin fusions see also US Patent No. 5,428,130 issued June 27, 1995.

I. Preparation of Anti-TAT Antibodies and TAT Polypeptides

The description below relates primarily to production of anti-TAT antibodies and TAT polypeptides by culturing cells transformed or transfected with a vector containing anti-TAT antibody- and TAT polypeptide-encoding nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare anti-TAT antibodies and TAT polypeptides. For instance, the appropriate amino acid sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart et al., Solid-Phase Peptide Synthesis, W.H. Freeman Co., San Francisco, CA (1969); Merrifield, J. Am. Chem. Soc., 85:2149-2154 (1963)]. *In vitro* protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, CA) using manufacturer's instructions. Various portions of the anti-TAT antibody or TAT polypeptide may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the desired anti-TAT antibody or TAT polypeptide.

1. Isolation of DNA Encoding Anti-TAT Antibody or TAT Polypeptide

DNA encoding anti-TAT antibody or TAT polypeptide may be obtained from a cDNA library prepared from tissue believed to possess the anti-TAT antibody or TAT polypeptide mRNA and to express it at a detectable level. Accordingly, human anti-TAT antibody or TAT polypeptide DNA can be conveniently obtained from a cDNA library prepared from human tissue. The anti-TAT antibody- or TAT polypeptide-encoding gene may also be obtained from a genomic library or by known synthetic procedures (e.g., automated

nucleic acid synthesis).

Libraries can be screened with probes (such as oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook et al., Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding anti-TAT antibody or TAT polypeptide is to use PCR methodology [Sambrook et al., supra; Dieffenbach et al., PCR Primer: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 1995)].

Techniques for screening a cDNA library are well known in the art. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like ³²P-labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook et al., supra.

Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined using methods known in the art and as described herein.

Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook et al., supra, to detect precursors and processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

2. Selection and Transformation of Host Cells

Host cells are transfected or transformed with expression or cloning vectors described herein for anti-TAT antibody or TAT polypeptide production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in Mammalian Cell Biotechnology: a Practical Approach, M. Butler, ed. (IRL Press, 1991) and Sambrook et al., supra.

Methods of eukaryotic cell transfection and prokaryotic cell transformation are known to the ordinarily skilled artisan, for example, CaCl₂, CaPO₄, liposome-mediated and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., supra, or electroporation is generally used for prokaryotes. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., Gene, 23:315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, Virology,

52:456-457 (1978) can be employed. General aspects of mammalian cell host system transfections have been described in U.S. Patent No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen et al., J. Bact., 130:946 (1977) and Hsiao et al., Proc. Natl. Acad. Sci. (USA), 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, e.g., polybrene, polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown et al., Methods in Enzymology, 185:527-537 (1990) and Mansour et al., Nature, 336:348-352 (1988).

Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635). Other suitable prokaryotic host cells include Enterobacteriaceae such as *Escherichia*, e.g., *E. coli*, *Enterobacter*, *Erwinia*, *Klebsiella*, *Proteus*, *Salmonella*, e.g., *Salmonella typhimurium*, *Serratia*, e.g., *Serratia marcescans*, and *Shigella*, as well as *Bacilli* such as *B. subtilis* and *B. licheniformis* (e.g., *B. licheniformis* 41P disclosed in DD 266,710 published 12 April 1989), *Pseudomonas* such as *P. aeruginosa*, and *Streptomyces*. These examples are illustrative rather than limiting. Strain W3110 is one particularly preferred host or parent host because it is a common host strain for recombinant DNA product fermentations. Preferably, the host cell secretes minimal amounts of proteolytic enzymes. For example, strain W3110 may be modified to effect a genetic mutation in the genes encoding proteins endogenous to the host, with examples of such hosts including *E. coli* W3110 strain 1A2, which has the complete genotype *tonA* ; *E. coli* W3110 strain 9E4, which has the complete genotype *tonA ptr3*; *E. coli* W3110 strain 27C7 (ATCC 55,244), which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT kar*; *E. coli* W3110 strain 37D6, which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT rbs7 ilvG kar*; *E. coli* W3110 strain 40B4, which is strain 37D6 with a non-kanamycin resistant *degP* deletion mutation; and an *E. coli* strain having mutant periplasmic protease disclosed in U.S. Patent No. 4,946,783 issued 7 August 1990. Alternatively, *in vitro* methods of cloning, e.g., PCR or other nucleic acid polymerase reactions, are suitable.

Full length antibody, antibody fragments, and antibody fusion proteins can be produced in bacteria, in particular when glycosylation and Fc effector function are not needed, such as when the therapeutic antibody is conjugated to a cytotoxic agent (e.g., a toxin) and the immunoconjugate by itself shows effectiveness in tumor cell destruction. Full length antibodies have greater half life in circulation. Production in *E. coli* is faster and more cost efficient. For expression of antibody fragments and polypeptides in bacteria, see, e.g., U.S. 5,648,237 (Carter et. al.), U.S. 5,789,199 (Joly et al.), and U.S. 5,840,523 (Simmons et al.) which describes translation initiation regio (TIR) and signal sequences for optimizing expression and secretion, these patents incorporated herein by reference. After expression, the antibody is isolated from the *E. coli* cell paste in a soluble fraction and can be purified through, e.g., a protein A or G column depending on the isotype. Final purification can be carried out similar to the process for purifying antibody expressed e.g., in CHO cells.

In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for anti-TAT antibody- or TAT polypeptide-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism. Others include *Schizosaccharomyces pombe* (Beach and Nurse, Nature, 290: 140 [1981]; EP 139,383 published 2 May 1985); *Kluyveromyces* hosts (U.S. Patent No. 4,943,529; Fleer et al., Bio/Technology, 9:968-975 (1991)) such as, e.g., *K. lactis* (MW98-8C, CBS683, CBS4574; Louvencourt et al., J. Bacteriol., 154(2):737-742 [1983]), *K. fragilis* (ATCC 12,424), *K. bulgaricus* (ATCC 16,045), *K. wickerhamii* (ATCC 24,178), *K. waltii* (ATCC 56,500), *K. drosophilae* (ATCC 36,906; Van den Berg et al., Bio/Technology, 8:135 (1990)), *K. thermotolerans*, and *K. marxianus*; *Yarrowia* (EP 402,226); *Pichia pastoris* (EP 183,070; Sreekrishna et al., J. Basic Microbiol., 28:265-278 [1988]); *Candida*; *Trichoderma reesei* (EP 244,234); *Neurospora crassa* (Case et al., Proc. Natl. Acad. Sci. USA, 76:5259-5263 [1979]); *Schwanniomyces* such as *Schwanniomyces occidentalis* (EP 394,538 published 31 October 1990); and filamentous fungi such as, e.g., *Neurospora*, *Penicillium*, *Tolypocladium* (WO 91/00357 published 10 January 1991), and *Aspergillus* hosts such as *A. nidulans* (Ballance et al., Biochem. Biophys. Res. Commun., 112:284-289 [1983]; Tilburn et al., Gene, 26:205-221 [1983]; Yelton et al., Proc. Natl. Acad. Sci. USA, 81: 1470-1474 [1984]) and *A. niger* (Kelly and Hynes, EMBO J., 4:475-479 [1985]). Methylotropic yeasts are suitable herein and include, but are not limited to, yeast capable of growth on methanol selected from the genera consisting of *Hansenula*, *Candida*, *Kloeckera*, *Pichia*, *Saccharomyces*, *Torulopsis*, and *Rhodotorula*. A list of specific species that are exemplary of this class of yeasts may be found in C. Anthony, The Biochemistry of Methylotrophs, 269 (1982).

Suitable host cells for the expression of glycosylated anti-TAT antibody or TAT polypeptide are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as *Drosophila* S2 and *Spodoptera* Sf9, as well as plant cells, such as cell cultures of cotton, corn, potato, soybean, petunia, tomato, and tobacco. Numerous baculoviral strains and variants and corresponding permissive insect host cells from hosts such as *Spodoptera frugiperda* (caterpillar), *Aedes aegypti* (mosquito), *Aedes albopictus* (mosquito), *Drosophila melanogaster* (fruitfly), and *Bombyx mori* have been identified. A variety of viral strains for transfection are publicly available, e.g., the L-1 variant of *Autographa californica* NPV and the Bm-5 strain of *Bombyx mori* NPV, and such viruses may be used as the virus herein according to the present invention, particularly for transfection of *Spodoptera frugiperda* cells.

However, interest has been greatest in vertebrate cells, and propagation of vertebrate cells in culture (tissue culture) has become a routine procedure. Examples of useful mammalian host cell lines are monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., J. Gen Virol. 36:59 (1977)); baby hamster kidney cells (BHK, ATCC CCL 10); Chinese hamster ovary cells/-DHFR (CHO, Urlaub et al., Proc. Natl. Acad. Sci. USA 77:4216 (1980)); mouse sertoli cells (TM4, Mather, Biol. Reprod. 23:243-251 (1980)); monkey kidney cells (CV1 ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL-1587); human cervical carcinoma cells (HELA, ATCC CCL 2); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2,

HB 8065); mouse mammary tumor (MMT 060562, ATCC CCL51); TRI cells (Mather et al., Annals N.Y. Acad. Sci. 383:44-68 (1982)); MRC 5 cells; FS4 cells; and a human hepatoma line (Hep G2).

Host cells are transformed with the above-described expression or cloning vectors for anti-TAT antibody or TAT polypeptide production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences.

3. Selection and Use of a Replicable Vector

The nucleic acid (e.g., cDNA or genomic DNA) encoding anti-TAT antibody or TAT polypeptide may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan.

The TAT may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the anti-TAT antibody- or TAT polypeptide-encoding DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence may be, e.g., the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces* α -factor leaders, the latter described in U.S. Patent No. 5,010,182), or acid phosphatase leader, the *C. albicans* glucoamylase leader (EP 362,179 published 4 April 1990), or the signal described in WO 90/13646 published 15 November 1990. In mammalian cell expression, mammalian signal sequences may be used to direct secretion of the protein, such as signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2 μ plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells.

Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*.

An example of suitable selectable markers for mammalian cells are those that enable the identification

of cells competent to take up the anti-TAT antibody- or TAT polypeptide-encoding nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., Proc. Natl. Acad. Sci. USA, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp1* gene present in the yeast plasmid YRp7 [Stinchcomb et al., Nature, 282:39 (1979); Kingsman et al., Gene, 7:141 (1979); Tschemper et al., Gene, 10:157 (1980)]. The *trp1* gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, Genetics, 85:12 (1977)].

Expression and cloning vectors usually contain a promoter operably linked to the anti-TAT antibody- or TAT polypeptide-encoding nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well known. Promoters suitable for use with prokaryotic hosts include the β -lactamase and lactose promoter systems [Chang et al., Nature, 275:615 (1978); Goeddel et al., Nature, 281:544 (1979)], alkaline phosphatase, a tryptophan (*trp*) promoter system [Goeddel, Nucleic Acids Res., 8:4057 (1980); EP 36,776], and hybrid promoters such as the *tac* promoter [deBoer et al., Proc. Natl. Acad. Sci. USA, 80:21-25 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding anti-TAT antibody or TAT polypeptide.

Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman et al., J. Biol. Chem., 255:2073 (1980)] or other glycolytic enzymes [Hess et al., J. Adv. Enzyme Reg., 7:149 (1968); Holland, Biochemistry, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

Anti-TAT antibody or TAT polypeptide transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

Transcription of a DNA encoding the anti-TAT antibody or TAT polypeptide by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α -fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the

late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the anti-TAT antibody or TAT polypeptide coding sequence, but is preferably located at a site 5' from the promoter.

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding anti-TAT antibody or TAT polypeptide.

Still other methods, vectors, and host cells suitable for adaptation to the synthesis of anti-TAT antibody or TAT polypeptide in recombinant vertebrate cell culture are described in Gething et al., Nature, 293:620-625 (1981); Mantei et al., Nature, 281:40-46 (1979); EP 117,060; and EP 117,058.

4. Culturing the Host Cells

The host cells used to produce the anti-TAT antibody or TAT polypeptide of this invention may be cultured in a variety of media. Commercially available media such as Ham's F10 (Sigma), Minimal Essential Medium ((MEM), (Sigma), RPMI-1640 (Sigma), and Dulbecco's Modified Eagle's Medium ((DMEM), Sigma) are suitable for culturing the host cells. In addition, any of the media described in Ham et al Meth. Enz. 58:44 (1979), Barnes et al., Anal. Biochem. 102:255 (1980), U.S. Pat. Nos. 4,767,704; 4,657,866; 4,927,762; 4,560,655; or 5,122,469; WO 90/03430; WO 87/00195; or U.S. Patent Re. 30,985 may be used as culture media for the host cells. Any of these media may be supplemented as necessary with hormones and/or other growth factors (such as insulin, transferrin, or epidermal growth factor), salts (such as sodium chloride, calcium, magnesium, and phosphate), buffers (such as HEPES), nucleotides (such as adenosine and thymidine), antibiotics (such as GENTAMYCIN™ drug), trace elements (defined as inorganic compounds usually present at final concentrations in the micromolar range), and glucose or an equivalent energy source. Any other necessary supplements may also be included at appropriate concentrations that would be known to those skilled in the art. The culture conditions, such as temperature, pH, and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

5. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, Proc. Natl. Acad. Sci. USA, 77:5201-5205 (1980)], dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence TAT polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence fused to TAT DNA and encoding a specific antibody epitope.

6. Purification of Anti-TAT Antibody and TAT Polypeptide

Forms of anti-TAT antibody and TAT polypeptide may be recovered from culture medium or from host cell lysates. If membrane-bound, it can be released from the membrane using a suitable detergent solution (e.g. Triton-X 100) or by enzymatic cleavage. Cells employed in expression of anti-TAT antibody and TAT polypeptide can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

It may be desired to purify anti-TAT antibody and TAT polypeptide from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the anti-TAT antibody and TAT polypeptide. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, Methods in Enzymology, 182 (1990); Scopes, Protein Purification: Principles and Practice, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular anti-TAT antibody or TAT polypeptide produced.

When using recombinant techniques, the antibody can be produced intracellularly, in the periplasmic space, or directly secreted into the medium. If the antibody is produced intracellularly, as a first step, the particulate debris, either host cells or lysed fragments, are removed, for example, by centrifugation or ultrafiltration. Carter et al., Bio/Technology 10:163-167 (1992) describe a procedure for isolating antibodies which are secreted to the periplasmic space of *E. coli*. Briefly, cell paste is thawed in the presence of sodium

acetate (pH 3.5), EDTA, and phenylmethylsulfonylfluoride (PMSF) over about 30 min. Cell debris can be removed by centrifugation. Where the antibody is secreted into the medium, supernatants from such expression systems are generally first concentrated using a commercially available protein concentration filter, for example, an Amicon or Millipore Pellicon ultrafiltration unit. A protease inhibitor such as PMSF may be included in any of the foregoing steps to inhibit proteolysis and antibiotics may be included to prevent the growth of adventitious contaminants.

The antibody composition prepared from the cells can be purified using, for example, hydroxylapatite chromatography, gel electrophoresis, dialysis, and affinity chromatography, with affinity chromatography being the preferred purification technique. The suitability of protein A as an affinity ligand depends on the species and isotype of any immunoglobulin Fc domain that is present in the antibody. Protein A can be used to purify antibodies that are based on human $\gamma 1$, $\gamma 2$ or $\gamma 4$ heavy chains (Lindmark et al., *J. Immunol. Meth.* 62:1-13 (1983)). Protein G is recommended for all mouse isotypes and for human $\gamma 3$ (Guss et al., *EMBO J.* 5:15671575 (1986)). The matrix to which the affinity ligand is attached is most often agarose, but other matrices are available. Mechanically stable matrices such as controlled pore glass or poly(styrenedivinyl)benzene allow for faster flow rates and shorter processing times than can be achieved with agarose. Where the antibody comprises a C_H3 domain, the Bakerbond ABX[™] resin (J. T. Baker, Phillipsburg, NJ) is useful for purification. Other techniques for protein purification such as fractionation on an ion-exchange column, ethanol precipitation, Reverse Phase HPLC, chromatography on silica, chromatography on heparin SEPHAROSE[™] chromatography on an anion or cation exchange resin (such as a polyaspartic acid column), chromatofocusing, SDS-PAGE, and ammonium sulfate precipitation are also available depending on the antibody to be recovered.

Following any preliminary purification step(s), the mixture comprising the antibody of interest and contaminants may be subjected to low pH hydrophobic interaction chromatography using an elution buffer at a pH between about 2.5-4.5, preferably performed at low salt concentrations (e.g., from about 0-0.25M salt).

J. Pharmaceutical Formulations

Therapeutic formulations of the anti-TAT antibodies, TAT binding oligopeptides, TAT binding organic molecules and/or TAT polypeptides used in accordance with the present invention are prepared for storage by mixing the antibody, polypeptide, oligopeptide or organic molecule having the desired degree of purity with optional pharmaceutically acceptable carriers, excipients or stabilizers (*Remington's Pharmaceutical Sciences* 16th edition, Osol, A. Ed. (1980)), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as acetate, Tris, phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine,

histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; tonicifiers such as trehalose and sodium chloride; sugars such as sucrose, mannitol, trehalose or sorbitol; surfactant such as polysorbate; salt-forming counter-ions such as sodium; metal complexes (e.g., Zn-protein complexes); and/or non-ionic surfactants such as TWEEN®, PLURONICS® or polyethylene glycol (PEG). The antibody preferably comprises the antibody at a concentration of between 5-200 mg/ml, preferably between 10-100 mg/ml.

The formulations herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. For example, in addition to an anti-TAT antibody, TAT binding oligopeptide, or TAT binding organic molecule, it may be desirable to include in the one formulation, an additional antibody, e.g., a second anti-TAT antibody which binds a different epitope on the TAT polypeptide, or an antibody to some other target such as a growth factor that affects the growth of the particular cancer. Alternatively, or additionally, the composition may further comprise a chemotherapeutic agent, cytotoxic agent, cytokine, growth inhibitory agent, anti-hormonal agent, and/or cardioprotectant. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

The active ingredients may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules) or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, 16th edition, Osol, A. Ed. (1980).

Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semi-permeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, e.g., films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and γ ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT® (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid.

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

K. Diagnosis and Treatment with Anti-TAT Antibodies, TAT Binding Oligopeptides and TAT Binding Organic Molecules

To determine TAT expression in the cancer, various diagnostic assays are available. In one embodiment, TAT polypeptide overexpression may be analyzed by immunohistochemistry (IHC). Paraffin embedded tissue sections from a tumor biopsy may be subjected to the IHC assay and accorded a TAT protein staining intensity criteria as follows:

Score 0 - no staining is observed or membrane staining is observed in less than 10% of tumor cells.

Score 1+ - a faint/barely perceptible membrane staining is detected in more than 10% of the tumor cells. The cells are only stained in part of their membrane.

Score 2+ - a weak to moderate complete membrane staining is observed in more than 10% of the tumor cells.

Score 3+ - a moderate to strong complete membrane staining is observed in more than 10% of the tumor cells.

Those tumors with 0 or 1+ scores for TAT polypeptide expression may be characterized as not overexpressing TAT, whereas those tumors with 2+ or 3+ scores may be characterized as overexpressing TAT.

Alternatively, or additionally, FISH assays such as the INFORM® (sold by Ventana, Arizona) or PATHVISION® (Vysis, Illinois) may be carried out on formalin-fixed, paraffin-embedded tumor tissue to determine the extent (if any) of TAT overexpression in the tumor.

TAT overexpression or amplification may be evaluated using an *in vivo* diagnostic assay, e.g., by administering a molecule (such as an antibody, oligopeptide or organic molecule) which binds the molecule to be detected and is tagged with a detectable label (e.g., a radioactive isotope or a fluorescent label) and externally scanning the patient for localization of the label.

As described above, the anti-TAT antibodies, oligopeptides and organic molecules of the invention have various non-therapeutic applications. The anti-TAT antibodies, oligopeptides and organic molecules of the present invention can be useful for diagnosis and staging of TAT polypeptide-expressing cancers (e.g., in radioimaging). The antibodies, oligopeptides and organic molecules are also useful for purification or immunoprecipitation of TAT polypeptide from cells, for detection and quantitation of TAT polypeptide *in vitro*, e.g., in an ELISA or a Western blot, to kill and eliminate TAT-expressing cells from a population of mixed cells as a step in the purification of other cells.

Currently, depending on the stage of the cancer, cancer treatment involves one or a combination of the following therapies: surgery to remove the cancerous tissue, radiation therapy, and chemotherapy. Anti-TAT antibody, oligopeptide or organic molecule therapy may be especially desirable in elderly patients who do not tolerate the toxicity and side effects of chemotherapy well and in metastatic disease where radiation therapy has limited usefulness. The tumor targeting anti-TAT antibodies, oligopeptides and organic molecules of the invention are useful to alleviate TAT-expressing cancers upon initial diagnosis of the disease or during relapse. For therapeutic applications, the anti-TAT antibody, oligopeptide or organic molecule can be used alone, or in combination therapy with, e.g., hormones, antiangiogens, or radiolabelled compounds, or with surgery, cryotherapy, and/or radiotherapy. Anti-TAT antibody, oligopeptide or organic molecule treatment can be administered in conjunction with other forms of conventional therapy, either consecutively with, pre- or post-conventional therapy. Chemotherapeutic drugs such as TAXOTERE® (docetaxel), TAXOL® (paclitaxel), estramustine and mitoxantrone are used in treating cancer, in particular, in good risk patients. In the present method of the invention for treating or alleviating cancer, the cancer patient can be administered anti-TAT

antibody, oligopeptide or organic molecule in conjunction with treatment with the one or more of the preceding chemotherapeutic agents. In particular, combination therapy with paclitaxel and modified derivatives (see, e.g., EP0600517) is contemplated. The anti-TAT antibody, oligopeptide or organic molecule will be administered with a therapeutically effective dose of the chemotherapeutic agent. In another embodiment, the anti-TAT antibody, oligopeptide or organic molecule is administered in conjunction with chemotherapy to enhance the activity and efficacy of the chemotherapeutic agent, e.g., paclitaxel. The Physicians' Desk Reference (PDR) discloses dosages of these agents that have been used in treatment of various cancers. The dosing regimen and dosages of these aforementioned chemotherapeutic drugs that are therapeutically effective will depend on the particular cancer being treated, the extent of the disease and other factors familiar to the physician of skill in the art and can be determined by the physician.

In one particular embodiment, a conjugate comprising an anti-TAT antibody, oligopeptide or organic molecule conjugated with a cytotoxic agent is administered to the patient. Preferably, the immunoconjugate bound to the TAT protein is internalized by the cell, resulting in increased therapeutic efficacy of the immunoconjugate in killing the cancer cell to which it binds. In a preferred embodiment, the cytotoxic agent targets or interferes with the nucleic acid in the cancer cell. Examples of such cytotoxic agents are described above and include maytansinoids, calicheamicins, ribonucleases and DNA endonucleases.

The anti-TAT antibodies, oligopeptides, organic molecules or toxin conjugates thereof are administered to a human patient, in accord with known methods, such as intravenous administration, e.g., as a bolus or by continuous infusion over a period of time, by intramuscular, intraperitoneal, intracerebrospinal, subcutaneous, intra-articular, intrasynovial, intrathecal, oral, topical, or inhalation routes. Intravenous or subcutaneous administration of the antibody, oligopeptide or organic molecule is preferred.

Other therapeutic regimens may be combined with the administration of the anti-TAT antibody, oligopeptide or organic molecule. The combined administration includes co-administration, using separate formulations or a single pharmaceutical formulation, and consecutive administration in either order, wherein preferably there is a time period while both (or all) active agents simultaneously exert their biological activities. Preferably such combined therapy results in a synergistic therapeutic effect.

It may also be desirable to combine administration of the anti-TAT antibody or antibodies, oligopeptides or organic molecules, with administration of an antibody directed against another tumor antigen associated with the particular cancer.

In another embodiment, the therapeutic treatment methods of the present invention involves the combined administration of an anti-TAT antibody (or antibodies), oligopeptides or organic molecules and one or more chemotherapeutic agents or growth inhibitory agents, including co-administration of cocktails of different chemotherapeutic agents. Chemotherapeutic agents include estramustine phosphate, prednimustine, cisplatin, 5-fluorouracil, melphalan, cyclophosphamide, hydroxyurea and hydroxyureataxanes (such as paclitaxel and doxorubicin) and/or anthracycline antibiotics. Preparation and dosing schedules for such chemotherapeutic agents may be used according to manufacturers' instructions or as determined empirically by the skilled practitioner. Preparation and dosing schedules for such chemotherapy are also described in Chemotherapy

Service Ed., M.C. Perry, Williams & Wilkins, Baltimore, MD (1992).

The antibody, oligopeptide or organic molecule may be combined with an anti-hormonal compound; e.g., an anti-estrogen compound such as tamoxifen; an anti-progesterone such as onapristone (see, EP 616 812); or an anti-androgen such as flutamide, in dosages known for such molecules. Where the cancer to be treated is androgen independent cancer, the patient may previously have been subjected to anti-androgen therapy and, after the cancer becomes androgen independent, the anti-TAT antibody, oligopeptide or organic molecule (and optionally other agents as described herein) may be administered to the patient.

Sometimes, it may be beneficial to also co-administer a cardioprotectant (to prevent or reduce myocardial dysfunction associated with the therapy) or one or more cytokines to the patient. In addition to the above therapeutic regimes, the patient may be subjected to surgical removal of cancer cells and/or radiation therapy, before, simultaneously with, or post antibody, oligopeptide or organic molecule therapy. Suitable dosages for any of the above co-administered agents are those presently used and may be lowered due to the combined action (synergy) of the agent and anti-TAT antibody, oligopeptide or organic molecule.

For the prevention or treatment of disease, the dosage and mode of administration will be chosen by the physician according to known criteria. The appropriate dosage of antibody, oligopeptide or organic molecule will depend on the type of disease to be treated, as defined above, the severity and course of the disease, whether the antibody, oligopeptide or organic molecule is administered for preventive or therapeutic purposes, previous therapy, the patient's clinical history and response to the antibody, oligopeptide or organic molecule, and the discretion of the attending physician. The antibody, oligopeptide or organic molecule is suitably administered to the patient at one time or over a series of treatments. Preferably, the antibody, oligopeptide or organic molecule is administered by intravenous infusion or by subcutaneous injections. Depending on the type and severity of the disease, about 1 µg/kg to about 50 mg/kg body weight (e.g., about 0.1-15mg/kg/dose) of antibody can be an initial candidate dosage for administration to the patient, whether, for example, by one or more separate administrations, or by continuous infusion. A dosing regimen can comprise administering an initial loading dose of about 4 mg/kg, followed by a weekly maintenance dose of about 2 mg/kg of the anti-TAT antibody. However, other dosage regimens may be useful. A typical daily dosage might range from about 1 µg/kg to 100 mg/kg or more, depending on the factors mentioned above. For repeated administrations over several days or longer, depending on the condition, the treatment is sustained until a desired suppression of disease symptoms occurs. The progress of this therapy can be readily monitored by conventional methods and assays and based on criteria known to the physician or other persons of skill in the art.

Aside from administration of the antibody protein to the patient, the present application contemplates administration of the antibody by gene therapy. Such administration of nucleic acid encoding the antibody is encompassed by the expression "administering a therapeutically effective amount of an antibody". See, for example, WO96/07321 published March 14, 1996 concerning the use of gene therapy to generate intracellular antibodies.

There are two major approaches to getting the nucleic acid (optionally contained in a vector) into the patient's cells; *in vivo* and *ex vivo*. For *in vivo* delivery the nucleic acid is injected directly into the patient,

usually at the site where the antibody is required. For *ex vivo* treatment, the patient's cells are removed, the nucleic acid is introduced into these isolated cells and the modified cells are administered to the patient either directly or, for example, encapsulated within porous membranes which are implanted into the patient (see, e.g., U.S. Patent Nos. 4,892,538 and 5,283,187). There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells *in vitro*, or *in vivo* in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells *in vitro* include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, etc. A commonly used vector for *ex vivo* delivery of the gene is a retroviral vector.

The currently preferred *in vivo* nucleic acid transfer techniques include transfection with viral vectors (such as adenovirus, Herpes simplex I virus, or adeno-associated virus) and lipid-based systems (useful lipids for lipid-mediated transfer of the gene are DOTMA, DOPE and DC-Chol, for example). For review of the currently known gene marking and gene therapy protocols see Anderson et al., *Science* 256:808-813 (1992). See also WO 93/25673 and the references cited therein.

The anti-TAT antibodies of the invention can be in the different forms encompassed by the definition of "antibody" herein. Thus, the antibodies include full length or intact antibody, antibody fragments, native sequence antibody or amino acid variants, humanized, chimeric or fusion antibodies, immunoconjugates, and functional fragments thereof. In fusion antibodies an antibody sequence is fused to a heterologous polypeptide sequence. The antibodies can be modified in the Fc region to provide desired effector functions. As discussed in more detail in the sections herein, with the appropriate Fc regions, the naked antibody bound on the cell surface can induce cytotoxicity, e.g., via antibody-dependent cellular cytotoxicity (ADCC) or by recruiting complement in complement dependent cytotoxicity, or some other mechanism. Alternatively, where it is desirable to eliminate or reduce effector function, so as to minimize side effects or therapeutic complications, certain other Fc regions may be used.

In one embodiment, the antibody competes for binding or bind substantially to, the same epitope as the antibodies of the invention. Antibodies having the biological characteristics of the present anti-TAT antibodies of the invention are also contemplated, specifically including the *in vivo* tumor targeting and any cell proliferation inhibition or cytotoxic characteristics.

Methods of producing the above antibodies are described in detail herein.

The present anti-TAT antibodies, oligopeptides and organic molecules are useful for treating a TAT-expressing cancer or alleviating one or more symptoms of the cancer in a mammal. Such a cancer includes prostate cancer, cancer of the urinary tract, lung cancer, breast cancer, colon cancer and ovarian cancer, more specifically, prostate adenocarcinoma, renal cell carcinomas, colorectal adenocarcinomas, lung adenocarcinomas, lung squamous cell carcinomas, and pleural mesothelioma. The cancers encompass metastatic cancers of any of the preceding. The antibody, oligopeptide or organic molecule is able to bind to at least a portion of the cancer cells that express TAT polypeptide in the mammal. In a preferred embodiment, the antibody, oligopeptide or organic molecule is effective to destroy or kill TAT-expressing tumor cells or inhibit

the growth of such tumor cells, *in vitro* or *in vivo*, upon binding to TAT polypeptide on the cell. Such an antibody includes a naked anti-TAT antibody (not conjugated to any agent). Naked antibodies that have cytotoxic or cell growth inhibition properties can be further harnessed with a cytotoxic agent to render them even more potent in tumor cell destruction. Cytotoxic properties can be conferred to an anti-TAT antibody by, e.g., conjugating the antibody with a cytotoxic agent, to form an immunoconjugate as described herein. The cytotoxic agent or a growth inhibitory agent is preferably a small molecule. Toxins such as calicheamicin or a maytansinoid and analogs or derivatives thereof, are preferable.

The invention provides a composition comprising an anti-TAT antibody, oligopeptide or organic molecule of the invention, and a carrier. For the purposes of treating cancer, compositions can be administered to the patient in need of such treatment, wherein the composition can comprise one or more anti-TAT antibodies present as an immunoconjugate or as the naked antibody. In a further embodiment, the compositions can comprise these antibodies, oligopeptides or organic molecules in combination with other therapeutic agents such as cytotoxic or growth inhibitory agents, including chemotherapeutic agents. The invention also provides formulations comprising an anti-TAT antibody, oligopeptide or organic molecule of the invention, and a carrier. In one embodiment, the formulation is a therapeutic formulation comprising a pharmaceutically acceptable carrier.

Another aspect of the invention is isolated nucleic acids encoding the anti-TAT antibodies. Nucleic acids encoding both the H and L chains and especially the hypervariable region residues, chains which encode the native sequence antibody as well as variants, modifications and humanized versions of the antibody, are encompassed.

The invention also provides methods useful for treating a TAT polypeptide-expressing cancer or alleviating one or more symptoms of the cancer in a mammal, comprising administering a therapeutically effective amount of an anti-TAT antibody, oligopeptide or organic molecule to the mammal. The antibody, oligopeptide or organic molecule therapeutic compositions can be administered short term (acute) or chronic, or intermittent as directed by physician. Also provided are methods of inhibiting the growth of, and killing a TAT polypeptide-expressing cell.

The invention also provides kits and articles of manufacture comprising at least one anti-TAT antibody, oligopeptide or organic molecule. Kits containing anti-TAT antibodies, oligopeptides or organic molecules find use, e.g., for TAT cell killing assays, for purification or immunoprecipitation of TAT polypeptide from cells. For example, for isolation and purification of TAT, the kit can contain an anti-TAT antibody, oligopeptide or organic molecule coupled to beads (e.g., sepharose beads). Kits can be provided which contain the antibodies, oligopeptides or organic molecules for detection and quantitation of TAT *in vitro*, e.g., in an ELISA or a Western blot. Such antibody, oligopeptide or organic molecule useful for detection may be provided with a label such as a fluorescent or radiolabel.

L. Articles of Manufacture and Kits

Another embodiment of the invention is an article of manufacture containing materials useful for the treatment of anti-TAT expressing cancer. The article of manufacture comprises a container and a label or

package insert on or associated with the container. Suitable containers include, for example, bottles, vials, syringes, etc. The containers may be formed from a variety of materials such as glass or plastic. The container holds a composition which is effective for treating the cancer condition and may have a sterile access port (for example the container may be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle). At least one active agent in the composition is an anti-TAT antibody, oligopeptide or organic molecule of the invention. The label or package insert indicates that the composition is used for treating cancer. The label or package insert will further comprise instructions for administering the antibody, oligopeptide or organic molecule composition to the cancer patient. Additionally, the article of manufacture may further comprise a second container comprising a pharmaceutically-acceptable buffer, such as bacteriostatic water for injection (BWFI), phosphate-buffered saline, Ringer's solution and dextrose solution. It may further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, and syringes.

Kits are also provided that are useful for various purposes, e.g., for TAT-expressing cell killing assays, for purification or immunoprecipitation of TAT polypeptide from cells. For isolation and purification of TAT polypeptide, the kit can contain an anti-TAT antibody, oligopeptide or organic molecule coupled to beads (e.g., sepharose beads). Kits can be provided which contain the antibodies, oligopeptides or organic molecules for detection and quantitation of TAT polypeptide *in vitro*, e.g., in an ELISA or a Western blot. As with the article of manufacture, the kit comprises a container and a label or package insert on or associated with the container. The container holds a composition comprising at least one anti-TAT antibody, oligopeptide or organic molecule of the invention. Additional containers may be included that contain, e.g., diluents and buffers, control antibodies. The label or package insert may provide a description of the composition as well as instructions for the intended *in vitro* or diagnostic use.

M. Uses for TAT Polypeptides and TAT-Polypeptide Encoding Nucleic Acids

Nucleotide sequences (or their complement) encoding TAT polypeptides have various applications in the art of molecular biology, including uses as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA probes. TAT-encoding nucleic acid will also be useful for the preparation of TAT polypeptides by the recombinant techniques described herein, wherein those TAT polypeptides may find use, for example, in the preparation of anti-TAT antibodies as described herein.

The full-length native sequence TAT gene, or portions thereof, may be used as hybridization probes for a cDNA library to isolate the full-length TAT cDNA or to isolate still other cDNAs (for instance, those encoding naturally-occurring variants of TAT or TAT from other species) which have a desired sequence identity to the native TAT sequence disclosed herein. Optionally, the length of the probes will be about 20 to about 50 bases. The hybridization probes may be derived from at least partially novel regions of the full length native nucleotide sequence wherein those regions may be determined without undue experimentation or from genomic sequences including promoters, enhancer elements and introns of native sequence TAT. By way of example, a screening method will comprise isolating the coding region of the TAT gene using the known DNA sequence to synthesize a selected probe of about 40 bases. Hybridization probes may be labeled by a variety

of labels, including radionucleotides such as ^{32}P or ^{35}S , or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the TAT gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine which members of such libraries the probe hybridizes to. Hybridization techniques are described in further detail in the Examples below. Any EST sequences disclosed in the present application may similarly be employed as probes, using the methods disclosed herein.

Other useful fragments of the TAT-encoding nucleic acids include antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target TAT mRNA (sense) or TAT DNA (antisense) sequences. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment of the coding region of TAT DNA. Such a fragment generally comprises at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

Binding of antisense or sense oligonucleotides to target nucleic acid sequences results in the formation of duplexes that block transcription or translation of the target sequence by one of several means, including enhanced degradation of the duplexes, premature termination of transcription or translation, or by other means. Such methods are encompassed by the present invention. The antisense oligonucleotides thus may be used to block expression of TAT proteins, wherein those TAT proteins may play a role in the induction of cancer in mammals. Antisense or sense oligonucleotides further comprise oligonucleotides having modified sugar-phosphodiester backbones (or other sugar linkages, such as those described in WO 91/06629) and wherein such sugar linkages are resistant to endogenous nucleases. Such oligonucleotides with resistant sugar linkages are stable *in vivo* (i.e., capable of resisting enzymatic degradation) but retain sequence specificity to be able to bind to target nucleotide sequences.

Preferred intragenic sites for antisense binding include the region incorporating the translation initiation/start codon (5'-AUG / 5'-ATG) or termination/stop codon (5'-UAA, 5'-UAG and 5'-UGA / 5'-TAA, 5'-TAG and 5'-TGA) of the open reading frame (ORF) of the gene. These regions refer to a portion of the mRNA or gene that encompasses from about 25 to about 50 contiguous nucleotides in either direction (i.e., 5' or 3') from a translation initiation or termination codon. Other preferred regions for antisense binding include: introns; exons; intron-exon junctions; the open reading frame (ORF) or "coding region," which is the region between the translation initiation codon and the translation termination codon; the 5' cap of an mRNA which comprises an N7-methylated guanosine residue joined to the 5'-most residue of the mRNA via a 5'-5' triphosphate linkage and includes 5' cap structure itself as well as the first 50 nucleotides adjacent to the cap; the 5' untranslated region (5'UTR), the portion of an mRNA in the 5' direction from the translation initiation codon, and thus including nucleotides between the 5' cap site and the translation initiation codon of an mRNA or corresponding nucleotides on the gene; and the 3' untranslated region (3'UTR), the portion of an mRNA in the 3' direction from the translation termination codon, and thus including nucleotides between the translation termination codon and 3' end of an mRNA or corresponding nucleotides on the gene.

Specific examples of preferred antisense compounds useful for inhibiting expression of TAT proteins include oligonucleotides containing modified backbones or non-natural internucleoside linkages. Oligonucleotides having modified backbones include those that retain a phosphorus atom in the backbone and those that do not have a phosphorus atom in the backbone. For the purposes of this specification, and as sometimes referenced in the art, modified oligonucleotides that do not have a phosphorus atom in their internucleoside backbone can also be considered to be oligonucleosides. Preferred modified oligonucleotide backbones include, for example, phosphorothioates, chiral phosphorothioates, phosphorodithioates, phosphotriesters, aminoalkylphosphotri-esters, methyl and other alkyl phosphonates including 3'-alkylene phosphonates, 5'-alkylene phosphonates and chiral phosphonates, phosphinates, phosphoramidates including 3'-amino phosphoramidate and aminoalkylphosphoramidates, thionophosphoramidates, thionoalkylphosphonates, thionoalkylphosphotriesters, selenophosphates and borano-phosphates having normal 3'-5' linkages, 2'-5' linked analogs of these, and those having inverted polarity wherein one or more internucleotide linkages is a 3' to 3', 5' to 5' or 2' to 2' linkage. Preferred oligonucleotides having inverted polarity comprise a single 3' to 3' linkage at the 3'-most internucleotide linkage i.e. a single inverted nucleoside residue which may be abasic (the nucleobase is missing or has a hydroxyl group in place thereof). Various salts, mixed salts and free acid forms are also included. Representative United States patents that teach the preparation of phosphorus-containing linkages include, but are not limited to, U.S. Pat. Nos.: 3,687,808; 4,469,863; 4,476,301; 5,023,243; 5,177,196; 5,188,897; 5,264,423; 5,276,019; 5,278,302; 5,286,717; 5,321,131; 5,399,676; 5,405,939; 5,453,496; 5,455,233; 5,466,677; 5,476,925; 5,519,126; 5,536,821; 5,541,306; 5,550,111; 5,563,253; 5,571,799; 5,587,361; 5,194,599; 5,565,555; 5,527,899; 5,721,218; 5,672,697 and 5,625,050, each of which is herein incorporated by reference.

Preferred modified oligonucleotide backbones that do not include a phosphorus atom therein have backbones that are formed by short chain alkyl or cycloalkyl internucleoside linkages, mixed heteroatom and alkyl or cycloalkyl internucleoside linkages, or one or more short chain heteroatomic or heterocyclic internucleoside linkages. These include those having morpholino linkages (formed in part from the sugar portion of a nucleoside); siloxane backbones; sulfide, sulfoxide and sulfone backbones; formacetyl and thioformacetyl backbones; methylene formacetyl and thioformacetyl backbones; riboacetyl backbones; alkene containing backbones; sulfamate backbones; methyleneimino and methylenehydrazino backbones; sulfonate and sulfonamide backbones; amide backbones; and others having mixed N, O, S and CH₂ component parts. Representative United States patents that teach the preparation of such oligonucleosides include, but are not limited to, U.S. Pat. Nos.: 5,034,506; 5,166,315; 5,185,444; 5,214,134; 5,216,141; 5,235,033; 5,264,562; 5,264,564; 5,405,938; 5,434,257; 5,466,677; 5,470,967; 5,489,677; 5,541,307; 5,561,225; 5,596,086; 5,602,240; 5,610,289; 5,602,240; 5,608,046; 5,610,289; 5,618,704; 5,623,070; 5,663,312; 5,633,360; 5,677,437; 5,792,608; 5,646,269 and 5,677,439, each of which is herein incorporated by reference.

In other preferred antisense oligonucleotides, both the sugar and the internucleoside linkage, i.e., the backbone, of the nucleotide units are replaced with novel groups. The base units are maintained for hybridization with an appropriate nucleic acid target compound. One such oligomeric compound, an oligonucleotide mimetic

that has been shown to have excellent hybridization properties, is referred to as a peptide nucleic acid (PNA). In PNA compounds, the sugar-backbone of an oligonucleotide is replaced with an amide containing backbone, in particular an aminoethylglycine backbone. The nucleobases are retained and are bound directly or indirectly to aza nitrogen atoms of the amide portion of the backbone. Representative United States patents that teach the preparation of PNA compounds include, but are not limited to, U.S. Pat. Nos.: 5,539,082; 5,714,331; and 5,719,262, each of which is herein incorporated by reference. Further teaching of PNA compounds can be found in Nielsen et al., Science, 1991, 254, 1497-1500.

Preferred antisense oligonucleotides incorporate phosphorothioate backbones and/or heteroatom backbones, and in particular $-\text{CH}_2\text{-NH-O-CH}_2-$, $-\text{CH}_2\text{-N(CH}_3\text{)-O-CH}_2-$ [known as a methylene (methylimino) or MMI backbone], $-\text{CH}_2\text{-O-N(CH}_3\text{)-CH}_2-$, $-\text{CH}_2\text{-N(CH}_3\text{)-N(CH}_3\text{)-CH}_2-$ and $-\text{O-N(CH}_3\text{)-CH}_2\text{-CH}_2-$ [wherein the native phosphodiester backbone is represented as $-\text{O-P-O-CH}_2-$] described in the above referenced U.S. Pat. No. 5,489,677, and the amide backbones of the above referenced U.S. Pat. No. 5,602,240. Also preferred are antisense oligonucleotides having morpholino backbone structures of the above-referenced U.S. Pat. No. 5,034,506.

Modified oligonucleotides may also contain one or more substituted sugar moieties. Preferred oligonucleotides comprise one of the following at the 2' position: OH; F; O-alkyl, S-alkyl, or N-alkyl; O-alkenyl, S-alkenyl, or N-alkenyl; O-alkynyl, S-alkynyl or N-alkynyl; or O-alkyl-O-alkyl, wherein the alkyl, alkenyl and alkynyl may be substituted or unsubstituted C_1 to C_{10} alkyl or C_2 to C_{10} alkenyl and alkynyl. Particularly preferred are $\text{O}[(\text{CH}_2)_n\text{O}]_m\text{CH}_3$, $\text{O}(\text{CH}_2)_n\text{OCH}_3$, $\text{O}(\text{CH}_2)_n\text{NH}_2$, $\text{O}(\text{CH}_2)_n\text{CH}_3$, $\text{O}(\text{CH}_2)_n\text{ONH}_2$, and $\text{O}(\text{CH}_2)_n\text{ON}[(\text{CH}_2)_m\text{CH}_3]_2$, where n and m are from 1 to about 10. Other preferred antisense oligonucleotides comprise one of the following at the 2' position: C_1 to C_{10} lower alkyl, substituted lower alkyl, alkenyl, alkynyl, alkaryl, aralkyl, O-alkaryl or O-aralkyl, SH, SCH_3 , OCN, Cl, Br, CN, CF_3 , OCF_3 , SOCH_3 , SO_2CH_3 , ONO_2 , NO_2 , N_3 , NH_2 , heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, an RNA cleaving group, a reporter group, an intercalator, a group for improving the pharmacokinetic properties of an oligonucleotide, or a group for improving the pharmacodynamic properties of an oligonucleotide, and other substituents having similar properties. A preferred modification includes 2'-methoxyethoxy (2'-O- $\text{CH}_2\text{CH}_2\text{OCH}_3$, also known as 2'-O-(2-methoxyethyl) or 2'-MOE) (Martin et al., Helv. Chim. Acta, 1995, 78, 486-504) i.e., an alkoxyalkoxy group. A further preferred modification includes 2'-dimethylaminoethoxyethoxy, i.e., a $\text{O}(\text{CH}_2)_2\text{ON}(\text{CH}_3)_2$ group, also known as 2'-DMAOE, as described in examples hereinbelow, and 2'-dimethylaminoethoxyethoxy (also known in the art as 2'-O-dimethylaminoethoxyethyl or 2'-DMAEOE), i.e., 2'-O- $\text{CH}_2\text{-O-CH}_2\text{-N(CH}_3)_2$.

A further preferred modification includes Locked Nucleic Acids (LNAs) in which the 2'-hydroxyl group is linked to the 3' or 4' carbon atom of the sugar ring thereby forming a bicyclic sugar moiety. The linkage is preferably a methylene ($-\text{CH}_2-$)_n group bridging the 2' oxygen atom and the 4' carbon atom wherein n is 1 or 2. LNAs and preparation thereof are described in WO 98/39352 and WO 99/14226.

Other preferred modifications include 2'-methoxy (2'-O- CH_3), 2'-aminopropoxy (2'-O $\text{CH}_2\text{CH}_2\text{CH}_2$

NH₂), 2'-allyl (2'-CH₂-CH=CH₂), 2'-O-allyl (2'-O-CH₂-CH=CH₂) and 2'-fluoro (2'-F). The 2'-modification may be in the arabino (up) position or ribo (down) position. A preferred 2'-arabino modification is 2'-F. Similar modifications may also be made at other positions on the oligonucleotide, particularly the 3' position of the sugar on the 3' terminal nucleotide or in 2'-5' linked oligonucleotides and the 5' position of 5' terminal nucleotide. Oligonucleotides may also have sugar mimetics such as cyclobutyl moieties in place of the pentofuranosyl sugar.

Representative United States patents that teach the preparation of such modified sugar structures include, but are not limited to, U.S. Pat. Nos.: 4,981,957; 5,118,800; 5,319,080; 5,359,044; 5,393,878; 5,446,137; 5,466,786; 5,514,785; 5,519,134; 5,567,811; 5,576,427; 5,591,722; 5,597,909; 5,610,300; 5,627,053; 5,639,873; 5,646,265; 5,658,873; 5,670,633; 5,792,747; and 5,700,920, each of which is herein incorporated by reference in its entirety.

Oligonucleotides may also include nucleobase (often referred to in the art simply as "base") modifications or substitutions. As used herein, "unmodified" or "natural" nucleobases include the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C) and uracil (U). Modified nucleobases include other synthetic and natural nucleobases such as 5-methylcytosine (5-me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-halouracil and cytosine, 5-propynyl (-C≡C-CH₃ or -CH₂-C≡CH) uracil and cytosine and other alkynyl derivatives of pyrimidine bases, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl and other 8-substituted adenines and guanines, 5-halo particularly 5-bromo, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylguanine and 7-methyladenine, 2-F-adenine, 2-amino-adenine, 8-azaguanine and 8-azaadenine, 7-deazaguanine and 7-deazaadenine and 3-deazaguanine and 3-deazaadenine. Further modified nucleobases include tricyclic pyrimidines such as phenoxazine cytidine(1H-pyrimido[5,4-b][1,4]benzoxazin-2(3H)-one), phenothiazine cytidine (1H-pyrimido[5,4-b][1,4]benzothiazin-2(3H)-one), G-clamps such as a substituted phenoxazine cytidine (e.g. 9-(2-aminoethoxy)-H-pyrimido[5,4-b][1,4]benzoxazin-2(3H)-one), carbazole cytidine (2H-pyrimido[4,5-b]indol-2-one), pyridoindole cytidine (H-pyrido[3',2':4,5]pyrrolo[2,3-d]pyrimidin-2-one). Modified nucleobases may also include those in which the purine or pyrimidine base is replaced with other heterocycles, for example 7-deaza-adenine, 7-deazaguanosine, 2-aminopyridine and 2-pyridone. Further nucleobases include those disclosed in U.S. Pat. No. 3,687,808, those disclosed in The Concise Encyclopedia Of Polymer Science And Engineering, pages 858-859, Kroschwitz, J. I., ed. John Wiley & Sons, 1990, and those disclosed by Englisch et al., Angewandte Chemie, International Edition, 1991, 30, 613. Certain of these nucleobases are particularly useful for increasing the binding affinity of the oligomeric compounds of the invention. These include 5-substituted pyrimidines, 6-azapyrimidines and N-2, N-6 and O-6 substituted purines, including 2-aminopropyladenine, 5-propynyluracil and 5-propynylcytosine. 5-methylcytosine substitutions have been shown to increase nucleic acid duplex stability by 0.6-1.2.degree. C. (Sanghvi et al, Antisense Research and Applications, CRC Press, Boca Raton, 1993, pp. 276-278) and are preferred base substitutions, even more particularly when combined with 2'-O-methoxyethyl sugar modifications. Representative United States patents

that teach the preparation of modified nucleobases include, but are not limited to: U.S. Pat. No. 3,687,808, as well as U.S. Pat. Nos.: 4,845,205; 5,130,302; 5,134,066; 5,175,273; 5,367,066; 5,432,272; 5,457,187; 5,459,255; 5,484,908; 5,502,177; 5,525,711; 5,552,540; 5,587,469; 5,594,121; 5,596,091; 5,614,617; 5,645,985; 5,830,653; 5,763,588; 6,005,096; 5,681,941 and 5,750,692, each of which is herein incorporated by reference.

5 Another modification of antisense oligonucleotides chemically linking to the oligonucleotide one or more moieties or conjugates which enhance the activity, cellular distribution or cellular uptake of the oligonucleotide. The compounds of the invention can include conjugate groups covalently bound to functional groups such as primary or secondary hydroxyl groups. Conjugate groups of the invention include intercalators, reporter molecules, polyamines, polyamides, polyethylene glycols, polyethers, groups that enhance the pharmacodynamic properties of oligomers, and groups that enhance the pharmacokinetic properties of
10 oligomers. Typical conjugates groups include cholesterol, lipids, cation lipids, phospholipids, cationic phospholipids, biotin, phenazine, folate, phenanthridine, anthraquinone, acridine, fluoresceins, rhodamines, coumarins, and dyes. Groups that enhance the pharmacodynamic properties, in the context of this invention, include groups that improve oligomer uptake, enhance oligomer resistance to degradation, and/or strengthen
15 sequence-specific hybridization with RNA. Groups that enhance the pharmacokinetic properties, in the context of this invention, include groups that improve oligomer uptake, distribution, metabolism or excretion. Conjugate moieties include but are not limited to lipid moieties such as a cholesterol moiety (Letsinger et al., Proc. Natl. Acad. Sci. USA, 1989, 86, 6553-6556), cholic acid (Manoharan et al., Bioorg. Med. Chem. Let., 1994, 4, 1053-1060), a thioether, e.g., hexyl-S-tritylthiol (Manoharan et al., Ann. N.Y. Acad. Sci., 1992, 660, 306-309;
20 Manoharan et al., Bioorg. Med. Chem. Let., 1993, 3, 2765-2770), a thiocholesterol (Oberhauser et al., Nucl. Acids Res., 1992, 20, 533-538), an aliphatic chain, e.g., dodecandiol or undecyl residues (Saison-Behmoaras et al., EMBO J., 1991, 10, 1111-1118; Kabanov et al., FEBS Lett., 1990, 259, 327-330; Svinarchuk et al., Biochimie, 1993, 75, 49-54), a phospholipid, e.g., di-hexadecyl-rac-glycerol or triethyl-ammonium 1,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate (Manoharan et al., Tetrahedron Lett., 1995, 36, 3651-3654;
25 Shea et al., Nucl. Acids Res., 1990, 18, 3777-3783), a polyamine or a polyethylene glycol chain (Manoharan et al., Nucleosides & Nucleotides, 1995, 14, 969-973), or adamantane acetic acid (Manoharan et al., Tetrahedron Lett., 1995, 36, 3651-3654), a palmityl moiety (Mishra et al., Biochim. Biophys. Acta, 1995, 1264, 229-237), or an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety. Oligonucleotides of the invention may also be conjugated to active drug substances, for example, aspirin, warfarin, phenylbutazone,
30 ibuprofen, suprofen, fenbufen, ketoprofen, (S)-(+)-pranoprofen, carprofen, dansylsarcosine, 2,3,5-triiodobenzoic acid, flufenamic acid, folinic acid, a benzothiadiazide, chlorothiazide, a diazepam, indomethacin, a barbiturate, a cephalosporin, a sulfa drug, an antidiabetic, an antibacterial or an antibiotic. Oligonucleotide-drug conjugates and their preparation are described in U.S. patent application Ser. No. 09/334,130 (filed Jun. 15, 1999) and United States patents Nos.: 4,828,979; 4,948,882; 5,218,105; 5,525,465;
35 5,541,313; 5,545,730; 5,552,538; 5,578,717; 5,580,731; 5,580,731; 5,591,584; 5,109,124; 5,118,802; 5,138,045; 5,414,077; 5,486,603; 5,512,439; 5,578,718; 5,608,046; 4,587,044; 4,605,735; 4,667,025;

4,762,779; 4,789,737; 4,824,941; 4,835,263; 4,876,335; 4,904,582; 4,958,013; 5,082,830; 5,112,963; 5,214,136; 5,082,830; 5,112,963; 5,214,136; 5,245,022; 5,254,469; 5,258,506; 5,262,536; 5,272,250; 5,292,873; 5,317,098; 5,371,241; 5,391,723; 5,416,203; 5,451,463; 5,510,475; 5,512,667; 5,514,785; 5,565,552; 5,567,810; 5,574,142; 5,585,481; 5,587,371; 5,595,726; 5,597,696; 5,599,923; 5,599,928 and 5,688,941, each of which is herein incorporated by reference.

5 It is not necessary for all positions in a given compound to be uniformly modified, and in fact more than one of the aforementioned modifications may be incorporated in a single compound or even at a single nucleoside within an oligonucleotide. The present invention also includes antisense compounds which are chimeric compounds. "Chimeric" antisense compounds or "chimeras," in the context of this invention, are antisense compounds, particularly oligonucleotides, which contain two or more chemically distinct regions, each
10 made up of at least one monomer unit, i.e., a nucleotide in the case of an oligonucleotide compound. These oligonucleotides typically contain at least one region wherein the oligonucleotide is modified so as to confer upon the oligonucleotide increased resistance to nuclease degradation, increased cellular uptake, and/or increased binding affinity for the target nucleic acid. An additional region of the oligonucleotide may serve as a substrate for enzymes capable of cleaving RNA:DNA or RNA:RNA hybrids. By way of example, RNase H is a cellular
15 endonuclease which cleaves the RNA strand of an RNA:DNA duplex. Activation of RNase H, therefore, results in cleavage of the RNA target, thereby greatly enhancing the efficiency of oligonucleotide inhibition of gene expression. Consequently, comparable results can often be obtained with shorter oligonucleotides when chimeric oligonucleotides are used, compared to phosphorothioate deoxyoligonucleotides hybridizing to the same target region. Chimeric antisense compounds of the invention may be formed as composite structures of two or more
20 oligonucleotides, modified oligonucleotides, oligonucleosides and/or oligonucleotide mimetics as described above. Preferred chimeric antisense oligonucleotides incorporate at least one 2' modified sugar (preferably 2'-O-(CH₂)₂-O-CH₃) at the 3' terminal to confer nuclease resistance and a region with at least 4 contiguous 2'-H sugars to confer RNase H activity. Such compounds have also been referred to in the art as hybrids or gapmers. Preferred gapmers have a region of 2' modified sugars (preferably 2'-O-(CH₂)₂-O-CH₃) at the 3'-terminal and
25 at the 5' terminal separated by at least one region having at least 4 contiguous 2'-H sugars and preferably incorporate phosphorothioate backbone linkages. Representative United States patents that teach the preparation of such hybrid structures include, but are not limited to, U.S. Pat. Nos. 5,013,830; 5,149,797; 5,220,007; 5,256,775; 5,366,878; 5,403,711; 5,491,133; 5,565,350; 5,623,065; 5,652,355; 5,652,356; and 5,700,922, each of which is herein incorporated by reference in its entirety.

30 The antisense compounds used in accordance with this invention may be conveniently and routinely made through the well-known technique of solid phase synthesis. Equipment for such synthesis is sold by several vendors including, for example, Applied Biosystems (Foster City, Calif.). Any other means for such synthesis known in the art may additionally or alternatively be employed. It is well known to use similar techniques to prepare oligonucleotides such as the phosphorothioates and alkylated derivatives. The compounds
35 of the invention may also be admixed, encapsulated, conjugated or otherwise associated with other molecules, molecule structures or mixtures of compounds, as for example, liposomes, receptor targeted molecules, oral,

rectal, topical or other formulations, for assisting in uptake, distribution and/or absorption. Representative United States patents that teach the preparation of such uptake, distribution and/or absorption assisting formulations include, but are not limited to, U.S. Pat. Nos. 5,108,921; 5,354,844; 5,416,016; 5,459,127; 5,521,291; 5,543,158; 5,547,932; 5,583,020; 5,591,721; 4,426,330; 4,534,899; 5,013,556; 5,108,921; 5,213,804; 5,227,170; 5,264,221; 5,356,633; 5,395,619; 5,416,016; 5,417,978; 5,462,854; 5,469,854; 5,512,295; 5,527,528; 5,534,259; 5,543,152; 5,556,948; 5,580,575; and 5,595,756, each of which is herein incorporated by reference.

Other examples of sense or antisense oligonucleotides include those oligonucleotides which are covalently linked to organic moieties, such as those described in WO 90/10048, and other moieties that increases affinity of the oligonucleotide for a target nucleic acid sequence, such as poly-(L-lysine). Further still, intercalating agents, such as ellipticine, and alkylating agents or metal complexes may be attached to sense or antisense oligonucleotides to modify binding specificities of the antisense or sense oligonucleotide for the target nucleotide sequence.

Antisense or sense oligonucleotides may be introduced into a cell containing the target nucleic acid sequence by any gene transfer method, including, for example, CaPO_4 -mediated DNA transfection, electroporation, or by using gene transfer vectors such as Epstein-Barr virus. In a preferred procedure, an antisense or sense oligonucleotide is inserted into a suitable retroviral vector. A cell containing the target nucleic acid sequence is contacted with the recombinant retroviral vector, either *in vivo* or *ex vivo*. Suitable retroviral vectors include, but are not limited to, those derived from the murine retrovirus M-MuLV, N2 (a retrovirus derived from M-MuLV), or the double copy vectors designated DCT5A, DCT5B and DCT5C (see WO 90/13641).

Sense or antisense oligonucleotides also may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell.

Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. The sense or antisense oligonucleotide-lipid complex is preferably dissociated within the cell by an endogenous lipase.

Antisense or sense RNA or DNA molecules are generally at least about 5 nucleotides in length, alternatively at least about 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710,

720, 730, 740, 750, 760, 770, 780, 790, 800, 810, 820, 830, 840, 850, 860, 870, 880, 890, 900, 910, 920, 930, 940, 950, 960, 970, 980, 990, or 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length.

The probes may also be employed in PCR techniques to generate a pool of sequences for identification of closely related TAT coding sequences.

5 Nucleotide sequences encoding a TAT can also be used to construct hybridization probes for mapping the gene which encodes that TAT and for the genetic analysis of individuals with genetic disorders. The nucleotide sequences provided herein may be mapped to a chromosome and specific regions of a chromosome using known techniques, such as *in situ* hybridization, linkage analysis against known chromosomal markers, and hybridization screening with libraries.

10 When the coding sequences for TAT encode a protein which binds to another protein (example, where the TAT is a receptor), the TAT can be used in assays to identify the other proteins or molecules involved in the binding interaction. By such methods, inhibitors of the receptor/ligand binding interaction can be identified. Proteins involved in such binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction. Also, the receptor TAT can be used to isolate correlative ligand(s).
15 Screening assays can be designed to find lead compounds that mimic the biological activity of a native TAT or a receptor for TAT. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules contemplated include synthetic organic or inorganic compounds. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays and
20 cell based assays, which are well characterized in the art.

Nucleic acids which encode TAT or its modified forms can also be used to generate either transgenic animals or "knock out" animals which, in turn, are useful in the development and screening of therapeutically useful reagents. A transgenic animal (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic
25 stage. A transgene is a DNA which is integrated into the genome of a cell from which a transgenic animal develops. In one embodiment, cDNA encoding TAT can be used to clone genomic DNA encoding TAT in accordance with established techniques and the genomic sequences used to generate transgenic animals that contain cells which express DNA encoding TAT. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S.
30 Patent Nos. 4,736,866 and 4,870,009. Typically, particular cells would be targeted for TAT transgene incorporation with tissue-specific enhancers. Transgenic animals that include a copy of a transgene encoding TAT introduced into the germ line of the animal at an embryonic stage can be used to examine the effect of increased expression of DNA encoding TAT. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression. In
35 accordance with this facet of the invention, an animal is treated with the reagent and a reduced incidence of the pathological condition, compared to untreated animals bearing the transgene, would indicate a potential

therapeutic intervention for the pathological condition.

Alternatively, non-human homologues of TAT can be used to construct a TAT "knock out" animal which has a defective or altered gene encoding TAT as a result of homologous recombination between the endogenous gene encoding TAT and altered genomic DNA encoding TAT introduced into an embryonic stem cell of the animal. For example, cDNA encoding TAT can be used to clone genomic DNA encoding TAT in accordance with established techniques. A portion of the genomic DNA encoding TAT can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see e.g., Thomas and Capecchi, *Cell*, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected [see e.g., Li et al., *Cell*, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras [see e.g., Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the TAT polypeptide.

Nucleic acid encoding the TAT polypeptides may also be used in gene therapy. In gene therapy applications, genes are introduced into cells in order to achieve *in vivo* synthesis of a therapeutically effective genetic product, for example for replacement of a defective gene. "Gene therapy" includes both conventional gene therapy where a lasting effect is achieved by a single treatment, and the administration of gene therapeutic agents, which involves the one time or repeated administration of a therapeutically effective DNA or mRNA. Antisense RNAs and DNAs can be used as therapeutic agents for blocking the expression of certain genes *in vivo*. It has already been shown that short antisense oligonucleotides can be imported into cells where they act as inhibitors, despite their low intracellular concentrations caused by their restricted uptake by the cell membrane. (Zamecnik *et al.*, *Proc. Natl. Acad. Sci. USA* 83:4143-4146 [1986]). The oligonucleotides can be modified to enhance their uptake, e.g. by substituting their negatively charged phosphodiester groups by uncharged groups.

There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells *in vitro*, or *in vivo* in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells *in vitro* include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, etc. The currently preferred *in vivo* gene transfer techniques include transfection with viral (typically retroviral) vectors and viral coat protein-liposome mediated transfection (Dzau

et al., Trends in Biotechnology 11, 205-210 [1993]). In some situations it is desirable to provide the nucleic acid source with an agent that targets the target cells, such as an antibody specific for a cell surface membrane protein or the target cell, a ligand for a receptor on the target cell, etc. Where liposomes are employed, proteins which bind to a cell surface membrane protein associated with endocytosis may be used for targeting and/or to facilitate uptake, e.g. capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half-life. The technique of receptor-mediated endocytosis is described, for example, by Wu et al., J. Biol. Chem. 262, 4429-4432 (1987); and Wagner et al., Proc. Natl. Acad. Sci. USA 87, 3410-3414 (1990). For review of gene marking and gene therapy protocols see Anderson et al., Science 256, 808-813 (1992).

The nucleic acid molecules encoding the TAT polypeptides or fragments thereof described herein are useful for chromosome identification. In this regard, there exists an ongoing need to identify new chromosome markers, since relatively few chromosome marking reagents, based upon actual sequence data are presently available. Each TAT nucleic acid molecule of the present invention can be used as a chromosome marker.

The TAT polypeptides and nucleic acid molecules of the present invention may also be used diagnostically for tissue typing, wherein the TAT polypeptides of the present invention may be differentially expressed in one tissue as compared to another, preferably in a diseased tissue as compared to a normal tissue of the same tissue type. TAT nucleic acid molecules will find use for generating probes for PCR, Northern analysis, Southern analysis and Western analysis.

This invention encompasses methods of screening compounds to identify those that mimic the TAT polypeptide (agonists) or prevent the effect of the TAT polypeptide (antagonists). Screening assays for antagonist drug candidates are designed to identify compounds that bind or complex with the TAT polypeptides encoded by the genes identified herein, or otherwise interfere with the interaction of the encoded polypeptides with other cellular proteins, including e.g., inhibiting the expression of TAT polypeptide from cells. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates.

The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays, and cell-based assays, which are well characterized in the art.

All assays for antagonists are common in that they call for contacting the drug candidate with a TAT polypeptide encoded by a nucleic acid identified herein under conditions and for a time sufficient to allow these two components to interact.

In binding assays, the interaction is binding and the complex formed can be isolated or detected in the reaction mixture. In a particular embodiment, the TAT polypeptide encoded by the gene identified herein or the drug candidate is immobilized on a solid phase, e.g., on a microtiter plate, by covalent or non-covalent attachments. Non-covalent attachment generally is accomplished by coating the solid surface with a solution of the TAT polypeptide and drying. Alternatively, an immobilized antibody, e.g., a monoclonal antibody, specific for the TAT polypeptide to be immobilized can be used to anchor it to a solid surface. The assay is performed by adding the non-immobilized component, which may be labeled by a detectable label, to the

immobilized component, e.g., the coated surface containing the anchored component. When the reaction is complete, the non-reacted components are removed, e.g., by washing, and complexes anchored on the solid surface are detected. When the originally non-immobilized component carries a detectable label, the detection of label immobilized on the surface indicates that complexing occurred. Where the originally non-immobilized component does not carry a label, complexing can be detected, for example, by using a labeled antibody specifically binding the immobilized complex.

If the candidate compound interacts with but does not bind to a particular TAT polypeptide encoded by a gene identified herein, its interaction with that polypeptide can be assayed by methods well known for detecting protein-protein interactions. Such assays include traditional approaches, such as, e.g., cross-linking, co-immunoprecipitation, and co-purification through gradients or chromatographic columns. In addition, protein-protein interactions can be monitored by using a yeast-based genetic system described by Fields and co-workers (Fields and Song, Nature (London), 340:245-246 (1989); Chien et al., Proc. Natl. Acad. Sci. USA, 88:9578-9582 (1991)) as disclosed by Chevray and Nathans, Proc. Natl. Acad. Sci. USA, 89: 5789-5793 (1991). Many transcriptional activators, such as yeast GAL4, consist of two physically discrete modular domains, one acting as the DNA-binding domain, the other one functioning as the transcription-activation domain. The yeast expression system described in the foregoing publications (generally referred to as the "two-hybrid system") takes advantage of this property, and employs two hybrid proteins, one in which the target protein is fused to the DNA-binding domain of GAL4, and another, in which candidate activating proteins are fused to the activation domain. The expression of a GAL1- *lacZ* reporter gene under control of a GAL4-activated promoter depends on reconstitution of GAL4 activity via protein-protein interaction. Colonies containing interacting polypeptides are detected with a chromogenic substrate for β -galactosidase. A complete kit (MATCHMAKER™) for identifying protein-protein interactions between two specific proteins using the two-hybrid technique is commercially available from Clontech. This system can also be extended to map protein domains involved in specific protein interactions as well as to pinpoint amino acid residues that are crucial for these interactions.

Compounds that interfere with the interaction of a gene encoding a TAT polypeptide identified herein and other intra- or extracellular components can be tested as follows: usually a reaction mixture is prepared containing the product of the gene and the intra- or extracellular component under conditions and for a time allowing for the interaction and binding of the two products. To test the ability of a candidate compound to inhibit binding, the reaction is run in the absence and in the presence of the test compound. In addition, a placebo may be added to a third reaction mixture, to serve as positive control. The binding (complex formation) between the test compound and the intra- or extracellular component present in the mixture is monitored as described hereinabove. The formation of a complex in the control reaction(s) but not in the reaction mixture containing the test compound indicates that the test compound interferes with the interaction of the test compound and its reaction partner.

To assay for antagonists, the TAT polypeptide may be added to a cell along with the compound to be screened for a particular activity and the ability of the compound to inhibit the activity of interest in the presence

of the TAT polypeptide indicates that the compound is an antagonist to the TAT polypeptide. Alternatively, antagonists may be detected by combining the TAT polypeptide and a potential antagonist with membrane-bound TAT polypeptide receptors or recombinant receptors under appropriate conditions for a competitive inhibition assay. The TAT polypeptide can be labeled, such as by radioactivity, such that the number of TAT polypeptide molecules bound to the receptor can be used to determine the effectiveness of the potential antagonist. The gene encoding the receptor can be identified by numerous methods known to those of skill in the art, for example, ligand panning and FACS sorting. Coligan et al., Current Protocols in Immun., 1(2): Chapter 5 (1991). Preferably, expression cloning is employed wherein polyadenylated RNA is prepared from a cell responsive to the TAT polypeptide and a cDNA library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the TAT polypeptide. Transfected cells that are grown on glass slides are exposed to labeled TAT polypeptide. The TAT polypeptide can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase. Following fixation and incubation, the slides are subjected to autoradiographic analysis. Positive pools are identified and sub-pools are prepared and re-transfected using an interactive sub-pooling and re-screening process, eventually yielding a single clone that encodes the putative receptor.

As an alternative approach for receptor identification, labeled TAT polypeptide can be photoaffinity-linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is resolved by PAGE and exposed to X-ray film. The labeled complex containing the receptor can be excised, resolved into peptide fragments, and subjected to protein micro-sequencing. The amino acid sequence obtained from micro-sequencing would be used to design a set of degenerate oligonucleotide probes to screen a cDNA library to identify the gene encoding the putative receptor.

In another assay for antagonists, mammalian cells or a membrane preparation expressing the receptor would be incubated with labeled TAT polypeptide in the presence of the candidate compound. The ability of the compound to enhance or block this interaction could then be measured.

More specific examples of potential antagonists include an oligonucleotide that binds to the fusions of immunoglobulin with TAT polypeptide, and, in particular, antibodies including, without limitation, poly- and monoclonal antibodies and antibody fragments, single-chain antibodies, anti-idiotypic antibodies, and chimeric or humanized versions of such antibodies or fragments, as well as human antibodies and antibody fragments. Alternatively, a potential antagonist may be a closely related protein, for example, a mutated form of the TAT polypeptide that recognizes the receptor but imparts no effect, thereby competitively inhibiting the action of the TAT polypeptide.

Another potential TAT polypeptide antagonist is an antisense RNA or DNA construct prepared using antisense technology, where, e.g., an antisense RNA or DNA molecule acts to block directly the translation of mRNA by hybridizing to targeted mRNA and preventing protein translation. Antisense technology can be used to control gene expression through triple-helix formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5' coding portion of the polynucleotide sequence, which encodes the mature TAT polypeptides herein, is used to design an antisense

RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res., 6:3073 (1979); Cooney et al., Science, 241: 456 (1988); Dervan et al., Science, 251:1360 (1991)), thereby preventing transcription and the production of the TAT polypeptide. The antisense RNA oligonucleotide hybridizes to the mRNA *in vivo* and blocks translation of the mRNA molecule into the TAT polypeptide (antisense - Okano, Neurochem., 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression (CRC Press: Boca Raton, FL, 1988). The oligonucleotides described above can also be delivered to cells such that the antisense RNA or DNA may be expressed *in vivo* to inhibit production of the TAT polypeptide. When antisense DNA is used, oligodeoxyribonucleotides derived from the translation-initiation site, e.g., between about -10 and +10 positions of the target gene nucleotide sequence, are preferred.

Potential antagonists include small molecules that bind to the active site, the receptor binding site, or growth factor or other relevant binding site of the TAT polypeptide, thereby blocking the normal biological activity of the TAT polypeptide. Examples of small molecules include, but are not limited to, small peptides or peptide-like molecules, preferably soluble peptides, and synthetic non-peptidyl organic or inorganic compounds.

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. Ribozymes act by sequence-specific hybridization to the complementary target RNA, followed by endonucleolytic cleavage. Specific ribozyme cleavage sites within a potential RNA target can be identified by known techniques. For further details see, e.g., Ross Current Biology, 4:469-471 (1994), and PCT publication No. WO 97/33551 (published September 18, 1997).

Nucleic acid molecules in triple-helix formation used to inhibit transcription should be single-stranded and composed of deoxynucleotides. The base composition of these oligonucleotides is designed such that it promotes triple-helix formation via Hoogsteen base-pairing rules, which generally require sizeable stretches of purines or pyrimidines on one strand of a duplex. For further details see, e.g., PCT publication No. WO 97/33551, *supra*.

These small molecules can be identified by any one or more of the screening assays discussed hereinabove and/or by any other screening techniques well known for those skilled in the art.

Isolated TAT polypeptide-encoding nucleic acid can be used herein for recombinantly producing TAT polypeptide using techniques well known in the art and as described herein. In turn, the produced TAT polypeptides can be employed for generating anti-TAT antibodies using techniques well known in the art and as described herein.

Antibodies specifically binding a TAT polypeptide identified herein, as well as other molecules identified by the screening assays disclosed hereinbefore, can be administered for the treatment of various disorders, including cancer, in the form of pharmaceutical compositions.

If the TAT polypeptide is intracellular and whole antibodies are used as inhibitors, internalizing antibodies are preferred. However, lipofections or liposomes can also be used to deliver the antibody, or an antibody fragment, into cells. Where antibody fragments are used, the smallest inhibitory fragment that specifically binds to the binding domain of the target protein is preferred. For example, based upon the variable-region sequences of an antibody, peptide molecules can be designed that retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology. See, *e.g.*, Marasco *et al.*, Proc. Natl. Acad. Sci. USA, 90: 7889-7893 (1993).

The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition may comprise an agent that enhances its function, such as, for example, a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

EXAMPLES

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Manassas, VA.

EXAMPLE 1: Analysis of Differential TAT Polypeptide Expression by GEPIS

An expressed sequence tag (EST) DNA database (LIFESEQ®, Incyte Pharmaceuticals, Palo Alto, CA) was searched and interesting EST sequences were identified by GEPIS. Gene expression profiling *in silico* (GEPIS) is a bioinformatics tool developed at Genentech, Inc. that characterizes genes of interest for new cancer therapeutic targets. GEPIS takes advantage of large amounts of EST sequence and library information to determine gene expression profiles. GEPIS is capable of determining the expression profile of a gene based upon its proportional correlation with the number of its occurrences in EST databases, and it works by integrating the LIFESEQ® EST relational database and Genentech proprietary information in a stringent and statistically meaningful way. In this example, GEPIS is used to identify and cross-validate novel tumor antigens, although GEPIS can be configured to perform either very specific analyses or broad screening tasks. For the initial screen, GEPIS is used to identify EST sequences from the LIFESEQ® database that correlate

to expression in a particular tissue or tissues of interest (often a tumor tissue of interest). Then, GEPIS was employed to generate a complete tissue expression profile for the various sequences of interest. Using this type of screening bioinformatics, various TAT polypeptides (and their encoding nucleic acid molecules) were identified as being significantly overexpressed in a particular type of cancer or certain cancers as compared to other cancers and/or normal non-cancerous tissues. The rating of GEPIS hits is based upon several criteria including, for example, tissue specificity, tumor specificity and expression level in normal essential and/or normal proliferating tissues. The following is a list of molecules whose tissue expression profile as determined by GEPIS evidences significant upregulation of expression in a specific tumor or tumors as compared to other tumor(s) and/or normal tissues and optionally relatively low expression in normal essential and/or normal proliferating tissues.

Under each tissue heading shown below is a list of the cDNA sequences that are detectably overexpressed in tumor tissue of the indicated tissue type as compared to normal non-tumor tissue of the same tissue type. As such, the molecules listed below (and the polypeptides they encode) are excellent nucleic acid (and polypeptide) targets for the diagnosis and therapy of cancer in mammals.

PERIPHERAL NERVOUS SYSTEM

DNA324303	DNA324573	DNA324681	DNA325296	DNA325405	DNA325407
DNA325408	DNA325409	DNA325410	DNA325449	DNA325503	DNA326083
DNA326231	DNA188229	DNA327080	DNA327081	DNA327082	

BRAIN

DNA323721	DNA323722	DNA323723	DNA323724	DNA323726	DNA323727
DNA323728	DNA323729	DNA323731	DNA323732	DNA287173	DNA151148
DNA323740	DNA323742	DNA323743	DNA323744	DNA323751	DNA323753
DNA323755	DNA323757	DNA323759	DNA323764	DNA323765	DNA323778
DNA323781	DNA323783	DNA323785	DNA323795	DNA323796	DNA323797
DNA323805	DNA323810	DNA323811	DNA323812	DNA323814	DNA83085
DNA323817	DNA323821	DNA273060	DNA323823	DNA323824	DNA256503
DNA323825	DNA323826	DNA323828	DNA323829	DNA323830	DNA323833
DNA103214	DNA323834	DNA323837	DNA323838	DNA323839	DNA323846
DNA323856	DNA323859	DNA323863	DNA323869	DNA323871	DNA323874
DNA323882	DNA323887	DNA323888	DNA323892	DNA323893	DNA323897
DNA323898	DNA323900	DNA323901	DNA323902	DNA323908	DNA210134
DNA323912	DNA323918	DNA323921	DNA323922	DNA323923	DNA323924
DNA323925	DNA323926	DNA257916	DNA323927	DNA323931	DNA323936
DNA323937	DNA323938	DNA323939	DNA323940	DNA323942	DNA226793
DNA294794	DNA323943	DNA323944	DNA323946	DNA323947	DNA323950

	DNA323951	DNA103436	DNA323953	DNA323958	DNA323959	DNA323961
	DNA226619	DNA323962	DNA323964	DNA323969	DNA323970	DNA323973
	DNA323974	DNA323975	DNA323976	DNA323977	DNA323979	DNA323980
	DNA323991	DNA323992	DNA323994	DNA323995	DNA324000	DNA324001
	DNA324002	DNA324003	DNA227246	DNA324004	DNA324008	DNA324009
5	DNA324010	DNA324011	DNA324012	DNA196344	DNA193882	DNA324024
	DNA324034	DNA324037	DNA324042	DNA324046	DNA324047	DNA324048
	DNA324050	DNA324051	DNA324055	DNA275195	DNA324059	DNA324060
	DNA275049	DNA324063	DNA324065	DNA324066	DNA324067	DNA324071
	DNA324072	DNA324073	DNA227165	DNA324074	DNA324076	DNA324077
10	DNA324078	DNA324079	DNA324080	DNA271243	DNA324081	DNA324082
	DNA324084	DNA324088	DNA324090	DNA324091	DNA324092	DNA324099
	DNA324101	DNA324106	DNA324109	DNA324111	DNA324112	DNA324121
	DNA324122	DNA324123	DNA324128	DNA324129	DNA227795	DNA324130
	DNA324131	DNA324132	DNA324133	DNA227528	DNA324134	DNA150725
15	DNA324136	DNA324138	DNA324139	DNA324141	DNA324146	DNA324152
	DNA324153	DNA324155	DNA324159	DNA324160	DNA324161	DNA324162
	DNA194740	DNA324166	DNA324175	DNA324176	DNA272127	DNA324177
	DNA324182	DNA324184	DNA324186	DNA324188	DNA324194	DNA324197
	DNA324198	DNA324203	DNA324204	DNA324207	DNA324209	DNA324210
20	DNA324216	DNA324218	DNA324220	DNA324221	DNA324222	DNA324223
	DNA324224	DNA324227	DNA324228	DNA194827	DNA324230	DNA324231
	DNA324233	DNA324234	DNA324235	DNA324237	DNA324239	DNA254204
	DNA324240	DNA189697	DNA324243	DNA324246	DNA324251	DNA324253
	DNA150884	DNA324256	DNA324258	DNA324260	DNA324262	DNA324264
25	DNA324269	DNA324270	DNA324271	DNA324274	DNA324275	DNA269910
	DNA324279	DNA324285	DNA324286	DNA324288	DNA324290	DNA270401
	DNA226547	DNA324295	DNA324296	DNA324299	DNA324300	DNA324304
	DNA324305	DNA324308	DNA324309	DNA324310	DNA324313	DNA324314
	DNA324315	DNA324316	DNA324317	DNA103505	DNA324318	DNA324319
30	DNA324320	DNA324323	DNA324327	DNA324328	DNA324329	DNA324330
	DNA324331	DNA324333	DNA324336	DNA324338	DNA324342	DNA324343
	DNA324353	DNA88547	DNA324356	DNA324358	DNA324359	DNA324361
	DNA324363	DNA324364	DNA324365	DNA324366	DNA324367	DNA324368
	DNA324369	DNA324371	DNA324377	DNA324387	DNA324388	DNA324389
35	DNA324390	DNA324397	DNA324398	DNA324410	DNA324411	DNA324412
	DNA324413	DNA254620	DNA324415	DNA324417	DNA324418	DNA89239

	DNA324420	DNA225592	DNA324422	DNA324428	DNA324429	DNA324434
	DNA324435	DNA324437	DNA324441	DNA324442	DNA324443	DNA324448
	DNA324449	DNA324457	DNA324465	DNA324466	DNA324467	DNA324472
	DNA257511	DNA324483	DNA324485	DNA324486	DNA225919	DNA324487
	DNA324491	DNA324495	DNA324496	DNA324497	DNA324498	DNA324510
5	DNA324512	DNA324513	DNA324516	DNA324518	DNA324519	DNA324521
	DNA324524	DNA324525	DNA227575	DNA324526	DNA225920	DNA324527
	DNA225921	DNA324528	DNA324531	DNA324532	DNA324533	DNA324534
	DNA324538	DNA324540	DNA324541	DNA324542	DNA324545	DNA324546
	DNA324548	DNA324558	DNA324559	DNA324564	DNA324577	DNA324578
10	DNA288259	DNA324590	DNA324591	DNA324595	DNA324596	DNA324597
	DNA324600	DNA324604	DNA324605	DNA324613	DNA324614	DNA324615
	DNA324616	DNA324618	DNA324619	DNA324620	DNA324624	DNA324625
	DNA83020	DNA324626	DNA103380	DNA226872	DNA324632	DNA324640
	DNA324642	DNA324643	DNA324645	DNA324646	DNA324647	DNA324649
15	DNA324651	DNA324652	DNA324653	DNA150679	DNA324654	DNA324655
	DNA324656	DNA324657	DNA324658	DNA324659	DNA324660	DNA324661
	DNA324662	DNA324663	DNA324664	DNA324665	DNA324666	DNA324667
	DNA324668	DNA324669	DNA324670	DNA324671	DNA324672	DNA324673
	DNA324674	DNA324675	DNA324676	DNA324678	DNA324681	DNA324682
20	DNA324685	DNA324686	DNA324691	DNA324694	DNA324696	DNA324697
	DNA324698	DNA324700	DNA324701	DNA324702	DNA324704	DNA324705
	DNA225909	DNA274206	DNA324706	DNA324707	DNA324710	DNA324711
	DNA324714	DNA324715	DNA324716	DNA270675	DNA324717	DNA269593
	DNA324718	DNA324719	DNA324720	DNA324721	DNA272171	DNA324728
25	DNA324729	DNA304680	DNA324730	DNA324734	DNA324736	DNA324737
	DNA227204	DNA324738	DNA324740	DNA287246	DNA324743	DNA324745
	DNA304716	DNA324748	DNA324749	DNA324750	DNA324751	DNA324755
	DNA324756	DNA324757	DNA324758	DNA227442	DNA324766	DNA324767
	DNA324768	DNA324769	DNA287227	DNA324771	DNA324772	DNA324773
30	DNA324774	DNA272263	DNA287319	DNA324777	DNA324778	DNA324779
	DNA324782	DNA324784	DNA324785	DNA324786	DNA324787	DNA271040
	DNA324789	DNA324791	DNA324792	DNA324794	DNA324796	DNA324797
	DNA324798	DNA324799	DNA324803	DNA324804	DNA324805	DNA324809
	DNA324810	DNA324812	DNA324817	DNA324819	DNA324820	DNA324821
35	DNA324826	DNA324830	DNA324836	DNA324837	DNA324838	DNA324840
	DNA324841	DNA324842	DNA324844	DNA324853	DNA324866	DNA324873

	DNA324876	DNA324877	DNA324878	DNA324879	DNA324884	DNA324885
	DNA324886	DNA324889	DNA324890	DNA324891	DNA324892	DNA324894
	DNA225631	DNA274326	DNA324895	DNA324896	DNA324899	DNA324902
	DNA324903	DNA324906	DNA324907	DNA324908	DNA324916	DNA324917
	DNA324918	DNA324920	DNA324922	DNA275334	DNA324924	DNA324925
5	DNA324929	DNA273865	DNA324931	DNA324932	DNA304707	DNA324938
	DNA324944	DNA324945	DNA324947	DNA324952	DNA324953	DNA324955
	DNA324960	DNA304710	DNA324962	DNA324963	DNA324965	DNA324966
	DNA324968	DNA324969	DNA324972	DNA324973	DNA324974	DNA324977
	DNA324978	DNA324979	DNA324980	DNA324982	DNA324984	DNA272090
10	DNA324988	DNA324989	DNA324990	DNA324996	DNA324997	DNA324998
	DNA324999	DNA325002	DNA325005	DNA325006	DNA325012	DNA325013
	DNA325014	DNA325015	DNA325019	DNA325020	DNA325024	DNA325026
	DNA325027	DNA325032	DNA325033	DNA325034	DNA325035	DNA325037
	DNA325040	DNA325041	DNA325043	DNA325044	DNA325045	DNA325046
15	DNA325047	DNA325050	DNA325052	DNA325054	DNA325062	DNA325064
	DNA325065	DNA274178	DNA325069	DNA83022	DNA325070	DNA325071
	DNA325072	DNA325073	DNA225671	DNA325075	DNA325076	DNA227267
	DNA325082	DNA325083	DNA325084	DNA325085	DNA325088	DNA325102
	DNA325103	DNA325105	DNA325106	DNA325111	DNA325112	DNA325116
20	DNA325117	DNA325118	DNA325119	DNA325126	DNA325128	DNA325132
	DNA325136	DNA325137	DNA325138	DNA325139	DNA325140	DNA325141
	DNA325143	DNA325144	DNA325145	DNA325146	DNA325147	DNA325148
	DNA325150	DNA325151	DNA325152	DNA325153	DNA325155	DNA325156
	DNA325157	DNA325160	DNA325161	DNA325163	DNA325164	DNA325165
25	DNA325166	DNA325167	DNA325168	DNA325170	DNA325171	DNA226345
	DNA325173	DNA325174	DNA325181	DNA227491	DNA254771	DNA89242
	DNA325182	DNA325184	DNA325187	DNA325190	DNA272655	DNA275322
	DNA325197	DNA325199	DNA325200	DNA272213	DNA325202	DNA325203
	DNA325204	DNA257309	DNA325206	DNA325209	DNA325211	DNA325212
30	DNA289530	DNA287271	DNA325214	DNA325216	DNA325217	DNA325218
	DNA325219	DNA325220	DNA325221	DNA325222	DNA218841	DNA325223
	DNA325226	DNA325229	DNA88350	DNA325235	DNA325236	DNA325237
	DNA325240	DNA325243	DNA325246	DNA325247	DNA325249	DNA325250
	DNA325252	DNA325253	DNA325257	DNA325258	DNA325261	DNA325262
35	DNA325264	DNA325265	DNA325266	DNA325267	DNA325268	DNA325269
	DNA325270	DNA325271	DNA325273	DNA325274	DNA325275	DNA325276

	DNA325278	DNA325279	DNA325283	DNA325288	DNA325290	DNA325292
	DNA325293	DNA325296	DNA325301	DNA325302	DNA325303	DNA325304
	DNA325307	DNA325309	DNA325310	DNA325312	DNA325314	DNA325315
	DNA325316	DNA325318	DNA325319	DNA325320	DNA325322	DNA325324
	DNA193957	DNA325325	DNA325326	DNA325328	DNA325329	DNA325331
5	DNA325333	DNA325334	DNA325335	DNA325336	DNA325337	DNA325338
	DNA325341	DNA304459	DNA325342	DNA325343	DNA325344	DNA325346
	DNA325347	DNA325348	DNA325349	DNA325355	DNA325360	DNA325361
	DNA325362	DNA325363	DNA325364	DNA325365	DNA325369	DNA325372
	DNA325375	DNA325381	DNA325384	DNA325385	DNA325393	DNA325395
10	DNA269952	DNA325396	DNA325397	DNA325400	DNA325402	DNA325403
	DNA325404	DNA325405	DNA325407	DNA325408	DNA325409	DNA325410
	DNA325413	DNA325414	DNA325415	DNA325417	DNA325418	DNA325423
	DNA325425	DNA325426	DNA325430	DNA325434	DNA97285	DNA325446
	DNA325451	DNA325452	DNA325453	DNA325456	DNA325457	DNA150974
15	DNA325458	DNA287417	DNA227088	DNA325462	DNA325464	DNA325465
	DNA325466	DNA325469	DNA287254	DNA325471	DNA325474	DNA325476
	DNA325477	DNA325479	DNA325480	DNA325481	DNA325482	DNA325483
	DNA325484	DNA325489	DNA325491	DNA325492	DNA325493	DNA325495
	DNA325496	DNA325497	DNA325498	DNA269803	DNA325500	DNA325501
20	DNA325503	DNA325505	DNA270721	DNA189687	DNA325506	DNA325511
	DNA325512	DNA325513	DNA103474	DNA325514	DNA325516	DNA325517
	DNA325518	DNA325519	DNA325520	DNA325521	DNA325522	DNA325523
	DNA88176	DNA325529	DNA325530	DNA325534	DNA325535	DNA325539
	DNA325540	DNA325541	DNA325544	DNA325545	DNA325546	DNA325547
25	DNA325549	DNA225752	DNA325551	DNA325553	DNA325554	DNA325557
	DNA325561	DNA325563	DNA325566	DNA325568	DNA325571	DNA325572
	DNA325573	DNA325574	DNA325575	DNA325579	DNA325580	DNA325583
	DNA325585	DNA325586	DNA325587	DNA88114	DNA325592	DNA325593
	DNA325596	DNA325597	DNA325600	DNA325601	DNA225632	DNA83180
30	DNA325603	DNA325608	DNA325618	DNA150997	DNA325625	DNA325631
	DNA325636	DNA325638	DNA325639	DNA325642	DNA325643	DNA325649
	DNA325650	DNA325651	DNA325652	DNA325653	DNA325654	DNA325655
	DNA325656	DNA325657	DNA325658	DNA325659	DNA325660	DNA325661
	DNA325664	DNA270458	DNA227092	DNA325665	DNA325669	DNA325670
35	DNA325673	DNA325674	DNA325675	DNA325676	DNA325677	DNA325679
	DNA325680	DNA325681	DNA325683	DNA325684	DNA325687	DNA325688

	DNA325689	DNA325690	DNA325691	DNA325695	DNA325698	DNA325702
	DNA325706	DNA79101	DNA325709	DNA325711	DNA325712	DNA325717
	DNA325720	DNA325721	DNA325723	DNA325724	DNA325731	DNA226014
	DNA325733	DNA325736	DNA325739	DNA325747	DNA325750	DNA325752
	DNA325755	DNA325758	DNA325761	DNA325762	DNA325763	DNA325766
5	DNA325768	DNA325773	DNA325775	DNA325776	DNA325782	DNA325786
	DNA325787	DNA302016	DNA325789	DNA325793	DNA325794	DNA325796
	DNA325797	DNA325802	DNA325806	DNA325807	DNA325808	DNA325809
	DNA226853	DNA325811	DNA325812	DNA325814	DNA325818	DNA325819
	DNA270254	DNA281436	DNA325837	DNA325838	DNA325840	DNA325843
10	DNA325844	DNA325850	DNA325851	DNA325852	DNA325855	DNA325856
	DNA325858	DNA325859	DNA325870	DNA325875	DNA325878	DNA325885
	DNA325895	DNA325902	DNA225649	DNA325913	DNA325915	DNA325918
	DNA325919	DNA325922	DNA325924	DNA325928	DNA325932	DNA325935
	DNA325938	DNA325942	DNA325943	DNA325946	DNA325947	DNA325949
15	DNA325950	DNA325951	DNA325956	DNA325960	DNA325974	DNA325975
	DNA325976	DNA325977	DNA325980	DNA325981	DNA325985	DNA325986
	DNA325991	DNA325992	DNA325994	DNA325995	DNA325996	DNA326002
	DNA326003	DNA326005	DNA326006	DNA326007	DNA326010	DNA326011
	DNA226646	DNA326022	DNA287331	DNA326024	DNA326025	DNA326026
20	DNA326028	DNA326029	DNA326030	DNA326032	DNA326034	DNA326038
	DNA326039	DNA326040	DNA326041	DNA326042	DNA326046	DNA326047
	DNA326049	DNA326052	DNA326053	DNA326057	DNA326061	DNA326062
	DNA326064	DNA326066	DNA326068	DNA275181	DNA326069	DNA326071
	DNA326075	DNA326076	DNA326078	DNA326079	DNA326080	DNA326085
25	DNA326086	DNA326087	DNA326091	DNA273839	DNA256844	DNA326092
	DNA326093	DNA256886	DNA326095	DNA254781	DNA326096	DNA326097
	DNA326098	DNA326099	DNA326100	DNA326102	DNA326103	DNA326109
	DNA326110	DNA326111	DNA326112	DNA326113	DNA326114	DNA326115
	DNA326116	DNA326117	DNA326120	DNA326121	DNA326122	DNA326123
30	DNA326124	DNA326125	DNA326128	DNA326129	DNA326130	DNA326132
	DNA326133	DNA326136	DNA326139	DNA326140	DNA326141	DNA326144
	DNA326145	DNA326146	DNA326147	DNA326149	DNA326154	DNA326156
	DNA326157	DNA326158	DNA254532	DNA326161	DNA326162	DNA326163
	DNA326168	DNA271171	DNA326170	DNA326171	DNA326174	DNA287355
35	DNA326177	DNA326178	DNA326182	DNA326185	DNA326186	DNA326188
	DNA326189	DNA326190	DNA326195	DNA326196	DNA326197	DNA326198

	DNA326200	DNA326201	DNA326202	DNA326204	DNA88261	DNA326205
	DNA326206	DNA326207	DNA326208	DNA326209	DNA326211	DNA326213
	DNA326214	DNA326218	DNA326219	DNA326221	DNA326222	DNA326226
	DNA326228	DNA326232	DNA326233	DNA326234	DNA326238	DNA326241
	DNA326242	DNA326248	DNA326250	DNA326251	DNA326252	DNA326253
5	DNA326254	DNA326257	DNA326258	DNA326260	DNA326264	DNA326266
	DNA97300	DNA326267	DNA326268	DNA326269	DNA326270	DNA326271
	DNA326273	DNA297388	DNA326274	DNA326276	DNA326277	DNA326278
	DNA326283	DNA254198	DNA326288	DNA326289	DNA326290	DNA326291
	DNA326292	DNA326294	DNA326295	DNA326296	DNA255414	DNA326298
10	DNA326299	DNA326300	DNA326303	DNA326307	DNA326308	DNA326311
	DNA326312	DNA326318	DNA326319	DNA326320	DNA326321	DNA326322
	DNA326323	DNA66475	DNA270979	DNA326328	DNA326329	DNA326330
	DNA272889	DNA326331	DNA326332	DNA326333	DNA226389	DNA326335
	DNA326336	DNA326337	DNA326340	DNA326342	DNA326343	DNA326345
15	DNA326346	DNA88378	DNA326347	DNA326350	DNA257428	DNA326353
	DNA326354	DNA326356	DNA326359	DNA326362	DNA196642	DNA270901
	DNA326363	DNA326366	DNA326367	DNA326368	DNA254791	DNA287425
	DNA326372	DNA326375	DNA326376	DNA326378	DNA326379	DNA287291
	DNA326381	DNA326382	DNA326383	DNA326384	DNA326386	DNA326387
20	DNA150457	DNA326389	DNA227055	DNA326392	DNA326394	DNA326396
	DNA326397	DNA326399	DNA326401	DNA326403	DNA88430	DNA326406
	DNA326411	DNA326412	DNA326413	DNA129504	DNA326415	DNA326416
	DNA326417	DNA326418	DNA326419	DNA326425	DNA326426	DNA326427
	DNA326428	DNA326429	DNA326430	DNA326431	DNA326434	DNA326438
25	DNA273694	DNA326439	DNA326449	DNA326450	DNA326451	DNA326452
	DNA326453	DNA326454	DNA326457	DNA326461	DNA326462	DNA326465
	DNA326470	DNA326471	DNA326478	DNA326481	DNA326482	DNA326483
	DNA326484	DNA326485	DNA326487	DNA326489	DNA326490	DNA326491
	DNA326492	DNA326493	DNA274101	DNA326494	DNA326495	DNA326496
30	DNA326499	DNA326502	DNA326505	DNA326506	DNA326509	DNA326510
	DNA326511	DNA326514	DNA287636	DNA326515	DNA326516	DNA326518
	DNA326519	DNA326520	DNA326521	DNA326522	DNA326523	DNA326528
	DNA326529	DNA326530	DNA326531	DNA326532	DNA326533	DNA326534
	DNA326535	DNA326536	DNA326537	DNA326538	DNA326540	DNA274761
35	DNA272421	DNA326542	DNA326546	DNA326547	DNA326548	DNA326550
	DNA326552	DNA326555	DNA326557	DNA326559	DNA227280	DNA326561

	DNA326563	DNA326569	DNA326570	DNA326571	DNA326572	DNA326575
	DNA218271	DNA326577	DNA326578	DNA326579	DNA103320	DNA326584
	DNA326585	DNA274034	DNA326586	DNA326587	DNA326588	DNA326589
	DNA326590	DNA326591	DNA326592	DNA326595	DNA326596	DNA326597
	DNA326598	DNA326599	DNA326600	DNA326601	DNA326602	DNA326603
5	DNA269630	DNA326604	DNA326605	DNA326609	DNA326610	DNA287240
	DNA326618	DNA326622	DNA326623	DNA326624	DNA326625	DNA227249
	DNA326626	DNA326628	DNA326633	DNA326634	DNA326638	DNA326641
	DNA326642	DNA326644	DNA326645	DNA326646	DNA326647	DNA256836
	DNA326648	DNA326650	DNA326653	DNA326654	DNA326656	DNA326657
10	DNA326658	DNA326659	DNA326662	DNA326663	DNA326664	DNA272347
	DNA326669	DNA326670	DNA256840	DNA326671	DNA326672	DNA326673
	DNA326674	DNA326677	DNA326679	DNA273600	DNA326680	DNA326682
	DNA326684	DNA326685	DNA326686	DNA326687	DNA326688	DNA326689
	DNA326691	DNA326692	DNA151808	DNA326696	DNA326698	DNA326699
15	DNA326700	DNA326702	DNA326705	DNA326706	DNA326710	DNA326711
	DNA326713	DNA88084	DNA256533	DNA251057	DNA326715	DNA326716
	DNA326717	DNA326718	DNA326721	DNA326722	DNA326723	DNA326726
	DNA326727	DNA326729	DNA326730	DNA326731	DNA326734	DNA326735
	DNA326736	DNA326737	DNA326739	DNA273066	DNA326742	DNA326743
20	DNA103239	DNA326744	DNA326745	DNA326746	DNA326747	DNA326748
	DNA326749	DNA269481	DNA326751	DNA326752	DNA326754	DNA326756
	DNA326758	DNA326760	DNA326761	DNA273346	DNA326763	DNA326765
	DNA326766	DNA272062	DNA326768	DNA326769	DNA326770	DNA326771
	DNA297288	DNA304662	DNA326772	DNA326774	DNA287270	DNA326780
25	DNA326781	DNA326783	DNA326785	DNA287261	DNA326789	DNA83170
	DNA326796	DNA326798	DNA326805	DNA326806	DNA150767	DNA326812
	DNA326813	DNA326817	DNA326818	DNA326819	DNA326820	DNA326821
	DNA226758	DNA194701	DNA326823	DNA326824	DNA326828	DNA326829
	DNA326831	DNA326833	DNA326835	DNA227472	DNA326836	DNA103525
30	DNA326840	DNA326841	DNA273320	DNA326842	DNA88569	DNA326843
	DNA326848	DNA326849	DNA326852	DNA326853	DNA326856	DNA326857
	DNA326861	DNA326862	DNA326863	DNA304670	DNA326864	DNA326866
	DNA103486	DNA326869	DNA326878	DNA326879	DNA326884	DNA326886
	DNA326887	DNA326888	DNA254572	DNA326889	DNA254994	DNA326891
35	DNA326894	DNA326896	DNA326897	DNA326901	DNA226409	DNA326908
	DNA326911	DNA326912	DNA326913	DNA326914	DNA326916	DNA255046

	DNA225954	DNA326921	DNA326922	DNA326928	DNA326929	DNA326930
	DNA257549	DNA304835	DNA326935	DNA326940	DNA269830	DNA326945
	DNA326946	DNA326948	DNA254141	DNA151882	DNA326949	DNA326950
	DNA326951	DNA326952	DNA326953	DNA326956	DNA326958	DNA188740
	DNA326959	DNA290259	DNA304719	DNA326963	DNA326964	DNA326965
5	DNA254240	DNA326970	DNA326972	DNA326973	DNA326974	DNA326976
	DNA326977	DNA326981	DNA219225	DNA270954	DNA326983	DNA326985
	DNA326988	DNA326989	DNA326990	DNA326991	DNA326992	DNA326993
	DNA256070	DNA327000	DNA327002	DNA327003	DNA327004	DNA327005
	DNA269793	DNA327011	DNA227689	DNA274829	DNA327022	DNA327023
10	DNA327024	DNA327025	DNA327028	DNA327030	DNA327034	DNA327035
	DNA327036	DNA327042	DNA271580	DNA327043	DNA273992	DNA327045
	DNA327046	DNA327047	DNA327051	DNA327054	DNA225721	DNA327058
	DNA327059	DNA327060	DNA327061	DNA327062	DNA327067	DNA327068
	DNA327075	DNA327076	DNA327077	DNA327078	DNA327085	DNA76504
15	DNA327093	DNA273487	DNA327098	DNA327099	DNA254783	DNA227917
	DNA327112	DNA327113	DNA327115	DNA327116	DNA227013	DNA225800
	DNA327118	DNA225655	DNA327119	DNA327120	DNA327126	DNA327127

HEAD AND NECK

20	DNA323805	DNA323843	DNA323861	DNA323883	DNA323899	DNA323907
	DNA323908	DNA323909	DNA323986	DNA324001	DNA324039	DNA270154
	DNA324139	DNA324202	DNA324258	DNA324263	DNA324325	DNA324338
	DNA324393	DNA272605	DNA324425	DNA324480	DNA324588	DNA324651
	DNA324721	DNA324751	DNA324784	DNA324812	DNA324830	DNA227924
25	DNA324874	DNA324884	DNA131588	DNA89242	DNA325196	DNA325303
	DNA325352	DNA325377	DNA325503	DNA189687	DNA325526	DNA325573
	DNA150978	DNA325624	DNA79313	DNA325655	DNA325656	DNA325657
	DNA325658	DNA325661	DNA227094	DNA254777	DNA325799	DNA325801
	DNA226853	DNA325832	DNA274058	DNA325857	DNA325917	DNA325941
30	DNA325953	DNA325968	DNA325989	DNA325991	DNA326015	DNA326048
	DNA326076	DNA326119	DNA326135	DNA326159	DNA326172	DNA287355
	DNA326316	DNA326324	DNA326329	DNA326331	DNA326332	DNA88457
	DNA88281	DNA226011	DNA326738	DNA273517	DNA326839	DNA326873
	DNA326884	DNA326958	DNA327038	DNA327078		

35

PLACENTA

	DNA323721	DNA323723	DNA323728	DNA323729	DNA323734	DNA287173
	DNA323736	DNA227821	DNA323738	DNA323739	DNA273712	DNA323741
	DNA323747	DNA323750	DNA323753	DNA323756	DNA323763	DNA323765
	DNA323766	DNA323773	DNA323776	DNA323777	DNA323778	DNA323781
	DNA323782	DNA323783	DNA323784	DNA196349	DNA323789	DNA323791
5	DNA323792	DNA323793	DNA323794	DNA323800	DNA323804	DNA227213
	DNA323809	DNA323811	DNA189315	DNA323817	DNA323819	DNA323820
	DNA323822	DNA274745	DNA273060	DNA272024	DNA323829	DNA323831
	DNA323832	DNA323833	DNA304686	DNA323834	DNA323835	DNA323839
	DNA323840	DNA323841	DNA323842	DNA323847	DNA323856	DNA323857
10	DNA323858	DNA323859	DNA226260	DNA323862	DNA323863	DNA323867
	DNA323868	DNA323869	DNA323870	DNA271003	DNA323871	DNA323872
	DNA323874	DNA323875	DNA323876	DNA323880	DNA323882	DNA323887
	DNA323888	DNA323891	DNA323892	DNA323896	DNA323900	DNA227529
	DNA323902	DNA323905	DNA323906	DNA227577	DNA323914	DNA323915
15	DNA323916	DNA323920	DNA323925	DNA323927	DNA226125	DNA323936
	DNA323940	DNA323941	DNA323944	DNA323947	DNA323952	DNA323954
	DNA323959	DNA323963	DNA323964	DNA323966	DNA323971	DNA323972
	DNA323973	DNA323974	DNA323980	DNA323981	DNA323996	DNA323999
	DNA324004	DNA324009	DNA324014	DNA324018	DNA324026	DNA324030
20	DNA324031	DNA324032	DNA324035	DNA324037	DNA324038	DNA324042
	DNA324043	DNA324044	DNA324047	DNA324048	DNA324049	DNA324054
	DNA275195	DNA324060	DNA324063	DNA324067	DNA324068	DNA324070
	DNA324072	DNA324073	DNA324089	DNA324090	DNA324091	DNA324092
	DNA324093	DNA324096	DNA324101	DNA275066	DNA324106	DNA324109
25	DNA324110	DNA324111	DNA324112	DNA324115	DNA324119	DNA227795
	DNA287167	DNA324130	DNA324133	DNA324134	DNA150725	DNA324140
	DNA324141	DNA324142	DNA324143	DNA324144	DNA324150	DNA324151
	DNA324152	DNA324153	DNA324154	DNA324156	DNA275240	DNA324169
	DNA324170	DNA324171	DNA324172	DNA324175	DNA324182	DNA324186
30	DNA304805	DNA324189	DNA324190	DNA324191	DNA324193	DNA324195
	DNA324199	DNA324200	DNA324201	DNA324203	DNA324204	DNA271608
	DNA324206	DNA324207	DNA324209	DNA324210	DNA324212	DNA324213
	DNA324214	DNA324215	DNA324218	DNA324219	DNA324224	DNA324226
	DNA324230	DNA189697	DNA324244	DNA324247	DNA324254	DNA324258
35	DNA324260	DNA324266	DNA324268	DNA324269	DNA324270	DNA324271
	DNA324272	DNA324274	DNA324276	DNA151017	DNA324277	DNA324281

	DNA324282	DNA324289	DNA271187	DNA269930	DNA324292	DNA324293
	DNA324294	DNA226547	DNA324295	DNA324298	DNA324302	DNA324308
	DNA324310	DNA324311	DNA324313	DNA324316	DNA150562	DNA254582
	DNA324320	DNA324322	DNA324326	DNA324337	DNA269730	DNA324338
	DNA324339	DNA324340	DNA324341	DNA324343	DNA324344	DNA324347
5	DNA324348	DNA324350	DNA324351	DNA324358	DNA324360	DNA324365
	DNA324368	DNA324373	DNA324375	DNA324376	DNA324379	DNA324380
	DNA269858	DNA324387	DNA324390	DNA324396	DNA324398	DNA324399
	DNA324400	DNA324402	DNA324405	DNA324408	DNA324409	DNA324411
	DNA324412	DNA324416	DNA324417	DNA324418	DNA324419	DNA324423
10	DNA324430	DNA324431	DNA324432	DNA324434	DNA324436	DNA324437
	DNA324444	DNA324445	DNA324446	DNA324447	DNA324448	DNA270615
	DNA324450	DNA324451	DNA324452	DNA324459	DNA324460	DNA324461
	DNA324463	DNA324464	DNA324468	DNA324469	DNA324472	DNA324473
	DNA324478	DNA324479	DNA257511	DNA324481	DNA324483	DNA324491
15	DNA324495	DNA324496	DNA324501	DNA324502	DNA324508	DNA324510
	DNA324512	DNA324519	DNA324520	DNA324521	DNA324525	DNA324529
	DNA324530	DNA324531	DNA324537	DNA324538	DNA324539	DNA324541
	DNA324542	DNA324543	DNA324544	DNA324545	DNA324547	DNA324549
	DNA324550	DNA324561	DNA324563	DNA324564	DNA324565	DNA227173
20	DNA324570	DNA324571	DNA324572	DNA287282	DNA324576	DNA324579
	DNA324581	DNA324582	DNA324583	DNA324584	DNA288259	DNA324586
	DNA324590	DNA324591	DNA324592	DNA324593	DNA324595	DNA324596
	DNA324597	DNA324598	DNA324599	DNA324600	DNA324601	DNA324603
	DNA324604	DNA257253	DNA324611	DNA324613	DNA324616	DNA324617
25	DNA324618	DNA324619	DNA324621	DNA324622	DNA324624	DNA103380
	DNA324629	DNA324630	DNA324631	DNA324632	DNA324633	DNA324634
	DNA324641	DNA324645	DNA324646	DNA324647	DNA302020	DNA324650
	DNA324677	DNA324678	DNA324680	DNA324682	DNA226418	DNA324685
	DNA324687	DNA324688	DNA324689	DNA324690	DNA324693	DNA227320
30	DNA324696	DNA324697	DNA324707	DNA324712	DNA324715	DNA324716
	DNA270675	DNA324717	DNA324720	DNA324722	DNA324723	DNA324725
	DNA324727	DNA304680	DNA324730	DNA324735	DNA324736	DNA324737
	DNA324741	DNA324742	DNA275630	DNA324745	DNA324746	DNA324751
	DNA324752	DNA324753	DNA324754	DNA324756	DNA324759	DNA324760
35	DNA324761	DNA324763	DNA324764	DNA324765	DNA304661	DNA324771
	DNA324775	DNA324776	DNA324777	DNA324778	DNA324779	DNA324780

	DNA324781	DNA324783	DNA304699	DNA324785	DNA271040	DNA324790
	DNA324794	DNA324796	DNA324797	DNA324806	DNA324811	DNA324818
	DNA324820	DNA324822	DNA324824	DNA324827	DNA324830	DNA324832
	DNA324833	DNA324835	DNA324840	DNA324841	DNA324844	DNA324846
	DNA271418	DNA324849	DNA324853	DNA324857	DNA324859	DNA324860
5	DNA324862	DNA324864	DNA324866	DNA324868	DNA324871	DNA324872
	DNA324889	DNA324891	DNA225631	DNA274326	DNA324895	DNA247595
	DNA324898	DNA324900	DNA324901	DNA324902	DNA324909	DNA324915
	DNA324916	DNA324917	DNA324920	DNA275334	DNA324925	DNA324926
	DNA324928	DNA324929	DNA273865	DNA324934	DNA324936	DNA324937
10	DNA287189	DNA324939	DNA324940	DNA103588	DNA324950	DNA324951
	DNA324952	DNA324961	DNA324965	DNA324966	DNA324967	DNA324968
	DNA324975	DNA324976	DNA324982	DNA324986	DNA272090	DNA324989
	DNA324990	DNA324991	DNA324992	DNA324993	DNA324994	DNA324995
	DNA270711	DNA325001	DNA325002	DNA325003	DNA325004	DNA325006
15	DNA325008	DNA325013	DNA325015	DNA325021	DNA325024	DNA325026
	DNA325027	DNA325028	DNA325030	DNA325033	DNA325034	DNA325042
	DNA325048	DNA226337	DNA325051	DNA325053	DNA325067	DNA325078
	DNA325079	DNA325080	DNA325081	DNA325087	DNA325088	DNA325095
	DNA325099	DNA325101	DNA325102	DNA325103	DNA325104	DNA325105
20	DNA325106	DNA226496	DNA325111	DNA325113	DNA325114	DNA325116
	DNA325117	DNA325118	DNA325119	DNA325123	DNA131588	DNA325126
	DNA325128	DNA325129	DNA325132	DNA325133	DNA325136	DNA325139
	DNA325140	DNA325141	DNA325144	DNA325146	DNA325150	DNA325152
	DNA325153	DNA325156	DNA325157	DNA325162	DNA325164	DNA325168
25	DNA271847	DNA270991	DNA325173	DNA325174	DNA325175	DNA325176
	DNA325179	DNA325181	DNA227491	DNA325182	DNA325183	DNA325184
	DNA325185	DNA325187	DNA325189	DNA325190	DNA325196	DNA325200
	DNA325201	DNA325202	DNA254543	DNA325206	DNA325209	DNA325213
	DNA325214	DNA325215	DNA325219	DNA325222	DNA325223	DNA325225
30	DNA325228	DNA325229	DNA325232	DNA325244	DNA325248	DNA325250
	DNA325253	DNA325259	DNA325260	DNA325263	DNA325265	DNA325272
	DNA325277	DNA325280	DNA325289	DNA325293	DNA273759	DNA325294
	DNA325301	DNA325303	DNA325305	DNA325308	DNA325311	DNA325326
	DNA325328	DNA325329	DNA325334	DNA103421	DNA325343	DNA325344
35	DNA325346	DNA325347	DNA325353	DNA325356	DNA325358	DNA325359
	DNA325360	DNA325364	DNA325366	DNA325370	DNA325375	DNA325378

	DNA325381	DNA273521	DNA325383	DNA325384	DNA325389	DNA325394
	DNA325395	DNA269431	DNA325405	DNA325412	DNA325418	DNA325424
	DNA325430	DNA325431	DNA325439	DNA325441	DNA325442	DNA325443
	DNA325444	DNA325445	DNA325447	DNA325448	DNA325451	DNA325452
	DNA325454	DNA325455	DNA325456	DNA270134	DNA325460	DNA287417
5	DNA325463	DNA325464	DNA325465	DNA325468	DNA325470	DNA325475
	DNA325478	DNA325479	DNA325480	DNA325483	DNA325486	DNA325487
	DNA325488	DNA325490	DNA325494	DNA325498	DNA325504	DNA270721
	DNA325506	DNA325507	DNA325508	DNA325513	DNA325522	DNA325523
	DNA325527	DNA325529	DNA325530	DNA325534	DNA325535	DNA325541
10	DNA325544	DNA271843	DNA325556	DNA325557	DNA325560	DNA325567
	DNA325570	DNA325576	DNA325582	DNA325584	DNA325587	DNA325589
	DNA325593	DNA325595	DNA325596	DNA325597	DNA254624	DNA325601
	DNA225632	DNA325602	DNA325610	DNA325611	DNA325616	DNA325618
	DNA325621	DNA325625	DNA325626	DNA325627	DNA325632	DNA325633
15	DNA271344	DNA325640	DNA325642	DNA325644	DNA325645	DNA325648
	DNA227191	DNA270458	DNA227092	DNA325666	DNA325674	DNA325680
	DNA325681	DNA304783	DNA325685	DNA325686	DNA325688	DNA325689
	DNA325695	DNA325699	DNA325700	DNA325701	DNA325704	DNA325707
	DNA325711	DNA325712	DNA325720	DNA325724	DNA325727	DNA325728
20	DNA325729	DNA304694	DNA325730	DNA227474	DNA325731	DNA227171
	DNA325732	DNA271492	DNA325733	DNA325736	DNA325737	DNA325739
	DNA325750	DNA325751	DNA325752	DNA325758	DNA325760	DNA325762
	DNA325763	DNA325772	DNA325773	DNA325775	DNA325776	DNA325782
	DNA325783	DNA325784	DNA325785	DNA325786	DNA270677	DNA325787
25	DNA302016	DNA325789	DNA325792	DNA325798	DNA325802	DNA325805
	DNA325806	DNA325809	DNA270015	DNA325810	DNA325811	DNA325812
	DNA325813	DNA325814	DNA325816	DNA325818	DNA325820	DNA304669
	DNA281436	DNA325828	DNA325829	DNA325830	DNA325833	DNA325834
	DNA325837	DNA325838	DNA325843	DNA325844	DNA325847	DNA325860
30	DNA325861	DNA325862	DNA325863	DNA325865	DNA325866	DNA325867
	DNA325872	DNA325874	DNA325876	DNA325877	DNA325880	DNA325881
	DNA325882	DNA325886	DNA325887	DNA325888	DNA325889	DNA325893
	DNA325900	DNA325903	DNA325904	DNA325906	DNA325908	DNA325910
	DNA325911	DNA325912	DNA325913	DNA325921	DNA269498	DNA325922
35	DNA325925	DNA325926	DNA325927	DNA325933	DNA325935	DNA325936
	DNA325939	DNA325941	DNA325944	DNA325947	DNA325948	DNA325949

	DNA325950	DNA103509	DNA325959	DNA325961	DNA325962	DNA325963
	DNA325965	DNA325966	DNA325972	DNA325973	DNA325980	DNA325982
	DNA325983	DNA227559	DNA325985	DNA325987	DNA325988	DNA325994
	DNA325995	DNA325997	DNA326001	DNA326002	DNA326003	DNA326010
	DNA326016	DNA326019	DNA326020	DNA326021	DNA326022	DNA326023
5	DNA287331	DNA326028	DNA326036	DNA326041	DNA326044	DNA326046
	DNA326047	DNA326050	DNA326051	DNA326056	DNA275144	DNA326058
	DNA326063	DNA326070	DNA326073	DNA326075	DNA326081	DNA326082
	DNA326084	DNA326088	DNA273839	DNA326094	DNA326097	DNA326099
	DNA326103	DNA326104	DNA326105	DNA326106	DNA326108	DNA326116
10	DNA326117	DNA326118	DNA326121	DNA326122	DNA326124	DNA326125
	DNA326128	DNA326129	DNA326134	DNA289522	DNA326136	DNA326150
	DNA326151	DNA274002	DNA326152	DNA326153	DNA326154	DNA326155
	DNA326156	DNA326157	DNA326167	DNA326168	DNA271171	DNA326173
	DNA287355	DNA326176	DNA326179	DNA194805	DNA326181	DNA326183
15	DNA326184	DNA326186	DNA326188	DNA326191	DNA326192	DNA326195
	DNA326196	DNA326197	DNA326198	DNA275408	DNA326200	DNA189703
	DNA326201	DNA326203	DNA304704	DNA326208	DNA326210	DNA326211
	DNA326212	DNA326214	DNA326217	DNA326222	DNA326223	DNA326224
	DNA326225	DNA326227	DNA227234	DNA326233	DNA326234	DNA326249
20	DNA326251	DNA326252	DNA326255	DNA326260	DNA326261	DNA326262
	DNA97300	DNA326268	DNA326272	DNA326273	DNA326278	DNA103401
	DNA326285	DNA326288	DNA290292	DNA326289	DNA326291	DNA326292
	DNA326296	DNA326305	DNA326311	DNA326313	DNA326314	DNA326315
	DNA326316	DNA287427	DNA326322	DNA326324	DNA326325	DNA326326
25	DNA326330	DNA326334	DNA326338	DNA326339	DNA326340	DNA326342
	DNA326343	DNA326344	DNA326356	DNA326361	DNA270901	DNA326364
	DNA97290	DNA227071	DNA326369	DNA287425	DNA326377	DNA326381
	DNA326384	DNA326385	DNA326387	DNA326388	DNA227055	DNA326395
	DNA326396	DNA326397	DNA150814	DNA326399	DNA326406	DNA326407
30	DNA326408	DNA326409	DNA326410	DNA326411	DNA129504	DNA326415
	DNA326421	DNA326424	DNA326427	DNA326430	DNA326435	DNA326445
	DNA326448	DNA326449	DNA326450	DNA326451	DNA326452	DNA326453
	DNA326454	DNA256813	DNA326457	DNA326459	DNA326463	DNA326464
	DNA326466	DNA326467	DNA326468	DNA326469	DNA326471	DNA326472
35	DNA326474	DNA326477	DNA326483	DNA326484	DNA326485	DNA326486
	DNA326487	DNA326488	DNA326489	DNA326490	DNA326491	DNA326495

	DNA326496	DNA326499	DNA326507	DNA326508	DNA326510	DNA326513
	DNA326514	DNA287636	DNA326515	DNA326516	DNA326518	DNA326520
	DNA326524	DNA326525	DNA326529	DNA326530	DNA326544	DNA326548
	DNA326549	DNA326551	DNA326553	DNA326557	DNA326559	DNA227280
	DNA270621	DNA326563	DNA326564	DNA326565	DNA326567	DNA326569
5	DNA326579	DNA326580	DNA326585	DNA287243	DNA326589	DNA326593
	DNA326594	DNA326595	DNA269894	DNA326596	DNA326597	DNA326603
	DNA326604	DNA326606	DNA326607	DNA326611	DNA326612	DNA326613
	DNA326616	DNA326624	DNA227249	DNA326626	DNA326627	DNA326631
	DNA326632	DNA326633	DNA326634	DNA326636	DNA326637	DNA326639
10	DNA326640	DNA326641	DNA326643	DNA326649	DNA326651	DNA326657
	DNA273474	DNA272347	DNA326669	DNA326671	DNA274139	DNA273600
	DNA326680	DNA326681	DNA326683	DNA326686	DNA326687	DNA326688
	DNA326689	DNA326690	DNA326691	DNA326695	DNA326698	DNA326702
	DNA326704	DNA326705	DNA326706	DNA326707	DNA103580	DNA256533
15	DNA326714	DNA274289	DNA326717	DNA326719	DNA326720	DNA326724
	DNA326727	DNA326728	DNA274823	DNA290260	DNA326733	DNA326736
	DNA273066	DNA326741	DNA326742	DNA326749	DNA326755	DNA326756
	DNA326757	DNA326758	DNA326760	DNA273346	DNA254548	DNA326767
	DNA326769	DNA297288	DNA326775	DNA326776	DNA326777	DNA326778
20	DNA287270	DNA326780	DNA326781	DNA326782	DNA326784	DNA326786
	DNA326787	DNA326788	DNA271010	DNA287290	DNA326793	DNA326794
	DNA326796	DNA326797	DNA326798	DNA326799	DNA326804	DNA326807
	DNA326808	DNA326809	DNA326812	DNA326814	DNA326815	DNA97298
	DNA326819	DNA326822	DNA194701	DNA326827	DNA326831	DNA103525
25	DNA326845	DNA326847	DNA326855	DNA326856	DNA326858	DNA326866
	DNA103486	DNA326870	DNA326871	DNA326873	DNA326877	DNA326879
	DNA326880	DNA326881	DNA269746	DNA326883	DNA326884	DNA326885
	DNA326886	DNA254572	DNA274129	DNA326895	DNA326899	DNA326900
	DNA326901	DNA326902	DNA326915	DNA226617	DNA326917	DNA326920
30	DNA326921	DNA326928	DNA326933	DNA326934	DNA326935	DNA326936
	DNA326937	DNA326938	DNA326940	DNA326941	DNA269830	DNA326943
	DNA326944	DNA103462	DNA326946	DNA326947	DNA254141	DNA270697
	DNA326952	DNA326953	DNA151752	DNA326956	DNA326957	DNA188740
	DNA326964	DNA326965	DNA254240	DNA326966	DNA326967	DNA326968
35	DNA326974	DNA326975	DNA326976	DNA326977	DNA326978	DNA254165
	DNA326980	DNA326981	DNA270954	DNA326983	DNA326984	DNA326985

	DNA326986	DNA326988	DNA326989	DNA326990	DNA326992	DNA326994
	DNA326996	DNA326997	DNA326999	DNA327003	DNA327005	DNA327015
	DNA327018	DNA327021	DNA327023	DNA327025	DNA327029	DNA327030
	DNA327031	DNA327032	DNA327037	DNA327039	DNA238039	DNA273992
	DNA327046	DNA327047	DNA327048	DNA327049	DNA327051	DNA327054
5	DNA327058	DNA327060	DNA327062	DNA327063	DNA327064	DNA327067
	DNA327068	DNA327069	DNA327070	DNA327071	DNA327073	DNA327074
	DNA327077	DNA327078	DNA327079	DNA254785	DNA327086	DNA327087
	DNA327088	DNA327094	DNA327095	DNA327096	DNA327097	DNA327103
	DNA327104	DNA327105	DNA327107	DNA327108	DNA327109	DNA327110
10	DNA254783	DNA327111	DNA327114	DNA327115	DNA327116	DNA327117
	DNA227013	DNA230792	DNA103558	DNA327122	DNA327123	

PINEAL GLAND

	DNA287173	DNA323879	DNA323924	DNA273088	DNA323988	DNA324002
15	DNA324042	DNA324048	DNA324090	DNA324091	DNA324092	DNA324216
	DNA324229	DNA324246	DNA324296	DNA324340	DNA324341	DNA324521
	DNA324554	DNA324561	DNA324575	DNA324636	DNA324642	DNA324731
	DNA324737	DNA227607	DNA304668	DNA287319	DNA324784	DNA324815
	DNA324816	DNA324872	DNA324885	DNA225631	DNA324905	DNA324930
20	DNA226416	DNA324940	DNA324943	DNA325026	DNA325027	DNA225671
	DNA325208	DNA325231	DNA325234	DNA325296	DNA325475	DNA271324
	DNA325601	DNA225632	DNA325642	DNA325644	DNA325786	DNA302016
	DNA325789	DNA325803	DNA325804	DNA325883	DNA325932	DNA326099
	DNA287355	DNA326363	DNA326543	DNA326672	DNA326909	DNA326910
25	DNA327009	DNA327023	DNA327025	DNA327121		

LYMPH NODE

	DNA227213	DNA323858	DNA323859	DNA323862	DNA323863	DNA323864
	DNA323866	DNA323872	DNA323887	DNA323925	DNA226619	DNA324056
30	DNA324091	DNA324092	DNA324099	DNA324100	DNA324113	DNA324154
	DNA324155	DNA324193	DNA324204	DNA324218	DNA324417	DNA324418
	DNA324434	DNA324472	DNA324495	DNA324501	DNA324503	DNA324504
	DNA324505	DNA324521	DNA324525	DNA324551	DNA324552	DNA324554
	DNA324555	DNA324556	DNA324557	DNA324558	DNA324574	DNA324575
35	DNA324595	DNA324596	DNA324613	DNA324632	DNA324645	DNA324682
	DNA324690	DNA304680	DNA324737	DNA324756	DNA324785	DNA324790

	DNA324828	DNA324829	DNA324841	DNA324904	DNA324905	DNA324906
	DNA324907	DNA324908	DNA324981	DNA324982	DNA324989	DNA324991
	DNA324992	DNA325006	DNA325079	DNA325111	DNA325126	DNA325156
	DNA325157	DNA325179	DNA287216	DNA288247	DNA325231	DNA325233
	DNA325234	DNA325235	DNA325236	DNA325250	DNA325326	DNA325346
5	DNA325347	DNA325360	DNA325384	DNA325389	DNA325535	DNA325576
	DNA325601	DNA225632	DNA325625	DNA325642	DNA325683	DNA325684
	DNA325750	DNA325752	DNA325758	DNA325786	DNA302016	DNA325789
	DNA325913	DNA151893	DNA325935	DNA325954	DNA325955	DNA325985
	DNA325991	DNA325994	DNA326002	DNA326022	DNA287331	DNA326041
10	DNA326046	DNA326047	DNA326075	DNA326095	DNA326099	DNA326121
	DNA326146	DNA97300	DNA270975	DNA326373	DNA326416	DNA326427
	DNA326449	DNA326457	DNA326459	DNA326463	DNA326633	DNA326742
	DNA326885	DNA326952	DNA326974	DNA327023	DNA327025	
15	<u>COLON</u>					
	DNA287173	DNA323865	DNA323867	DNA323871	DNA323947	DNA323964
	DNA324039	DNA324048	DNA324090	DNA324091	DNA324092	DNA324111
	DNA324112	DNA227795	DNA324155	DNA226547	DNA324417	DNA324418
	DNA324423	DNA324437	DNA324495	DNA324496	DNA324501	DNA324502
20	DNA324504	DNA324505	DNA324521	DNA324525	DNA324550	DNA324552
	DNA324556	DNA324557	DNA324558	DNA324575	DNA324604	DNA324613
	DNA324624	DNA324697	DNA324717	DNA324720	DNA304680	DNA324737
	DNA324756	DNA324785	DNA324790	DNA324828	DNA324829	DNA324865
	DNA324904	DNA324905	DNA324906	DNA324907	DNA324908	DNA324989
25	DNA325026	DNA325027	DNA325033	DNA325068	DNA325104	DNA325105
	DNA325106	DNA325116	DNA325128	DNA325129	DNA325156	DNA325157
	DNA325182	DNA325183	DNA325184	DNA325231	DNA325232	DNA325233
	DNA325234	DNA325235	DNA325236	DNA325250	DNA325326	DNA325347
	DNA325358	DNA325414	DNA325418	DNA189687	DNA325570	DNA325601
30	DNA225632	DNA325605	DNA325619	DNA256072	DNA325642	DNA325644
	DNA270458	DNA227092	DNA325731	DNA226014	DNA325786	DNA302016
	DNA325789	DNA325810	DNA325811	DNA325812	DNA325913	DNA325914
	DNA325941	DNA325985	DNA326002	DNA287331	DNA326099	DNA326121
	DNA326122	DNA326124	DNA326136	DNA326330	DNA326396	DNA326457
35	DNA326529	DNA326617	DNA326633	DNA326634	DNA326651	DNA290260
	DNA273517	DNA326886	DNA226409	DNA326958	DNA327025	DNA327029

DNA327067

PANCREAS

	DNA323732	DNA287173	DNA323745	DNA323778	DNA323781	DNA323783
	DNA323803	DNA323806	DNA323808	DNA323815	DNA103253	DNA304686
5	DNA323856	DNA323864	DNA323866	DNA323878	DNA323882	DNA210134
	DNA323920	DNA323923	DNA323927	DNA323951	DNA226619	DNA226005
	DNA83046	DNA324017	DNA324042	DNA324048	DNA324073	DNA324091
	DNA324092	DNA324119	DNA227795	DNA227528	DNA324139	DNA324155
	DNA324193	DNA324195	DNA324197	DNA324216	DNA324220	DNA324221
10	DNA324229	DNA324317	DNA324320	DNA324340	DNA324341	DNA324352
	DNA324364	DNA324366	DNA324367	DNA324380	DNA324398	DNA324412
	DNA324417	DNA324418	DNA324495	DNA324501	DNA324504	DNA324505
	DNA324521	DNA324536	DNA324552	DNA324557	DNA324558	DNA288259
	DNA324591	DNA83020	DNA324636	DNA324642	DNA324697	DNA324702
15	DNA324715	DNA324716	DNA324717	DNA304680	DNA324737	DNA227204
	DNA324744	DNA324756	DNA324770	DNA272263	DNA324784	DNA324790
	DNA324795	DNA324824	DNA324828	DNA324829	DNA324850	DNA324858
	DNA324880	DNA324884	DNA324885	DNA324891	DNA225631	DNA274326
	DNA324896	DNA324904	DNA324906	DNA324922	DNA324930	DNA324935
20	DNA304710	DNA324962	DNA324963	DNA324972	DNA324973	DNA324977
	DNA272090	DNA83141	DNA325009	DNA325027	DNA325033	DNA304685
	DNA325064	DNA325079	DNA325099	DNA325104	DNA325105	DNA325106
	DNA325126	DNA325136	DNA325146	DNA325156	DNA325157	DNA290319
	DNA254771	DNA89242	DNA325184	DNA325185	DNA325202	DNA325229
25	DNA88350	DNA325233	DNA325235	DNA325236	DNA325247	DNA325254
	DNA325262	DNA325268	DNA325296	DNA325330	DNA325332	DNA325335
	DNA325336	DNA287237	DNA325355	DNA325360	DNA325384	DNA325398
	DNA325403	DNA325405	DNA325411	DNA325414	DNA325418	DNA325428
	DNA97285	DNA325450	DNA325453	DNA325475	DNA325493	DNA325506
30	DNA325532	DNA325548	DNA325596	DNA325601	DNA225632	DNA226771
	DNA325642	DNA325655	DNA325656	DNA325657	DNA325658	DNA325660
	DNA325661	DNA325663	DNA270458	DNA227092	DNA196351	DNA325680
	DNA325740	DNA325741	DNA325742	DNA325743	DNA325744	DNA325745
	DNA325746	DNA325750	DNA325752	DNA325757	DNA325758	DNA325760
35	DNA325775	DNA325776	DNA325786	DNA325788	DNA325803	DNA325804
	DNA325826	DNA325912	DNA103509	DNA325952	DNA325953	DNA326003

	DNA326016	DNA287331	DNA326047	DNA326053	DNA326055	DNA326058
	DNA150485	DNA326060	DNA326072	DNA326092	DNA326099	DNA326110
	DNA326129	DNA326157	DNA326165	DNA326166	DNA287355	DNA326210
	DNA326220	DNA326233	DNA326234	DNA97300	DNA326288	DNA326291
	DNA326292	DNA326300	DNA326328	DNA326330	DNA326331	DNA326333
5	DNA326352	DNA326370	DNA326378	DNA326397	DNA88430	DNA326410
	DNA326415	DNA326416	DNA326426	DNA326480	DNA326481	DNA326482
	DNA256555	DNA326523	DNA326563	DNA326577	DNA326603	DNA326604
	DNA326615	DNA326621	DNA326625	DNA227249	DNA326646	DNA326657
	DNA326663	DNA326664	DNA326665	DNA326666	DNA326667	DNA272347
10	DNA326668	DNA326669	DNA326671	DNA274139	DNA326675	DNA326680
	DNA326692	DNA326698	DNA326712	DNA326717	DNA304658	DNA326752
	DNA326760	DNA326762	DNA273346	DNA254548	DNA326769	DNA326776
	DNA326777	DNA287270	DNA326790	DNA326803	DNA326818	DNA326829
	DNA194807	DNA103525	DNA326860	DNA326879	DNA226409	DNA326907
15	DNA326911	DNA326912	DNA326913	DNA326952	DNA326955	DNA304719
	DNA327023	DNA327025	DNA327042	DNA273254	DNA327116	DNA227013
	DNA103558	DNA327120				
	<u>PROSTATE</u>					
20	DNA287173	DNA323749	DNA323774	DNA323779	DNA323780	DNA323806
	DNA323820	DNA304686	DNA323850	DNA323864	DNA323866	DNA323867
	DNA323871	DNA323877	DNA323882	DNA227529	DNA323925	DNA323927
	DNA323944	DNA226619	DNA323964	DNA323980	DNA323982	DNA271986
	DNA324001	DNA324004	DNA83046	DNA324023	DNA227504	DNA324027
25	DNA324042	DNA324048	DNA324057	DNA324058	DNA324073	DNA324090
	DNA324091	DNA324092	DNA324101	DNA324111	DNA324112	DNA324115
	DNA324116	DNA324117	DNA227795	DNA324154	DNA324155	DNA324178
	DNA324203	DNA324219	DNA324230	DNA324260	DNA324293	DNA226547
	DNA324301	DNA227307	DNA324335	DNA324340	DNA324341	DNA324354
30	DNA324406	DNA324412	DNA324417	DNA324418	DNA324437	DNA324458
	DNA324472	DNA324494	DNA324502	DNA324503	DNA324504	DNA324505
	DNA324521	DNA324525	DNA324541	DNA324550	DNA324551	DNA324552
	DNA324554	DNA324555	DNA324556	DNA324557	DNA324558	DNA324561
	DNA324566	DNA324567	DNA324575	DNA324576	DNA288259	DNA324587
35	DNA324595	DNA324596	DNA254147	DNA324604	DNA324605	DNA324613
	DNA324624	DNA324631	DNA324632	DNA324636	DNA324645	DNA324682

	DNA324690	DNA324712	DNA324715	DNA324716	DNA324720	DNA324722
	DNA304680	DNA324737	DNA324785	DNA324793	DNA324796	DNA324797
	DNA150772	DNA324825	DNA324828	DNA324829	DNA324830	DNA324841
	DNA324844	DNA324847	DNA324856	DNA324866	DNA225631	DNA193955
	DNA324904	DNA324905	DNA324906	DNA227929	DNA324910	DNA324911
5	DNA324912	DNA324926	DNA103588	DNA324961	DNA325006	DNA325015
	DNA325026	DNA325027	DNA325079	DNA325086	DNA151010	DNA325098
	DNA325105	DNA325106	DNA325115	DNA325116	DNA131588	DNA325126
	DNA325127	DNA272050	DNA325129	DNA325131	DNA325156	DNA325157
	DNA325179	DNA325182	DNA325184	DNA325187	DNA325202	DNA325210
10	DNA325231	DNA325232	DNA325233	DNA325234	DNA325235	DNA325236
	DNA325250	DNA325303	DNA325326	DNA227172	DNA325335	DNA103421
	DNA325347	DNA226217	DNA325349	DNA325351	DNA325360	DNA325398
	DNA325414	DNA325432	DNA325472	DNA325475	DNA325535	DNA325558
	DNA325570	DNA325576	DNA325601	DNA225632	DNA325618	DNA325642
15	DNA325644	DNA325645	DNA325655	DNA270458	DNA325667	DNA325668
	DNA325680	DNA325681	DNA325723	DNA325731	DNA325749	DNA325750
	DNA325752	DNA325786	DNA302016	DNA325789	DNA325801	DNA325806
	DNA325811	DNA325812	DNA325814	DNA325815	DNA281436	DNA325836
	DNA325841	DNA325844	DNA325853	DNA325854	DNA325906	DNA325907
20	DNA325908	DNA325913	DNA325927	DNA325984	DNA325985	DNA325994
	DNA325998	DNA326002	DNA234442	DNA287331	DNA326041	DNA326046
	DNA326054	DNA326075	DNA326099	DNA326122	DNA326124	DNA326129
	DNA326136	DNA326155	DNA287355	DNA326194	DNA326201	DNA326233
	DNA326234	DNA326245	DNA326254	DNA97300	DNA326291	DNA326292
25	DNA326302	DNA326332	DNA326340	DNA97290	DNA326370	DNA326456
	DNA326457	DNA326459	DNA326481	DNA326482	DNA326529	DNA326599
	DNA326608	DNA326634	DNA326645	DNA326686	DNA326687	DNA326688
	DNA326692	DNA103580	DNA150784	DNA270931	DNA254548	DNA326839
	DNA326884	DNA326893	DNA326921	DNA326974	DNA327005	DNA327012
30	DNA327023	DNA327025	DNA327039	DNA273254	DNA327067	
<u>LIVER</u>						
	DNA323720	DNA323733	DNA287173	DNA323758	DNA323767	DNA323778
	DNA323783	DNA188748	DNA323808	DNA227213	DNA323810	DNA323817
35	DNA323820	DNA273060	DNA323852	DNA269708	DNA323864	DNA323865
	DNA323866	DNA323867	DNA323871	DNA323894	DNA323895	DNA274759

	DNA323913	DNA323917	DNA323922	DNA323927	DNA323934	DNA323936
	DNA323948	DNA323960	DNA226619	DNA323964	DNA323968	DNA323971
	DNA323972	DNA323973	DNA323974	DNA323983	DNA323984	DNA323989
	DNA324019	DNA254346	DNA324039	DNA324042	DNA82328	DNA324048
	DNA324053	DNA275195	DNA324063	DNA324069	DNA324090	DNA324091
5	DNA324092	DNA324095	DNA271060	DNA324111	DNA324112	DNA324118
	DNA324124	DNA324125	DNA227795	DNA287167	DNA227528	DNA324134
	DNA324139	DNA324141	DNA324154	DNA324155	DNA324158	DNA324174
	DNA324181	DNA324195	DNA324199	DNA324200	DNA324201	DNA324203
	DNA324204	DNA324205	DNA271608	DNA324208	DNA324217	DNA324229
10	DNA324238	DNA324245	DNA324258	DNA324283	DNA252367	DNA324293
	DNA226547	DNA324312	DNA324313	DNA324320	DNA324321	DNA324326
	DNA324340	DNA324341	DNA324349	DNA324351	DNA324355	DNA324370
	DNA324378	DNA324386	DNA324414	DNA324417	DNA324418	DNA324437
	DNA324439	DNA324464	DNA324474	DNA324476	DNA324481	DNA225919
15	DNA324492	DNA324495	DNA324496	DNA324501	DNA324502	DNA324503
	DNA324504	DNA324505	DNA225584	DNA324521	DNA324525	DNA324541
	DNA324550	DNA324551	DNA324552	DNA324554	DNA324555	DNA324556
	DNA324557	DNA324558	DNA324561	DNA324569	DNA324575	DNA324576
	DNA324580	DNA324581	DNA324582	DNA288259	DNA324591	DNA324596
20	DNA324600	DNA324606	DNA324613	DNA324618	DNA103380	DNA324632
	DNA324635	DNA324636	DNA324638	DNA324648	DNA324685	DNA324687
	DNA324690	DNA324695	DNA324700	DNA324702	DNA324713	DNA324717
	DNA324722	DNA324724	DNA324726	DNA324727	DNA304680	DNA324732
	DNA324733	DNA324736	DNA324737	DNA275630	DNA324744	DNA304716
25	DNA324751	DNA324753	DNA324756	DNA287319	DNA324780	DNA324781
	DNA324783	DNA304699	DNA324785	DNA324790	DNA324802	DNA324824
	DNA324828	DNA324829	DNA324844	DNA324866	DNA324881	DNA225631
	DNA274326	DNA324902	DNA324904	DNA324905	DNA324906	DNA324907
	DNA324908	DNA324915	DNA324916	DNA324917	DNA324922	DNA324927
30	DNA324931	DNA103588	DNA324944	DNA324950	DNA324951	DNA324961
	DNA304710	DNA324962	DNA324963	DNA324968	DNA324971	DNA324974
	DNA324977	DNA272090	DNA324989	DNA324991	DNA324992	DNA325009
	DNA325013	DNA325018	DNA325026	DNA325027	DNA325033	DNA325036
	DNA325039	DNA325078	DNA325079	DNA325080	DNA325081	DNA32509
35	DNA325091	DNA325092	DNA325104	DNA325105	DNA325106	DNA325113
	DNA325117	DNA325118	DNA325119	DNA131588	DNA325126	DNA325135

	DNA325152	DNA325153	DNA325156	DNA325157	DNA325162	DNA325177
	DNA325179	DNA89242	DNA325182	DNA325184	DNA325185	DNA325188
	DNA325194	DNA325231	DNA325232	DNA325233	DNA325234	DNA325235
	DNA325236	DNA325250	DNA325280	DNA325281	DNA325282	DNA325287
	DNA325296	DNA325326	DNA325332	DNA325334	DNA325335	DNA325339
5	DNA325340	DNA103506	DNA325343	DNA325344	DNA325347	DNA325352
	DNA325358	DNA325360	DNA325368	DNA325388	DNA255696	DNA325403
	DNA325408	DNA325409	DNA325410	DNA325411	DNA325414	DNA325418
	DNA97285	DNA325456	DNA226080	DNA325471	DNA325473	DNA325475
	DNA325485	DNA270721	DNA325506	DNA325524	DNA325535	DNA325536
10	DNA325537	DNA325564	DNA325565	DNA325570	DNA325571	DNA325590
	DNA325591	DNA325596	DNA325599	DNA325601	DNA225632	DNA226771
	DNA325625	DNA325633	DNA325637	DNA325642	DNA325644	DNA325645
	DNA270458	DNA227092	DNA325674	DNA290294	DNA325678	DNA325680
	DNA325681	DNA325686	DNA325692	DNA325693	DNA325694	DNA325722
15	DNA325731	DNA325732	DNA325750	DNA325752	DNA325756	DNA325758
	DNA325778	DNA325779	DNA325780	DNA325786	DNA302016	DNA325789
	DNA325803	DNA325804	DNA325809	DNA325811	DNA325812	DNA325814
	DNA325823	DNA325837	DNA325838	DNA325842	DNA325845	DNA325849
	DNA325853	DNA325854	DNA325863	DNA325868	DNA325869	DNA325871
20	DNA325882	DNA325887	DNA325896	DNA325906	DNA325908	DNA325912
	DNA325929	DNA325931	DNA325935	DNA226324	DNA325949	DNA325971
	DNA325978	DNA325979	DNA325985	DNA325999	DNA326002	DNA326003
	DNA326006	DNA326017	DNA287331	DNA326069	DNA326099	DNA326101
	DNA326121	DNA326122	DNA326124	DNA326127	DNA326129	DNA326136
25	DNA326156	DNA326164	DNA287355	DNA326193	DNA326196	DNA189703
	DNA326220	DNA326233	DNA326234	DNA326239	DNA326242	DNA326246
	DNA326247	DNA326254	DNA326256	DNA97300	DNA326273	DNA326278
	DNA254198	DNA326289	DNA326291	DNA326292	DNA326325	DNA326330
	DNA326334	DNA326339	DNA326341	DNA88378	DNA326347	DNA326352
30	DNA326357	DNA326370	DNA326380	DNA227055	DNA326406	DNA274755
	DNA326411	DNA326416	DNA326423	DNA326426	DNA326427	DNA326430
	DNA326434	DNA326437	DNA326440	DNA326449	DNA326450	DNA326451
	DNA326452	DNA326453	DNA326454	DNA326457	DNA326476	DNA326481
	DNA326482	DNA326484	DNA326485	DNA326489	DNA326497	DNA326498
35	DNA326539	DNA326548	DNA326563	DNA326579	DNA326580	DNA326586
	DNA326625	DNA227249	DNA326626	DNA326633	DNA326634	DNA326646

	DNA326651	DNA326671	DNA326678	DNA326680	DNA326698	DNA326701
	DNA326702	DNA326703	DNA326705	DNA326706	DNA103580	DNA326713
	DNA88084	DNA326727	DNA290260	DNA326736	DNA326741	DNA326742
	DNA326752	DNA326756	DNA326758	DNA326762	DNA254548	DNA326769
	DNA304662	DNA326772	DNA326776	DNA326777	DNA227348	DNA326819
5	DNA194701	DNA326826	DNA326831	DNA326832	DNA326850	DNA326851
	DNA269526	DNA326867	DNA326870	DNA326871	DNA269746	DNA326885
	DNA326886	DNA326905	DNA326923	DNA326924	DNA326939	DNA269830
	DNA326947	DNA326958	DNA188740	DNA326964	DNA326974	DNA326977
	DNA326981	DNA270954	DNA326983	DNA326987	DNA326992	DNA327003
10	DNA327005	DNA327010	DNA327013	DNA327014	DNA327016	DNA327023
	DNA327025	DNA327027	DNA327050	DNA327052	DNA327053	DNA273254
	DNA327065	DNA327067	DNA327068	DNA327069	DNA327091	DNA227656
	DNA327106	DNA327114	DNA327116	DNA227013		
15	<u>BONE MARROW</u>					
	DNA323735	DNA323762	DNA323770	DNA323771	DNA323774	DNA323775
	DNA323784	DNA323804	DNA272748	DNA323880	DNA323903	DNA323904
	DNA323964	DNA323982	DNA324015	DNA324023	DNA324056	DNA324057
	DNA324076	DNA324086	DNA324100	DNA324139	DNA324154	DNA324173
20	DNA324178	DNA324200	DNA324211	DNA324230	DNA324242	DNA324248
	DNA324249	DNA324250	DNA324260	DNA88100	DNA324301	DNA324364
	DNA324381	DNA324382	DNA324383	DNA324420	DNA324484	DNA324495
	DNA324507	DNA324551	DNA324554	DNA324575	DNA324605	DNA324637
	DNA324644	DNA324690	DNA304680	DNA324746	DNA324825	DNA324848
25	DNA324854	DNA324856	DNA324858	DNA324905	DNA324910	DNA325011
	DNA325031	DNA325086	DNA151010	DNA325127	DNA272050	DNA325133
	DNA325169	DNA325184	DNA325231	DNA325234	DNA325241	DNA325242
	DNA325299	DNA287642	DNA325345	DNA325351	DNA325354	DNA325356
	DNA325392	DNA325399	DNA325428	DNA325461	DNA272413	DNA325576
30	DNA325668	DNA325726	DNA325733	DNA325811	DNA325901	DNA325953
	DNA151831	DNA325998	DNA234442	DNA326035	DNA326095	DNA326138
	DNA326365	DNA326373	DNA326390	DNA326391	DNA326416	DNA326417
	DNA326449	DNA326450	DNA326451	DNA326942	DNA327111	
35	<u>TESTIS</u>					
	DNA287173	DNA323761	DNA323770	DNA323771	DNA323774	DNA323775

	DNA226262	DNA323778	DNA323790	DNA323804	DNA323817	DNA323820
	DNA323829	DNA103214	DNA304686	DNA272748	DNA323844	DNA323845
	DNA323851	DNA323856	DNA323858	DNA323859	DNA323861	DNA323864
	DNA323865	DNA323866	DNA323867	DNA323869	DNA323871	DNA323872
	DNA323877	DNA323880	DNA323922	DNA323943	DNA323947	DNA323956
5	DNA323964	DNA323967	DNA323968	DNA323973	DNA323985	DNA323993
	DNA323998	DNA324004	DNA324009	DNA324015	DNA324023	DNA324048
	DNA324054	DNA324058	DNA324063	DNA324090	DNA324091	DNA324092
	DNA324100	DNA324103	DNA324111	DNA324112	DNA324114	DNA324117
	DNA324118	DNA227795	DNA150725	DNA324147	DNA324149	DNA324154
10	DNA324155	DNA324164	DNA324165	DNA324170	DNA324173	DNA324178
	DNA324187	DNA304805	DNA324196	DNA324199	DNA324200	DNA324201
	DNA299899	DNA324204	DNA271608	DNA324207	DNA324208	DNA324210
	DNA324213	DNA324214	DNA324218	DNA324219	DNA324229	DNA324230
	DNA324276	DNA324281	DNA324282	DNA324284	DNA324285	DNA324291
15	DNA324293	DNA226547	DNA324295	DNA324301	DNA324312	DNA324313
	DNA324326	DNA324357	DNA324358	DNA324373	DNA324381	DNA324382
	DNA324383	DNA324384	DNA324385	DNA324390	DNA324395	DNA324398
	DNA324403	DNA324404	DNA324417	DNA324418	DNA324423	DNA324433
	DNA324434	DNA324436	DNA324437	DNA324438	DNA324455	DNA324468
20	DNA324469	DNA324472	DNA324478	DNA324479	DNA324481	DNA324483
	DNA324490	DNA324491	DNA324495	DNA324496	NA324499	DNA324500
	DNA324501	DNA324502	DNA324503	DNA324504	DNA324505	DNA324507
	DNA324509	DNA324511	DNA324512	DNA324514	DNA324521	DNA324522
	DNA324525	DNA324531	DNA324541	DNA324549	DNA324550	DNA324551
25	DNA324552	DNA324554	DNA324555	DNA324556	DNA324557	DNA324558
	DNA324568	DNA324574	DNA324575	DNA324576	DNA324579	DNA324583
	DNA324584	DNA324585	DNA324590	DNA324591	DNA324592	DNA324595
	DNA324596	DNA324597	DNA324598	DNA324599	DNA324600	DNA324601
	DNA324605	DNA269816	DNA324612	DNA324613	DNA324616	DNA324622
30	DNA324624	DNA324628	DNA324632	DNA271931	DNA324642	DNA324645
	DNA324682	DNA324683	DNA324684	DNA324685	DNA324687	DNA324690
	DNA324697	DNA324717	DNA324720	DNA304680	DNA324737	DNA324742
	DNA275630	DNA324746	DNA324751	DNA324785	DNA324790	DNA324800
	DNA324801	DNA324803	DNA150772	DNA324811	DNA324828	DNA324829
35	DNA324831	DNA324840	DNA324841	DNA324843	DNA324844	DNA324845
	DNA324846	DNA324855	DNA324858	DNA324866	DNA324867	DNA324882

	DNA324883	DNA225631	DNA324902	DNA324904	DNA324905	DNA324906
	DNA324907	DNA324908	DNA324909	DNA324910	DNA324913	DNA324914
	DNA324915	DNA324916	DNA324917	DNA324926	DNA324928	DNA324941
	DNA324950	DNA324951	DNA324954	DNA304710	DNA324962	DNA324963
	DNA324965	DNA324966	DNA324967	DNA324968	DNA324982	DNA324989
5	DNA325002	DNA325003	DNA325006	DNA325007	DNA226560	DNA325010
	DNA325011	DNA325025	DNA325026	DNA325027	DNA325028	DNA325034
	DNA325049	DNA325078	DNA325079	DNA325080	DNA325081	DNA325086
	DNA325095	DNA325096	DNA151010	DNA325097	DNA325098	DNA325107
	DNA325111	DNA325116	DNA325117	DNA325118	DNA325119	DNA325123
10	DNA325124	DNA325125	DNA131588	DNA325127	DNA325134	DNA325141
	DNA325146	DNA325152	DNA325153	DNA325154	DNA325155	DNA325156
	DNA325157	DNA325158	DNA325159	DNA325164	DNA325169	DNA325179
	DNA325182	DNA325183	DNA325184	DNA325196	DNA325202	DNA325206
	DNA325222	DNA325229	DNA325231	DNA325232	DNA325233	DNA325234
15	DNA325235	DNA325236	DNA325250	DNA325281	DNA325282	DNA325289
	DNA325291	DNA325297	DNA325298	DNA325301	DNA287642	DNA325326
	DNA325339	DNA325340	DNA103421	DNA325345	DNA325347	DNA325349
	DNA325351	DNA325357	DNA325358	DNA325360	DNA325376	DNA325387
	DNA325392	DNA325395	DNA269952	DNA255078	DNA325428	DNA325430
20	DNA325433	DNA325434	DNA325435	DNA325436	DNA325437	DNA325438
	DNA97285	DNA325439	DNA325445	DNA254186	DNA325523	DNA325534
	DNA325535	DNA325541	DNA325549	DNA272413	DNA325564	DNA325565
	DNA325570	DNA257965	DNA325576	DNA325589	DNA325601	DNA225632
	DNA325613	DNA325615	DNA325622	DNA325625	DNA325629	DNA325630
25	DNA325632	DNA325633	DNA325635	DNA325642	DNA325644	DNA325645
	DNA325668	DNA325672	DNA325674	DNA325680	DNA325685	DNA325697
	DNA325711	DNA325720	DNA325731	DNA325732	DNA325736	DNA325748
	DNA325750	DNA325752	DNA325753	DNA325754	DNA325758	DNA325762
	DNA325782	DNA325786	DNA302016	DNA325789	DNA325806	DNA325809
30	DNA325810	DNA325811	DNA325812	DNA325814	DNA325821	DNA304669
	DNA325824	DNA325825	DNA325827	DNA325829	DNA325831	DNA325837
	DNA325838	DNA325843	DNA325844	DNA325848	DNA325860	DNA227321
	DNA325879	DNA325882	DNA325886	DNA325887	DNA325888	DNA325897
	DNA325898	DNA325901	DNA325905	DNA325906	DNA325908	DNA325913
35	DNA325922	DNA325933	DNA325934	DNA325935	DNA325939	DNA325940
	DNA325965	DNA325969	DNA325985	DNA325991	DNA325994	DNA325998

	DNA326002	DNA326003	DNA326009	DNA234442	DNA326020	DNA326021
	DNA326022	DNA287331	DNA326035	DNA326041	DNA326045	DNA326046
	DNA326047	DNA326070	DNA326075	DNA326099	DNA326128	DNA326129
	DNA326155	DNA326156	DNA274180	DNA326187	DNA326214	DNA326228
	DNA326233	DNA326234	DNA326251	DNA97300	DNA304715	DNA290292
5	DNA326289	DNA326291	DNA326292	DNA326311	DNA326364	DNA326373
	DNA326390	DNA326391	DNA326397	DNA326400	DNA326410	DNA326426
	DNA287234	DNA326449	DNA326450	DNA326451	DNA326452	DNA326453
	DNA326454	DNA326457	DNA326463	DNA326471	DNA326557	DNA326559
	DNA326579	DNA326580	DNA326603	DNA326633	DNA326634	DNA326642
10	DNA326651	DNA326686	DNA326687	DNA326688	DNA326691	DNA326692
	DNA326698	DNA290260	DNA304658	DNA326762	DNA326769	DNA326790
	DNA326791	DNA326792	DNA326796	DNA326798	DNA326837	DNA326854
	DNA326858	DNA326884	DNA326885	DNA326886	DNA326940	DNA326941
	DNA269830	DNA254240	DNA326974	DNA327005	DNA327019	DNA327020
15	DNA327021	DNA327025	DNA327026	DNA327027	DNA327029	DNA327039
	DNA327044	DNA327060	DNA327062	DNA273254	DNA327066	DNA327067
	DNA327072	DNA327077	DNA327078	DNA327079	DNA327083	DNA327084
	DNA327098	DNA327100	DNA327114			
20	<u>CERVIX</u>					
	DNA324417	DNA324418	DNA324557	DNA324828	DNA324829	DNA324904
	DNA324905	DNA324906	DNA325231	DNA325234		
	<u>NERVOUS</u>					
25	DNA287173	DNA323760	DNA103253	DNA323848	DNA323864	DNA323865
	DNA323866	DNA323867	DNA323877	DNA323878	DNA323882	DNA323887
	DNA323925	DNA323966	DNA324107	DNA227795	DNA324135	DNA227190
	DNA324155	DNA271608	DNA324219	DNA324259	DNA324320	DNA324351
	DNA324364	DNA270615	DNA324504	DNA324505	DNA324551	DNA324552
30	DNA324554	DNA324555	DNA324556	DNA324557	DNA324558	DNA324575
	DNA324756	DNA324790	DNA324828	DNA324829	DNA324904	DNA324905
	DNA324906	DNA324907	DNA324908	DNA324982	DNA325079	DNA325187
	DNA325231	DNA325232	DNA325233	DNA325234	DNA325235	DNA325236
	DNA325416	DNA325419	DNA325432	DNA325562	DNA325602	DNA325607
35	DNA226028	DNA325647	DNA325704	DNA325759	DNA287331	DNA326077
	DNA326196	DNA326198	DNA326215	DNA326362	DNA326459	DNA326752

	DNA326846	DNA226409	DNA326956	DNA326983	DNA327058	DNA327099
	<u>EYE</u>					
	DNA323721	DNA287173	DNA323747	DNA323763	DNA323769	DNA226262
	DNA323778	DNA323799	DNA323807	DNA227213	DNA323817	DNA323818
5	DNA323820	DNA323829	DNA323835	DNA323839	DNA323856	DNA323858
	DNA323859	DNA323864	DNA323865	DNA323866	DNA323869	DNA323871
	DNA323872	DNA323875	DNA323887	DNA323891	DNA323892	DNA323906
	DNA323914	DNA323923	DNA323925	DNA323928	DNA323932	DNA323935
	DNA323936	DNA323947	DNA323964	DNA323971	DNA323972	DNA323973
10	DNA323974	DNA323988	DNA256905	DNA324004	DNA324009	DNA324010
	DNA247474	DNA324022	DNA324023	DNA324025	DNA324028	DNA324029
	DNA324037	DNA324048	DNA324049	DNA103217	DNA275195	DNA324059
	DNA324060	DNA324061	DNA275049	DNA324062	DNA273800	DNA324076
	DNA324083	DNA324085	DNA324087	DNA324090	DNA324091	DNA324092
15	DNA324096	DNA324100	DNA226428	DNA275066	DNA324104	DNA324106
	DNA324108	DNA324110	DNA324111	DNA324112	DNA324127	DNA227795
	DNA287167	DNA324155	DNA324157	DNA324163	DNA324164	DNA324165
	DNA324167	DNA275240	DNA324170	DNA324175	DNA324185	DNA324186
	DNA324193	DNA324199	DNA324200	DNA324201	DNA324203	DNA324204
20	DNA324207	DNA324209	DNA324210	DNA324212	DNA324213	DNA324214
	DNA324217	DNA324218	DNA324219	DNA324224	DNA324230	DNA324280
	DNA324281	DNA324282	DNA226547	DNA324295	DNA324306	DNA324307
	DNA324312	DNA324313	DNA324320	DNA324322	DNA324329	DNA324330
	DNA324331	DNA273919	DNA324332	DNA324334	DNA324338	DNA324344
25	DNA324345	DNA324347	DNA324358	DNA324359	DNA324365	DNA324372
	DNA324374	DNA324390	DNA324417	DNA324418	DNA324423	DNA324434
	DNA324436	DNA324437	DNA324448	DNA324458	DNA324461	DNA324463
	DNA324470	DNA324478	DNA324479	DNA324481	DNA324482	DNA324483
	DNA324491	DNA324495	DNA324496	DNA324501	DNA324504	DNA324505
30	DNA324510	DNA324512	DNA324519	DNA324521	DNA324525	DNA324535
	DNA324541	DNA324552	DNA324555	DNA324556	DNA324557	DNA324558
	DNA324575	DNA324584	DNA324589	DNA324590	DNA324591	DNA324594
	DNA324595	DNA324596	DNA324597	DNA324598	DNA324599	DNA324600
	DNA254147	DNA324607	DNA290231	DNA324608	DNA324609	DNA324613
35	DNA324623	DNA324624	DNA324625	DNA324632	DNA324645	DNA324682
	DNA324687	DNA324690	DNA324697	DNA324710	DNA324711	DNA324717

	DNA324718	DNA324720	DNA304680	DNA324737	DNA270613	DNA324742
	DNA287246	DNA324745	DNA304716	DNA324747	DNA324751	DNA324756
	DNA324766	DNA304661	DNA324777	DNA324778	DNA324779	DNA324785
	DNA324788	DNA324790	DNA324811	DNA324828	DNA324829	DNA324830
	DNA324839	DNA324841	DNA324844	DNA324866	DNA324902	DNA324904
5	DNA324906	DNA324907	DNA324908	DNA324915	DNA324916	DNA324917
	DNA324942	DNA103588	DNA324948	DNA324949	DNA324950	DNA324951
	DNA324965	DNA324966	DNA324967	DNA324968	DNA324982	DNA324989
	DNA325002	DNA325003	DNA325005	DNA325006	DNA325013	DNA325015
	DNA325024	DNA325025	DNA325026	DNA325027	DNA325034	DNA325058
10	DNA325066	DNA325078	DNA325079	DNA325080	DNA325081	DNA325093
	DNA325098	DNA325110	DNA325111	DNA325116	DNA325117	DNA325118
	DNA325119	DNA325124	DNA325127	DNA325128	DNA325130	DNA325146
	DNA325152	DNA325153	DNA325155	DNA325156	DNA325157	DNA325164
	DNA325172	DNA325179	DNA325182	DNA325183	DNA325184	DNA325190
15	DNA325191	DNA325192	DNA325193	DNA325196	DNA325198	DNA325202
	DNA325206	DNA271722	DNA325207	DNA325209	DNA325222	DNA325233
	DNA325235	DNA325236	DNA325247	DNA325256	DNA325283	DNA325289
	DNA325293	DNA325298	DNA325300	DNA325301	DNA325311	DNA325313
	DNA325317	DNA325321	DNA325323	DNA325347	DNA325351	DNA325364
20	DNA325370	DNA325376	DNA325378	DNA325382	DNA227509	DNA325389
	DNA325390	DNA325395	DNA325427	DNA325430	DNA97285	DNA325439
	DNA325442	DNA325445	DNA325451	DNA325452	DNA270134	DNA325459
	DNA272728	DNA325478	DNA325479	DNA325499	DNA270721	DNA325506
	DNA325523	DNA325526	DNA325534	DNA325535	DNA325540	DNA325542
25	DNA325543	DNA271843	DNA325559	DNA325576	DNA325577	DNA325578
	DNA325584	DNA325587	DNA325593	DNA325596	DNA325598	DNA325601
	DNA225632	DNA325607	DNA226028	DNA325612	DNA325614	DNA325625
	DNA325627	DNA325628	DNA325632	DNA325642	DNA325647	DNA325674
	DNA290294	DNA325678	DNA325680	DNA325682	DNA325683	DNA325684
30	DNA325685	DNA325688	DNA325690	DNA325695	DNA325713	DNA325719
	DNA325720	DNA325731	DNA325733	DNA325736	DNA274361	DNA325752
	DNA325757	DNA325762	DNA325769	DNA325773	DNA325775	DNA325776
	DNA325782	DNA325784	DNA325786	DNA302016	DNA325789	DNA325800
	DNA325810	DNA325811	DNA325812	DNA325817	DNA325818	DNA304669
35	DNA281436	DNA325835	DNA325837	DNA325838	DNA325843	DNA325844
	DNA210180	DNA325872	DNA325882	DNA325889	DNA325891	DNA325892

	DNA325899	DNA325906	DNA325908	DNA325922	DNA325924	DNA325933
	DNA325935	DNA325945	DNA325964	DNA325965	DNA325975	DNA325978
	DNA325979	DNA325985	DNA325988	DNA326000	DNA326002	DNA326004
	DNA326008	DNA234442	DNA326013	DNA326016	DNA326020	DNA326021
	DNA326022	DNA326031	DNA326033	DNA255370	DNA273014	DNA326037
5	DNA326047	DNA326050	DNA326058	DNA326061	DNA326072	DNA326097
	DNA326099	DNA326104	DNA326105	DNA326116	DNA326121	DNA326122
	DNA326124	DNA326129	DNA326133	DNA326136	DNA326156	DNA326167
	DNA326175	DNA326196	DNA326197	DNA326198	DNA326214	DNA326221
	DNA326222	DNA326229	DNA326243	DNA326244	DNA326251	DNA326260
10	DNA326264	DNA326265	DNA97300	DNA297388	DNA326288	DNA290292
	DNA326289	DNA326294	DNA326296	DNA326316	DNA326322	DNA326334
	DNA326339	DNA326343	DNA326344	DNA227873	DNA326348	DNA326360
	DNA97290	DNA227071	DNA227764	DNA326376	DNA326381	DNA326393
	DNA326394	DNA326398	DNA326402	DNA326405	DNA326406	DNA326413
15	DNA326418	DNA326420	DNA326427	DNA326435	DNA326436	DNA326445
	DNA326447	DNA274690	DNA326449	DNA326450	DNA326451	DNA326452
	DNA326453	DNA326454	DNA326455	DNA326458	DNA326459	DNA326463
	DNA326466	DNA326467	DNA326473	DNA326488	DNA326520	DNA326526
	DNA326527	DNA326534	DNA326559	DNA326560	DNA326574	DNA326576
20	DNA326579	DNA326580	DNA326615	DNA326617	DNA326633	DNA326634
	DNA326642	DNA326663	DNA326664	DNA272347	DNA326669	DNA326671
	DNA326691	DNA326694	DNA326697	DNA326705	DNA326706	DNA256533
	DNA326717	DNA326718	DNA326719	DNA326720	DNA326749	DNA326753
	DNA273346	DNA326769	DNA287270	DNA326779	DNA326780	DNA326781
25	DNA326787	DNA326795	DNA326796	DNA326798	DNA326819	DNA326830
	DNA326858	DNA254572	DNA326892	DNA326894	DNA326904	DNA326919
	DNA326931	DNA326932	DNA326935	DNA326940	DNA326941	DNA269830
	DNA326946	DNA326952	DNA326956	DNA326962	DNA254240	DNA326974
	DNA326983	DNA327005	DNA327006	DNA327007	DNA327017	DNA327019
30	DNA327021	DNA327023	DNA327025	DNA327026	DNA327027	DNA327029
	DNA327046	DNA327058	DNA327060	DNA327062	DNA273254	DNA327067
	DNA327070	DNA327072	DNA327077	DNA327078	DNA327079	DNA227181
	DNA327099	DNA327114	DNA103558	DNA327125		
35	<u>Ovary</u>					
	DNA287173	DNA323865	DNA323867	DNA324048	DNA324148	DNA324295

DNA324340	DNA324341	DNA324642	DNA324694	DNA324697	DNA324737
DNA324874	DNA325601	DNA225632	DNA325720	DNA325786	DNA287331
DNA326099	DNA326657	DNA327025			

ADIPOSE

5	DNA325952	DNA325957	DNA325958		
---	-----------	-----------	-----------	--	--

WHOLE BLOOD

	DNA323718	DNA323719	DNA323752	DNA323754	DNA323788	DNA83085
	DNA323886	DNA323889	DNA323890	DNA323911	DNA323957	DNA323980
10	DNA324002	DNA324020	DNA324021	DNA324033	DNA324040	DNA324041
	DNA324052	DNA324240	DNA324296	DNA225910	DNA324317	DNA324320
	DNA324515	DNA324560	DNA324562	DNA324722	DNA324742	DNA324784
	DNA324861	DNA324875	DNA324884	DNA324885	DNA324887	DNA324888
	DNA324923	DNA325016	DNA325017	DNA325038	DNA325055	DNA325056
15	DNA325057	DNA325059	DNA325060	DNA325061	DNA325063	DNA325177
	DNA325255	DNA88562	DNA325335	DNA325360	DNA325401	DNA325516
	DNA325609	DNA325623	DNA325631	DNA325641	DNA290294	DNA325678
	DNA226014	DNA325750	DNA325758	DNA325764	DNA325803	DNA281436
	DNA325829	DNA226105	DNA325912	DNA326089	DNA326090	DNA326113
20	DNA326115	DNA326160	DNA326240	DNA326254	DNA88378	DNA88554
	DNA326371	DNA326479	DNA326655	DNA326802	DNA326834	DNA88239
	DNA326906	DNA326958	DNA326977	DNA327052	DNA327116	

THYROID

25	DNA323717	DNA188748	DNA323867	DNA324154	DNA324216	DNA324295
	DNA324501	DNA324503	DNA324550	DNA324551	DNA324554	DNA324565
	DNA324697	DNA324873	DNA324874	DNA324905	DNA325191	DNA325192
	DNA325232	DNA325234	DNA325335	DNA325503	DNA325720	DNA325845
	DNA326259	DNA326275	DNA326862	DNA326863	DNA304670	DNA326864

30

PITUITARY GLAND

	DNA323717	DNA323967	DNA103593	DNA324100	DNA324293	DNA324326
	DNA324610	DNA324720	DNA324801	DNA324846	DNA324874	DNA325089
	DNA325523	DNA325533	DNA325589	DNA325617	DNA325967	DNA325970

35

SKIN

	DNA323717	DNA323721	DNA323730	DNA287173	DNA227821	DNA323764
	DNA323778	DNA323782	DNA323783	DNA323798	DNA323817	DNA323820
	DNA323822	DNA274745	DNA323829	DNA323833	DNA323856	DNA323858
	DNA323859	DNA323862	DNA323863	DNA323872	DNA323874	DNA323878
	DNA227529	DNA227577	DNA323925	DNA323927	DNA323947	DNA226619
5	DNA323980	DNA324004	DNA324009	DNA324042	DNA324047	DNA324048
	DNA324049	DNA324060	DNA324067	DNA324102	DNA227795	DNA324134
	DNA150725	DNA324153	DNA324178	DNA324204	DNA324207	DNA324210
	DNA324218	DNA324224	DNA324225	DNA324229	DNA254204	DNA324258
	DNA324294	DNA324316	DNA324317	DNA324334	DNA324338	DNA324339
10	DNA324340	DNA324341	DNA324358	DNA324371	DNA324372	DNA324379
	DNA324380	DNA324382	DNA324383	DNA324390	DNA324392	DNA324398
	DNA324401	DNA324407	DNA324412	DNA79129	DNA324434	DNA324472
	DNA324479	DNA324491	DNA324495	DNA324496	DNA324509	DNA324512
	DNA225584	DNA324521	DNA324525	DNA324541	DNA324564	DNA288259
15	DNA324590	DNA324591	DNA324592	DNA324595	DNA324596	DNA324597
	DNA324598	DNA324599	DNA324600	DNA324604	DNA324613	DNA324632
	DNA324645	DNA324678	DNA324682	DNA324687	DNA324690	DNA324692
	DNA324697	DNA324698	DNA324704	DNA324712	DNA324714	DNA324715
	DNA324716	DNA324717	DNA324720	DNA304680	DNA324736	DNA324737
20	DNA324751	DNA324756	DNA272263	DNA324780	DNA324781	DNA324785
	DNA324790	DNA324819	DNA324844	DNA324858	DNA324863	DNA324866
	DNA324874	DNA225631	DNA324902	DNA324907	DNA324908	DNA324919
	DNA324920	DNA324926	DNA227268	DNA103588	DNA324952	DNA324962
	DNA324965	DNA324966	DNA324967	DNA324968	DNA324982	DNA272090
25	DNA324989	DNA325006	DNA304685	DNA325078	DNA325079	DNA325080
	DNA325081	DNA325090	DNA325091	DNA325092	DNA325108	DNA325111
	DNA325116	DNA325117	DNA325118	DNA325119	DNA325126	DNA325132
	DNA325136	DNA325141	DNA325152	DNA325153	DNA325164	DNA325177
	DNA325183	DNA325206	DNA325209	DNA325222	DNA325223	DNA88350
30	DNA325230	DNA325245	DNA325250	DNA325280	DNA325293	DNA325296
	DNA325301	DNA325303	DNA325326	DNA325343	DNA325347	DNA325389
	DNA325395	DNA325403	DNA325411	DNA325412	DNA325430	DNA97285
	DNA325441	DNA325442	DNA325467	DNA325506	DNA325523	DNA325534
	DNA325535	DNA325570	DNA325576	DNA325596	DNA325601	DNA225632
35	DNA325605	DNA325606	DNA325610	DNA325625	DNA325633	DNA325642
	DNA325644	DNA325655	DNA325656	DNA325657	DNA227092	DNA325674

	DNA325680	DNA325695	DNA325700	DNA325702	DNA325711	DNA325712
	DNA325724	DNA325733	DNA325736	DNA325738	DNA325752	DNA325770
	DNA325773	DNA325775	DNA325776	DNA325777	DNA325786	DNA325805
	DNA325810	DNA325818	DNA325837	DNA325838	DNA325890	DNA325900
	DNA325906	DNA325908	DNA325909	DNA325913	DNA325920	DNA269498
5	DNA325922	DNA325925	DNA325935	DNA325941	DNA103509	DNA325965
	DNA227559	DNA325985	DNA325994	DNA326002	DNA326003	DNA326022
	DNA287331	DNA326027	DNA326036	DNA326041	DNA326046	DNA326047
	DNA326056	DNA326076	DNA273839	DNA326099	DNA326107	DNA326116
	DNA326118	DNA326121	DNA326122	DNA326124	DNA326128	DNA326129
10	DNA326133	DNA326136	DNA326142	DNA326156	DNA326168	DNA326173
	DNA287355	DNA326178	DNA326196	DNA326197	DNA275408	DNA326251
	DNA326254	DNA97300	DNA326272	DNA326273	DNA326278	DNA326288
	DNA290292	DNA326296	DNA326311	DNA326316	DNA326324	DNA326329
	DNA326343	DNA88378	DNA326354	DNA326355	DNA326358	DNA326362
15	DNA227071	DNA326384	DNA227055	DNA326396	DNA326397	DNA326406
	DNA326408	DNA326415	DNA326416	DNA326426	DNA326449	DNA326450
	DNA326451	DNA326452	DNA326453	DNA326454	DNA326457	DNA326463
	DNA326475	DNA326490	DNA326499	DNA326525	DNA326539	DNA326559
	DNA270621	DNA326562	DNA326579	DNA326580	DNA326595	DNA326597
20	DNA326599	DNA326603	DNA326651	DNA272347	DNA274139	DNA326680
	DNA326691	DNA326704	DNA326709	DNA304658	DNA326742	DNA326752
	DNA326760	DNA273346	DNA254548	DNA326769	DNA287270	DNA326780
	DNA326781	DNA326790	DNA326796	DNA326798	DNA150548	DNA326803
	DNA326819	DNA326821	DNA194701	DNA326825	DNA326872	DNA326884
25	DNA326886	DNA254572	DNA326901	DNA226617	DNA326921	DNA326935
	DNA326941	DNA326947	DNA326949	DNA326950	DNA326952	DNA326956
	DNA326963	DNA326967	DNA326974	DNA326981	DNA219225	DNA326983
	DNA326984	DNA326985	DNA326995	DNA327003	DNA327023	DNA327025
	DNA227943	DNA327056	DNA327057	DNA327060	DNA327062	DNA273254
30	DNA327068	DNA327101	DNA327107	DNA327110	DNA327114	DNA327115
	DNA227013					
<u>THYMUS</u>						
	DNA324063	DNA324197	DNA324641	DNA324685	DNA324926	DNA325038
35	DNA325195	DNA325238	DNA325405	DNA325420	DNA325421	DNA325422
	DNA325506	DNA325645	DNA325809	DNA325930	DNA326089	DNA326090

DNA326243 DNA326554 DNA326563 DNA326747

MUSCLE

	DNA323725	DNA323732	DNA287173	DNA323736	DNA323737	DNA323740
	DNA171408	DNA323746	DNA323748	DNA323749	DNA323753	DNA323765
5	DNA323766	DNA323767	DNA323768	DNA323778	DNA323779	DNA323780
	DNA323782	DNA323784	DNA323789	DNA323792	DNA323794	DNA323798
	DNA323801	DNA323802	DNA323804	DNA227213	DNA323810	DNA323813
	DNA323816	DNA323817	DNA274487	DNA323820	DNA323821	DNA323826
	DNA323827	DNA323829	DNA323830	DNA323833	DNA103214	DNA323837
10	DNA323839	DNA323852	DNA323853	DNA323854	DNA323855	DNA323858
	DNA323859	DNA323860	DNA323862	DNA323863	DNA323864	DNA323865
	DNA323866	DNA323867	DNA323869	DNA323870	DNA323871	DNA275139
	DNA323872	DNA323874	DNA323881	DNA323882	DNA323885	DNA323887
	DNA227529	DNA225809	DNA323914	DNA323925	DNA323929	DNA323930
15	DNA323933	DNA323934	DNA323936	DNA194600	DNA323947	DNA323949
	DNA323955	DNA323964	DNA323971	DNA323972	DNA323973	DNA323974
	DNA323977	DNA323978	DNA323981	DNA323987	DNA323995	DNA323997
	DNA290234	DNA324001	DNA256905	DNA324004	DNA324007	DNA324014
	DNA324016	DNA324039	DNA324045	DNA324048	DNA324049	DNA324054
20	DNA275195	DNA324058	DNA324059	DNA324060	DNA324063	DNA324064
	DNA273800	DNA324090	DNA324091	DNA324092	DNA324097	DNA324098
	DNA324109	DNA324111	DNA324112	DNA324120	DNA324126	DNA227795
	DNA324133	DNA324135	DNA324137	DNA324141	DNA324145	DNA324154
	DNA324155	DNA255531	DNA275240	DNA324168	DNA324170	DNA324182
25	DNA324183	DNA88051	DNA324197	DNA324199	DNA324200	DNA324201
	DNA324203	DNA324204	DNA324207	DNA324210	DNA324217	DNA324230
	DNA324232	DNA189697	DNA324241	DNA324243	DNA324252	DNA324255
	DNA324257	DNA324260	DNA324263	DNA324267	DNA324269	DNA324270
	DNA324271	DNA324278	DNA324282	DNA324287	DNA324294	DNA226547
30	DNA324295	DNA324297	DNA324313	DNA324318	DNA324323	DNA324324
	DNA324329	DNA324330	DNA324331	DNA324338	DNA324340	DNA324341
	DNA324358	DNA324371	DNA324390	DNA324398	DNA324400	DNA324414
	DNA324417	DNA324418	DNA324421	DNA324423	DNA324434	DNA324437
	DNA324440	DNA324454	DNA324456	DNA324461	DNA324462	DNA324469
35	DNA324472	DNA324478	DNA324479	DNA324483	DNA324488	DNA324493
	DNA324495	DNA324496	DNA324501	DNA324502	DNA324503	DNA324504

	DNA324505	DNA324510	DNA324521	DNA324523	DNA324525	DNA324538
	DNA324541	DNA324550	DNA324551	DNA324552	DNA324554	DNA324556
	DNA324557	DNA324558	DNA324564	DNA324575	DNA324583	DNA324584
	DNA288259	DNA324590	DNA324591	DNA324592	DNA324595	DNA324596
	DNA324597	DNA324598	DNA324599	DNA324600	DNA324602	DNA324604
5	DNA324608	DNA324613	DNA324624	DNA324626	DNA324627	DNA269809
	DNA324632	DNA324633	DNA324634	DNA324636	DNA324645	DNA271626
	DNA324675	DNA324678	DNA324682	DNA324685	DNA324690	DNA324696
	DNA324697	DNA274206	DNA324707	DNA324708	DNA324709	DNA324710
	DNA324711	DNA324715	DNA324716	DNA270675	DNA324717	DNA324720
10	DNA324722	DNA324723	DNA304680	DNA324737	DNA324739	DNA324744
	DNA304460	DNA324751	DNA324756	DNA324763	DNA324764	DNA324769
	DNA324770	DNA324780	DNA324781	DNA324783	DNA304699	DNA324784
	DNA324785	DNA324790	DNA324791	DNA290264	DNA324794	DNA324811
	DNA324813	DNA324815	DNA324823	DNA324827	DNA324828	DNA324829
15	DNA103471	DNA324834	DNA324840	DNA324841	DNA324844	DNA324846
	DNA324851	DNA324852	DNA324866	DNA324880	DNA324884	DNA324893
	DNA225631	DNA274326	DNA324896	DNA324897	DNA324902	DNA324904
	DNA324905	DNA324906	DNA324907	DNA324908	DNA324915	DNA324916
	DNA324917	DNA324921	DNA324926	DNA324932	DNA324933	DNA287189
20	DNA103588	DNA324950	DNA324951	DNA324952	DNA324957	DNA324958
	DNA324959	DNA324965	DNA324966	DNA324967	DNA324968	DNA324972
	DNA324973	DNA324977	DNA324982	DNA324983	DNA324985	DNA324989
	DNA324990	DNA324991	DNA324992	DNA325002	DNA325006	DNA325013
	DNA325015	DNA325021	DNA325022	DNA325023	DNA325024	DNA325026
25	DNA325027	DNA325034	DNA325039	DNA325045	DNA226337	DNA325062
	DNA325077	DNA325078	DNA325079	DNA325080	DNA325081	DNA325094
	DNA325095	DNA325100	DNA325103	DNA325109	DNA226496	DNA325111
	DNA325116	DNA325117	DNA325118	DNA325119	DNA325122	DNA131588
	DNA325152	DNA325153	DNA325156	DNA325157	DNA325164	DNA325168
30	DNA325174	DNA325178	DNA325179	DNA325182	DNA325183	DNA325184
	DNA287216	DNA288247	DNA325187	DNA325190	DNA325196	DNA325200
	DNA325202	DNA325205	DNA325206	DNA325210	DNA325214	DNA225630
	DNA325216	DNA325222	DNA325223	DNA325227	DNA325231	DNA325232
	DNA325233	DNA325234	DNA325235	DNA325236	DNA325239	DNA325245
35	DNA325247	DNA325250	DNA325295	DNA325296	DNA325301	DNA325303
	DNA325308	DNA325326	DNA325327	DNA325344	DNA304488	DNA325346

	DNA325347	DNA325358	DNA325360	DNA325362	DNA325367	DNA325371
	DNA325373	DNA144601	DNA325375	DNA325380	DNA325384	DNA325389
	DNA325406	DNA325407	DNA325408	DNA325409	DNA325410	DNA325411
	DNA325429	DNA325440	DNA325451	DNA325452	DNA325459	DNA272728
	DNA325463	DNA325469	DNA325474	DNA325478	DNA325494	DNA325498
5	DNA270721	DNA325515	DNA325523	DNA325531	DNA325534	DNA325535
	DNA325538	DNA325552	DNA325555	DNA325560	DNA325576	DNA325577
	DNA325580	DNA325581	DNA297398	DNA325582	DNA325584	DNA325585
	DNA325587	DNA325588	DNA325594	DNA325597	DNA254624	DNA325601
	DNA225632	DNA188396	DNA226028	DNA325618	DNA325620	DNA325625
10	DNA325627	DNA325633	DNA325637	DNA272379	DNA325642	DNA325644
	DNA325645	DNA325646	DNA325671	DNA325674	DNA325680	DNA227094
	DNA325695	DNA325703	DNA137231	DNA325704	DNA325705	DNA325706
	DNA325708	DNA79101	DNA325709	DNA325710	DNA325711	DNA325712
	DNA325714	DNA325715	DNA325716	DNA325718	DNA325720	DNA325724
15	DNA325725	DNA325731	DNA325733	DNA325734	DNA325750	DNA325752
	DNA325758	DNA325762	DNA325767	DNA325768	DNA325771	DNA325773
	DNA325775	DNA325776	DNA325781	DNA325784	DNA325786	DNA302016
	DNA325789	DNA325790	DNA325791	DNA325795	DNA325806	DNA325808
	DNA325809	DNA325810	DNA325811	DNA325812	DNA325814	DNA325815
20	DNA325826	DNA325830	DNA325837	DNA325838	DNA325843	DNA325844
	DNA325857	DNA325867	DNA325873	DNA325874	DNA225865	DNA325879
	DNA325882	DNA325889	DNA325891	DNA325906	DNA325908	DNA325910
	DNA325911	DNA325912	DNA325913	DNA325925	DNA325933	DNA151893
	DNA325935	DNA325937	DNA103509	DNA325954	DNA325955	DNA325965
25	DNA325966	DNA325985	DNA325994	DNA326002	DNA255340	DNA326012
	DNA326014	DNA326018	DNA326022	DNA287331	DNA326027	DNA326036
	DNA326040	DNA326041	DNA326046	DNA326047	DNA326058	DNA326059
	DNA326065	DNA326067	DNA326074	DNA326075	DNA326099	DNA326104
	DNA326105	DNA326121	DNA326122	DNA326123	NA326124	DNA326126
30	DNA326128	DNA326129	DNA326131	DNA326133	DNA326136	DNA326137
	DNA326143	DNA326147	DNA326148	DNA274002	DNA326156	DNA326157
	DNA194805	DNA326180	DNA326183	DNA326186	DNA326193	DNA326195
	DNA326196	DNA326197	DNA326199	DNA326216	DNA326235	DNA326236
	DNA326263	DNA97300	DNA297388	DNA326278	DNA326279	DNA326288
35	DNA326289	DNA326292	DNA326293	DNA326294	DNA227084	DNA326296
	DNA326298	DNA326299	DNA326301	DNA326304	DNA326305	DNA326306

	DNA326309	DNA326310	DNA326311	DNA326316	DNA326317	DNA270979
	DNA326328	DNA326333	DNA326338	DNA326343	DNA326349	DNA326351
	DNA326356	DNA326362	DNA270901	DNA326374	DNA326375	DNA326378
	DNA326381	DNA326397	DNA326406	DNA326411	DNA129504	DNA326416
	DNA326420	DNA326423	DNA326426	DNA326427	DNA326430	DNA326443
5	DNA326444	DNA326449	DNA326450	DNA326451	DNA326452	DNA326453
	DNA326454	DNA326457	DNA326460	DNA326463	DNA326469	DNA326487
	DNA326500	DNA326501	DNA326503	DNA326504	DNA326512	DNA326533
	DNA326539	DNA326548	DNA326550	DNA326556	DNA326558	DNA326566
	DNA326568	DNA326573	DNA326577	DNA326578	DNA326579	DNA326586
10	DNA326595	DNA326596	DNA326599	DNA326603	DNA269630	DNA326607
	DNA326614	DNA326621	DNA326625	DNA326629	DNA326630	DNA326633
	DNA326634	DNA326648	DNA326651	DNA326652	DNA273474	DNA326671
	DNA326676	DNA326680	DNA326691	DNA326693	DNA326695	DNA326698
	DNA32670	DNA326703	DNA326704	DNA326705	DNA326706	DNA326707
15	DNA326708	DNA326709	DNA257531	DNA256533	DNA326717	DNA326718
	DNA326725	DNA290260	DNA326740	DNA326745	DNA326749	DNA326752
	DNA326756	DNA326758	DNA273346	DNA326764	DNA297288	DNA287270
	DNA326789	DNA326790	DNA326796	DNA326800	DNA326805	DNA326808
	DNA326809	DNA326810	DNA326811	DNA326818	DNA326819	DNA326821
20	DNA194701	DNA326829	DNA326831	DNA103525	DNA326838	DNA326841
	DNA88239	DNA326845	DNA326850	DNA326851	DNA269526	DNA326868
	DNA326874	DNA326875	DNA326876	DNA326879	DNA326882	DNA326884
	DNA326886	DNA188732	DNA254572	DNA326890	DNA151898	DNA326894
	DNA326898	DNA326901	DNA326904	DNA226409	DNA326906	DNA326909
25	DNA326915	DNA326921	DNA326925	DNA226561	DNA326926	DNA326927
	DNA326936	DNA326937	DNA326941	DNA269830	DNA326946	DNA326952
	DNA326953	DNA326954	DNA326956	DNA326958	DNA188740	DNA326960
	DNA254240	DNA326974	DNA326977	DNA326979	DNA326981	DNA326982
	DNA326989	DNA326990	DNA237931	DNA326998	DNA327001	DNA327003
30	DNA327005	DNA327008	DNA327013	DNA327023	DNA327025	DNA327029
	DNA327031	DNA327033	DNA327041	DNA227943	DNA327051	DNA327058
	DNA327060	DNA327067	DNA327068	DNA270496	DNA327077	DNA327078
	DNA327079	DNA327086	DNA327089	DNA327093	DNA327099	DNA327102
	DNA327104	DNA227013	DNA327120	DNA327122	DNA327124	DNA327125

35

ENDOCRINE

DNA323772	DNA323943	DNA323976	DNA254298	DNA324100	DNA227528
DNA324139	DNA324285	DNA79129	DNA324484	DNA290585	DNA324550
DNA324642	DNA324692	DNA324910	DNA324964	DNA325350	DNA325549
DNA325615	DNA325884	DNA325916	DNA325991	DNA326003	DNA188351
DNA326328	DNA326619	DNA304658	DNA326790	DNA83170	

5

KIDNEY

DNA287173	DNA103253	DNA323858	DNA323859	DNA323869	DNA323871
DNA323872	DNA323927	DNA323947	DNA226619	DNA323964	DNA324042
DNA324048	DNA324063	DNA324090	DNA324092	DNA324111	DNA324112
DNA324193	DNA324210	DNA324218	DNA324294	DNA226547	DNA324338
DNA324340	DNA324341	DNA324347	DNA324398	DNA324417	DNA324418
DNA324424	DNA324426	DNA324427	DNA324434	DNA324437	DNA324472
DNA324521	DNA324525	DNA324561	DNA324595	DNA324604	DNA324613
DNA83020	DNA324639	DNA324641	DNA324645	DNA324685	DNA324715
DNA324716	DNA324717	DNA324720	DNA324722	DNA324727	DNA304680
DNA324737	DNA324751	DNA304661	DNA324790	DNA324798	DNA324830
DNA324844	DNA225631	DNA274326	DNA324922	DNA324926	DNA304710
DNA324963	DNA324989	DNA324998	DNA325026	DNA325028	DNA325104
DNA325105	DNA325106	DNA325111	DNA325126	DNA325152	DNA325153
DNA325182	DNA325184	DNA325222	DNA325296	DNA325303	DNA325326
DNA325334	DNA325347	DNA325360	DNA325384	DNA325389	DNA325414
DNA325446	DNA325475	DNA325523	DNA325535	DNA325601	DNA225632
DNA325633	DNA325642	DNA325644	DNA270458	DNA325731	DNA325750
DNA325752	DNA325758	DNA325786	DNA302016	DNA325789	DNA325804
DNA325809	DNA325810	DNA325811	DNA325812	DNA281436	DNA325935
DNA325952	DNA325985	DNA326002	DNA326003	DNA326022	DNA287331
DNA326041	DNA326046	DNA326047	DNA326099	DNA326233	DNA326234
DNA326237	DNA97300	DNA326291	DNA326292	DNA326311	DNA326370
DNA326397	DNA326422	DNA326463	DNA326469	DNA326559	DNA326586
DNA326603	DNA326633	DNA326634	DNA326692	DNA326769	DNA287270
DNA326884	DNA326885	DNA326886	DNA326952	DNA326974	DNA327023
DNA327025	DNA327029	DNA327067	DNA327085	DNA327116	

LUNG

DNA323717	DNA323718	DNA323719	DNA287173	DNA323740	DNA226262
DNA323778	DNA323783	DNA274745	DNA323829	DNA323832	DNA323839

	DNA323841	DNA323856	DNA323858	DNA323859	DNA323862	DNA323863
	DNA323864	DNA323865	DNA323866	DNA323867	DNA323871	DNA323872
	DNA323878	DNA323887	DNA323892	DNA227529	DNA323902	DNA290284
	DNA323910	DNA304666	DNA304720	DNA323922	DNA323925	DNA323927
	DNA323936	DNA226793	DNA323944	DNA323945	DNA323947	DNA323954
5	DNA323959	DNA323964	DNA323965	DNA323995	DNA324005	DNA324006
	DNA324020	DNA324021	DNA324033	DNA324036	DNA324039	DNA324040
	DNA324041	DNA324042	DNA324044	DNA324047	DNA324048	DNA324049
	DNA324052	DNA324054	DNA324060	DNA324063	DNA324067	DNA324073
	DNA324090	DNA324091	DNA324092	DNA324094	DNA324101	DNA324105
10	DNA324109	DNA324111	DNA324112	DNA227795	DNA324134	DNA324148
	DNA324155	DNA324170	DNA324182	DNA324203	DNA324204	DNA324207
	DNA324210	DNA324218	DNA324232	DNA324261	DNA324265	DNA324273
	DNA324293	DNA324294	DNA226547	DNA324295	DNA324320	DNA324326
	DNA324338	DNA324339	DNA324340	DNA324341	DNA324358	DNA324365
15	DNA324380	DNA324412	DNA324414	DNA324416	DNA324417	DNA324418
	DNA324434	DNA324436	DNA324437	DNA324444	DNA324453	DNA324454
	DNA324472	DNA324475	DNA324483	DNA324491	DNA290585	DNA324502
	DNA324504	DNA324505	DNA324510	DNA324515	DNA324521	DNA324525
	DNA324541	DNA324549	DNA324552	DNA324557	DNA324558	DNA324561
20	DNA324564	DNA324579	DNA324584	DNA324591	DNA324592	DNA324596
	DNA324597	DNA324598	DNA324599	DNA324600	DNA324604	DNA324613
	DNA324633	DNA324641	DNA324643	DNA324685	DNA324697	DNA324699
	DNA324700	DNA324702	DNA324703	DNA324707	DNA324714	DNA324715
	DNA324716	DNA324717	DNA324720	DNA304680	DNA324736	DNA324737
25	DNA324745	DNA324749	DNA324751	DNA324755	DNA324756	DNA227442
	DNA324771	DNA324784	DNA324785	DNA324790	DNA324796	DNA324797
	DNA324803	DNA290785	DNA324814	DNA324815	DNA324816	DNA324819
	DNA324828	DNA324829	DNA324841	DNA324844	DNA324846	DNA271418
	DNA324870	DNA324873	DNA324874	DNA324875	DNA324884	DNA324885
30	DNA324887	DNA324888	DNA324889	DNA274326	DNA324896	DNA324900
	DNA324904	DNA324906	DNA324907	DNA324908	DNA275334	DNA324925
	DNA324926	DNA273865	DNA103588	DNA324945	DNA324946	DNA324956
	DNA324961	DNA304710	DNA324962	DNA324963	DNA324965	DNA324966
	DNA324967	DNA324968	DNA324982	DNA324983	DNA272090	DNA324989
35	DNA325002	DNA325015	DNA325016	DNA325017	DNA325024	DNA325026
	DNA325027	DNA325029	DNA325033	DNA325034	DNA325039	DNA325055

	DNA325056	DNA325057	DNA325078	DNA325079	DNA325080	DNA325081
	DNA325100	DNA325104	DNA325105	DNA325106	DNA226496	DNA325116
	DNA325117	DNA325118	DNA325119	DNA325128	DNA325141	DNA325146
	DNA325152	DNA325153	DNA325156	DNA325157	DNA226345	DNA325173
	DNA290319	DNA325182	DNA325183	DNA325184	DNA325190	DNA325196
5	DNA325209	DNA325214	DNA325217	DNA325222	DNA325233	DNA325235
	DNA325236	DNA325246	DNA325247	DNA325250	DNA325278	DNA325284
	DNA325285	DNA325286	DNA325303	DNA325305	DNA325326	DNA325334
	DNA304459	DNA325343	DNA325344	DNA325347	DNA325353	DNA325358
	DNA325360	DNA325379	DNA325384	DNA325389	DNA325401	DNA325414
10	DNA325418	DNA325441	DNA325451	DNA325452	DNA325456	DNA325463
	DNA325475	DNA325479	DNA325483	DNA325502	DNA325506	DNA325509
	DNA325510	DNA325516	DNA325522	DNA325523	DNA325527	DNA325534
	DNA325535	DNA325550	DNA325569	DNA325570	DNA325584	DNA325593
	DNA325595	DNA151827	DNA325601	DNA225632	DNA103514	DNA325604
15	DNA325618	DNA325625	DNA325633	DNA325634	DNA271344	DNA325642
	DNA325644	DNA325645	DNA325658	DNA325659	DNA325660	DNA325662
	DNA270458	DNA227092	DNA325674	DNA325680	DNA325686	DNA325695
	DNA325704	DNA325711	DNA325712	DNA325720	DNA325731	DNA325750
	DNA325752	DNA325755	DNA325757	DNA325758	DNA325773	DNA325775
20	DNA325776	DNA325786	DNA302016	DNA325789	DNA325806	DNA325809
	DNA325810	DNA325811	DNA325812	DNA325814	DNA325818	DNA325822
	DNA325837	DNA325838	DNA325843	DNA325844	DNA325864	DNA325891
	DNA325894	DNA325913	DNA325920	DNA269498	DNA325923	DNA325933
	DNA325935	DNA325945	DNA103509	DNA325952	DNA325953	DNA325957
25	DNA325958	DNA325965	DNA325985	DNA325988	DNA325994	DNA326002
	DNA226646	DNA326022	DNA287331	DNA326041	DNA326046	DNA326047
	DNA326099	DNA326102	DNA326116	DNA326121	DNA326122	DNA326124
	DNA326128	DNA326129	DNA326133	DNA289522	DNA326136	DNA326146
	DNA326155	DNA326156	DNA326168	DNA326169	DNA287355	DNA326177
30	DNA326186	DNA326194	DNA326214	DNA326230	DNA326233	DNA326234
	DNA326256	DNA326260	DNA97300	DNA326273	DNA326278	DNA326279
	DNA326287	DNA326288	DNA326289	DNA326291	DNA326292	DNA326296
	DNA326297	DNA326300	DNA326309	DNA326311	DNA326330	DNA272889
	DNA270975	DNA326347	DNA270901	DNA326381	DNA326384	DNA326396
35	DNA326404	DNA129504	DNA326414	DNA326415	DNA326416	DNA326426
	DNA326427	DNA326429	DNA326430	DNA326432	DNA326433	DNA326440

	DNA326441	DNA326442	DNA326446	DNA326449	DNA326450	DNA326451
	DNA326452	DNA326453	DNA326454	DNA271841	DNA326457	DNA326459
	DNA326463	DNA326479	DNA326481	DNA326482	DNA326484	DNA326485
	DNA326487	DNA326499	DNA326512	DNA287636	DNA326516	DNA326523
	DNA326559	DNA326562	DNA326573	DNA326579	DNA326581	DNA326582
5	DNA326583	DNA326584	DNA326585	DNA274034	DNA326596	DNA326597
	DNA326603	DNA326615	DNA326625	DNA326626	DNA326633	DNA326634
	DNA326642	DNA326651	DNA326657	DNA326660	DNA326661	DNA274139
	DNA326676	DNA326683	DNA326684	DNA326685	DNA326687	DNA326688
	DNA326690	DNA326691	DNA326692	DNA326698	DNA326702	DNA103580
10	DNA326726	DNA326727	DNA326731	DNA290260	DNA326736	DNA326739
	DNA326741	DNA326742	DNA326756	DNA326758	DNA326761	DNA273346
	DNA254548	DNA326769	DNA326773	DNA287270	DNA326781	DNA326782
	DNA326787	DNA326789	DNA326798	DNA326801	DNA326808	DNA326818
	DNA326819	DNA273517	DNA194701	DNA103525	DNA326844	DNA326884
15	DNA326885	DNA326886	DNA254572	DNA326901	DNA326902	DNA326921
	DNA326937	DNA269830	DNA326952	DNA326953	DNA326972	DNA326974
	DNA326981	DNA326983	DNA327005	DNA327023	DNA327025	DNA327029
	DNA327033	DNA327054	DNA327060	DNA327067	DNA327068	DNA327077
	DNA327078	DNA327079	DNA327085	DNA327111	DNA227013	
20	<u>BREAST</u>					
	DNA323717	DNA273712	DNA226262	DNA323778	DNA323784	DNA323804
	DNA323805	DNA323817	DNA323820	DNA323829	DNA323836	DNA323845
	DNA323858	DNA323859	DNA323862	DNA323863	DNA323867	DNA323868
25	DNA323869	DNA323870	DNA323871	DNA323872	DNA323919	DNA323922
	DNA323936	DNA323943	DNA323944	DNA323947	DNA323953	DNA323964
	DNA323980	DNA323990	DNA323998	DNA324004	DNA324009	DNA324013
	DNA324042	DNA324047	DNA324054	DNA324063	DNA324075	DNA324090
	DNA324091	DNA324092	DNA324101	DNA324103	DNA324110	DNA324111
30	DNA324112	DNA227795	DNA324134	DNA227190	DNA324149	DNA324154
	DNA324159	DNA324170	DNA324178	DNA324189	DNA324192	DNA324193
	DNA324207	DNA324210	DNA324218	DNA324224	DNA324230	DNA324236
	DNA324243	DNA324276	DNA324285	DNA226547	DNA324295	DNA150976
	DNA324320	DNA324338	DNA324340	DNA324341	DNA324346	DNA324347
35	DNA324373	DNA324390	DNA324391	DNA324394	DNA324412	DNA324417
	DNA324418	DNA324423	DNA324434	DNA324437	DNA324438	DNA139747

	DNA253804	DNA324471	DNA324472	DNA324478	DNA324479	DNA324483
	DNA324489	DNA324495	DNA324502	DNA324503	DNA324506	DNA324509
	DNA324511	DNA324512	DNA225584	DNA324517	DNA324521	DNA324525
	DNA324549	DNA324550	DNA324551	DNA324554	DNA324561	DNA324564
	DNA324565	DNA324568	DNA324574	DNA324576	DNA324577	DNA324579
5	DNA324591	DNA324592	DNA324595	DNA324596	DNA324597	DNA324599
	DNA324600	DNA324601	DNA324605	DNA324613	DNA324624	DNA103380
	DNA324632	DNA324633	DNA324641	DNA324643	DNA324645	DNA324679
	DNA324682	DNA324684	DNA324685	DNA324690	DNA324712	DNA324714
	DNA324717	DNA324720	DNA324727	DNA304680	DNA324736	DNA324737
10	DNA324746	DNA324749	DNA324751	DNA324755	DNA304661	DNA287227
	DNA324773	DNA324785	DNA324790	DNA324796	DNA324797	DNA324807
	DNA324810	DNA324811	DNA324824	DNA324827	DNA324841	DNA324844
	DNA324858	DNA324866	DNA324874	DNA324878	DNA324879	DNA225631
	DNA324902	DNA324905	DNA324910	DNA324928	DNA324945	DNA304710
15	DNA324963	DNA324966	DNA324967	DNA324968	DNA304801	DNA272090
	DNA324987	DNA324989	DNA325000	DNA325006	DNA325010	DNA325015
	DNA325024	DNA325026	DNA325027	DNA325034	DNA325078	DNA325079
	DNA325080	DNA325081	DNA325099	DNA325101	DNA325103	DNA325104
	DNA325106	DNA325111	DNA325113	DNA325116	DNA325117	DNA325118
20	DNA325119	DNA325120	DNA325121	DNA325123	DNA325127	DNA325141
	DNA325152	DNA325153	DNA325155	DNA325156	DNA325157	DNA325162
	DNA325164	DNA325179	DNA325180	DNA325182	DNA325183	DNA325184
	DNA325190	DNA325200	DNA325202	DNA325206	DNA325209	DNA325222
	DNA325229	DNA325231	DNA325232	DNA325234	DNA325250	DNA325278
25	DNA325291	DNA325292	DNA325295	DNA325301	DNA325326	DNA325339
	DNA325340	DNA325343	DNA325344	DNA325346	DNA325347	DNA325356
	DNA325358	DNA325374	DNA325381	DNA325386	DNA325389	DNA325391
	DNA325395	DNA325428	DNA325430	DNA325431	DNA325436	DNA325437
	DNA97285	DNA325442	DNA325451	DNA325452	DNA75863	DNA325475
30	DNA325483	DNA325523	DNA325525	DNA325528	DNA325535	DNA325549
	DNA325576	DNA325584	DNA325596	DNA325601	DNA225632	DNA325618
	DNA325625	DNA325633	DNA325642	DNA325644	DNA325645	DNA325662
	DNA270458	DNA227092	DNA325674	DNA325680	DNA325696	DNA325697
	DNA325711	DNA325712	DNA325731	DNA325736	DNA325757	DNA325762
35	DNA325765	DNA325783	DNA325786	DNA302016	DNA325789	DNA325804
	DNA325806	DNA325809	DNA325810	DNA325811	DNA325812	DNA325814

	DNA325837	DNA325838	DNA325839	DNA325843	DNA325844	DNA325848
	DNA325900	DNA325906	DNA325907	DNA325908	DNA325913	DNA325922
	DNA325930	DNA325933	DNA325935	DNA325966	DNA227559	DNA325985
	DNA325986	DNA227206	DNA325990	DNA325991	DNA219233	DNA325994
	DNA325998	DNA326000	DNA326002	DNA326022	DNA326041	DNA326046
5	DNA326047	DNA326075	DNA326079	DNA326099	DNA326113	DNA326115
	DNA97293	DNA326122	DNA326124	DNA326128	DNA326129	DNA326136
	DNA326156	DNA287355	DNA326187	DNA326233	DNA326234	DNA326251
	DNA326254	DNA326260	DNA97300	DNA326273	DNA326278	DNA326280
	DNA326281	DNA304715	DNA326282	DNA326286	DNA290292	DNA326289
10	DNA326291	DNA326292	DNA66475	DNA326324	DNA326326	DNA326327
	DNA326364	DNA326378	DNA326381	DNA326396	DNA326415	DNA326449
	DNA326450	DNA326451	DNA326452	DNA326453	DNA326454	DNA326457
	DNA326463	DNA326469	DNA326499	DNA287636	DNA326529	DNA326541
	DNA270315	DNA326546	DNA326557	DNA326559	DNA326562	DNA326579
15	DNA326615	DNA326620	DNA227249	DNA326633	DNA326634	DNA326635
	DNA326651	DNA326657	DNA272347	DNA326669	DNA326686	DNA326687
	DNA326688	DNA326698	DNA326732	DNA290260	DNA326741	DNA326742
	DNA83154	DNA326756	DNA326758	DNA326759	DNA326769	DNA326777
	DNA287270	DNA326792	DNA326796	DNA326798	DNA326799	DNA326816
20	DNA194701	DNA103525	DNA326841	DNA326862	DNA326863	DNA304670
	DNA326864	DNA326866	DNA326870	DNA326885	DNA326886	DNA326903
	DNA326921	DNA326952	DNA326969	DNA326971	DNA326974	DNA326981
	DNA327016	DNA327023	DNA327025	DNA327029	DNA273992	DNA327060
	DNA327062	DNA273254	DNA327067	DNA327068	DNA327073	DNA327085
25	DNA327087	DNA327090	DNA327092	DNA276159	DNA327127	
<u>STOMACH</u>						
	DNA287173	DNA323805	DNA323849	DNA323864	DNA323865	DNA323866
	DNA323873	DNA323884	DNA323920	DNA323925	DNA323934	DNA323990
30	DNA324028	DNA324029	DNA324039	DNA324048	DNA324065	DNA227545
	DNA227795	DNA324155	DNA324179	DNA324180	DNA324216	DNA324243
	DNA324244	DNA324294	DNA324362	DNA324364	DNA324398	DNA324417
	DNA324418	DNA324471	DNA324504	DNA324541	DNA324552	DNA324555
	DNA324556	DNA324558	DNA324624	DNA324630	DNA304680	DNA324756
35	DNA324769	DNA324790	DNA324808	DNA324850	DNA225631	DNA324906
	DNA324907	DNA324908	DNA324922	DNA304710	DNA324962	DNA324963

	DNA324972	DNA324973	DNA324982	DNA324997	DNA325033	DNA325074
	DNA325078	DNA325079	DNA325104	DNA325105	DNA325106	DNA325148
	DNA325149	DNA325156	DNA325157	DNA89242	DNA325186	DNA325191
	DNA325192	DNA325202	DNA325224	DNA325233	DNA325235	DNA325236
	DNA325251	DNA325262	DNA325268	DNA325306	DNA325316	DNA325318
5	DNA325320	DNA325368	DNA325418	DNA97285	DNA325441	DNA325442
	DNA325444	DNA325446	DNA325474	DNA325480	DNA325506	DNA325534
	DNA325535	DNA325570	DNA325601	DNA225632	DNA325642	DNA325644
	DNA325645	DNA270458	DNA227092	DNA325773	DNA325775	DNA325776
	DNA325803	DNA325804	DNA274058	DNA325843	DNA325873	DNA325941
10	DNA325986	DNA325993	DNA326019	DNA287331	DNA326043	DNA326133
	DNA326196	DNA326284	DNA326311	DNA326333	DNA326347	DNA326397
	DNA326427	DNA326517	DNA326603	DNA326641	DNA326642	DNA326698
	DNA326750	DNA326791	DNA326846	DNA326859	DNA326862	DNA326863
	DNA304670	DNA326864	DNA326865	DNA326918	DNA326961	DNA326977
15	DNA326983	DNA327040	DNA327042	DNA327055	DNA273254	DNA327099
	DNA327116	DNA327127				
	<u>BONE</u>					
	DNA323765	DNA323817	DNA323820	DNA323829	DNA323864	DNA323867
20	DNA323869	DNA323871	DNA323914	DNA323947	DNA323964	DNA324004
	DNA324009	DNA324090	DNA324091	DNA324092	DNA324111	DNA324112
	DNA324154	DNA324155	DNA324200	DNA324201	DNA324210	DNA324230
	DNA324293	DNA226547	DNA324295	DNA324326	DNA324347	DNA324390
	DNA324417	DNA324418	DNA324423	DNA324437	DNA324472	DNA324483
25	DNA324488	DNA324501	DNA324502	DNA324503	DNA324504	DNA324505
	DNA324512	DNA324521	DNA324525	DNA324541	DNA324549	DNA324550
	DNA324551	DNA324554	DNA324555	DNA324556	DNA324557	DNA324558
	DNA324575	DNA324576	DNA324579	DNA324595	DNA324596	DNA324604
	DNA324613	DNA324624	DNA324632	DNA324641	DNA324645	DNA324682
30	DNA324687	DNA324697	DNA324717	DNA324720	DNA324737	DNA324756
	DNA304661	DNA324785	DNA324796	DNA324797	DNA150772	DNA324828
	DNA324829	DNA324844	DNA324866	DNA324902	DNA324904	DNA324905
	DNA324906	DNA324926	DNA324989	DNA325015	DNA325024	DNA325026
	DNA325027	DNA325034	DNA325111	DNA325116	DNA131588	DNA325156
35	DNA325157	DNA325164	DNA325179	DNA325182	DNA325183	DNA325184
	DNA325202	DNA325206	DNA325222	DNA325229	DNA325231	DNA325232

	DNA325234	DNA325236	DNA325250	DNA325301	DNA325303	DNA325326
	DNA325339	DNA325340	DNA325347	DNA325358	DNA325395	DNA325430
	DNA325437	DNA325451	DNA325452	DNA325523	DNA325558	DNA325570
	DNA325576	DNA325601	DNA225632	DNA325633	DNA325731	DNA325733
	DNA325736	DNA325762	DNA325786	DNA302016	DNA325789	DNA325806
5	DNA325810	DNA325811	DNA325812	DNA325843	DNA325844	DNA325906
	DNA325908	DNA325913	DNA325922	DNA325935	DNA325985	DNA326002
	DNA326041	DNA326046	DNA326099	DNA326233	DNA326234	DNA326251
	DNA97300	DNA304715	DNA326286	DNA326289	DNA326381	DNA326457
	DNA326580	DNA326633	DNA326634	DNA326635	DNA326651	DNA290260
10	DNA326796	DNA326884	DNA326886	DNA326974	DNA326977	DNA327005
	DNA327025	DNA327060	DNA327062	DNA327067	DNA327114	

EXAMPLE 2: Use of TAT as a hybridization probe

15 The following method describes use of a nucleotide sequence encoding TAT as a hybridization probe for, i.e., diagnosis of the presence of a tumor in a mammal.

DNA comprising the coding sequence of full-length or mature TAT as disclosed herein can also be employed as a probe to screen for homologous DNAs (such as those encoding naturally-occurring variants of TAT) in human tissue cDNA libraries or human tissue genomic libraries.

Hybridization and washing of filters containing either library DNAs is performed under the following high stringency conditions. Hybridization of radiolabeled TAT-derived probe to the filters is performed in a solution of 50% formamide, 5x SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH 6.8, 2x Denhardt's solution, and 10% dextran sulfate at 42°C for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1x SSC and 0.1% SDS at 42°C.

DNAs having a desired sequence identity with the DNA encoding full-length native sequence TAT can then be identified using standard techniques known in the art.

EXAMPLE 3: Expression of TAT in *E. coli*

This example illustrates preparation of an unglycosylated form of TAT by recombinant expression in *E. coli*.

The DNA sequence encoding TAT is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., Gene, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the TAT coding region, lambda transcriptional terminator, and an argU gene.

The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., supra. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized TAT protein can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

TAT may be expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA encoding TAT is initially amplified using selected PCR primers. The primers will contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged sequences are then ligated into an expression vector, which is used to transform an *E. coli* host based on strain 52 (W3110

fuhA(tonA) lon galE rpoHts(htpRts) clpP(lacIq). Transformants are first grown in LB containing 50 mg/ml carbenicillin at 30°C with shaking until an O.D.600 of 3-5 is reached. Cultures are then diluted 50-100 fold into CRAP media (prepared by mixing 3.57 g (NH₄)₂SO₄, 0.71 g sodium citrate•2H₂O, 1.07 g KCl, 5.36 g Difco yeast extract, 5.36 g Sheffield hycase SF in 500 mL water, as well as 110 mM MPOS, pH 7.3, 0.55% (w/v) glucose and 7 mM MgSO₄) and grown for approximately 20-30 hours at 30°C with shaking. Samples are removed to verify expression by SDS-PAGE analysis, and the bulk culture is centrifuged to pellet the cells. Cell pellets are frozen until purification and refolding.

E. coli paste from 0.5 to 1 L fermentations (6-10 g pellets) is resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1M and 0.02 M, respectively, and the solution is stirred overnight at 4°C. This step results in a denatured protein with all cysteine residues blocked by sulfitolization. The solution is centrifuged at 40,000 rpm in a Beckman Ultracentrifuge for 30 min. The supernatant is diluted with 3-5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. The clarified extract is loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate column buffer. The column is washed with additional buffer containing 50 mM imidazole (Calbiochem, Utrol grade), pH 7.4. The protein is eluted with buffer containing 250 mM imidazole. Fractions containing the desired protein are pooled and stored at 4°C. Protein concentration is estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

The proteins are refolded by diluting the sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM cysteine, 20 mM glycine and 1 mM EDTA. Refolding volumes are chosen so that the final protein concentration is between 50 to 100 micrograms/ml. The refolding solution is stirred gently at 4°C for 12-36 hours. The refolding reaction is quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the solution is filtered through a 0.22 micron filter and acetonitrile is added to 2-10% final concentration. The refolded protein is chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions with A280 absorbance are analyzed on SDS polyacrylamide gels and fractions containing homogeneous refolded protein are pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile since those species are the most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded forms of proteins from the desired form, the reversed phase step also removes endotoxin from the samples.

Fractions containing the desired folded TAT polypeptide are pooled and the acetonitrile removed using a gentle stream of nitrogen directed at the solution. Proteins are formulated into 20 mM Hepes, pH 6.8 with 0.14 M sodium chloride and 4% mannitol by dialysis or by gel filtration using G25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

Certain of the TAT polypeptides disclosed herein have been successfully expressed and purified using

this technique(s).

EXAMPLE 4: Expression of TAT in mammalian cells

This example illustrates preparation of a potentially glycosylated form of TAT by recombinant expression in mammalian cells.

5 The vector, pRK5 (see EP 307,247, published March 15, 1989), is employed as the expression vector. Optionally, the TAT DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the TAT DNA using ligation methods such as described in Sambrook et al., supra. The resulting vector is called pRK5-TAT.

10 In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 µg pRK5-TAT DNA is mixed with about 1 µg DNA encoding the VA RNA gene [Thimmappaya et al., Cell, 31:543 (1982)] and dissolved in 500 µl of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M CaCl₂. To this mixture is added, dropwise, 500µl of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM NaPO₄, and a precipitate is allowed to form for 10 minutes at 25°C. The
15 precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37°C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200 µCi/ml ³⁵S-cysteine and 200 µCi/ml ³⁵S-methionine.
20 After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of TAT polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

In an alternative technique, TAT may be introduced into 293 cells transiently using the dextran sulfate
25 method described by Sompariyac et al., Proc. Natl. Acad. Sci., 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 µg pRK5-TAT DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 µg/ml bovine insulin and
30 0.1 µg/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed TAT can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

In another embodiment, TAT can be expressed in CHO cells. The pRK5-TAT can be transfected into
35 CHO cells using known reagents such as CaPO₄ or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as ³⁵S-methionine. After determining the presence of TAT polypeptide, the culture medium may be replaced

with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed TAT can then be concentrated and purified by any selected method.

Epitope-tagged TAT may also be expressed in host CHO cells. The TAT may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged TAT insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged TAT can then be concentrated and purified by any selected method, such as by Ni^{2+} -chelate affinity chromatography.

TAT may also be expressed in CHO and/or COS cells by a transient expression procedure or in CHO cells by another stable expression procedure.

Stable expression in CHO cells is performed using the following procedure. The proteins are expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g. extracellular domains) of the respective proteins are fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or is a poly-His tagged form.

Following PCR amplification, the respective DNAs are subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., Current Protocols of Molecular Biology, Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used expression in CHO cells is as described in Lucas et al., Nucl. Acids Res. 24:9 (1774-1779 (1996), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits selection for stable maintenance of the plasmid following transfection.

Twelve micrograms of the desired plasmid DNA is introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect[®] (Quiagen), Dosper[®] or Fugene[®] (Boehringer Mannheim). The cells are grown as described in Lucas et al., supra. Approximately 3×10^7 cells are frozen in an ampule for further growth and production as described below.

The ampules containing the plasmid DNA are thawed by placement into water bath and mixed by vortexing. The contents are pipetted into a centrifuge tube containing 10 mLs of media and centrifuged at 1000 rpm for 5 minutes. The supernatant is aspirated and the cells are resuspended in 10 mL of selective media (0.2 μm filtered PS20 with 5% 0.2 μm diafiltered fetal bovine serum). The cells are then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells are transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37°C. After another 2-3 days, 250 mL, 500 mL and 2000 mL spinners are seeded with 3×10^5 cells/mL. The cell media is exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in U.S. Patent No. 5,122,469, issued June 16, 1992 may actually be used. A 3L production spinner is seeded at 1.2×10^6 cells/mL. On day 0, the cell number pH is determined. On day

1, the spinner is sampled and sparging with filtered air is commenced. On day 2, the spinner is sampled, the temperature shifted to 33°C, and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion) taken. Throughout the production, the pH is adjusted as necessary to keep it at around 7.2. After 10 days, or until the viability dropped below 70%, the cell culture is harvested by centrifugation and filtering through a 0.22 μ m filter. The filtrate was
5 either stored at 4°C or immediately loaded onto columns for purification.

For the poly-His tagged constructs, the proteins are purified using a Ni-NTA column (Qiagen). Before purification, imidazole is added to the conditioned media to a concentration of 5 mM. The conditioned media is pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After loading, the column is washed with additional
10 equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein is subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

Immunoadhesin (Fc-containing) constructs are purified from the conditioned media as follows. The conditioned medium is pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column is washed extensively with equilibration buffer
15 before elution with 100 mM citric acid, pH 3.5. The eluted protein is immediately neutralized by collecting 1 ml fractions into tubes containing 275 μ L of 1 M Tris buffer, pH 9. The highly purified protein is subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity is assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation.

20 Certain of the TAT polypeptides disclosed herein have been successfully expressed and purified using this technique(s).

EXAMPLE 5: Expression of TAT in Yeast

The following method describes recombinant expression of TAT in yeast.

25 First, yeast expression vectors are constructed for intracellular production or secretion of TAT from the ADH2/GAPDH promoter. DNA encoding TAT and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of TAT. For secretion, DNA encoding TAT can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, a native TAT signal peptide or other mammalian signal peptide, or, for example, a yeast alpha-factor or invertase secretory
30 signal/leader sequence, and linker sequences (if needed) for expression of TAT.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

35 Recombinant TAT can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The

concentrate containing TAT may further be purified using selected column chromatography resins.

Certain of the TAT polypeptides disclosed herein have been successfully expressed and purified using this technique(s).

EXAMPLE 6: Expression of TAT in Baculovirus-Infected Insect Cells

The following method describes recombinant expression of TAT in Baculovirus-infected insect cells.

The sequence coding for TAT is fused upstream of an epitope tag contained within a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the sequence encoding TAT or the desired portion of the coding sequence of TAT such as the sequence encoding an extracellular domain of a transmembrane protein or the sequence encoding the mature protein if the protein is extracellular is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector.

Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (Pharmlingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4 - 5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression are performed as described by O'Reilley et al., Baculovirus expression vectors: A Laboratory Manual, Oxford: Oxford University Press (1994).

Expressed poly-his tagged TAT can then be purified, for example, by Ni²⁺-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert et al., Nature, **362**:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM MgCl₂; 0.1 mM EDTA; 10% glycerol; 0.1 % NP-40; 0.4 M KCl), and sonicated twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% glycerol, pH 7.8) and filtered through a 0.45 µm filter. A Ni²⁺-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A₂₈₀ with loading buffer, at which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching A₂₈₀ baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or Western blot with Ni²⁺-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His₆-tagged TAT are pooled and dialyzed against loading buffer.

Alternatively, purification of the IgG tagged (or Fc tagged) TAT can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

Certain of the TAT polypeptides disclosed herein have been successfully expressed and purified using

this technique(s).

EXAMPLE 7: Preparation of Antibodies that Bind TAT

This example illustrates preparation of monoclonal antibodies which can specifically bind TAT.

Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, *supra*. Immunogens that may be employed include purified TAT, fusion proteins containing TAT, and cells expressing recombinant TAT on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

Mice, such as Balb/c, are immunized with the TAT immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-TAT antibodies.

After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of TAT. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

The hybridoma cells will be screened in an ELISA for reactivity against TAT. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against TAT is within the skill in the art.

The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-TAT monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

EXAMPLE 8: Purification of TAT Polypeptides Using Specific Antibodies

Native or recombinant TAT polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-TAT polypeptide, mature TAT polypeptide, or pre-TAT polypeptide is purified by immunoaffinity chromatography using antibodies specific for the TAT polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-TAT polypeptide antibody to an activated chromatographic resin.

Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium

sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CnBr-activated SEPHAROSE™ (Pharmacia LKB Biotechnology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

Such an immunoaffinity column is utilized in the purification of TAT polypeptide by preparing a fraction from cells containing TAT polypeptide in a soluble form. This preparation is derived by solubilization of the whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble TAT polypeptide containing a signal sequence may be secreted in useful quantity into the medium in which the cells are grown.

A soluble TAT polypeptide-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of TAT polypeptide (*e.g.*, high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/TAT polypeptide binding (*e.g.*, a low pH buffer such as approximately pH 2-3, or a high concentration of a chaotrope such as urea or thiocyanate ion), and TAT polypeptide is collected.

EXAMPLE 9: *In Vitro* Tumor Cell Killing Assay

Mammalian cells expressing the TAT polypeptide of interest may be obtained using standard expression vector and cloning techniques. Alternatively, many tumor cell lines expressing TAT polypeptides of interest are publicly available, for example, through the ATCC and can be routinely identified using standard ELISA or FACS analysis. Anti-TAT polypeptide monoclonal antibodies (and toxin conjugated derivatives thereof) may then be employed in assays to determine the ability of the antibody to kill TAT polypeptide expressing cells *in vitro*.

For example, cells expressing the TAT polypeptide of interest are obtained as described above and plated into 96 well dishes. In one analysis, the antibody/toxin conjugate (or naked antibody) is included throughout the cell incubation for a period of 4 days. In a second independent analysis, the cells are incubated for 1 hour with the antibody/toxin conjugate (or naked antibody) and then washed and incubated in the absence of antibody/toxin conjugate for a period of 4 days. Cell viability is then measured using the CellTiter-Glo Luminescent Cell Viability Assay from Promega (Cat# G7571). Untreated cells serve as a negative control.

EXAMPLE 10: *In Vivo* Tumor Cell Killing Assay

To test the efficacy of conjugated or unconjugated anti-TAT polypeptide monoclonal antibodies, anti-TAT antibody is injected intraperitoneally into nude mice 24 hours prior to receiving tumor promoting cells subcutaneously in the flank. Antibody injections continue twice per week for the remainder of the study. Tumor volume is then measured twice per week.

The foregoing written specification is considered to be sufficient to enable one skilled in the art to

practice the invention. The present invention is not to be limited in scope by the construct deposited, since the deposited embodiment is intended as a single illustration of certain aspects of the invention and any constructs that are functionally equivalent are within the scope of this invention. The deposit of material herein does not constitute an admission that the written description herein contained is inadequate to enable the practice of any aspect of the invention, including the best mode thereof, nor is it to be construed as limiting the scope of the claims to the specific illustrations that it represents. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

5

WHAT IS CLAIMED IS:

1. Isolated nucleic acid having a nucleotide sequence that has at least 80% nucleic acid sequence identity to:

(a) a DNA molecule encoding the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) a DNA molecule encoding the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) a DNA molecule encoding an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) a DNA molecule encoding an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(f) the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(g) the complement of (a), (b), (c), (d), (e) or (f).

2. Isolated nucleic acid having:

(a) a nucleotide sequence that encodes the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) a nucleotide sequence that encodes the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) a nucleotide sequence that encodes an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) a nucleotide sequence that encodes an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(f) the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(g) the complement of (a), (b), (c), (d), (e) or (f).

3. Isolated nucleic acid that hybridizes to:

(a) a nucleic acid that encodes the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) a nucleic acid that encodes the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) a nucleic acid that encodes an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) a nucleic acid that encodes an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

- (e) the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);
- (f) the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or
- (g) the complement of (a), (b), (c), (d), (e) or (f).
4. The nucleic acid of Claim 3, wherein the hybridization occurs under stringent conditions.
5. The nucleic acid of Claim 3 which is at least about 5 nucleotides in length.
6. An expression vector comprising the nucleic acid of Claim 1, 2 or 3.
7. The expression vector of Claim 6, wherein said nucleic acid is operably linked to control sequences recognized by a host cell transformed with the vector.
8. A host cell comprising the expression vector of Claim 7.
9. The host cell of Claim 8 which is a CHO cell, an *E. coli* cell or a yeast cell.
10. A process for producing a polypeptide comprising culturing the host cell of Claim 8 under conditions suitable for expression of said polypeptide and recovering said polypeptide from the cell culture.
11. An isolated polypeptide having at least 80% amino acid sequence identity to:
- (a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);
- (b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;
- (c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;
- (d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;
- (e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or
- (f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).
12. An isolated polypeptide having:
- (a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);
- (b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;
- (c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;
- (d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;
- (e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or
- (f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

13. A chimeric polypeptide comprising the polypeptide of Claim 11 or 12 fused to a heterologous polypeptide.

14. The chimeric polypeptide of Claim 13, wherein said heterologous polypeptide is an epitope tag sequence or an Fc region of an immunoglobulin.

15. An isolated antibody that binds to a polypeptide having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

16. An isolated antibody that binds to a polypeptide having:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

17. The antibody of Claim 15 or 16 which is a monoclonal antibody.

18. The antibody of Claim 15 or 16 which is an antibody fragment.

19. The antibody of Claim 15 or 16 which is a chimeric or a humanized antibody.

20. The antibody of Claim 15 or 16 which is conjugated to a growth inhibitory agent.

21. The antibody of Claim 15 or 16 which is conjugated to a cytotoxic agent.

22. The antibody of Claim 21, wherein the cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

23. The antibody of Claim 21, wherein the cytotoxic agent is a toxin.

24. The antibody of Claim 23, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

25. The antibody of Claim 23, wherein the toxin is a maytansinoid.

26. The antibody of Claim 15 or 16 which is produced in bacteria.

27. The antibody of Claim 15 or 16 which is produced in CHO cells.

28. The antibody of Claim 15 or 16 which induces death of a cell to which it binds.

29. The antibody of Claim 15 or 16 which is detectably labeled.

30. An isolated nucleic acid having a nucleotide sequence that encodes the antibody of Claim 15 or 16.

31. An expression vector comprising the nucleic acid of Claim 30 operably linked to control sequences recognized by a host cell transformed with the vector.

32. A host cell comprising the expression vector of Claim 31.

33. The host cell of Claim 32 which is a CHO cell, an *E. coli* cell or a yeast cell.

34. A process for producing an antibody comprising culturing the host cell of Claim 32 under conditions suitable for expression of said antibody and recovering said antibody from the cell culture.

35. An isolated oligopeptide that binds to a polypeptide having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

36. An isolated oligopeptide that binds to a polypeptide having:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355

(SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

37. The oligopeptide of Claim 35 or 36 which is conjugated to a growth inhibitory agent.

38. The oligopeptide of Claim 35 or 36 which is conjugated to a cytotoxic agent.

39. The oligopeptide of Claim 38, wherein the cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

40. The oligopeptide of Claim 38, wherein the cytotoxic agent is a toxin.

41. The oligopeptide of Claim 40, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

42. The oligopeptide of Claim 40, wherein the toxin is a maytansinoid.

43. The oligopeptide of Claim 35 or 36 which induces death of a cell to which it binds.

44. The oligopeptide of Claim 35 or 36 which is detectably labeled.

45. A TAT binding organic molecule that binds to a polypeptide having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

46. The organic molecule of Claim 45 that binds to a polypeptide having:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown

in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

47. The organic molecule of Claim 45 or 46 which is conjugated to a growth inhibitory agent.

48. The organic molecule of Claim 45 or 46 which is conjugated to a cytotoxic agent.

49. The organic molecule of Claim 48, wherein the cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

5 50. The organic molecule of Claim 48, wherein the cytotoxic agent is a toxin.

51. The organic molecule of Claim 50, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

52. The organic molecule of Claim 50, wherein the toxin is a maytansinoid.

53. The organic molecule of Claim 45 or 46 which induces death of a cell to which it binds.

10 54. The organic molecule of Claim 45 or 46 which is detectably labeled.

55. A composition of matter comprising:

(a) the polypeptide of Claim 11;

(b) the polypeptide of Claim 12;

(c) the chimeric polypeptide of Claim 13;

15 (d) the antibody of Claim 15;

(e) the antibody of Claim 16;

(f) the oligopeptide of Claim 35;

(g) the oligopeptide of Claim 36;

(h) the TAT binding organic molecule of Claim 45; or

20 (i) the TAT binding organic molecule of Claim 46; in combination with a carrier.

56. The composition of matter of Claim 55, wherein said carrier is a pharmaceutically acceptable carrier.

57. An article of manufacture comprising:

(a) a container; and

25 (b) the composition of matter of Claim 55 contained within said container.

58. The article of manufacture of Claim 57 further comprising a label affixed to said container, or a package insert included with said container, referring to the use of said composition of matter for the therapeutic treatment of or the diagnostic detection of a cancer.

30 59. A method of inhibiting the growth of a cell that expresses a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

35 (c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-

6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising contacting said cell with an antibody,
5 oligopeptide or organic molecule that binds to said protein, the binding of said antibody, oligopeptide or organic molecule to said protein thereby causing an inhibition of growth of said cell.

60. The method of Claim 59, wherein said antibody is a monoclonal antibody.

61. The method of Claim 59, wherein said antibody is an antibody fragment.

62. The method of Claim 59, wherein said antibody is a chimeric or a humanized antibody.

10 63. The method of Claim 59, wherein said antibody, oligopeptide or organic molecule is conjugated to a growth inhibitory agent.

64. The method of Claim 59, wherein said antibody, oligopeptide or organic molecule is conjugated to a cytotoxic agent.

15 65. The method of Claim 64, wherein said cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

66. The method of Claim 64, wherein the cytotoxic agent is a toxin.

67. The method of Claim 66, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

68. The method of Claim 66, wherein the toxin is a maytansinoid.

20 69. The method of Claim 59, wherein said antibody is produced in bacteria.

70. The method of Claim 59, wherein said antibody is produced in CHO cells.

71. The method of Claim 59, wherein said cell is a cancer cell.

72. The method of Claim 71, wherein said cancer cell is further exposed to radiation treatment or a chemotherapeutic agent.

25 73. The method of Claim 71, wherein said cancer cell is selected from the group consisting of a breast cancer cell, a colorectal cancer cell, a lung cancer cell, an ovarian cancer cell, a central nervous system cancer cell, a liver cancer cell, a bladder cancer cell, a pancreatic cancer cell, a cervical cancer cell, a melanoma cell and a leukemia cell.

30 74. The method of Claim 71, wherein said protein is more abundantly expressed by said cancer cell as compared to a normal cell of the same tissue origin.

75. The method of Claim 59 which causes the death of said cell.

76. The method of Claim 59, wherein said protein has:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

35 (b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures

1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

77. A method of therapeutically treating a mammal having a cancerous tumor comprising cells that express a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising administering to said mammal a therapeutically effective amount of an antibody, oligopeptide or organic molecule that binds to said protein, thereby effectively treating said mammal.

78. The method of Claim 77, wherein said antibody is a monoclonal antibody.

79. The method of Claim 77, wherein said antibody is an antibody fragment.

80. The method of Claim 77, wherein said antibody is a chimeric or a humanized antibody.

81. The method of Claim 77, wherein said antibody, oligopeptide or organic molecule is conjugated to a growth inhibitory agent.

82. The method of Claim 77, wherein said antibody, oligopeptide or organic molecule is conjugated to a cytotoxic agent.

83. The method of Claim 82, wherein said cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

84. The method of Claim 82, wherein the cytotoxic agent is a toxin.

85. The method of Claim 84, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

86. The method of Claim 84, wherein the toxin is a maytansinoid.

87. The method of Claim 77, wherein said antibody is produced in bacteria.

88. The method of Claim 77, wherein said antibody is produced in CHO cells.

89. The method of Claim 77, wherein said tumor is further exposed to radiation treatment or a chemotherapeutic agent.

90. The method of Claim 77, wherein said tumor is a breast tumor, a colorectal tumor, a lung tumor, an ovarian tumor, a central nervous system tumor, a liver tumor, a bladder tumor, a pancreatic tumor, or a cervical tumor.

5 91. The method of Claim 77, wherein said protein is more abundantly expressed by the cancerous cells of said tumor as compared to a normal cell of the same tissue origin.

92. The method of Claim 77, wherein said protein has:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

10 (b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

15 (e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

20 93. A method of determining the presence of a protein in a sample suspected of containing said protein, wherein said protein has at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

25 (c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

30 (f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising exposing said sample to an antibody, oligopeptide or organic molecule that binds to said protein and determining binding of said antibody, oligopeptide or organic molecule to said protein in said sample, wherein binding of the antibody, oligopeptide or organic molecule to said protein is indicative of the presence of said protein in said sample.

35 94. The method of Claim 93, wherein said sample comprises a cell suspected of expressing said protein.

95. The method of Claim 94, wherein said cell is a cancer cell.

96. The method of Claim 93, wherein said antibody, oligopeptide or organic molecule is detectably labeled.

97. The method of Claim 93, wherein said protein has:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

5 (b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

10 (d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

15 98. A method of diagnosing the presence of a tumor in a mammal, said method comprising determining the level of expression of a gene encoding a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

20 (b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

25 (e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

30 (f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), in a test sample of tissue cells obtained from said mammal and in a control sample of known normal cells of the same tissue origin, wherein a higher level of expression of said protein in the test sample, as compared to the control sample, is indicative of the presence of tumor in the mammal from which the test sample was obtained.

99. The method of Claim 98, wherein the step of determining the level of expression of a gene encoding said protein comprises employing an oligonucleotide in an *in situ* hybridization or RT-PCR analysis.

35 100. The method of Claim 98, wherein the step determining the level of expression of a gene encoding said protein comprises employing an antibody in an immunohistochemistry or Western blot analysis.

101. The method of Claim 98, wherein said protein has:

- (a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);
- (b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;
- (c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;
- 5 (d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;
- (e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or
- 10 (f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

102. A method of diagnosing the presence of a tumor in a mammal, said method comprising contacting a test sample of tissue cells obtained from said mammal with an antibody, oligopeptide or organic molecule that binds to a protein having at least 80% amino acid sequence identity to:

- (a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);
- 15 (b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;
- (c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;
- (d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;
- 20 (e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or
- (f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), and detecting the formation of a complex between said antibody, oligopeptide or organic molecule and said protein in the test sample, wherein the formation of a complex is indicative of the presence of a tumor in said mammal.
- 25

103. The method of Claim 102, wherein said antibody, oligopeptide or organic molecule is detectably labeled.

104. The method of Claim 102, wherein said test sample of tissue cells is obtained from an individual suspected of having a cancerous tumor.

30

105. The method of Claim 102, wherein said protein has:

- (a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);
- (b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;
- 35 (c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

106. A method for treating or preventing a cell proliferative disorder associated with increased expression or activity of a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising administering to a subject in need of such treatment an effective amount of an antagonist of said protein, thereby effectively treating or preventing said cell proliferative disorder.

107. The method of Claim 106, wherein said cell proliferative disorder is cancer.

108. The method of Claim 106, wherein said antagonist is an anti-TAT polypeptide antibody, TAT binding oligopeptide, TAT binding organic molecule or antisense oligonucleotide.

109. A method of binding an antibody, oligopeptide or organic molecule to a cell that expresses a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising contacting said cell with an antibody,

oligopeptide or organic molecule that binds to said protein and allowing the binding of the antibody, oligopeptide or organic molecule to said protein to occur, thereby binding said antibody, oligopeptide or organic molecule to said cell.

110. The method of Claim 109, wherein said antibody is a monoclonal antibody.

111. The method of Claim 109, wherein said antibody is an antibody fragment.

5 112. The method of Claim 109, wherein said antibody is a chimeric or a humanized antibody.

113. The method of Claim 109, wherein said antibody, oligopeptide or organic molecule is conjugated to a growth inhibitory agent.

114. The method of Claim 109, wherein said antibody, oligopeptide or organic molecule is conjugated to a cytotoxic agent.

10 115. The method of Claim 114, wherein said cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

116. The method of Claim 114, wherein the cytotoxic agent is a toxin.

117. The method of Claim 116, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

15 118. The method of Claim 116, wherein the toxin is a maytansinoid.

119. The method of Claim 109, wherein said antibody is produced in bacteria.

120. The method of Claim 109, wherein said antibody is produced in CHO cells.

121. The method of Claim 109, wherein said cell is a cancer cell.

20 122. The method of Claim 121, wherein said cancer cell is further exposed to radiation treatment or a chemotherapeutic agent.

123. The method of Claim 121, wherein said cancer cell is selected from the group consisting of a breast cancer cell, a colorectal cancer cell, a lung cancer cell, an ovarian cancer cell, a central nervous system cancer cell, a liver cancer cell, a bladder cancer cell, a pancreatic cancer cell, a cervical cancer cell, a melanoma cell and a leukemia cell.

25 124. The method of Claim 123, wherein said protein is more abundantly expressed by said cancer cell as compared to a normal cell of the same tissue origin.

125. The method of Claim 109 which causes the death of said cell.

126. Use of a nucleic acid as claimed in any of Claims 1 to 5 or 30 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

30 127. Use of a nucleic acid as claimed in any of Claims 1 to 5 or 30 in the preparation of a medicament for treating a tumor.

128. Use of a nucleic acid as claimed in any of Claims 1 to 5 or 30 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

35 129. Use of an expression vector as claimed in any of Claims 6, 7 or 31 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

130. Use of an expression vector as claimed in any of Claims 6, 7 or 31 in the preparation of

medicament for treating a tumor.

131. Use of an expression vector as claimed in any of Claims 6, 7 or 31 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

132. Use of a host cell as claimed in any of Claims 8, 9, 32, or 33 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

5

133. Use of a host cell as claimed in any of Claims 8, 9, 32 or 33 in the preparation of a medicament for treating a tumor.

134. Use of a host cell as claimed in any of Claims 8, 9, 32 or 33 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

135. Use of a polypeptide as claimed in any of Claims 11 to 14 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

136. Use of a polypeptide as claimed in any of Claims 11 to 14 in the preparation of a medicament for treating a tumor.

137. Use of a polypeptide as claimed in any of Claims 11 to 14 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

138. Use of an antibody as claimed in any of Claims 15 to 29 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

139. Use of an antibody as claimed in any of Claims 15 to 29 in the preparation of a medicament for treating a tumor.

140. Use of an antibody as claimed in any of Claims 15 to 29 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

141. Use of an oligopeptide as claimed in any of Claims 35 to 44 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

142. Use of an oligopeptide as claimed in any of Claims 35 to 44 in the preparation of a medicament for treating a tumor.

143. Use of an oligopeptide as claimed in any of Claims 35 to 44 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

144. Use of a TAT binding organic molecule as claimed in any of Claims 45 to 54 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

145. Use of a TAT binding organic molecule as claimed in any of Claims 45 to 54 in the preparation of a medicament for treating a tumor.

146. Use of a TAT binding organic molecule as claimed in any of Claims 45 to 54 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

147. Use of a composition of matter as claimed in any of Claims 55 or 56 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

148. Use of a composition of matter as claimed in any of Claims 55 or 56 in the preparation of a medicament for treating a tumor.

149. Use of a composition of matter as claimed in any of Claims 55 or 56 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

150. Use of an article of manufacture as claimed in any of Claims 57 or 58 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

151. Use of an article of manufacture as claimed in any of Claims 57 or 58 in the preparation of a medicament for treating a tumor.

152. Use of an article of manufacture as claimed in any of Claims 57 or 58 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

153. A method for inhibiting the growth of a cell, wherein the growth of said cell is at least in part dependent upon a growth potentiating effect of a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

5 (b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

10 (d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

15 (f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising contacting said protein with an antibody, oligopeptide or organic molecule that binds to said protein, thereby inhibiting the growth of said cell.

154. The method of Claim 153, wherein said cell is a cancer cell.

155. The method of Claim 153, wherein said protein is expressed by said cell.

156. The method of Claim 153, wherein the binding of said antibody, oligopeptide or organic molecule to said protein antagonizes a cell growth-potentiating activity of said protein.

20 157. The method of Claim 153, wherein the binding of said antibody, oligopeptide or organic molecule to said protein induces the death of said cell.

158. The method of Claim 153, wherein said antibody is a monoclonal antibody.

159. The method of Claim 153, wherein said antibody is an antibody fragment.

160. The method of Claim 153, wherein said antibody is a chimeric or a humanized antibody.

25 161. The method of Claim 153, wherein said antibody, oligopeptide or organic molecule is conjugated to a growth inhibitory agent.

162. The method of Claim 153, wherein said antibody, oligopeptide or organic molecule is conjugated to a cytotoxic agent.

30 163. The method of Claim 162, wherein said cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

164. The method of Claim 162, wherein the cytotoxic agent is a toxin.

165. The method of Claim 164, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

166. The method of Claim 164, wherein the toxin is a maytansinoid.

35 167. The method of Claim 153, wherein said antibody is produced in bacteria.

168. The method of Claim 153, wherein said antibody is produced in CHO cells.

169. The method of Claim 153, wherein said protein has:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

170. A method of therapeutically treating a tumor in a mammal, wherein the growth of said tumor is at least in part dependent upon a growth potentiating effect of a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising contacting said protein with an antibody, oligopeptide or organic molecule that binds to said protein, thereby effectively treating said tumor.

171. The method of Claim 170, wherein said protein is expressed by cells of said tumor.

172. The method of Claim 170, wherein the binding of said antibody, oligopeptide or organic molecule to said protein antagonizes a cell growth-potentiating activity of said protein.

173. The method of Claim 170, wherein said antibody is a monoclonal antibody.

174. The method of Claim 170, wherein said antibody is an antibody fragment.

175. The method of Claim 170, wherein said antibody is a chimeric or a humanized antibody.

176. The method of Claim 170, wherein said antibody, oligopeptide or organic molecule is conjugated to a growth inhibitory agent.

177. The method of Claim 170, wherein said antibody, oligopeptide or organic molecule is conjugated to a cytotoxic agent.

178. The method of Claim 177, wherein said cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

179. The method of Claim 177, wherein the cytotoxic agent is a toxin.

180. The method of Claim 179, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

5 181. The method of Claim 179, wherein the toxin is a maytansinoid.

182. The method of Claim 170, wherein said antibody is produced in bacteria.

183. The method of Claim 170, wherein said antibody is produced in CHO cells.

184. The method of Claim 170, wherein said protein has:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

10 (b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

15 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

1/6881
FIGURE 1

ATCACATGCCTATCATATAGTAAAACCCAGCCCATGGCCCCTAACAGGGGCCCTCTCAGCCCTCCTAATGACCTC
CGGCCTAGCCATGTGATTTCACTTCCACTCCACAACCCTCCTCATACTAGGCCTACTAACCAACACACTAACCAT
ATACCAATGATGGCGCGATGTAACACGAGAAAGCACATACCAAGGCCACCACACACCACCTGTCCAGAAAGGCCT
TCGATACGGGATAATCCTATTTATTACCTCAGAAGTTTTTTTCTTCGCAGGATTTTTCTGAGCCTTTTACCACTC
CAGCCTAGCTCCCACCCCCCAACTAGGGGGACACTGGCCCCCAACAGGCATCACCCCGCTAAATCCCCTAGAAGT
CCCACTCCTAAACACATCCGTATTACTCGCATCAGGGGTATCAATCACCTGAGCTCACCATAGTCTAATAGTCTA
TTTTACCCTCCTACAAGCCTCAGAGTACTTCGAG

2/6881
FIGURE 2

TCTAATACCTATTGATCTGTCACTTTCTCCCATCACGCTCAGGTGGGACCATTTCAGTTGCAGGAAAACAAGCTTA
ACACGCCCCACTAATTCTACATTATGGTGAGTTCTATAATTATTTTATTATATATTACAGTGTAATAATGGAAATA
AAGTGCCTAATAAATGCAAATGTGCTTACATCTTTTGGCCCAGCTCCTACCTCCCGGCAGCCTCTCCAGGCCCAG
AACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCACAATGGCCTATTTAGGCCCATAACCTATGTCAC
GGCAGCCTCCGCAGATGAGGCTACTGCCTCACAAACAGCCTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTT
TAGACCCAGCTCCTGCCTCCCAGCCTTCTCTCCAGGCCCTGAACTTTCTCAAGTCGACCTCACCAGGCCCAGCTC
ATGCTTCTTTGCAGCCTCTCCAGGCCCAGCTCCTGCATCTTGGTGGCCCCCTCCAGGCCCAGCCTCTGCCTCCCGT
CAGCCTCTACAGTCCCAAAGTCTGCCTCACAGCAGATTCTTCACGCCCAGCATCTACCTCACTTGGACCCCTCCAG
ACCCAGATGGTGTCTCACTGTGGCATCCTCAGGCGAAGCTCCTGCCTTTCGGCAGCCTCTCCAGGCCCAGCTCCT
CCTGCCTCCCAGTGGCCTCTTTCGGCCCAGCCCAGCTCATGCCTCCCGGCGGCCTTCCCAAGCCCCGCTTTTGAC
TTTCGGTGGCCTCTGCAGGCCTCGACAAGGCCAGCCTCCTGCCTCCCGAAGGCCTGCACAGGCCCAGCCTCTGC
CTCACAGCGGACTCTC

3/6881
FIGURE 3

CAAGCTCATGACTCACAATGGCCTATTTAGGCCCATACCCTACGTACGGCAGCCTCCGCAGATGAGCCTACTGC
CTCACAACAGCCTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTTTAGACCCAGCTCCTGCCTCCCAGCCTT
CTCTCCAGGCTCTGAACTTTCTCAGGTCTCCCTCTGTTGTCCAAGGCTGGAGTGTAGTAGTGCTATCGCAGCTGA
CTGCAGCCTCAACCTTCCAGGCTGAAGCGATCCTCCACCTCAACCTCCCACGTGGCTGAGACTACAGGTGCTTG
CCACTATGCCCAACTAACATTTGGAATTTTCGTATACGTGGATTCCAGAGGGGTGACAGCGAAACGTGGGACCAT
TCAGTTGCAGGAAAACAAGCTTAACACGCCCACTAATTCTACATTATGCTCCTACCTCCCGGCAGCCTCTCCAGG
CCCAGAACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCACAATG

4/6881
FIGURE 4

CGTCGGCCCCCGGCCCCCAGCAGCCTCCAAAGCCCTGTGACTCACAGCCCTGCTTCCACGGGGGGACCTGCCAG
GACTGGGCATTGGGCGGGGGCTTCACCTGCAGCTGCCCCGCAGGCAGGGGAGGCGCCGTCTGTGAGAAGGTGCTT
GGCGCCCCCTGTGCCGGCCTTCGAGGGCCGCTCCTTCTGGCCTTCCCCACTCTCCGCGCCTACCACACGCTGCGC
CTGGCACTGGAATTCCGGGCGCTGGAGCCTCAGGGGCTGCTGCTGTACAATGGCAACGCCCCGGGGCAAGGACTTC
CTGGCATTGGCGCTGCTAGATGGCCGCTGCAGCTCAGGTTTGACACAGGTTTCGGGGCCGGCGGTGCTGACCAGT
GCCGTGCCGGTAGAGCCGGGCCAGTGGCACCGCCTGGAGCTGTCCCGGCACTGGCGCCGGGGCACCCCTCTCGGTG
GATGGTGAGACCCCTGTTCTGGGCGAGAGTCCCAGTGGCACCGACGGCCTCAACCTGGACACAGACCTCTTTGTG
GGCGGCGTACCCGAGGACCAGGCTGCCGTGGCGCTGGAGCGGACCTTCGTGGGCGCCGGCCTGAGGGGGTGCATC
CGTTTGCTGGACGTCAACAACCAGCGCCTGGAGCTTGGCATTGGGCCCGGGGGCTGCCACCCGAGGCTCTGGCGTG
GGCAAGTGCGGGGACCACCCCTGCCTGCCCAACCCCTGCCATGGCGGGGGCCCCATGCCAGAACCTGGAGGCTGGA
AGGTTCCATTGCCAGTGCCCCGCCCCGGCCGCTCGGACCAACCTGTGCCGATGAGAAGAGCCCCCTGCCAGCCCAAC
CCCTGCCATGGGGCGGGCGCCCTGCCGTGTGCTGCCCGAGGGTGGTGCTCAGTGCGAGTGCCCCCTGGGGCGTGAG
GGCACCTTCTGCCAGACAGCCTCGGGGCAGGACGGCTCTGGGCCCTTCTGGCTGACTTCAACGGCTTCTCCAC
CTGGAGCTGAGAGGCCTGCACACCTTTGCACGGGACCTGGGGGAGAAGATGGCGCTGGAGGTCGTGTTCTGGCA
CGAGGCCCCAGCGGCCTCCTGCTCTACAACGGGCAGAAGACGGACGGCAAGGGGGACTTCGTGTCGCTGGCACTG
CGGGACCGCCGCTGGAGTTCCGCTACGACCTGGGCAAGGGGGCAGCGGTATCAGGAGCAGGGAGCCAGTCACC
CTGGGAGCCTGGACCAGGGTCTCACTGGAGCGAAACGGCCGCAAGGGTGCCCTGCGTGTGGGCGACGGCCCCCGT
GTGTTGGGGGAGTCCCCGTTCCGCACACCGTCTCAACCTGAAGGAGCCGCTCTACGTAGGGGGCGCTCCCGAC
TTCAGCAAGCTGGCCCGTGCTGCTGCCGTGTCTCTGGCTTCGACGGTGCCATCCAGCTGGTCTCCCTCGGAGGC
CGCCAGCTGCTGACCCCGGAGCACGTGCTGCGGCAGGTGGACGTCACGTCCTTTGCAGGTACCCCTGCACCCGG
GCTCAGGCCACCCCTGCCTCAATGGGGCCTCCTGCGTCCCAGGGAGGCTGCCTATGTGTGCCTGTGTCCCGGG
GGATTCTCAGGACCGCACTGCGAGAAGGGGCTGGTGGAGAAGTCAGCGGGGGACGTGGATACCTTGGCCTTTGAC
GGGCGGACCTTTGTGAGTACCTCAACGCTGTGACCGAGAGCGAGAAGGCACTGCAGAGCAACCCTTTGAACTG
AGCCTGCGCACTGAGGCCACGCAGGGGCTGGTGCTCTGGAGTGGCAAGGCCACGGAGCGGGCAGACTATGTGGCA
CTGGCCAATTGTGGACGGGCACCTGCAACTGAGCTACAACCTGGGCTCCCAGCCCGTGGTGCTGCGTTCCACCGTG
CCCGTCAACACCAACCGCTGGTTGCGGGTCTGTGGCACATAGGGAGCAGAGGGAAGGTTCCCTGCAGGTGGGCAAT
GAGGCCCCCTGTGACCGGCTCCTCCCCGCTGGGCGCCACGCAGCTGGACACTGATGGAGCCCTGTGGCTTGGGGGC
CTGCCGGAGCTGCCCCGTGGGCCAGCACTGCCCAAGGCCTACGGCACAGGCTTTGTGGGCTGCTTGCGGGACGTG
GTGGTGGGCCGGCACCCGCTGCACCTGCTGGAGGACGCCGTACCAAGCCAGAGCTGCGGCCCTGCCCCACCCCA
TGAGCTGGCACCAGAGCCCCGCGCCCGCTGTAATTATTTTCTATTTTTGTAAACTTGTTGCTTTTTGATATGATT
TTCTTGCTGAGTGTGGCCGGAGGACTGCTGGCCCCGGCCTCCCTTCCGTCCAGGCAGCCGTGCTGCAGACAGA
CCTAGTGCCGAGGGATGGACAGGCGAGGTGGCAGCGTGGAGGGCTCGGCGTGGATGGCAGCCTCAGGACACACAC
CCCTGCCTCAAGGTGCTGAGCCCCCGCCTTGCACTGCGCCTGCCCCACGGTGTCCCCGCGGGAAGCAGCCCCGG
CTCCTGAATCACCCCTCGCTCCGTGAGGCGGGACTCGTGTCAGAGAGGAAGGGGCTGCTGAGGTCTGATGGGGC
CCTTCTCCTCGGGTGACCCACAGGGCCTTTCCAAGCCCCCATTTGAGCTGCTCCTTCTGTGTGTGCTCTGGGCC
CTGCCTCGGCCTCCTGCGCCAATACTGTGACTTCCAACAATGTTACTGCTGGGCACAGCTCTGCGTTGCTCCCG
TGCTGCTGCGCCAGCCCCAGGCTGCTGAGGAGCAGAGGCCAGACCAGGGCCGATCTGGGTGTCTGACCCCTCAG
CTGGCCCTGCCCAGCCACCCCTGGACATGACCGTATCCCTCTGCCACACCCAGGCCCTGCGAGGGGCTATCGAGA
GGAGCTCACTGTGGGATGGGGTGTGACCTCTGCCGCTGCTGGGTATCTGGGCCTGGCCATGGCTGTGTTCTTCA
TGTGTTGATTTTATTTGACCCCTGGAGTGGTGGGTCTCATCTTTCCCATCTCGCCTGAGAGCGGCTGAGGGCTGC
CTCACTGCAAACTCCTCCCCACAGCGTCAGTGAAAGTCGTCTTGTCTCAGAATGACCAGGGGCCAGCCAGTGTCT
GACCAAGGTCAAGGGGCAGGTGCAGAGGTGGCAGGGATGGCTCCGAAGCCAGAAATGCCTTAAACTGCAACGTCC
CGTCCCTTCCCCACCCCCATCCCATCCCCACCCCCAGCCCCAGCCAGTCTCCTAGGAGCAGGACCCGATGAAG
CGGGCGGCGGTGGGGCTGGGTGCCGTGTTACTAACTCTAGTATGTTTCTGTGTCAATCGCTGTGAAATAAAGTCT
GAAAACTTT

5/6881
FIGURE 5

MLNSSLMRITLRLNLEEVEFCVEDKPGTHFTPVPPPTPDACRGMLCGFGAVCEPNAEGPGRASCVCCKKSPCPSVVA
PVCGSDASTYSNECELQRAQCSQQRRIRLLSRGPCGSRDPCSNTVCSFGSTCARSADGLTASCLCPATCRGAPEG
TVCGSDGADYPGECQLLRRACARQENVFKKFDGPCDPCQALPDPSSRCRVNPRTRRPEMLLRPESCPARQAPVC
GDDGVITYENDCVMGRSGAARGLLLQKVRSGQCQGRDQCPEPCRFNAVCLSRGRPRCSCDRVTCDGAYRPVCAQD
GRTYDSDCWRRQQAECRQQRAIPSKHQGPCDQAPSPCLGVQCAFATCAVKNGQAACECLQACSSLYDPVCGSDGV
TYGSACELEATACTLGREIQVARKGPCDRCGQCRFGALCEAETGRCVCPSECVALAQPVCGSDGHTYPTSECMLHV
HACTHQISLHVASAGPCETCGDAVCAFGAVCSAGQVCPCREHPPPGPVCGSDGVITYGSACELREAACLQQTQIE
EARAGPCEQAECGSGSGSGEDGDCEQELCRQRGGIWDDESEDGPCVCDFFSCQSVPGSPVCGSDGVITYSTECCLK
KARCESQRGLYVAAQGACRGPTFAPLPPVAPLHCAQTPYGCCQDNITAAARGVGLAGCPSACQCNPHGSYGGTCDP
ATGQCSCRPGVGGRLRCDRCEPGFWNFRGIVTDGRSGCTPCSCDPQGAVRDDCEQMTGLCSCKPGVAGPKCGQCPD
GRALGPAGCEADASAPATCAEMRCEFGARCVEESGSAHCVCPLMTCPEANATKVCGSDGVITYGNECQLKTIACRQ
GLQISIQSLGPCQEAVAPSTHTPSASVTVTTPGLLLSQALPAPPALPLAPSSTAHSQTTTPPPSSRPRTTASVPR
TTVWPVLTVPPTAPSPAPSLVASAFGESGSTDGSSDEELSGDQEASGGGSGGLEPLEGSSVATPGPPVERASCYN
SALGCCSDGKTPSLDAEGSNCPATKVFQGVLELEGVGQELFYTPEMADPKSELFGETARSIESTLDDLFRNSDV
KKDFRSVRLRDLGPGKSVRAIVDVHFDPTTAFRAPDVARALLRQIQVSRRRSLGVRRPLQEHVRFMDFDWFFAFI
TGATSGAIAAGATARATTASRLPSSAVTPRAPHPSHTSQPVAKTTAAPTRRPPTTAPSRVPGRRPPAPQQPPKP
CDSQPCFHGGTCQDWALGGGFTCSCPAGRGGAUCEKVLGAPVPAFEGRSFLAFPTLRAHYTLRLALEFRALEPQG
LLLYNGNARGKDFLALALLDGRVQLRFDTGSGPAVLTSAVPVEPGQWHRLRLSRHWRRTLSVDGETPVLGESPS
GTDGLNLDTDLFVGGVPEDQAAVALERTFVGAGLRGCIRLLDVNNQRLELGIGPGAATRGSGVGKCGDHPCLPNP
CHGGAPCQNL EAGRFHCQCPPGRVGFCADEKSPCQPNPCHGAAPCRVLP EGGAQCECPLGREGTFCQTASGQDG
SGPFLADFN GFSHLELRGLHTFARDLGEKMALEVVF LARGPSGLLLYNGQKTDGKGD FVS LALRDRRLEFRYDLG
KGA AVIRSREPVT LGAWTRVSLERNGRKGALRVGDGPRVLGESPVPH TVLNLKEFLYVGGAPDFSKLARAAAVSS
GFDGAIQLVSLGGRQLLTPEHVL RQVDVTSFAGHPCTRASGHPCLNGASCVPREAA YVCLCPGGFSGPHCEKGLV
EKSAGD VDTLAFDGRTFVEYLN AVTESEKALQSNHFELSLRTEATQGLVLWSGKATERADYVALAIVDGH LQLSY
NLGSQPVVLRSTVPVNTNRWLRVVAHREQREGSLQVGNEAPVTGSSPLGATQLD TDGALWLGGLP ELPVGPALPK
AYGTGFV GCLRDVVVGRHPLHLL EDAVTKEP LRPCPTP

6/6881
FIGURE 6

ACAGAGACCCCGAGTTCTACAAGTTCTGCAGGAGAATGACCAGAGCCTGCTAAACTTCAGCGACTCGGACAGCT
CTGAGGAGGAAGAGGGGCCGTTCCACTCCCTGCCAGATGTGCTGGAGGAAGCCAGTGAGGAGGAGGATGGAGCGG
AGGAAGGAGAAGATGGGGACAGAGTCCCCAGAGGGCTGAAGGGGAAGAAGATTCTGTTCTGTGACCGTTCGCCA
TGTTGAGAGATGGAAGCAGGCAGCAAAGCAACGCCTCACTCCAAAGCTGTTCCATGAAGTGGTACAGGCGTTCC
GAGCAGCTGTGGCCACCACCCGAGGGGACCAGGAAAGTGCTGAGGCCAACAAATTCCAGGTCACGGACAGTGCTG
CATTCAATGCTCTGGTTACCTTCTGCATCAGAGACCTCATTGGCTGTCTCCAGAAGCTGCTGTTTGAAAGGTGG
CAAAGGATAGCAGCAGGATGCTGCAGCCGTCCAGCAGCCCGCTCTGGGGGAAGCTTCGTGTGGACATCAAGGCTT
ACCTGGGCTCGGCCATACAGCTGGTGTCTGTCTGTCGGAGACGACGGTGTGGCGGCCGTGCTGCGGCACATCA
GCGTGCTGGTGCCCTGCTTCCTGACCTTCCCCAAGCAGTGCCGCATGCTGCTCAAGAGAATGGTGATCGTATGGA
GCACTGGGGAAGAGTCTCTGCGGGTGCTGGCTTTCTGGTCTCTCAGCAGAGTCTGCCGGCACAAGAAGGACACTT
TCCTTGGCCCCGTCTCAAGCAAATGTACATCACGTATGTGAGGAAGTCAAGTTCACCTCGCCTGGTGCCCTCC
CCTTCATCAGTTTCATGCAGTGACCTTGACGGAGCTGCTGGCCCTGGAGCCGGGTGTGGCCTACCAGCACGCCT
TCCTCTACATCCGCCAGCTCGCCATACACCTGCGCAACGCCATGACCACTCGCAAGAAGGAAACATACCAGTCTG
TGTAACAAGTGGCAGTATGTGCACTGCCTCTTCCTGTGGTGCCGGGTCTGAGCACTGCGGGCCCCAGCGAAGCCC
TCCAGCCCTTGGTCTACCCCTTGCCCAAGTCATCATTGGCTGTATCAAGCTCATCCCCACTGCCCGCTTCTACC
CGCTGCGAATGCACTGCATCCGTGCCCTGACGCTGCTCTCGGGGAGCTCGGGGGCCTTCATCCCGGTGCTGCCTT
TCATCCTGGAGATGTTCCAGCAGGTGCACTTCAACAGGAAGCCAGGGCGCATGAGCTCAAGCCCATCAACTTCT
CCGTGATCCTGAAGCTGTCCAATGTCAACCTGCAGGAGAAGGCGTACCGGGACGGCCTGGTGGAGCAGCTGTACG
ACCTCACCTTGGAGTACCTGCACAGCCAGGCACACTGCATCGGCTTCCCGGAGCTGGTGCTGCCTGTGGTCTCTGC
AGCTGAAGTCGTTCTCCGGGAGTGCAAGGTGGCCAACTACTGCCGGCAGGTGCAGCAGCTGCTTGGGAAGGTTT
AGGAGAAGTTCGGCATACTCTGCAGCCGCCGCCAGAGGGTTTCCTTCGGCGTCTCTGAGCAGCAGGCAGTGGAAG
CCTGGGAGAAGCTGACCCGGGAAGAGGGGACACCCCTGACCTTGTACTACAGCCACTGGCGCAAGCTGCGTGACC
GGGAGATCCAGCTGGAGATCAGTGGCAAAGAGCGGCTGGAAGACCTGAACTTCCCTGAGATCAAACGAAGGAAGA
TGGCTGACAGGAAGGATGAGGACAGGAAGCAATTTAAAGACCTCTTTGACCTGAACAGCTCTGAAGAGGACGACA
CCGAGGGATTCTCGGAGAGAGGGATACTGAGGCCCTGAGCACTCGGCATGGGGTGGAAGACGATGAAGAGGACG
AGGAGGAGGGCGAGGAGGACAGCAGCAACTCGGAGGATGGAGACCCAGACGCAGAGGCGGGGCTGGCCCCCTGGGG
AGCTGCAGCAGCTGGCCCAGGGGCCGGAGGACGAGCTGGAGGATCTGCAGCTCTCAGAGGACGACTGAGGCAGCC
CATCTGGGGGGCCTGTAGGGGCTGCCGGGCTGGTGGCCAGTGTTCACCTCCCTGGCAGTCAGGCCTAGAGGCT
GGCGTCTGTGCAGTTGGGGGAGGCAGTAGACACGGGACAGGCTTTATTATTATTTTTCAGCATGAAAGACCAAA
CGTATCGAGAGCTGGGCTGGGCTGGGCTGGTGTGGCTGCTGAAGCCCCACAGCTGTGGGCTGCTGAAGTCAGCTC
CGCGGGGGAGCTGACCTGACGTCAGCAGACCGAGACCAGTCCCAGTTCCAGGGGGAGGCCTGCAGGCCCTGGC
CCCTTCCACCACCTCTGCCCTCCGTCTGCAGACCTCGTCCATCTGCACCAGGCTCTGCCTTCACTCCCCAAGTC
TTTGAAAATTTGTTCTTTCTTTGAAGTCACATTTTCTTTTAAATTTTTTGTGTTTGCATCCGAAACCGAAAGA
AATAAAGCGGTGGGAGGCAGGGCCATTGTGTTG

7/6881
FIGURE 7

MAAAGSRKRRLAELTVDEF LASGFDSESESESESENSPQAETREAREEAARSPDKPGGSPSASRRKGRASEHKDQLSR
LKDRDPEFYKFLQENDQSLLNFSDSDSSEEEEGPFHSLPDVLEEASEEEDGAEEGEDGDRVPRGLKGKKNSVPVT
VAMVERWKQAAKQRLTPKLFHEVVQAFRAAVATTRGDQESAEANKFQVTD SAAFNALVTFCIRD LIGCLQKLLFG
KVAKDSSRMLQPSSSPLWGKLRVDIKAYLGSATQLVSC LSETTVLAAVLRHISVLVPCFLTTFPKQCRMLLKRMVI
VWSTGEESLRVLAFLVLSRVCRHKKDTFLGPVLKQMYITYVRNCKFTSPGALPFISFMQWTLTELLALEPGVAYQ
HAFLYIRQLAIHLRNAMTTRKKETYQSVYNWQYVHCLFLWCRVLSTAGPSEALQPLVYPLAQV IIGCIKLIPTAR
FYPLRMHCIRALTLLSGSSGAFIPVLPFILEMFQQVDFNRKPGRMSSKPINFSVILKLSNVNLQEKAYRDGLVEQ
LYDLTLEYLHSQAHCIGFPELVLPVVLQLKSFLRECKVANYCRQVQQLLGKVQENSAYICSRQRVSFGVSEQQA
VEAWEKLTREEGTPLTLYYSHWRKLRDREIQLEISGKERLEDLNFPEIKRRKMADRKDED RKQFKDLFDLNSSEE
DDTEGFSERGILRPLSTRHGVEDDEEDEEEGEEDSSNSE DGDPAEAGLAPGELQQLAQGPEDLEDLQLSEDD

8/6881
FIGURE 8

GTGTACGAAAGAGAAACCCGGAGGGCGCCGGGGACTGGGCCGGGGTCTGCAGGGCTCAGCTGAGCCCATGAGCTC
CCAGAGCTAACCCTGAACACCCAGGCGGGCAAAGGGCTGATGTCGGTAGTCCCCATCCTGGAGGGGAGGCTCT
GCGCATCTGCTCCTGGC**ATG**GCGCTGCGGCACCTCGCCCTCCTGGCTGGCCTTCTCGTGGGAGTCGCCAGCAAGT
CCATGGAGAACACGGCCCAGCTGCCCCAGTGCTGTGTGGATGTGGTGGGCGTCAACGCCAGCTGCCAGGCGCAA
GTCTGTGTGGTCCAGGCTGTTACAGGCGCTGGAACGCGGACGGGAGCGCCAGCTGCGTCCGCTGTGGGAACGGAA
CCCTCCCAGCCTACAACGGCTCCGAGTGTTAGAAAGCTTTGCTGGCCCGGGTGCGCCATTCCCCATGAACAGAAGCT
CAGGGACCCCCGGGCGGCCACATCCTGGGGCTCCGCGCGTGGCCGCTCCCTCTTCTGGGCACGTTCTTCATTA
GCTCCGGCCTCATCCTCTCCGTAGCTGGGTTCTTCTACCTCAAGCGCTCCAGTAAACTCCCCAGGGCCTGCTACA
GAAGAAACAAAGCTCCGGCCCTGCAGCCTGGCGAAGCCGCTGCAATGATCCCCCGCCACAGTCCCTCAGTACGGA
AGCCGCGCTACGTCAGGCGGGAGCGGCCCTGGACAGGGCCACGGATCCCGCTGCCTTCCCGGGGGAGGCCCCGTA
TCAGCAATGTC**TGA**CCTGGAGGCGGAGACCACGCCACGCACTTGGCGGCAGGGACCCGGAGGCCGACCCCTTGGC
GGGAACCAGCACAAAGTGTTGGCATCGCCCGGCGCCCGGGACAGTCTGGGCACAGCCTCGGCTCTGGGTCCCTC
CGCCTCCCAGCGACGGACGCCAAAGGGTCCCGGGCCGCTGAGGCTCCTCCCCACCACAGCCATCTCGTTTATCG
GACCAGGAGCAGGCATCCATGAGACCTCAGAGCTTCAGATCGAGGCCTTGGGGGGTCCGGGCCCCCCCCAGGAAAC
ACGGTGAGGCCCCAGCGCCTGCAGCCAAAGCTGGCACGATCTATGGGGCAGGTGCCGCTCTGCCTAGAAAAGCCA
GGGGCTCTGCTGCCGTGCCCTCCAGAGCCACAGCGGGCAGGACTCCTCCAGCACCACCACACCCAGTGGCCCGA
GACCCCTCTGAGAACAGTGAGGCTGGTCCTCGTGCCGTTCCAGCCGGTGCCCGGCCAGTGGGGAGGACACAGCCT
AGGAACCAGCTGCCTGAGACCAGGGTGCTCTGGGCTGTCTCCCGCTGGCGGAGACCCCAAGCACGCAGCCAC
CCATTTCCGGAGCTGCAGGATAGAGCTTCTCTTGATCTCTGTTTTTAAGCAGAAATTCATTGTGCTGAAAAGTC
CTCCAGAGCTCTGTGGCCCCGCTCGGATCCGCTGGACCCCCATGCCCTGGCTGATCCCTGCCACGTGGGGCAGGC
CCACATCTAACCCCCACAAGTCACTGCCTCACTGCACCTGCCAAGGCTGCCCTGGCGCTGAGTCTTGGGGTCCCT
CCCGGAGTTCTGGGAGAAAGGCGCCGTCGTGGCCGCTCCCGCACGCCAGGCCCGGGCTCCACCGTGGGTCTCA
GACGCCCTGCGGCACCGGCACCGTCTGCTTTAGCATGGGACCCCCATCTGAGGGGTGGCCTGGCCTTCGGGGTCC
CCACGCTCCTTTGCGAAGTCCACTGTGGGTGCCATCATGGTCTCCGGGACCTGGGCCAGCGGAACGTGGGGGCA
CTGGGTGTGCTGATATAAAGTCGGCATTACTCAAAAAAAAAAAAAAAAAAAAAA

9/6881
FIGURE 9

MALRHLALLAGLLVGVASKSMентаQLPECCVDVVGVNASCPGASLCGPGCYRRWNADGSASCVRCGNGTLPAYN
GSECRSFAGPGAPFFPMNRSSGTPGRPHPGAPRVAASLFLGTFFISSGLILSVAGFFYLKRSSKLPRACYRRNKAP
ALQPGEEAAMIPFPQSSVRKPRYVRRERPLDRATDPAAFPGEARISNV

10/6881
FIGURE 10

AAAAAAAAAAAAAAAAACCGGCTCGCGGCGCGTGGAGGCTGCTCCCAGCCGCGCGAGTCAGACTCGGGTGGGGG
TCCCGGCGGCGGTAGCGGCGGCGGCGGTGCGAGC**ATGT**CGTGGCTCTTCGGCATTAAACAAGGGCCCCAAGGGTGA
AGGCGCGGGGCGCGCCGCCCTTTGCCGCCCGCGCAGCCCGGGGCCGAGGGCGGCGGGGACCGCGGCTTGGGAGA
CCGGCCGGCGCCCAAGGACAAATGGAGCAACTTCGACCCACCGGCCCTGGAGCGCGCCGCCAAGGCGGCGCGCGA
GCTGGAGCACTCGCGTTATGCCAAGGACGCCCTGAATCTGGCACAGATGCAGGAGCAGACGCTGCAGTTGGAGCA
ACAGTCCAAGCTCAAAGAGTATGAGGCCGCCGTGGAGCAGCTCAAGAGCGAGCAGATCCGGGCGCAGGCTGAGGA
GAGGAGGAAGACCCTGAGCGAGGAGACCGGCAGCACCAGGCCAGGGCCAGTATCAAGACAAGCTGGCCCCGGCA
GCGCTACGAGGACCAACTGAAGCAGCAGCAACTTCTCAATGAGGAGAATTTACGGAAGCAGGAGGAGTCCGTGCA
GAAGCAGGAAGCCATGCGGCGAGCCACCGTGGAGCGGGAGATGGAGCTGCGGCACAAGAATGAGATGCTGCGAGT
GGAGGCCGAGGCCCGGGCGCGCGCCAAGGCCGAGCGGGAGAATGCAGACATCATCCGCGAGCAGATCCGCCTGAA
GGCGGCCGAGCACCGTCAGACCGTCTTGGAGTCCATCAGGACGGCTGGCACCTTGTTTGGGGAAGGATTCCGTGC
CTTTGTGACAGACTGGGACAAAGTGACAGCCACGGTGGCTGGGCTGACGCTGCTGGCTGTTGGGGTCTACTCAGC
CAAGAATGCCACGCTTGTCGCCCGGCCGCTTCATCGAGGCTCGGCTGGGGAAGCCGTCCCTAGTGAGGGAGACGTC
CCGCATCACGGTGCTTGAGGCGCTGCGGCACCCCATCCAGGTCAGCCGGCGGCTCCTCAGTCGACCCACAGGACGC
GCTGGAGGGTGTTGTGCTCAGTCCCAGCCTGGAAGCACGGGTGCGCGACATCGCCATAGCAACAAGGAACACCAA
GAAGAACCGCAGCCTGTACAGGAACATCCTGATGTACGGGCCACAGGCACCGGGAAGACGCTGTTTGCCAAGAA
ACTCGCCCTGCACTCAGGCATGGAATACGCCATCATGACAGGCGGGGACGTGGCCCCCATGGGGCGGGAAGGCGT
GACCGCCATGCACAAGCTCTTTGACTGGGCCAATACCAGCCGGCGCGGCTCCTGCTCTTTGTGGATGAAGCGGA
CGCCTTCCTTCGGAAGCGAGCCACCGAGAAGATAAGCGAGGACCTCAGGGCCACACTGAACGCCTTCCTGTACCG
CACGGGCCAGCACAGCAACAAGTTCATGCTGGTCTTGCCAGGCAACCAACCAGAGCAGTTCGACTGGGCCATCAA
TGACCGCATCAATGAGATGGTCCACTTCGACCTGCCAGGGCAGGAGGAACGGGAGCGCCTGGTGAGAATGTATTT
TGACAAGTATGTTCTTAAGCCGGCCACAGAAGGAAAGCAGCGCCTGAAGCTGGCCAGTTTGACTACGGGAGGAA
GTGCTCGGAGGTGCTCGGCTGACGGAGGGCATGTGCGGCGGGAGATCGCTCAGCTGGCCGTGCTCCTGGCAGGC
CACGGCGTATGCCTCCGAGGACGGGGTCTGACCGAGGCCATGATGGACACCCGCGTGCAAGATGCTGTCCAGCA
GCACCAGCAGAAGATGTGCTGGCTGAAGGCGGAAGGGCTGGGCGTGGGGACGAGCCTTCCCCATCC**TG**AGTCCA
CAGGGAGATCCACAGCTCACGGAGCCTGGCCGCGGACCCCTCCACCCCTGCCTTGCCGGCCCCCTGCACATTTAG
GATATGCTCCTGGGTGGGACTGGGCTGTGCCCAGGGCCTCTGTCCCCCAGGATGTCTTGTTGGTGCGGGTTCGGCC
GTTCTGCCCCCAGGGCACCCCTGTTGTAGGCACTGGCTAGGGAGGGGCAGGCCTCCTTCCTGCCCCCTCGAGAC
ACTCTTGGGAGATGCATTTTCCGTCTGGCTCACAGGGGGAGGGTGAGGCTTTGCACCCACAGCCCTGCCAGGCC
ACTGTGAGGGTGGGTGCTGGCTGACCCCCCGGGGCAGCAGGAGCCAGGCAGGTGATGTCTTTGTTCTCGGCTCCC
ACAGCAGAGCCAGGTGAGGGGGCGCCTGCCAGGGCCAGACCCAGGTGGGGCAGCCTGAACCCTGCTTCCCCCTGT
GGCCGGCATGCCCCGATCTTTCACACACTGGTGACCCTGAGAGAGGAGGGAGGAGGAACCTGGCGGGGGTGTCT
GAGGCCGCACTGTCAGCTGGCCGGTCCAAGCCTGTGGCTGGAGCTGGGGTCTGTTTACCTAATAAAGTCCACAG
GTGCCTCATT

11/6881
FIGURE 11

MSWLFGINKGPKGEGAGPPPLPPAQPGAEGGGDRGLGDRPAPKDKWSNFDPTGLERAAKAARELEHSRYAKDAL
NLAQMQEQTLLQLEQQSKLKEYEAAVEQLKSEQIRAQAEERRKTLSEETRQHQAQYQDKLARQRYEDQLKQQQL
LNEENLRKQEEVQKQEQAMRRATVEREMELRHKNEMLRVEAEARARAKAERENADIIREQIRLKAAEHRQTVLES
IRTAGTLFGEGFRAFVTDWDKVTATVAGLTLLAVGVYSAKNATLVAGRFIEARLGKPSLVRETSRITVLEALRHP
IQVSRRLLSRPQDALEGVVLSPSLEARVRDIAIATRNTKKNRSLYRNILMYGPPGTGKTLFAKKLALHSGMDYAI
MTGGDVAPMGREGVTAMHKLFDWANTSRRGLLLFVDEADAF LRKRATEKISED LRATLNAFLYRTGQHSNKFMLV
LASNQPEQFDWAINDRINEMVHFDLPGQEERERLVRMYFDKYVLKPATEGKQRLKLAQFDYGRKCSEVARLTEGM
SGREIAQLAVSWQATAYASEDGVLTEAMMDTRVQDAVQQHQQKMCWLKAEGPGRGDEPSPS

12/6881
FIGURE 12

ATCAGTTCTCGCCCGTCTGGGCGTGGGCGTGGCCGGCGTGGCTGCTCGGGACCACCCGAACCCGCGGCCATGGCC
CCGGCCCGCCGAGCCCCCGGAGGTGATCCGCGCGGCGCAGAAGGACGAGTACTACCGCGGTGGGCTGCGGAGC
GCGGCGGGCGGCCCTGCACAGCCTGGCGGGTGCGAGGAAGTGGCTGGAGTGGAGGAAGGAGGTTGAGCTGCTC
TCAGATGTGGCCTACTTTGGCCTCACCACACTTGCAGGCTACCAGACCCTGGGGGAGGAGTACGTCAGCATCATC
CAGGTGGACCCATCGCGGATACATGTGCCCTCCTCGCTGCGCCGTGGCGTGCTGGTGACGCTGCATGCCGTCTTG
CCCTACCTGCTGGACAAGGCCCTGCTCCCCCTGGAGCAGGAGCTGCAGGCTGACCCCGACAGTGGGCGACCCCTG
CAGGGGAGCCTGGGGCCAGGTGGGCGTGGCTGCTCAGGGGCGCGGCGCTGGATGCGTCAACACACGGCCACCCCTG
ACTGAGCAGCAGAGGAGGGCGCTGCTGCGGGCGGTCTTCGTCTCAGACAGGGCCTCGCCTGCCTCCAGCGGCTA
CATGTTGCCTGGTTTTACATCCACGGTGTCTTCTACCACCTGGCCAAGAGGCTCACGGGGATCACGTACCTCCGT
GTCCGCAGCCTGCCCCGAGAGGACCTGAGGGCCCGTGTAGCTACAGGCTGCTGGGGGTTCATCTCACTGCTGCAC
CTGGTGCTGTCCATGGGGCTGCAGCTGTACGGTTTTAGGCAGCGGCAGCGAGCCAGGAAGGAGTGGAGGCTGCAC
CGCGGCCTGTCTCACCGCAGGGCCTCCTTGGAGGAGAGAGCCGTTTCCAGAAACCCCTGTGCACCCTGTGCCTG
GAGGAGCGCAGGCACCCAACAGCCACGCCCTGCGGCCACCTGTTCTGCTGGGAGTGCATCACCGCGTGGTGCAGC
AGCAAGGCGGAGTGTCCCCTCTGCCGGGAGAAGTTCCTCCCCAGAAGCTCATCTACCTTCGGCACTACCGCTGA

GCCGGCGCCCGGGTGGGCCTGGACACAGATGACCTCTACGGGAGTCTGAACGCCAAGATTTAGTCTCAGGATTAA
CCTTGCTTGACAGAAAGTTAGAACACTCTCAGTTTTTTGTGATGTAAGATACTAACCTAGCCACCCTGGGAGAGA
ACAGAAAGCTGTCCCTGGCTGCGCTTTCTCAGCCCTGGGAGGGGCGCCTGAACCCAGAACATTTCCCTAACCCCA
ACCTGGTAGGACTCAGCCACTTCTTCAGGAATTTCACTTATTTGGACGGGATTTTAGGTTTCCCTCCCTTCCCCA
AACCATACAGTTGAGAAGTAATTCAGAAAGTAGGCCAGAAACACTTTATTCGTTTATATTGTGAGAAAACAGCCC
CATCAGGCTTGTTGTTAAGGCAATGGACTGAATGAGTGCCTGCTGGGTGGGGTGGGGCACGGAGGCTGGCGGGTTG
CTTCAGCCAGTGCAGTGAGAACAGCAGCCCCACGGCCCCATGGGAGGCGGCGCTGCTCTCCCCGAGGGCGGCTGG
GCAGAGCACATCCCCAGGACTTGATGACCACACGGGGCAGAGAGAAACCAACCAAGGCCAGCACCTCCGTGCGA
AGCATTTGGCACACACACCTTCAATACACGTCAAGGTCGCTTCCAGTTTTAGAAAAACAGAAATCTGCATCTCAGC
CTGAGACGCACAGAGAGGTCTCTTCTGACCCAGACGCACTCACGAGCCAGGTCTTGGGGGTATGGGGGCTGCCA
GGGGCGCCCGAGCCCTCTCTGGGGGGCCTGCTGGGCAGGCGACCTGCTGACCCACGGTCACTGCTGTGTTTACG
CCCTCAGCTCGGCCCCAGCCTATTTCCCGCCTCCATTTGATGTTTCCAGGTTTTCAAAACTGCATTTAACCTGCG
CCAGAGAGTTACCGTAGGCATCTTTAATAAACTAACTCCAGCAAAAAAAAAAAAAA

13/6881
FIGURE 13

MAPAAASPPEVIRAAQKDEYYRGGLRSAAGGALHSLAGARKWLEWRKEVELLSDVAYFGLTTLAGYQTLGEEYVS
IIQVDPSRIHVPSSLRRGVLVTLHAVLPYLLDKALLPLEQELQADPDSEGRPLQGSLGPGGRGCSGARRWMRHHTA
TLTEQQRRALLRAVFVLRQGLACLQRLHVAWFYIHGVFYHLAKRLTGITYLRVRSPLGEDLRARVSYRLLGVISL
LHLVLSMGLQLYGFRQQRARKEWRLHRGLSHRRASLEERAVSRNPLCTLCEERRHPTATPCGHLFCWECITAW
CSSKAECPLCREKFPPQKLIYLRHYR

14/6881
FIGURE 14

GGGCGGCGAGTGGGGAGCGGGGCCGGGAGTGGAGCAGCCGCCGCGGGCGGGACTGGACCGAGCCTCGCCGGCGCGC
ACCTGCCCCGAGCGCCCCGCGGAGCGCGCAGCGCGGCCCGAGCGCGACGACCTGCCGAGCGGGCGGCCGAGGCGGGCG
GTGTGGGCGCGTCAAGGCCGCGACGAGGGCGCTGAGACAAATTTACATGTATTGGAGACCAGACCAGAAGCCCTTC
TGAATTAAGATCTCACATTCTTGAAGGTGGCATTGAAGAGCACTAAGATCGGAAGATGAGTGAGCTTGACCAGTT
ACGGCAGGAGGCCGAGCAACTTAAGAACCAGATTTCGAGACGCCAGGAAAGCATGTGCAGATGCAACTCTCTCTCA
GATCACAAACAACATCGACCCAGTGGGAAGAATCCAAATGCGCACGAGGAGGACACTGCGGGGGCACCTGGCCAA
GATCTACGCCATGCACTGGGGCACAGACTCCAGGCTTCTCGTCAGTGCCTCGCAGGATGGTAAACTTATCATCTG
GGACAGCTACACCACCAACAAGGTCCACGCCATCCCTCTGCGCTCCTCCTGGGTGATGACCTGTGCATATGCCCC
TTCTGGGAACATATGTGGCCTGCGGTGGCCTGGATAACATTTGCTCCATTTACAATCTGAAAACCTCGTGAGGGGAA
CGTGCGCGTGAGTCGTGAGCTGGCAGGACACACAGGTTACCTGTCTGTGCTGCCGATTCTTGATGACAATCAGAT
CGTCACCAGCTCTGGAGACACCACGTGTGCCCTGTGGGACATCGAGACCGGCCAGCAGACGACCACGTTTACCGG
ACACACTGGAGATGTCATGAGCCTTTCTCTGTCTCTGACACCAGACTGTTTCGTCTCTGGTGCTTGTGATGCTTC
AGCCAAACTCTGGGATGTGCGAGAAGGCATGTGCCGGCAGACCTTCACTGGCCACGAGTCTGACATCAATGCCAT
TTGCTTCTTTCCAAATGGCAATGCATTTGCCACTGGCTCAGACGACGCCACCTGCAGGCTGTTTGACCTTCGTGC
TGACCAGGAGCTCATGACTTACTCCCATGACAACATCATCTGCGGGATCACCTCTGTCTCCTTCTCCAAGAGCGG
GCGCCTCCTCCTTGCTGGGTACGACGACTTCAACTGCAACGTCTGGGATGCACTCAAAGCCGACCGGGCAGGTGT
CTTGGCTGGGCATGACAACCGCGTCAGCTGCCTGGGCGTGACTGACGATGGCATGGCTGTGGCGACAGGGTCTCTG
GGATAGCTTCTCAAGATCTGGAACAAACGCCAGTAGCATGTGGATGCCATGGAGACTGGAAGACCATTCCAACCT
TGGACGCGTTACCATGAGAGCATATCCTATCCAACCGTACTAACGTGGACACCCTACACCTCCCCCTCAGAACTTC
AAAAGGGCAAGATCTTTTTTCTTCACTTATTGCTGAAACCAAGAGCACAATTCCCATTGAGAGAAAGATCTCTG
TGCTGTAAACTAAAACAAATTGTGCATTCCCTCCGGGGCCATCGTCTTTGTTTTCTTTTTTGTCTTGAATGAATT
TTAAAGGAAATATATAATAAAAAATGTTAACCAGAAGGTAAACTTGAGTGTAAATTGTCAGACAGACACACTTTTC
CACCAGTGTATTTGAATTTTAGACCAGTGACCTGTTTTGTGGCATTTCATGCAAAACATGCTGAGGGCTTTGTTTC
ATCTGGTCATCGTGTCCAAATTTAGTCATGTTTGTAGCAAGATTTTGAAGCATTTCATATTTCTTTTTTAAAT
GTATTCCTTTGTGTTCAACAGTTAATCAAAACCAGAGAGTCTAGGGCAGCCTCTCTGATGTTGTCAATGATGTAA
ATTAGTCCCTGGTTTTTAATTTTCTGTCTGATGTACAGATCATTGTTGCACACAAACGTGGCATAGAAAAGAA
CATGTTTCAAGCCATGGGGCCAAGCACATGCGGGGACGGTCTCAAATGCGTGATCAGAGAATCCTTCACCTTTG
CTGAAAAGTGAGCTCAGATCCAGCACCATGTTCCCTCCTGACCCATCCTGTCTATCTTCTCAGTTGAGTTTTTAAT
CTCACTTTGGGTTTCTTGTGAAGTTGGAGGGAAGTTTATAATAGCCTAACACTACCCACCCCCAACCTAGGAGG
AACCTCTGTTTTCAAGAGAGATGCCTGTCTGTGCTTGGATAGTCAGTCAATTATTTGTGTATGAAACAATGTAC
AAATCAATGTTTTGAAAATAATGATCTCAGACTTTCTAAGTTAAATTTTAAAAATTTTGATTGTTTGCATATTG
GGTGGGTTTACTCTTAGAATCGCATGCTGTAGAAATGCTCAAAAGTGCATATGGGACTCAGTCCTTAGGTGTTCT
TTTTCTTTTAAGAAATAACCTCTTACAGTTGTAACCATTGCGGCTCTGTCCACTTCTCGTTGCTGCTCTGTGGCA
CATATCGGAAGCAGTACAGCGCGCGGCTCTACACGCTTGGGTAGCGGGATAAGTCACTGTTTTCTTTATTTCTTT
AAAAAAAAAAAAAGTTCTGTTGCAACGACTGCTGTTGGATTCTGAGGGTGGGGAGGGAGAGAGAGGGAGGGAGAG
GGAGTGAAGAGCCTGCCCTCCTATATGGATTCTTCAGGGCCCTCCACATCTGAGGTGGCTCATTCCCATCACACA
CAGATTGTCTGGTGTTCATTTCAAGGCCAGTGTTTCAGCAGCAGCGTTTGGAAAGCAGGTTCTGTGGGACCCCCC
GCCCCGCCCCCGCACTCCTTCATAGCAGCAGTAGTGGCTTCTCCATCCTGTTTTCTGCAACATTTCTATACAAA
CTGTGCTGTGACCTTGCGGTAGGCCTGGATCTGGCAAAGAGAATACAAATGAAACCCCTTCTTTCTTTTCCGTC
CAACAACCTCTGTAGAGCTCTCTGCACCCCTTACCCCTTTCCACCTTTTGTATTTAATTTTAAAGTCAGTGTACTGC
AAGGAAGCTGGATGCAAGATAGATACTATATTAACTGTACTGTTATTTAAGATGTAATAAAGCAGTTTGACATG

15/6881
FIGURE 15

ATCAAACCACCCCAGCAAATGTCTCGGAAAGAAAAAGTTCATCACAGAAAAGATGAAAAGAGAAAAGAAAAATGT
AGGCATCATAGCCATTCAGCAGAAGGGGGGAAGCATGCTAGAGTGAAAGAAAGAGAGCACGAACGTCGGAAACGA
CATCGAGAAGAACAGGATAAAGCTCGCCGGGAATGGGAAAGACAGAAGAGAAGGGAAATGGCAAGGGAGCATTCC
AGGAGAGAAAGGGACCGCTTGAGCAGTTAGAAAGGAAGCGGGAGCGGGAGCGCAAGATGCGGGAGCAGCAGAAG
GAGCAGCAGTCAAGAAGATGACCTTCAGCGAGCACCCCTACAACAACCTCCGCAAGCGCTTCGGGGCTCTGCTCT
CAGACCAGGGCTTCGACCTCATGAACAAGTTCCTGACCTACTTCCCCGGGAGGAGGATCAGCGCTGAGGACGGCC
TCAAGCATGAGTATTTCCGCGAGACCCCCCTCCCCATCGACCCCTCCATGTTCCCCACGTGGCCCGCCAAGAGCG
AGCAGCAGCGTGTGAAGCGGGGCACCAGCCCGAGGCCCCCTGAGGGAGGCCTGGGCTACAGCCAGCTGGGTGACG
ACGACCTGAAGGAGACGGGCTTCACCTTACCACCACGAACCAGGGGGCCTCTGCCGCGGGCCCCGGCTTCAGCC
TCAAGTTCTGAAGGTCAGAGTGGACCCCGTCATGGGG

16/6881
FIGURE 16

MGKTEEKGNKGAFQERKGPLGAVRKEAGAGAQDAGAAEGAAVKKMTFSEHPYNNLRKRFGALLSDQGFDLMNKF
LTYFPGRRI SAEDGLKHEYFRETPLPIDPSMFPTWPAKSEQQRVKRGTSPRPPEGGLGYSQLGDDDLKETGFHLT
TTNQGASAAGPGFSLKF

17/6881
FIGURE 17

TCGCGCGGAAGCCGCGGTAGGGTGGGAACCCAAGCGGGAGAGCCGCGGGATTTCGGGCCGCCGCC**ATG**CCGTCGT
CCCCGCTGCGGGTGGCGGTGGTGTGCTCGAGCAACCAGAACCGGAGCATGGAGGCGCACAAACATCCTCAGCAAAC
GGGGATTACGCGTCCGATCCTTTGGAACAGGGACTCACGTGAAGCTTCCAGGACCAGCTCCCGACAAGCCCAATG
TTTATGATTTCAAACACATATGACCAGATGTACAATGATCTTCTTAGGAAAGACAAAGAACTCTATACACAGA
ATGGGATTTTACATATGCTGGACAGAAATAAGAGAATCAAGCCCCGGCCAGAAAGATTCCAGAACTGCAAAGACC
TGTTTGATCTGATCCTCACTTGCGAAGAGAGAGTGTATGACCAGGTGGTGGGAAGATCTGAATTCCAGAGAACAGG
AGACCTGCCAGCCCGTGCACGTGGTCAATGTGGACATCCAGGACAACCACGAGGAGGCCACCCTGGGGGCGTTTC
TCATCTGTGAGCTCTGCCAGTGTATCCAGCACACGGAAGACATGGAGAACGAGATCGACGAGCTGCTGCAGGAGT
TCGAGGAGAAGAGTGGCCGCACCTTTCTGCACACCGTCTGCTTCTAC**TGAG**CCCCAGCGCCCGCATGGAGCCGCCT
CTGGAGCTTCCTGTTGTTTCATACTTTTTTCTTCTGACATTTGTTTTTACTTACAGGTGTTCTGCTGGTGACGGT
AGCATTACCCAAATAAACTGTGCATATGAAATGGGAGAGGAGATGCCAAAACGCCAGATGAAAGCAATCAAGTTT
CTTCTTTTCCACTTTTACTTATGAGCGGGATATTGATTACAAAGTTTTTCTTCTTTAACCAAAAAGGAAAGACAA
CGGTTTGTGTGCACTTCCCGACATACCTGTGTCTTCGTGTGCCTGCCTTCCCTCCCTCCTCCCCACCGGGCCGGA
CTGTACAGAGCCCTGCTGCGGCGTGTTAGGAATGACCTGGAATTGTCAATAAACAGATGCTGCTGTCAAAAAAAA
AAAAAAA

18/6881
FIGURE 18

MPSSPLRVAVVCSSNQNRSM EAHNILSKRGFSVRSFGTGTHVKLPGPAPDKPNVYDFKTTYDQMYNDLLRKDKEL
YTQNGILHMLDRNKRIKPRPERFQNC KDLFDLILTCEERVYDQVVEDLNSREQETCQPVHVVNVDIQDNHEEATL
GAFLICELCQCIQHTEDMENEIDELLQEFEEKSGRTFLHTVCFY

19/6881
FIGURE 19

CCTGGCCACCGGCTCGCGGCGCGTGGAGGCTGCTCCCAGCCGCGCCCGAGTCAGACTCGGGTGGGGGTCCCGGCG
GCGGTAGCGGCGGCGGCGGTGCGAGCATGTCGTGGCTCTTCGGCGTTAACAAGGGCCCCAAGGGTGAAGGCGCGG
GGCCGCGCGCCCTTTGCCGCGCGCGCAGCCGGGGCCGAGGGCGGCGGGGACCGCGGTTTGGGAGACCGGCGCG
CGCCCAAGGACAAATGGAGCAACTTCGACCCACCGGCCTGGAGCGCGCCGCCAAGGCGGCGCGCGAGCTGGAGC
ACTCGCGTTACGCCAAGGAGGCCCTGAATCTGGCGCAGATGCAGGAGCAGACGCTGCAGTTGGAGCAACAGTCCA
AGCTCAAAGAGTATGAGGCGCGCGTGGAGCAGCTCAAGAGCGAGCAGATCCGGGCGCAGGCTGAGGAGAGGAGGA
AGACCCTGAGCGAGGAGACCCGGCAGCACCAGGCCAGGGCCCAGTATCAAGACAAGCTGGCCCCGGCAGCGCTACG
AGGACCAACTGAAGCAGCAGCAACTTCTCAATGAGGAGAATTTACGGAAGCAGGAGGAGTCCGTGCAGAAGCAGG
AAGCCATGCGGCGAGCCACCGTGGAGCGGGAGATGGAGCTGCGGCACAAGAATGAGATGCTGCGAGTGGAGACCG
AGGCCCGGGCGCGCCCAAGGCCGAGCGGGAGAATGCAGACATCATCCGCGAGCAGATCCGCCTGAAGGCGTCCG
AGCACCGTCAGACCGTCTTGAGTCCATCAGGACGGCTGGCACCTTGTTGGGGAAGGATTCCGTGCCTTTGTGA
CAGACCGGGACAAAGTGACAGCCACGGTGGCTGGGCTGACGCTGCTGGCTGTCGGGTCTACTCAGCCAAGAATG
CGACAGCCGTCACTGGCCGCTTCATCGAGGCTCGGCTGGGGAAGCCGTCCCTAGTGAGGGAGACGTCCCGCATCA
CGGTGCTGGAGGCGCTGCGGCACCCCATCCAGGTCAGCCGGCGGCTCCTCAGTCGACCCCAGGACGTGCTGGAGG
GTGTTGTGCTTAGTCCCAGCCTGGAAGCACGGGTGCGCGACATCGCCATAGCAACCAGGAACACCAAGAAGAACC
GGGGCCTGTACAGGCACATCCTGCTGTATGGGCCACCAGGCACCGGGAAGACGCTGTTTGCCAAGAACTCGCCC
TGCACTCAGGCATGGACTACGCCATCATGACAGGCGGGGACGTGGCCCCCATGGGGCGGGAAGGCGTGACCGCCA
TGCACAAGCTCTTTGACTGGGCCAATACCAGCCGGCGCGGCCTCCTGCTCTTCATGGATGAAGCAGACGCCTTCC
TTCGGAAGCGAGCCACTGAGGAGATAAGCAAGGACCTCAGAGCCACACTGAACGCCTTCCTGTACCACATGGGCC
AACACAGCAACAAATTCATGCTGGTCCTGGCCAGCAATCTGCCTGAGCAGTTCGACTGTGCCATCAACAGCCGCA
TTGACGTGATGGTCCACTTCGACCTGCCGACGAGGAGCGGGAGCGCCTGGTGAGACTGCATTTTGACAAC
GTGTTCTTAAGCCGGCCACAGAAGGAAAACGGCGCCTGAAGCTGGCCCAGTTTGACTACGGGAGGAAGTGCTCGG
AGGTGCTCGGCTGACGGAGGGCATGTGCGGCGGGGAGATCGCTCAGCTGGCCGTGTCTTGGCAGGCCACGGCAT
ATGCCTCCAAGGACGGGGTCTCACTGAGGCCATGATGGACGCCTGTGTGCAAGATGCTGTCCAGCAGTACCGAC
AGAAGATGCGCTGGCTGAAGGCGGAGGGGCTGGGCGCGGGGTCGAGCACCCCTATCCGGAGTCCAAGGCGAGA
CCCTCACCTCATGGAGCCTGGCCACGGACCCCTCCTACCCCTGCCTTGCCGGCCCCCTGCACATTTAGGATATGCT
CCTGGATGGGGACTGGGCTGTGCCAGGGCCTCTGTCCCCCAGGATGTCTTGTGGTGGCGGTTCGGCCGTTCTGCC
CCCCAGGGCACCCCTGTTGTAGGCACTGGCTAGGGAGGGGAGGCCTCCTTCCTGCCCCTCGAGACACTCTTGG
GAGATGCATTTTCCGTCTGGCTCACAGGGGGAGGGTGAGGCTTTGTACCCAGCCCTGCCCAGGCCACTGTGAG
GGTGGGTGCTGGCTGAGCCCTGGGGCAGAAGGAGTGGGGCAGGCGGGGTCTTTGTTCTCGGCTCCCACAGCAGA
GCCAGGTGAGGGGGGCGCTGCCAGGACTAGACAGAAGTGGGGCGGC

20/6881
FIGURE 20

ATGAGGCTGCAGAGTGATGTGGGGGCCAGCGGTGACTTCATGACCACACTGCGCCCAGGTGTAAGAGGGCACGCT
TCTGCCCAGGCATCGTCCATGGAAGACACGCAGTCGGCCACTGCAGCCTCGGTCCTGGGTGCCCTGGGGCTGGGT
CACTGGGGGCCACAGGCCACACTGAGAGACCACAGTCCTGGCATGCCATGCAGCTCCCTGTCCCCAGAGGCCATG
TCAAAGGACGCCCTGAATCTGGCGCAGATGCAGGAGCAGACGCTGCAGTTGGAGCAACAGTCCAAGCTCAAAACA
CTTGTCATGAGGATTTACGGAAGCAGGAGGAGTCCGTGCAGAAGCACCATCAGACCTTCTTGGAGTCCATCAGG
GCGGCTGGCACCTTGTTTGGGGAAGGATTCCGTGCCTTTGTGACAGACCGGGACAAAGTGACAGCCACGGTGGCT
GGGCTGACGCTGCTGGCTGTCGGGGTCTACTCAGCCAAGAATGCGACAGCCGTCCTGAGGCGCTACATCGAGGCT
CGGCTGGGGAAGCCGTCCTAGTGAGGGAGACGTCCCGCATCACGGTGCTTGAGGCGCTGCGGCACCCCATCCAG
CAGGTCAGCCGGCGGCTCCTCAGTCGACCCCAGGACGTGCTGGAGGGTGTTGTGCTTAGTCCCAGCCTGGAAGCA
CGGCTGCGCGACATCGCCATAATGACAAGGAACATCAAGAAGAACCGGGGCCTGTACAGGCACATCCTGCTGTAC
GGGCCACCAGGCACCGGGAAGACGCTGTTTGCCAAGAACTCGCCCTGCACTCAGGCATGGACTACGCCATCATG
ACAGGCGGGGACGTGGCCCCCATGGGGCGGGGAAGGCGTGACCGCCATGCACAAGCTCTTTGACTGGGCCAATACC
AGCCGGCGCGGCCTCCTGCTCTTTGTGGATGAAGCGGACGCCTTCCTTCGGAAGCGAGCCACTGAGAAGATAAGC
GAGGACCTCAGGGCCACACTGAACGCCTTCCTGTACCGCACGGGCCAGCACAGCAACAAATTCATGCTGATCCTG
GCCAGCTGCCACCCCGAGCAGTTTCGACTGGGCCATCAATGCCTGCATCGACGTGATGGTCCACTTCGACCTGCCA
GGGCAGGAGGAGCGGGCGCGCCTGGGATTGGAGGGAGAGGCTCCTCATGAGACCCCATGTGCGGACTAGAGGGA
GAGGCTCCTCATGGTCCACTGCTGGCTTCTGGCCTGGCCTCCCTGCAGCTGCCACACCCGGCCCTGGAGCCTCGT
GGTGTGGGGCGCGGCTCTTGCTTCCTGCTGCACATGTGCCTTGAGGCTGTCAGGCTCCCTGTTGCTGGCGGGCCC
CGGTTTCTGAGTCCTTCTGTGCACCTGACCCAAATCCCTGCTGTGCCAGTGACGACAAAAGCTGCTCTGTTCCA
AAGAGAGCCTGGTTCTCCCTGCCGACCCCTCCACTGCCGCCTGCTCCATGCTAGACCAGCTTTCCGGGCGTCTG
AAGCTGGCCCAGTTTGACTACGGGAGGAAGTGCTTAGAGATCGCTCGGCTGACAGAGGGCATGTCATGCCGGAAG
ATCGCACAGCTGGCCGTGTCCTGGCAGGCCACGGCGTATGCCTCCAAGGACGGGGTCTGACCGAGGCCATGATG
GACGCCTGCGTGCAAGACTTTGTCCAGCAGCACCAGCAGATGATGCGCTGGCTGAAGGGGGAGAGGCCTGGGCCC
GAGGACGAGCAACCCTCATCCTTGA

21/6881
FIGURE 21

MRLQSDVGASGDFMTTLRPGVRGHASQAASSMEDTQSATAASVLGALGLGHWGPQATLRDHSPGMPCSSLSPEAM
SKDALNLAQMQEQTLEQQSKLKQLVNEDLRKQEE SVQKHHQTFLESIRAAGTLFGEGFRAFVTDRDKVTATVA
GLTLLAVGVYSAKNATAVTGRYIEARLGKPSLVRETSRITVLEALRHP IQQVSRLLSRPQDVLEGVVLSPSLEA
RVRDIAIMTRNIKKNRGLYRHILLYGPPGTGKTLFAKKLALHSGMDYAIMTGGDVAPMGREGVTAMHKLFDWANT
SRRGLLLFVDEADAF LRKRATEKISED LRATLNAFLYRTGQHSNKFMLILASCHPEQFDWAINACIDVMVHFDLP
GQEERARLGLEGEAPHETPMSGLEGEAPHGPLLASGLASLQLPHPALEPRGVGRGSCFLLHMCLEAVRLPVAGGP
RFLSPSVHLTQIPAVASDDKSCSVPKRAWFSPADPSTAACSM LDQLSGRLKLAQFDYGRKCLEIARLTEGMSCRK
IAQLAVSWQATAYASKDGVLTEAMMDACVQDFVQQHQMMRWLKG ERP GPED EQPSS

22/6881
FIGURE 22

AAGTGCCCGAGGGCGGCCGCAGAACGGTCAATTTGAGCCGCGTCGAGCTCCCCTGGGACCTGTGGCCGCGCCCA
CAGACCATGCTCCTGGGGCGCCTGACTTCCCAGCTGTTGAGGGCCGTTCCCTTGGGCAGGCGGCCGCGCCCTTGG
CCCGTCTCTGGAGTGCTGGGCAGCCGGGTCTGCGGGCCCCCTTTACAGCACATCGCCGGCCGGCCAGGTAGGGCG
GCCTCTCTCCCTCGCAAGGGGGGCCAGCTGGAGCTGGAGGAGATGCTGGTCCCCAGGAAGATGTCCGTCAGCCCC
CTGGAGAGCTGGCTCACGGCCCCGCTGCTTCCTGCCCAGACTGGATAACGGGACCGCAGGGACTGTGGCTCCACCG
CAATCCTACCAGTGTCGCCCCAGCCAGATAGGGGAAGGGGCGGAGCAGGGGGATGAAGGCGTCGCGGATGCGCCT
CAAATTCAGTGCAAAAACGTGCTGAAGATCCGCCGGCGGAAGATGAACCACCACAAGTACCGGAAGCTGGTGAAG
AAGACGCGGTTTCTGCGGAGGAAGGTCCAGGAGGGACGCCTGAGACGCAAGCAGATCAAGTTCGAGAAAGACCTG
AGGCGCATCTGGCTGAAGGCGGGGCTAAAGGAAGCCCCGAAGGCTGGCAGACCCCCAAGATCTACCTGCGGGGC
AAATGAAGTCTGGCGCCGCCCTTCCCGCCCGTTGCTGCTGTGATCCGTAGTAATAAATTCTCAGAGGACTCAGCCT
TTAAA

23/6881
FIGURE 23

MLLGRLTSQLLRAVPWAGGRPPWPVSGVLGSRVCGPLYSTSPAGPGRAASLPRKGAQLELEEMLVPRKMSVSPLE
SWLTARCFLEPRLDGTAGTVAPPQSYQCPSQIGEGAEQGDEGVADAPQIQCKNVLKIRRRKMNNHHKYRKLVKKT
RFLRRKVQEGRLRRKQIKFEKDLRRIWLKAGLKEAPEGWQTPKIYLRGK

24/6881
FIGURE 24

GCGGTGCGGGCCGGGCGGGGCGCAGGCGGGCGGGCGGGTAGCGCCCCGCGTCCGAGCCCCGGGCGGGCCCTGAG
CGCGCGGGCTCCGCGCCGCGCCGCGGCCATGGCGGAGACCAAGATTATCTACCACATGGACGAGGAGGAGACGCC
GTACCTGGTCAAGCTGCCCCGTGGCCCCGAGCGCGTCACGCTGGCCGACTTCAAGAACGTGCTCAGCAACCGGCC
CGTGACACGCCTACAAATTCTTCTTTAAGTCCATGGACCAGGACTTCGGGGTGGTGAAGGAGGAGATCTTTGATGA
CAATGCCAAGCTTCCCTGCTTCAACGGCCGCGTGGTCTCCTGGCTGGTCTGGCTGAGGGTGCTCACTCGGATGC
GGGGTCCCAGGGCACGGACAGCCACACAGACCTGCCCCGCTCTTGAGCGGACAGGCGGCATCGGGGACTCCCG
GCCCCCTCCTTCCACCCAAATGTGGCCAGCAGCCGTGACGGGATGGACAACGAGACAGGCACGGAGTCCATGGT
CAGTCACCGGCGGGAGCGTGCCCGACGCCGAACCGCGAGGAGGCCGCCGACCAATGGGCACCCAAGGGGAGA
CCGACGGCGGGATGTGGGGCTGCCCCAGACAGCGCGTCCACCGCCCTCAGCAGCGAGCTTGAGTCCAGCAGCTT
TGTGGACTCGGACGAGGATGGCAGCACGAGCAGGCTCAGCAGCTCCACGGAGCAGAGCACCTCATCCAGACTCAT
CCGGAAGCACAAACGCCGGCGGAGGAAGCAGCGCCTTCGGCAGGCGGACCGGGCTCCTCCTTCAGCAGCATAAC
CGACTCCACCATGTCCCTCAACATCGTCACTGTACGCTCAACATGGAAAGACATCACTTTCTGGGCATCAGCAT
CGTGGGGCAGAGCAACGACCGTGGAGACGGCGGCATCTACATTGGCTCCATCATGAAGGGCGGGGCTGTGGCCGC
TGACGGCCGCATCGAGCCCGCGACATGTTGCTGCAGGTGAATGACGTGAACCTTTGAGAACATGAGCAATGACGA
TGCCGTGCGGGTGCTGCGGGAGATCGTTTCCCAGACGGGGCCCATCAGCCTCACTGTGGCCAAGTGCTGGGACCC
AACGCCCCGAAGCTACTTACCGTCCCACGGGCTGACCCGGTGCGGCCATCGACCCCGCCGCTGGCTGTCCCA
CACGGCGGCACTGACAGGAGCCCTGCCCCGCTACGAGCTGGAAGAGGCGCCGCTGACGGTGAAGAGTGACATGAG
CGCCGTGCTCCGGGTATGACAGCTGCCAGACTCGGGACTGGAGATCCGCGACCGCATGTGGCTCAAGATCACCAT
CGCCAATGCCGTATCGGGGCGGACGTGGTGGACTGGCTGTACACACACGTGGAGGGCTTCAAGGAGCGGCGGGA
GGCCCGGAAGTACGCCAGCAGCTTGCTGAAGCACGGCTTCCTGCGGCACACGGTCAACAAGATCACCTTCTCCGA
GCAGTGCTACTACGTCTTCGGGGATCTCTGCAGCAATCTCGCCACCCTGAACCTCAACAGTGGCTCCAGTGGGAC
TTCGATCAGGACACGCTGGCCCCGCTGCCCCACCGGCTGCCCCCTGGCTCTGGGTGAGGGCTACCCCTACCA
GTACCCGGGACCCCCACCCTGCTTCCCGCTGCCTACCAGGACCCGGGCTTTAGCTATGGCAGCGGCAGCACCGG
GAGTCAGCAGAGTGAAGGGAGCAAAAGCAGTGGGTCCACCCGGAGCAGCCGCCGGGCCCCGGGCGGTGAGAAGGA
GCGTCGGGCGGCGGGAGCTGGGGGAGTGGCAGTGAATCGGATCACACGGCACCGAGTGGGGTGGGGAGCAGCTG
GCGAGAGCGTCCGGCCGGCCAGCTCAGCCGTGGCAGCAGCCACGCAGTCAGGCCTCGGCTACCGCCCCGGGGCT
CCCCCGCCCCACCCACGACCAAGGCCTATACAGTGGTGGGGGGGCCACCCGGGGGACCCCTGTCCGGGAGCT
GGCTGCCGTCCCCCGGAATTGACAGGCAGCCGCCAGTCTTCCAGAAGGCTATGGGGAACCCCTGCGAGTTCTT
CGTGGACATCATGTGACTCGTGGCGCATGCCCCAGCCCTGCCTGAGGTGGGAGCTGGCGGTCTGCCGCATGCA
GAGCTCGCGTGGGCTTGCTTTCGTGGGGGCCAGGACGGGAGGCAGGGTGGGGGAGGCTGGACCACCACCATCT
GCCCTGGCAGCCTGGCTGCTCCAGCTCCTGACAGCACCTGTGTCTGAGCAGCCGTGTTGGGGGCGCTCCCTCTCT
GCCCCCTCAGCGAGAGCCTCGGACCTCCCAACCCCTTGTGTCTGGTGGGGATCCCTCCTGGGATGAGGAAGACCCC
CTCGGGCTCTCGGCTGACCCCCACCTCCTGCACAGCTGTGCCAGGCCCCAGGGTGGTCCATGCGGGGCAACCC
CCTGCGGTGCACAGGCCCCCTGTCTGGAGTAGGGATCTAATTTATTTATTTATTTGCTGGCCGGTGACTCGGGGG
AGGAGGCGACCCCTGTCATCTGTCCACCTGCTGCTGCCCCCTGGAGCAGCCTGCACCTTCTCTCCTCCCATCCGG
CAACAGTCTGAAAGTACGTGGAGGACGGGACCGGAAGACGAGAGAGGGCTGGACATCCTGCCCACCGTGTCCAG
CCAGGGCAGGGAGGGACCATGGCCCGCAGGGTCAAGGGGCCCGATGTGCACAGCTGCCACAGGGAGGGAGGTCT
TGGGGAGATGGGCAGTCAGGTGGCCCGTCTTGGTGAGTGACACACTGCGCGCACACATCGCGGCCCTTCTGGC
TTCTCTGGCCCCACGTGTCTGTGCTGTAGATACTGTATCAAAGTCCAGCGTTTAGATGGTTAACATAGAGCTG
CTTCTGTGTAAATGCTGCTTATTTTAAACATAAAAAGCGTTTAATTTTATGGG

25/6881
FIGURE 25

MAETKIIYHMDEEETPYLVKLPVAPERVTLADFKNVLSNRPVHAYKFFFKSMDQDFGVVKEEIFDDNAKLPCFNG
RVVSWLVLAEGAHS DAGS QGTDSHTDLPPPLERTGGIGDSRPPSFHPNVASSRDGMDNETGTESMVSHRRERARR
RNREEAARTNGHPRGDRRRDVGLPPDSASTALSSELESSSFVDSDEDGSTSRLSSSTEQSTSSRLIRKHKRRRRK
QRLRQADRASSFSITDSTMSLNIVTVTLNMERHHFLGISIVGQSNDRGDGGIYIGSIMKGGAVAADGRIEPGDM
LLQVNDVNFENMSNDDAVRVLREIVSQTGPISLTVAKCWDPTPRSYFTVPRADPVRPIDPAAWLSHTAALTGALP
RYELEEEAPLTVKSDMSAVVRVMQLPD SGLEIRDRMWLKITIANAVIGADVVDWLYTHVEGFKERREARKYASSLL
KHGFLRH TVNKITFSEQCYVFGDLCSNLATLNLNSGSSGTSDQDTLAPLPHPAAPWPLGQGYPYQYPGPPPCFP
PAYQDPGFSYGSGSTGSQQSEGSKSSGSTRSSRRAPGREKERRAAGAGGSGSESDHTAPSGVGSSWRERPAGQLS
RGSSPRSQASATAPGLPPPHTTKAYTVVGGPPGPPVRELA AVPELTGSRQSFQKAMGNPCEFFVDIM

26/6881
FIGURE 26

GCACCGCCCCCGCCGCAAGAAAGATGGCAGTGGCCTGATCCGGGGCCCGTTGGCGGCGTCACTGACGCTTCGCTC
CGGTCCCTCGGATCCCGAGCGCGGGGAGGCAGACCGACTGTGAGCTGCTTGTCCCCATCCTGCGGCCGTCCTGGGG
ACACAGAGCCCTCCGTGGTGCCCGGGGATTGGATTGGAGCCAGGACCTCACTTCCTCCTCTGCCCCCTGCCCTGC
CCCTCCCAGCACCTGGCCACACCCCTGCAGCCCGCCCCATGGTCTGGCCCTGGGTGGCGATGGCGTCCAGGTGGG
GTCCCCTCATTGGCCTGGCTCCGTGCTGCCTCTGGCTCCTGGGGGCGAGTCCTTCTGATGGACGCGTCTGCACGGC
CTGCCAACCCTCGTCCACTCGAGAGAGAGTAGCCAACAGGGAGGAGAATGAGATCCTGCCCCCAGACCACCTGA
ACGGGGTGAAGCTGGAGATGGACGGGCACCTCAATCGCGGCTTCCACCAGGAGGTCTTCTAGGCAAGGACCTGG
GTGGCTTTGATGAGGACGCGGAGCCGCGGCGGAGCCGGAGGAAGCTGATGGTCATCTTTTCCAAGGTGGATGTGA
ACACTGACCGGAAGATCAGTGCCAAGGAGATGCAGCGCTGGATCATGGAGAAGACGGCCGAGCACTTCCAGGAGG
CCATGGAGGAGAGCAAGACACACTTCCGCGCCGTGGACCCTGACGGGGACGGTCACGTGTCTTGGGACGAGTATA
AGGTGAAGTTTTTGGCGAGTAAAGGCCATAGCGAGAAGGAGGTTGCCGACGCCATCAGGCTCAACGAGGAACTCA
AAGTGGACGAGGAAACACAGGAAGTCTTGAGAACCTGAAGGACCGCTGGTACCAGGCGGACAGCCCCCTGCAG
ACCTGCTGCTGACGGAGGAGGAGTTCTGTGCTTCCTCCACCCCGAGCACAGCCGGGGAATGCTCAGGTTTCATGG
TGAAGGAGATCGTCCGGGACCTGGACCAGGACGGTGACAAGCAGCTCTCTGTGCCCGAGTTCATCTCCCTGCCCG
TGGGCACCGTGGAGAACCAGCAGGGCCAGGACATTGACGACAACTGGGTGAAAGACAGAAAAAAGGAGTTTGAGG
AGCTCATTGACTCCAACCACGACGGCATCGTGACCGCCGAGGAGCTGGAGAGCTACATGGACCCCATGAACGAGT
ACAACGCGCTGAACGAGGCCAAGCAGATGATCGCCGTGCGCGACGAGAACCAGAACCACCACTGGAGCCCCGAGG
AGGTGCTCAAGTACAGCGAGTTCTTACGGGCAGCAAGCTGGTGGACTACGCGCGCAGCGTGCACGAGGAGTTTTT
GAGCGCCCGGCCGCGCCCCGCGCCGCCCCCACGCAACCACGGGGCGGCCCTCGCGGGTGACTCCGGGGCTCCGTGG
CTGTCCCGGACCCACCTCTTCCCTGCCGCCGCCACCGGCCGACCGACCGCGGCTGCCCCAGTTGATGAGCGGC
GTGTCCCCTCTGCAGCGCGCACCCCGCGGGGCTTTGGCTGTGACGCGGTGCGGGGCGCGGGGCTGGGCTGTGGCC
CCGCGGCGCCGCTCCTCCCTGGTCCCTCGAAATCGTGGCATCTCACTTCTGAGAACGAAATCTCGCTTCAGTCA
CTCTGCCGAAGGCGCTGACGGCATCGCGGCCGGAACCTCTGGGCCCCGCCCCCTCCAGGGCCGCGCTCCGTGGG
AAAAACAGCTCCTCCATTTCCTTGAAAACCTGAACGATTATTAATAATAGATTAACTTCGCTGGAAATGAGTAG
CCAGGAAGTTCAGGGGAGGGTGCCGGGTCTTCCCGGCCCTGGCGTGTGCGAGCCACCCAGGTCCCGCAGCTGCC
GCTGAGAAAATGCAAATATTTGTTGTGACAAGAATCACATACATTTACTTTAAATATAGTTGCCTTTTTTGGTCA
GCTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

27/6881
FIGURE 27

MVWPWVAMASRWGPELIGLAPCCLWLLGAVLLMDASARPANHSSTRERVANREENEILPPDHLNGVKLEMDGHLNR
GFHQEVFLGKDLGGFDEDAEPRRSRRKLMVIFSKVDVNTDRKISAKEMQRWIMEKTAEHFQEAMEESKTHFRAVD
PDGDGHVSWDEYKVKFLASKGHSEKEVADAIRLNEELKVDEETQEVLENLKDRWYQADSPADLLLTEEEFLSFL
HPEHSRGMLRFRMVKEIVRDLDDQDGDKQLSVPEFISLPVGTVENQQGQDIDDNWVKDRKKEFEELIDSNHDGIVTA
EELESYMDPMNEYNALNEAKQMIAVADENQNHLEPEEVLKYSEFFTGSKLVDYARSVHEEF

28/6881
FIGURE 28

AAGGGGCCAAAAGGTCCACCTGATGAACCTGTTGCACGCGAAAAGTTCAGAACCACTGCTGCCAAGATGCTGACA
GAAGCCTTGAGAAGCACCTGCTGCGGGAAAAGACGTGCAGGCCTCACAGGTGCAGTGCGGTCTTCAGCGCGCTTG
AAAGCACGAAGTTGTTTCGGCAGCCAGGTTGGCCTCTGCCCAGGAAGTTGCTGGTTCCACGTCTGCCAAGACAGCA
TGTCTGACCCGGGCCCTGATCCTAGCACCCGCCCACCCGTGTACTTCCTCATCCCACAAAGCCACAGACACGCGA
ACGTCCAAGAAGTTCAAATGTGACAAAGGACATCTTGTGAAGTCAGAATTACAGAAGCTTGTCCCTAAGAATGAC
AGCGCTTCTTTGCCAAAAGTGACACCTGAGACCCCTTGTGAAAATGAGTTTGCTGAAGGCAGTGCCCTTGCTTCCA
GGCAGCGAGGCTGGCGTTTCTGTGCAGCAGGGGGCTGCAAGTCTTCCTCTCGGTGGCTGCAGAGTTGTGAGTGAC
TCTCGCTTAGCAAAGACTAGAGATGGCCTGTCCGTGCCAAAACACAGTGCCGGGTCCGGAGCAGAAGAATCCAAC
AGCAGCTCCACTGTGCAGAAGCAGAATGAGCCAGGGCTACAGACAGAGGATGTGCAGAAGCCACCACTTCAGATG
GACAACAGCGTCTTTCTAGATGACGACAGCAATCAGCCAATGCCCCGTGAGCCGGTTCTTTGGAAACGTTGAGCTC
ATGCAGGCCATAGAGAGGTCCGTGTGCAGCTGCCTGACGAGAACTGCATTCCCCAGCCCCAGCGGCGTCAGGGAG
CACCTCACCGTGTGTTCTCGCCCAGGGCAGTGGAGACAAGCCATTGGGAGTGCTCTCTCCATGGCCTCTTCCTGC
CGCCACCTGCACATAGAAGCTGAGTGGACCAACCAGGAGCAAGCTGGGGTCCCCGGGTGA

29/6881
FIGURE 29

AGAGGCGAGAACGACCCCGGGACCGACCAAAGCCCCGCGCGCCGCGCATCCCGCGTACAGCACCTACATCCCGCC
ACCGTCACCGCCACCACCATGCCCAAGAGAAAGGCTGAAGGGGATGCTAAAGGAGGTAAAGCCAAGGTGAAGGAC
GAACCACAGAGAAGGTCTGCAAGGTTGTCTGCTAAACCTGCTCCTCCAAAGCCAGAGCCCAAGCCTAAAAAGACC
CCTGCAAAGAAGGCAGAGAAGGTACCCAAAGGGAAAAAGGGAAAAGCTGATGCCCAGGAGGAGGGATTCCCTGAC
TTTGACACACATGGCCACCTTGGCACAAAAGCCTTGTGGTGTGGAAAAACAAATTTGTTTTTATGTCCTCTTCTC
CCTTTCCATCTTTCAGCATAGACTTAACTCCTTTAATCCCAGGCATCTGTTGGGACCTGACCCCTAGTCATTGGT
TACCAGTGTGTCAGGCAATCTGGACTTTCCAGTGATGCCACTGAGATGGCACCTGTCAAAGAGCAGTGGTTCCA
TTTCTAGATTGTGGATCTTCAGATAAATTCTGCCATTTTCAATTCCTGAAAGTCAGAGTCGGCTTGTGAA
AAGTTGTTAAACAACATGCTAAATGTGAAATGTCAACCCTCACTCTAAACTTTCCCTGTTTCAGAGCATGAGATGA
AGACTTCTTTGGGTTTTATAGCGGCTTTCTGATTTTTCGTAGTCCATTGAAGAAGGGAGTTTGAAAGTTGTTGTA
TACTGTAAACAATTGTCTGCCCATGTCCTGCCTGAAATACCA

30/6881
FIGURE 30

MPKRKAEGDAKGGKAKVKDEPQRRSARLSAKPAPPKPEPKPKKTPAKKAEKVPKGKKGKADVDTHGHLGTKALWC
GKTNLFLCPLLPHLSA

31/6881
FIGURE 31

TAGCTAGGCAGGAAGTCGGCGCGGGCGGGCGGACAGTATCTGTGGGTACCCGGAGCACGGAGATCTCGCCGGCT
TTACGTTACCTCGGTGTCTGCAGCACCCCTCCGCTTCTCTCCTAGGCGACGAGACCCAGTGGCTAGAAGTTCAC
CATGTCTATTCTCAAGATCCATGCCAGGGAGATCTTTGACTCTCGCGGGAATCCCAGTGTGAGGTTGATCTCTT
CACCTCAAAGGTCTCTTCAGAGCTGCTGTGCCCAGTGGTGCTTCAACTGGTATCTATGAGGCCCTAGAGCTCCG
GGACAATGATAAGACTCGCTATATGGGGAAGGGTGTCTCAAAGGCTGTTGAGCACATCAATAAACTATTGCGCC
TGCCCTGGTTAGCAAGAACTGAACGTCACAGAACAAGAGAAGATTGACAACTGATGATCGAGATGGATGGAAC
AGAAAATAAATCTAAGTTTGGTGCGAACGCCATTCTGGGGGTGTCCCTTGCCGTCTGCAAAGCTGGTGCCGTTGA
GAAGGGGTCCCCCTGTACCGCCACATCGCTGACTTGGCTGGCAACTCTGAAGTCATCCTGCCAGTCCCGGCGTT
CAATGTCATCAATGGCGGTTCTCATGCTGGCAACAAGCTGGCCATGCAGGAGTTTCATGATCCTCCCAGTCCGTTGC
AGCAAACCTTCAGGGAAGCCATGCGCATTGGAGCAGAGGTTTACCACAACCTGAAGAATGTCATCAAGGAGAAATA
TGGGAAAGATGCCACCAATGTGGGGGATGAAGGCGGGTTTGCTCCCAACATCCTGGAGAATAAAGAAGGCCTGGA
GCTGCTGAAGACTGCTATTGGGAAAGCTGGCTACACTGATAAGGTGGTTCATCGGCATGGACGTAGCGGCCTCCGA
GTTCTTCAGGTCTGGGAAGTATGACCTGGACTTCAAGTCTCCCGATGACCCAGCAGGTACATCTCGCCTGACCA
GCTGGCTGACCTGTACAAGTCCCTTCATCAAGGACTACCCAGTGGTGTCTATCGAAGATCCCTTTGACCAGGATGA
CTGGGGAGCTTGGCAGAAGTTCACAGCCAGTGCAGGAATCCAGGTAGTGGGGGATGATCTCACAGTGACCAACCC
AAAGAGGATCGCCAAGGCCGTGAACGAGAAGTCTGCAACTGCCTCCTGCTCAAAGTCAACCAGATTGGCTCCGT
GACCGAGTCTCTTCAGGCGTGCAAGCTGGCCCAGGCCAATGGTTGGGGCGTCATGGTGTCTCATCGTTCGGGGGA
GACTGAAGATACCTTCATCGCTGACCTGGTTGTGGGGCTGTGCACTGGGCAGATCAAGACTGGTGCCCCCTTGCCG
ATCTGAGCGCTTGGCCAAGTACAACCAGCTCCTCAGAATTGAAGAGGAGCTGGGCAGCAAGGCTAAGTTTGCCGG
CAGGAACTTCAGAAACCCCTTGGCCAAGTAAGCTGTGGGCAGGCAAGCCCTTCGGTCACCTGTTGGCTACACAGA
CCCCCTCCCCCTCGTGTGAGCTCAGGCAGCTCGAGGCCCCCGACCAACACTTGCAAGGGGTCCCTGCTAGTTAGCGCC
CCACCGCCGTGGAGTTCGTACCGCTTCCTTAGAACTTCTACAGAAGCCAAGCTCCCTGGAGCCCTGTTGGCAGCT
CTAGCTTTGCAGTCGTGTAATTGGCCCAAGTCATTGTTTTTCTCGCCTCACTTTCCACCAAGTGTCTAGAGTCAT
GTGAGCCTCGTGTATCTCCGGGGTGGCCACAGGCTAGATCCCCGGTGGTTTTGTGCTCAAAAATAAAAAGCCTCA
GTGACCCATGAG

32/6881
FIGURE 32

MSILKIHAREIFDSRGNPTVEVDLFTSKGLFRAAVPSGASTGIYEALERDNDKTRYMGKGVSKAVEHINKTIAP
ALVSKKLVNTEQEKIDKLMIEDGTENKSKFGANAILGVSLAVCKAGAVEKGVPLYRHIADLAGNSEVILPVPF
NVINGGSHAGNKLAMQEFMILPVGAANFREAMRIGAEVYHNLKNVIKEKYGKDATNVGDEGGFAPNILENKEGLE
LLKTAIGKAGYTDKVVIGMDVAASEFFRSGKYDLDFKSPDDPSRYISPDQLADLYKSFIKDYPVVSIEDPFDQDD
WGAWQKFTASAGIQVVGDDLTVTNPKRIAKAVNEKSCNCLLLKVNQIGSVTESLQACKLAQANGWGMVSHRSGE
TEDTFIADLVVGLCTGQIKTGAPCRSERLAKYNQLLRIEEEELGSKAKFAGRNFRNPLAK

33/6881
FIGURE 33

TGGTCCCAAGGCGCGTGCTTTGCAGCAGATGTGTGACCTGGCGTTCCCTGAGTGCTCGGAAAATGGCCTTGCTCT
CCGGTCGTTCCCCTTCAGGAGCAGAATTTTCCCACTGTAAAAAACCGAGCAAGTCTGGATAAGTGAGGCTGGCTC
CATGTATCCAGAATCAACGACGGGCTCCCCGGCTCGGCTCTCGCTGCGGCAGACGGGCTCCCCGGGATGATCTA
CAGTACTCGGTATGGGAGTCCCAAAAGACAGCTCCAGTTTTACAGGAACCTGGGCAAGTCTGGCCTGCGGGTCTC
CTGCCTGGGACTTGGAACATGGGTGACCTTCGGAGGCCAGATCACCGATGAGATGGCAGAGCAGCTCATGACCTT
GGCCTATGATAATGGCATCAACCTCTTCGATACAGCAGAAGTCTACGCAGCCGGCAAGGCTGAAGTGGTACTGGG
AAACATCATTAAGAAGAAAGGATGGAGGCGGTCCAGCCTCGTCATCACCACCAAGATCTTCTGGGGCGGAAAGGC
GGAGACGGAGCGGGGCTGTCCAGGAAGCACATAATCGAAGGTCTGAAAGCTTCCCTGGAGCGACTGCAGCTGGA
GTACGTGGATGTGGTGTGTTGCCAACCGCCCGGACCCCAACACCCCGATGGAAGAGACCGTCCGCGCCATGACCCA
CGTCATCAACCAGGGGATGGCCATGTACTGGGGCACGTACGCTGGAGCTCCATGGAGATCATGGAGGCCTACTC
CGTGGCCCGGCAGTTCAACCTGACCCCGCCCATCTGCGAGCAGGCTGAGTACCACATGTTCCAGCGTGAGAAAGT
GGAGGTGCAGCTGCCGGAGCTGTTCCACAAGATAGGAGTGGGCGCCATGACCTGGTCCCCTCTGGCCTGTGGCAT
TGTTTTCTGGCAAGTACGACAGTGGCATCCCACCCTACTCAAGAGCCTCCTTGAAGGGCTACCAGTGGCTGAAGGA
CAAGATCCTCAGTGAGGAGGGCCGGCGCCAGCAAGCCAAGCTGAAGGAGCTGCAGGCCATCGCCGAGCGCCTGGG
CTGCACCCTGCCCCAGCTGGCCATAGCCTGGTGCCTGAGGAATGAGGGAGTCAGCTCCGTGCTCCTGGGGGCCTC
CAATGCGGACCAGCTCATGGAGAACATTGGGGCAATACAGGTCCTTCCGAAACTGTCATCTTCCATTATCCACGA
GATTGATAGTATTTTGGGCAATAAACCTACAGCAAAAAGGACTACAGATCCTAAGCCGCCCCCGCCGCTGCT
CGGACAGTTTCCGTTCCCTCCTAGTCTCTGTTTCGCTCGCTTAAGCTGTTTTGAAGCCAAGTGAAAGAGTGTGGTTT
GCATCCAAGAGAAAACACCACACTGTGATGTATCGGGAAATGATCTCCCAAGTCGCTGCCAGACACCACCCACT
GCTTCGCCGGACAATGTGCAAGTCCAGTCTGTGCCGGGGAAGGCACTGGTTAGGAAGGATGTTCAAACGGTCCCA
CCCAAGCCTGTCACCTCTGCTCATCTCCAAGACCACCCAGCTTTCTCCAGCCACAGCCAAGATTCCCAAAGTC
AAGGCCCAAAGATTTCCAAGTTCCCAAAGTCAAGGCCAGGCCAAGGCCTGGTTGGGTCTTGGGGCGGGCAGGG
CCAGCCTCTCCTCTGCTGAGAATCCCCACTTGGTGTAGGGGGAGAGGGGAAAGGGGTCTGGCCCATCGAGGGGCC
CCTTCTGCCAGGGCCTTGGTTGCTGGGGCAGGGCCTCCCCACTGGGGGTCTTCTCCACCTCCCACTTTCCAAGG
GCTCCAGGAATCTGGGGCCTGACCACAGATTCTCTCCCATCTTTTCTGCTCCAACCTGCCCCACTGGGTCCCG
GCAGGGGCCATGCCTACCAAGCTCGAGCTGGCCCTTGACCCACCCACCCACCCCTTGTGTCAGGGGCAGGG
ACCCACAGGGGGATTGACTCTGCAGTTTGGGAGCCACAAAAGCGTAGCGGTGTGATTTCTAGCTCAGCCTCCAC
CGTCTTCTCCTACACACCAATGATGAGCCTCATGCCAGTGAGGCCCGGAGCGCTTGGGAGGGGTCCCAGTGGGG
CAGGCCCCCTCTGTCTGGCCACCCCTCTGTCTGGCCCCGGAAGGCCCTGTGGTCATGTGCTCCTAGCTGCACGGT
GGCTGCTGGCCACACCACGGCAAGTGGCAGCAGGGGCGGGCCCTGTGCACAAGGATGCACTCCTCTCGGCCCTG
TAGACTTTCTCTAAAGCCGCCCGCCAGCCCAGGCCGCTGCTCTGCACCGAGCTGGTGGGCTTGGGTTTTGTGGAG
CGCATGCTTGGACCTTTTCAGTAAGGAAGGGTCTTTGGGGTTTTCTGTGCCATGACTTGGGGGTGCACCCCCA
CAGCACCCCCACAATGTAGGAAAAGACCTCAGGGAACCTCTCCCTGGAAAGACGGGCAGGGCTGGTTAGCCCCTC
CCTGCTGACACCTGGGACAGGCTGGGCAGAGGGGAGAGAGGGCAGGACAGGCCAGAGTGACGCCCCCGTGCA
GCTTGGGGCCGGAGGGCAAGGGATGCCAGTAAGTCTGCAGGTGCGGGGTGCCACCTACAGGCCCAGGCCCTGTGTCC
CAAGCAGTACCCAGGCTTTGCAGACCACGCGGGGCAGGGCTCCACTGAAGCCACCCCCACCCCTCGCCAGCTAGC
TCCATAGGGAAGCCTGTGTCTCCTGCCCCCAGGGCGCACCCCTCAGTGCAGGCACCTCTGTTCCCGCTTTGCCCT
GGAGGAGCCACTATTCCAGAAGGCTCCACCCTGCCGTCTGCGGGAGCCTGCTGTCCAGTCTTGGCCGGGCCAAG
GCCTGGGAAACTGTGAAAGTCAGAAAGGCCAGCGGGGAGAGGCTGGGGCGAGGGGAGGAGGGGGATCAGCTTCTG
CTATTACCGACCCCCCTTCATGCTGCCCCCTGGCGCCTAGAACCCTTGCCCTCCTCATAGACCAAGTCCCGGGGG
TCTCCACTCAGTCTGCTGCTGCTTACCAGAAGCAGCCCTGTGAGTGTGGGGTGGGGAAGTCCCTTCCCAACG
GAGGTCCCAGCCTATGGCCCTGGGGCCAGGTGGGGGTGCCTGCTTCCCTCCCGACAGGGTCTTGCA

34/6881
FIGURE 34

CCTTTCTAACTCCGCTGCCGCCATGGCTCCTGTGAAAAAGCTTGTGGTGAAGGGGGGCAAAAAAAGAAGCAAGT
TCTGAAGTTCACCTCTTGATTGCACCCACCCTGTAGAAGATGGAATCATGGATGCTGCCAATTTTGAGCAGTTTTT
GCAAGAAAGGATCAAAGTGAACGGAAGCTGGGAACCTTGGTGGAGGGGTGGTGACCATCGAAAGGAGCAAGAG
CAAGATCACCGTGACATCCGAGGTGCCTTTCTCCAAAAGGTATTTGAAATATCTCACCAAAAAATATTTGAAGAA
GAATAATCTACGTGACTGGTTGCGCGTAGTTGCTAACAGCAAAGAGAGTTACGAATTACGTTACTTCCAGATTAA
CCAGGACGAAGAAGAGGAGGAAGACGAGGATTAAATTTTCAATTTATCTGGAAAATTTGTATGAGTTCTTGAATAA
AACTTGGGAACCAAAATGGTGGTTTATCCTTGTATCTCTGCAGTGTGGATTGAACAGAAAATTGGAAATCATAGT
CAAAGGGCTTCCCTTGGTTCGCCACTCATTTATTTGTAACTTGACTTCT

35/6881
FIGURE 35

MAPVKKLVVKGKKKKQVLKFTLDCTHPVEDGIMDAANFEQFLQERIKVNGKAGNLGGGVVTIERSKSKITVTSE
VPFSKRYLKYLTKKYLKKNNLRDWLRVVANSKESYELRYFQINQDEEEEEDED

36/6881
FIGURE 36A

CGCGCTCGCGGGGGCGGTGGCGCCCGGCACAGAGGGGTAAAGGGGGCGGTGCAGACGTCTCCCCGCCCATCCCCG
CCCCTCGAGAGCCGCGGCGCCCCGCCCTATTTATAGCAGCGGTGCCTAGCGCGCCGCGTCTCTCCGCGAGGCCCCG
GCCGCGGCGTCTCTGACAACTATCGAAGGCGCC**ATCG**AGCGACCGGCGCCCCCTGGCCGCTGCTTCCCTTCTCGGA
CCCCGCGCACGCCCTGAGCCTGCTGCGCGGCCTGAGCCAGCTGCGCGCCGAGCGCAAGTTCTTGGACGTGACCCT
GGAGGCGGCGGGCGGGCGCGACTTCCCGGCGCACCGTGCCTGCTGGCCGCCGCCAGCCCCCTACTTCCGCGCCAT
GTTTCGCGGGGCGAGCTGCGCGAGAGCCGCGCCGAGCGGGTGCCTGCGCTGCACGGAGTGCCTCCCGACATGCTGCAGCT
GCTGCTGGACTTCAGCTACACGGGCGCGTGGCGGTAAGCGGCGACAACGCTGAGCCGCTGCTGCGCGCCGCCGA
CCTGCTGCAGTTCCCGGCCGTGAAGGAGGCGTGCGGGGCCTTCTGCGAGCAGCAGCTCGACCTGGCCAACTGCCT
GGACATGCAGGACTTCGCTGAGGCCTTCAGCTGCTCGGGACTGGCGAGCGCGGCGCAGCGGTTTATTCTGCGCCA
CGTGGGCGAGCTGGGCGCCGAGCAGCTGGAGCGGCTGCCACTGGCGCGCTGCTGCGCTACCTGCGGGACGACGG
GCTGTGTGTGCCAAGGAGGAGGCCGCCTACCAGCTGGCGCTGCGCTGGGTCCGCGCTGACCCGCCGCGCCGCGC
CGCGCACTGGCCGCGAGCTGCTGGAGGCGTGCCTGCGCTTCTGCGCGCTTCTACCTGTTGGCGCACGTGCA
GGCCGAGCCGCTGGTGGCGCGTGCCACCCTGCCTGCGCTGCTGCGGAGGCGCGCACTTCAGGCGGCGCG
CTACGACCGCCACGACCGCGGGCCCTGTCCCCGAATGCGTCTCGCCGTCACCGGTCTCGCCGAGATCCTCGT
GCTCGTGGGCGGCTGCGACCAGGACTGTGACGAGCTGGTCACTGTGACTGCTACAACCCGCGAGACGGGTCACTG
GCGCTACCTGGCCGAGTTCCAGACCACCTGGGCGGAGGCTACAGCATCGTGGCGCTGGGCAATGACATCTACGT
GACGGGTGGGTCCGATGGCTCCCGGCTCTATGACTGCGTGTGGAGGTACAACCTCAAGCGTGAATGAGTGGGCGGA
GGTGGCGCCCATGCTGAAGGCCGCGAGTACCACAGCTCCTCTGTGCTGGACGGACTGCTGTACGTGGTGGCCGC
CGACAGCACCGAGCGCTATGACCACACCACTGACTCCTGGGAGGCCCTGCAGCCCATGACCTACCCCATGGACAA
CTGCTCCACCACTGCGTGCCGTGGCCGGCTCTATGCCATCGGCTCCCTGGCTGGCAAGGAGACCATGGTGATGCA
GTGCTACGACCCGGACACCGACCTGTGGTCTGCTGGTGGACTGCGGCCAGCTCCCGCCCTGGTCTTCCGCCCAA
GACTGCGACTCTAAACGGACTCATGTACTTTGTGAGGATGACTCCGCTGAGGTGGACGTGTACAACCCGACGAG
GAACGAATGGGACAAGATCCCGTCCATGAATCAGGTAAATTTTCAGGCGGGCCAGCATTGGAAGCACAGGCTGGT
CCTGATTTTGAACCCAAGTGTATCGTGATGAGTGTGTTGGGATCCACAGCCATGATGGATGGGTCTCATCTCAA
TTAATAGAAGGCTGCTCTTACCCTTATTTTGCACCTAAGGCTCACTGAGACACAGATGTTAAGTAATACCCTATG
ATTACACAGCTTAGTACACATTTGAGCAGTGTGTTATTGAGTATCTGCTGTGAGCCAGAGAGCAGAAGGAAGTGAG
GGAGCAAGGCATACAGTCATCTGGGGACACCTGTTCCAGAGAGGGACAGCAGGTACAGAGGCCCTGCAGCAGGGC
ACCTTGGCGTGTCTTAGATACACCAGCAGCCCATGTGGCCGAGCAGAGTCAGCATGAGGTCTGTGACCTACCT
TTTTTATTTTTGAGACAGGGTCTTGTCTGTACCCAGGCTGGAGTGCAGTGGTACAATCATGGCTCACTGCAGC
CTCCACCTCCTTGACTCGCAGTCTCCACCGCACCTTCTGAATAGCTGAGACTACAGGCGTGTGCCACCACAC
CCAGTAATTTTTTTTCTCATATGTAGATACAAAAGGATATTCTTAAATTTTTATAGAGACAGGGTCTTGCTGTG
TTACCCAGGCTGGTCTCACACTCCTGGCCTCAAGTGACCCTCCTGTCTCAGCCTCCCAAAGTGCTAGGATTATAG
GCGTGAACCACCACGCCCAGCTGGTTCCCTGAGGAAGTCAGTGTGGGAATACTTTTTTTTTTTTATACGGAGTCT
CGCTCTGTACCCAGGCTGGAGTGCAGTGGCACGATCTCGGCTCACTGCAAGCTCCATCTCCAGGTTACGCCA
TTCCTCCGCGCTCAACCTCCCGAGTAGCTGGGACTACAGGTACCCACCACCACGCCCAGCTAATTTTGTGTTGTGA
TTTTTAGTAGAGACGGGATTTCACTGTGTTAGCCAGGATGGTCTGGATCTCCTGACCTTGTGATCTGCCTGGCTC
AGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCATGCCAGCCCACTGTGGGAATACTTGTGTTGAGCAC
TTGCTGTGTGTTCTGAATAGGACAACCAGGGTCCACCCCTTCTCTCTGGGCTTGTGAGAAGAGGGGTGCCAGC
CTGACAGTGATGGGACAGGGAGGCTTCAGTGCCATTTGGCCATGTGAGCAGTGTTAGTCTGAGGTACACATCATA
TTGCCTACAGCCTTCTTCTGTGTGTCTGTAAACATTTCCAAACCTACACTCCGTGACATCCAGCCTCACAGCT
TACATCACAGCTTAATGTCTTGGCATTAAAGAGACCCAGCGTCTGTCTTCCCGCAGTAAGCTGCACATAGTCA
TAGCGAATTTGGGAAAGATGGAAGGAATCATCCAGCCTCGCGGTTAGAGCCCAGCTCTGCCACTGTCAGCCATG
CAAGCCTCAGTTTTTCCATCTGTAACATGGGGAGAACAGCACTGCTCAGCCCAGAGGGCCACTGCAGAGATTCTG
AGAGAGAACGTAGGAAGCGCTGCTCGGCACGACCTGCACACGGGGAGGCCTGGCGCTGCAGCGGGCACCCCTCATC
ACCATAGGGAAGGCCAGCTGCCTCCGGGGAGGCCCGTTCTCTAGGCAGGGTGTGGAAGGGGTGGCCTCTC
TGCTGCTTTCTGGGAGAGCCAAGGCCACCCCTCTGGGGTACTGACAGGGCATGCCTTGTCTCCAGTGGTTCCTCA
GGTGGGGCCCTGCCCTACCCTCTCCTCTGACCTCCACTCACTCATCCCTTTGGCCACAGGTACATGTGGGGGGC
AGCCTGGCCGTCTTGGGGGAAGCTGTACGTCTCTGGGGGATACACAATACATTTGAACCTCTCGACGTGGTA

37/6881
FIGURE 36B

GAGGCCTATGACCCAGAGACTCGCGCGTGGAGCGTGGTGGGGCGGCTCCAGAAACCCACCTTCTGGCATGGCAGT
GTCAGCATCTTCCGCCAGTTTCATGCCCCAGACCTTCTCGGGTGGGCGTGGCTTCGAGTTGGACAGTGGCAGCGAT
GACATGGACCCAGGCCGACCCCGGCCGCGCGGGACCCCGATGAGCTGCACTAGCCCCAGTCTGGCCCCGGCACGG
GCCTCGGTGCAGGTAACCTGGCACCTCTGCGGGGCAGTGCCCCACTCCTTTGTGCACAAGGACACGTTGGGCTCAC
AGGAGGAGCACAGGCTCTTGGGTGGCGAAGCCAGCCAGGATCCATTACCTGGAAGGTTTCTGTACCTTGAGAGC
CTGAATCAGAGGCCGTCGGGAACGCCCTCCCTGCAGTTGAGGAAGAGCCACTTTCTGCCAGCACATGTTTCTGG
GTCTTGGAGGTCACCCCCACCCGCGGATCACAGCTACCCACGCGGCGCACACCCCTCCTGCCGTTGTCATCTG
CACCTACTTGTTCACCTTGGGAGAGGACGATGACTTGGGAGGGACGCGTGAAGGGAGAAGGGGTCTCTCCCATG
AGGCTGAGGATGGCCTGAACCTGGAGCAGCGGACCAGGCAGACGGGCTGAAGTGGGGTCCCAAATTCCATGTCCA
GAGGTGTGGGGAGCCTGCCTCCCTAGCTCCTGGCCCCCTGCCAGGGGCTTACATCAAAACACCTCAGAGGGCTGCC
CTCCAGAGGCTGCACCCAGAACAGTGGGACATGAGCAGGGGTGTGGGCTTGGAGGGTGAAGAGGATGTGGTCCTA
TCAGATGCTGGGCCTCCTCAGCCATAGCCCCCTGCTCCTACCCCCCTGACTGGCTCTTGCGTCTCACCCTCTCACC
CTCTCCTTCCCGGGAGGCCCTGGGAGGTGATCATTGACACCCAGCCAAGCAGACAGCTGCGGGTGCCCAAGCCCT
TGCTGGGCCTGCGCGTGAGGAGTCCCACTGCTTCTAAAGGAAGTCTGGGCAGGAGGTGGCTTTGGTGGTTGGTT
CCAAAGTTGAAAATGCTTGCAGTTTGACCTTAGAAGAAGTGGGAAGAAGAAGGAGCTCTACAGGGTCAGCTTTGT
TTGATTTGTCCAGTCTAAGAAGTCCCATTGCCAAAGCTTTCTGCAGGAGGGTGAATGCCGAGCTTGGCAGCCCC
TGGGTTTCTCTTGGAAATGGTCAGTTTCCCTCAAAGTACCCAAAGTAGCCTTGGCTTGAGTTTTTGTCTTGCC
TCCTTTTTAGAGAAGAGGGCATTAGACTGCATTTTCTGGTTAAAGAAGTTAAAGCAAATGTTTATTGCCTTT
TCTAGTGAACCTAAGTTCGTAGAGATGTTCTCAGCAGGAAGACAGTCTTAGCACTGTCACTTAGCAGATTGCACTTA
AGTCCCTTGTGCTGGCCAGATGGCGTGGCTGGTTGCCTTAATATGTCCAGGACCCCTGACAGGGCTGCCTGGCC
TCTCCCTCGTGCTCCTCAAGAGCCCAGTCCATACACTGTGGATGTCAATTGCTGTGCGGTTAGGAAGTCTGTCT
AGAACGCCCTGGCTGGTATGACCACAGTTTCATGGCGGCTCTTCTCGCTTGGGTGATGGTCATCTTCCAGCACCTG
CTGTGCTGGGAAGGCCGAGGATGGGGGCCAGCACTGTCCAGGCCTGCTGGGGCCTGGCTGGGAGTCTGTGGGC
AGCATGGAACATGCAGCTGGGCTTCTGTGACCAGGCACCTCTGGCACTGTTGCTTGCCCTGTGCCCTGGACCT
TTTCTGCCCCCTCTCCTTCTCTGCTCCCTTGGGGCTACCCCTTGGCCCCCTCCTGGTCTGTGCAAACTCCCTCAG
GGAGCCCCCTGCCCTGTAGCTCTCGCTTAACTTCTAGGGGCTGCTGAGCCACCCAGAGGTTGTTGGAGTTCA
GCGGGGCAGCTTGTCTCCCTTGTGAGCAGGGGCGTAAGGGCTGGGTTTGGCCATACAAGGTTGGCTACGCCCTCA
ATCCCTGACCGTTCCAGGCACTGAGCTGGGCACCCACGGAAGGACATGCTGTCCAGACTGTGATGACTGCCAGCA
CAGGGCATCTCGGGCTTGGCTGGTCTGCGAGGCCTTGCCCCCTGTGGAACCTGGGTTTCTGTTTCTCAGTCTTT
TTTGC GGCTTTGCTGTGGTTGGCAGCTGCCGTA CTCCAGGCTTGTGTGCGGCACTCAGATGAGGGCTGTGGTGGC
AGCCAGTGCAGGAGAGCTGCGCTTGGGATTGTGCCCTCTCCTGTGTCTGTCCTCCGGACCTACCCAGGTCTCCAC
CATCAGGACCCTGTCTTTGGGTTTAGAAGACCAAGTATGGGGAAAACAGGCACCAGCCTCTGCAGCAATGGGTC
CCTCTAGCCTGTGGACACCAGCTGGGGGATCCAGGGTCAGGCCCCCTCCTCTCCCCAGTTTCCCTCTGCTGTGGG
TTCTGGGCTGTGATGTCTCCACCACTTAAGGATGTCTTTACACTGACTTCAGGATAGATGTTGGGATGCCTGGGC
ATGGCCACATGTTACATGTACAGAACTTTGTCTACAGCACAAATTAAGTTATATAAACACAGTACTGGTATTTA
ATGCTGATCTACTATAAGGTATTCTATATTTATATGACTTCAGAGACGCGTATGTAATAAAGGACGCCCTCCCTC
CAGTGTCCACATCCAGTTACCCCCAGAGGGTCGGGCAGGTTGACATATTTATTTTGTCTATTCTGTAGGCTTCC
ATGTCCAGAATCCTGCTTAAGGTTTTAGGGTACCTTCAGTACTTTTTGCAATAAAAGTATTTCTATCCATTTGG

38/6881

FIGURE 37

MERPAPLAVLPFSDPAHALSLLRGLSQLRAERKFLDVTLEAAGGRDFPAHRAVLAAASPYFRAMFAGQLRESRAE
RVRLHGVPPDMLQLLLDFSYTGRVAVSGDNAEPLLRADLLQFPVKEACGAFLLQQQLDLANCLDMQDFAEAFSC
SGLASAAQRFILRHVGELGAEQLERLPLARLLRYLRDDGLCVPKEEAAYQLALRWVRADPPRRAAHWPQLLEAVR
LPFVRRFYLLAHVEAEPLVARCPPCLRLLREARDFQAARYDRHDRGPCPRMRPRPSTGLAEILVLVGGCDQDCDE
LVTVDCYNPQTGWRYLAEPDHLGGYSIVALGNDIYVTGGSDGSRLYDCVWRYNSSVNEWAEVAPMLKAREYH
SSSVLDGLLYVVAADSTERYDHTTDSWEALQPMTYPMDNCSTTACRGRLYAIGSLAGKETMVMQCYDPDIDLWSL
VDCGQLPPWSFAPKTATLNGLMYFVRDDSAEVDVYNPTRNEWDKIPSMNQVNFQAGQHWKHRLVLILQPKCHRDE
CLGSTAMMDGSHLN

39/6881
FIGURE 38A

CCCGCGGCCGAGCCGGCGCGGGCCCCCGCACCTCCCCCGCTCGCGCGGCCTCGAGTCCAGAAGACCCGCTCCAC
ACACCGGGGCCCGCCGCGGAGCCTCATGGGGGTTGGAGTCCCCAAGGTTTCCTTTGTGCGCAGTATTGGCGGG
GCCTTGGACTIONACACTCCCAAGGCACCGCGCCCGCTCCCGCGCCACGCCCCCTCGCCGCTGGCTTCCAGTCG
CCACCCAGACTACATTTCCCGACAGGCCTCCCGGCTCTCCCGCCCTCCCTCCCGAGACACGAGCCGAACATGGGCG
TCAGGTGCGGGGAGCCGGTCGGGTTCCCGCTCACCGCCGCGCGCCGCCCCCTGCAGCCACTCTCCCGCCTCTAC
CGCCGCGGGGAGCTGCATCGTCCACTCCGGTCGGCGGTGGAACCGCCAGTCCGGGGTACACAGAGCTTGAGAAGCGA
CGCGCTGAGCCCCCATCACCTCCAGCCCGGGCGACCCCTCCCGGGTCCGCCCTCGCCCTGCGCAGCCGCCCCGAG
CCCCCAGCCCCGGGCGGCCCGCTCCAGCATCCAGCTCCTGCACTCTCGCAGCCGCGCGCCCCCGCCCCGGA
ACATGGACTCTGACTCTTGCGCCGCGCCCTTCCACCCGGAGGAATACTCCCCAGTTGCAAGAGGCGCAGGACCG
TGGAAGACTTCAACAAATTCTGCACCTTTGTCTTGCCCTATGCTGGCTACATCCCTTATCCGAAGGAGGAACCTC
CTTTAAGGAGCAGCCCCAGCCCTGCTAACAGCACTGCTGGTACCATTGACAGCGACGGCTGGGACGCGGGTTTCT
CAGACATCGCGTCTCTCAGTGCCTTTGCCAGTCTCTGACCGCTGCTTTAGCCACCTGCAGCCTACTCTCTTGACG
GAGCCAAGCCAGTAACCTTCTGCTGGACAGAAAAGAAAACGGACAAGCTGAAGAAGAAGAAGAAGAGGAAGCGCA
GGGACAGTGATGCGCTGGGAAAGAGGGGTACAGGGGGGGCTTGCTGAAGCTGGAAGCCGCTGACCCCTACGTGG
AGACCCCCACGAGTCCACCTTGCAGGATATCCCCAGGCTCCAGCGACCCCTGCTCGGGCTGGGACTCCGATA
CTCCCTCGAGTGGATCTTGTGCCACTGTGTACCTGATCAGGTCAAAGAAATAAAAACTGAAGGCAAACGGACTA
TCGTCCGGCAGGGAAAGCAGGTGGTGTTCGAGATGAGGACAGCACTGGCAATGATGAGGACATCATGGTGGACT
CAGATGACGATTCTGGGACCTCGTGACCTGCTTCTGCATGAAGCCATTTGCCGGCCGCCCATGATCGAGTGTA
ATGAGTGCCACACCTGGATTACCTGTCTGTGCGAAAATCCGGAAATCCAATGTTCCAGAAGTGTTTGTCTGCC
AAAAGTGCCGGGACTCCAAGTTTGACATCCGCCGTTCCAACCGCTCGCGGACGGGCTCCCGGAAGCTGTTCTCTGG
ACTGACTGCTGGCTGGCGAGGAGGCTGCGAGCGTGGAATCGGAAGCGACCGCGGGCTTTTTTGCCCTTCTCTTAG
TTGAGCACAGAACCCTCAGCTCTGGTGCGGGCAGATCCCTGCCATTTAGGTGCCTAAGCAAAAGGACAGGCTGTCT
CAAGGTAGAACTGTACATAGCCGGTGACCGAATGCGACCTTTGCCAGCCAGAGCTGCTGCCAGAGCTGCGTTCC
CTGCAGTGGAGGTGGACTGGACACCCACGTGCAGCGGGTTTGCTCATTTGAAAATGAGGGTCCGTGGTAGCTGT
GCGTTTTGCTATCATTTGCTAAGAGATTCCCGCTGATTGGGCTCAGTGCCAGCTGTTATTCTGCTTCCACTGTGTT
GGGGAGAGGTGTTTCGGTTTCCCCAGCCTGTTAATGAACAGCCATACGTGTAAGCTTTTTCTTGAGTGTTAAGTCT
TTTACCAAAAGTGTTCTGTACAGCAGCCATCCAAGTTGCCCTACTTAGTGGCTTGCCCTCTGCCTGCCTCAGCTG
CTGCCTGACCGGCTGGGGGAGGCACTGGCGGGAGGCCTCGGGCTCCCCTGGAAGGGCGCTGGGCTGGCGGGTCAG
CTGGTGGTTCTTAGGTTTTCTTCTGTTTGTAAAAGGGACAATGTGGCCACTTCTCTGTGGAAAGGGAGTTGGTT
GGGGGGTTGAGATGGCCCGTGTTTCTAATACTCAGTTTCTGTTTTGCACGATGTAAAAACCCCTGTCTTTTTGCACG
ATACAGCCAAAAGTATTGGCTGATTTCTTGCTGAGTGCCCTCTTAGTTGGTGTGTGAGGTCTTGGTGGGCTCAGG
CCAGCTGTTTTGCGAGTGTGGGAACCATAGGTTCTGTCTTTGTCTCTTCCCTTTCACCTCATTCTGGTAGCAGCAT
AAAGGTTAGGCAATCACTGGGACCCGCATGGTGTCTCTCAAAGAATAGGGTAAAGGAGAGCTGGGAGGGAGCCC
TCTCCGTTGGGTGACTCTTGTGTGCCCTTTAGACAGGCTGGCCTGCCGTTCCACAGGGTACAGTTAGGACTTGA
GTCTTTCTTTTTCTGTTTTGAGTTGGTGAGTGATAGGGTAACATGGGCCTTCAGGATGACCCCTTGGAACCT
GTGCCGAGTTCCTTAAATCTCAGCTGGGATCCTGGACCTGGGAGGCCCCCTGTGAGGGCCAGCTCTGAAAAACCT
GGGAGTTGATGCCGGAGGCTGTGGAAGAACTCTGCTCGAGGGCAGGGTGCCCTGGAACACTGGTAGTTCTGGGGC
TGGGAGGGAGAGGGGCTCCGGCTTCTCTGAAATGAACACTGCTCTTCAGCAGTTCAAGTACTTGTTCTCAAAAC
ATTTTCTAATTGATTGGTAGGTTTTCTAAGCATTGTTTCTTTAAGGCATGGAAAGGGAAGAATGCTCAAGCAAG
TCATGTTTGTTTTCTAGTGGGATGGGCCCGCTTCTCACTGCTGGGGGCTTCCCTTCATGTGGCACCTTTGTGCC
AGGCCACCAGGCAGACTCTTCCACCTTCTCCCACTGAAGCACCAAGGGCTTGAACCGTAATTTGGCTAATCAG
AGGCATTTTTTTTTGTCTAGTATCTTTCACACTTGTCCAACCGTCTTATTTTTTAAAGTTCTGTTGCTTGTAT
TAACACGAACTAGAGAGAAATAGTTTCTGAAGCCAGTTTATTGTGAAGATCCCCAAGGGGGAGGTTCCGGTAGAG
AAAAATAGTAAGCTGGTTTAGAACTGACGAGGGCAAACAGCCAGGACGCATTGGAGAGGAATTTGCCAAAGATC
TACCCTGAGATAACGCCTGTCCAGTGTCTTACCACGTGAATAACCAGCGCTCCAAAGTGTTTTTCTGCTTTGAA
AAAAAAAATTCCACAAGCTTTTAAAGGTGCATTTAAGAATCCATGTGACTTTAGAATGGAACCTGCCGGCCCTGG
CAACTGTACGCTGTGCTAGAAGGTTTCATGCCTCTGGAATGCATGTGATACTCATCTCCATTTTGTTCCTTGAT
TGCATTTTTGTCTTTTAGCAGATCTGTCCCTGTGGGTGGTGTCTAAGAAGTCGGACACCTTGGTTTTTGTGTTA

40/6881
FIGURE 38B

GATTGAGCTGGGCAGCTGCAATCAGCTTCTTTATATGCAAATTAGGCACGACCCATCTGTGGTTCCTGGTTGGTG
GCTAATGAAGTGAGGGGAGGGAGGGATGTCACCCCAAAGTAGGCCCTCCCATTTGGCTTTGGCCAGGCCAGACAC
TTCACATCGTTTACATGGTTCTGTGTAATTTAAAGTTTATGTGTATAAAGCGAAGCTGTTTCTGTGAACTGTA
TATTTTGTAATAAATATATTGCTACTTTGAGGTTTCATGATTCAAGGTTTCAGGCGATTGCGTTCTGTGCTGAAGG
A

41/6881

FIGURE 39

MDSDSCAAAFHP EEYSPSCKRRRTVEDFNKFCTFVLAYAGYIPYPKEELPLRSSPSPANSTAGTIDSDGWDAGFS
DIASSVPLPVSDRCF SHLQPTLLQRAKPSNFLDRKKTDKLKKKKKKRKRSDAPGKEGYRGGLLKLEAADPYVE
TPTSPTLQDIPQAPSDPCSGWSDTPSSGSCATVSPDQVKEIKTEGKRTIVRQKQVVFREDEDSTGNDEDIMVDS
DDDSWDLVTCTFCMKPFAGRPMIECNECHTWIHLSCAKIRKSNVPEVFVCQKCRDSKFDIRRSNRSRTGSRKLF LD

42/6881
FIGURE 40

GACGGCTCCGGGCCGCCAGGGGCCGCTGTGGCGCAGCCGGGCTGGCCCCGCGCTGTCCCTGACGCGGATCACTGGC
CCCTCTTGAGCACGGCCTTGCCGGTTTGGCGGGGTGAAAGGTTGCGAAGATGGCGACGGCCTTGAGCGAGGAGGA
GCTGGACAATGAAGACTATTACTCGTTGCTGAACGTGCGCAGGGAGGCCCTCTTCTGAAGAGCTGAAAGCTGCCTA
CCGGAGGGCTCTGTATGCTCTACCATCCAGACAAGCACAGAGACCCAGAGCTCAAGTCACAGGCGGAACGACTGTT
TAACCTTGTTTACCAGGCTTATGAAGTGCTTAGTGACCCCCAAACCAGGGCCATCTATGATATATATGGGAAGAG
AGGACTGGAAATGGAAGGATGGGAGGTTGTGGAAAGGAGGAGAACCCCTGCTGAAATTCGAGAGGAGTTTGAGCG
GCTGCAGAGAGAGAGAGAAGAGAGGAGATTGCAGCAGCGAACCAATCCCAAGGGAACGATCAGCGTTGGAGTAGA
TGCCACCGACCTTTTTGATCGCTATGATGAGGAGTATGAAGATGTGTCCGGCAGTAGCTTTCCGCAGATTGAAAT
TAATAAAATGCACATATCCCAGTCCATTGAGGCACCCCTTGACAGCGACAGACACAGCCATCCTCTCTGGAAGCCT
CTCAACCCAGAATGGAAATGGAGGAGGTTCCATTAACTTTGCGCTCAGACGAGTAACTTCGGCAAAGGGATGGGG
AGAGTTGGAATTTGGAGCTGGAGACCTACAGGGGCCTTTGTTTCGGTCTCAAGCTGTTCCGTAATCTCACACCAAG
ATGCTTTGTGACAACAACTGTGCTCTGCAGTTTTTCATCCCGTGGAATCCGACCCGGCCTGACCACTGTCTTAGC
TCGGAACCTAGACAAGAACACCGTGGGCTACCTGCAGTGGCGATGGGGTATCCAGTCAGCCATGAACACTAGCAT
CGTCCGAGACACTAAAACCAGCCACTTCACTGTGGCCCTGCAGCTGGGAATCCCTCACTCCTTTGCACTGATCAG
CTATCAGCACAAATTCGAAGATGACGATCAGACTCGTGTGAAAGGATCCCTCAAAGCAGGCTTCTTTGGGACGGT
GGTGGAGTACGGAGCTGAGAGGAAGATCTCCAGGCACAGCGTTTTGGGTGCAGCTGTCAGCGTTGGAGTTCACA
GGGTGTTTTCTCTCAAAGTCAAGCTCAACAGGGCCAGTCAGACATACTTCTTCCCTATTCACTTGACGGACCAGCT
TCTGCCCAGCGCCATGTTCTATGCCACCGTGGGGCCTCTAGTGCTTACTTTGCCATGCACCGTCTGATCATCAA
ACCATACCTCAGGGCTCAGAAAGAGAAGGAATTGGAGAAGCAGAGGGAAGCGCCGCCACCGATGTGCTGCAGAA
GAAGCAAGAGGCGGAGTCCGCTGTCCGGCTGATGCAGGAATCTGTCCGAAGGATAATTGAGGCAGAAGAGTCCAG
AATGGGCCTCATCATCGTCAATGCCTGGTACGGGAAGTTTGTCAATGACAAGAGCAGGAAGAGCGAGAAGGTGAA
GGTGATTGACGTGACTGTGCCCCCTGCAGTGCCTGGTGAAGGACTCGAAGCTCATCCTCACGGAGGCCTCCAAGGC
TGGGCTGCCTGGCTTTTATGACCCGTGTGTGGGGGAAGAGAAGAACCTGAAAGTGCTCTATCAGTTCCGGGGCGT
CCTGCATCAGGTGATGGTGCTGGACAGTGAAGCCCTCCGGATACCAAAGCAGTCCCACAGGATCGATACAGATGG
ATAAACTGCCAAGAACCAGATTTTTTAAAGGCCGCAAAAAATCTTTTCTGGGAGTCTACAAATTTGGAAATGAA
AAAACCCAGACATCAGATGTTTTTATTTTATATTATTATATAGAAGGTGGTACCATTATCAATTATGTGAAGGG
ACATGCAGACACCCAGCTTTTGAAGGTGCTGGGGGTAGGACTGAGGCAGCCCCACTGGGAACCAGACTGCAGCC
TGGCCCATGGCTGTTTTTCCAAGGATCAGTTCCTGGAGGGAAGGGCTCTGGCCCTGACTCCGCTGTGTCCCGAGC
ACACGTGCTGACCGCAGCCCCGCCGCCCTGTAGTTCTTGGCTGGGTCTGGAGGTGTCTGTGGAGCACCCCTGCCCTC
ACCACAGGAGCGTGAGCCACTTCTGCAGTCCACGCTGAACATGGGAAAACAACCTGAAAAGCAGGCAGGCCTCCCCG
GTCAGGGAGCCTCTGCTGTGCTGGCTTCCCATGACCACCTCCTCTTGCTGAAATATTACTGCTTGAATCTGGAGC
AGATTGCGGGTTTATAAACTGCTTTTTTATCTGAGAACAAACGGGTTTGGAATTAGTCGCTTTTTTTCCCCACT
CCCAGAGCTGCTCAAGTCATTCCACCGGCCCTCGGCTTGGGACAGGGTAGTGTAACCTCCCGATCCCAGGGCCT
AGCCCTGACACAGGTGGCTTCCCGTATCCCGGTGGGAAAACGCCCTGCCACCAGCGGGCTTGAGCTGGCCTGTGT
CCCTCCACCGCCTGCACCACCCACCTCCAGAGTGCAGTGTGTTGGCAAGGGCAGCTCAAGAGGACAGGACCAGGCG
CTTGGCAAGACATCAGACACACCCAACCAAGGCGTGGACCCAGGCCCGGCCGTGGTACCCAGCAGGTGGCA
CTGCAGCTCCCCGCTCCTGCAGGTCCAGCGTCTCACAGGAACACCAGGGCCTGTGCTCCGGAGCCTTCCTTCAG
ACCTTCTCTCCACGTGCCCACTTGGGATGCAGAATGCAGCGGAGCTAGGACCCCTCCACGGCCTGGACCTCGGC
TGCAGTAAAGTTACGTGAGGCCTGTCTCTCGGGGCCTGGAAGTGCCAGCCATCAGTTGCTCTTGCTGACCCCTCG
GAGCAAGCGCCGCACAGGTGGTGGCTGAGACAGCTGGCGCGGGGGGGCCCCAAGCTGCGCCGGCCTCCAGCCCACC
CACAGCTGTTGCTGAAGTCAGGCCTCCCTCCCCAGCACTGGTATCTGAGTAACGGCTAAGAACCTCCTTCTCTG
GTTTTGAAAAGCAGTTCGGGTGTCCAATTCTGTAACTTATCTCCATTTTTTAAAAAGGTTTCTCTGACGGCC
CCACGGCCCCGAGCCGCGGTGAGCGTCGTGTTGCATGAGCCTGGGCCCCGGGCTTCCCGTGCGCCTCTGCCGCAGG
TGCTTCTGGGCACCCATCCTCTGCGTTTCATTTGCAGTCGACTGTACAGAAGGCACTCACCACAATAAACCTTTC
CTGAAAGC

43/6881
FIGURE 41

TGCGAGGCAGAGTGCTAGCGGGAGCGCGAGCCAGCAAGAGGCGCCTGCGCGATGTCCGGGCCCCCTGAGCCCGCGG
CGCTGAGCCAGCCGGGACGGACATGCGCGGGAGGGCGCCGCGGGGAGCCGCGCTCCTCCGGGGGAATGAAAGC
TACTGGTTGATTTTAAAGTGCCTGGGCCTCACAGGTTTGGAGATGTCCCAGAATAAGGCACAATGTCAATAGCAG
GAGTTGCTGCTCAGGAGATCAGAGTCCCATTAAAAACTGGATTTCTACATAATGGCCGAGCCATGGGGAATATGA
GGAAGACCTACTGGAGCAGTCGAGTGAGTTTAAAAACAACCTTTTTAAATATTGACCCGATAACCATGGCCTACA
GTCTGAACTCTTCTGCTCAGGAGCGCCTAATACCACTTGGGCATGCTTCCAAATCTGCTCCGATGAATGGCCACT
GCTTTGCAGAAAATGGTCCATCTCAAAAGTCCAGCTTGCCCCCTCTTCTTATTCCCCCAAGTGAAAACCTTGGGAC
CACATGAAGAGGATCAAGTTGTATGTGGTTTAAAGAACTCACAGTGAATGGGGTTTGTGCTTCCACCCCTCCAC
TGACACCCATAAAAACTCCCCCTTCCCTTTTCCCCTGTGCCCCCTCTTTGTGAACGGGGTTCTAGGCCTCTTCCAC
CGTTGCCAATCTCTGAAGCCCTCTCTCTGGATGACACAGACTGTGAGGTGGAATTCCTAACTAGCTCAGATACAG
ACTTCCTTTTAGAAGACTCTACACTTTCTGATTTCAAATATGATGTTCTTGGCAGGCGAAGCTTCCGTGGGTGTG
GACAAATCAACTATGCATATTTTGATACCCAGCTGTTTCTGCAGCAGATCTCAGCTATGTGTCTGACCAAAATG
GAGGTGTCCAGATCCAAATCCTCCTCCACCTCAGACCCACCGAAGATTAAAGAAGGTCTCATTGGGACCAGCTG
GCTCCTTTAACAAGCCAGCCATAAGGATATCCAAGTGTGTATACACAGAGCTTCTCCTAACTCCGATGAAGACA
AACCTGAGGTTCCCCCAGAGTTCCCATACCTCCTAGACCAGTAAAGCCAGATTATAGAAGATGGTCAGCAGAAG
TTACTTCGAGCACCTATAGTGATGAAGACAGGCCTCCCAAAGTACCGCCAAGAGAACCTTTGTACCGAGTAAC
CGCGCACACCGAGTCCCAAAGCCTTCCGCTTACCTCAATGGGGTCATGCCCCGACACAGAGCTTTGCCCTG
ATCCCAAGTATGTCAGCAGCAAAGCACTGCAAAGACAGAACAGCGAAGGATCTGCCAGTAAGGTTTCCTTGCAATC
TGCCCATATTGAAAATGGGAAGAAGGTTAGTTCAACACATTATTACCTACTACCTGAACGACCACCATACCTGG
ACAAATATGAAAATTTTTTAGGGAAGCAGAAGAAACAAATGGAGGCGCCCAAATCCAGCCATTACCTGCTGACT
GCGGTATATCTTCAGCCACAGAAAAGCCAGACTCAAAAACAAAAATGGATCTGGGTGGCCACGTGAAGCGTAAAC
ATTTATCCTATGTGGTTTCTCCTTAGACCTTGGGGTCATGGTTCAGCAGAGGTTACATAGGAGCAAATGGTTCTC
AATTTTCCAGTTTGATTGAAGTGCAGAGAAAATCCCTTAGATTGCAAAATAAAATAGTTGAACTCTCTGTCTTC
ATGTGGAAGGTTTAGAGCAGTTGTGAGATGCTGTTATGCTGAGAAACCCTGACTTTGTTAGTGTGGAAAAAAGT
CTTACAAGTCTATAATTTAAAGATGTGATGGTGGGGAGGGGAGGATGGGGAAGCTTTTTATATATGCATACATTA
CATACCTATATATAAACTTGTGGTATAACCATAGACCATAGCTGCAGGTTAACCAATTAGTTACTATCGTAGAGT
AATATATATTGAGAATAATAAACTCAAGCTGGAGAAATGAGTCCTGATAGACTGAAAATTGAGCAAATGGAAGAA
GATACAGTATTGTTTAGATCAGAATCATTAAAAAATATTTTTGTTTAGTAAGTTTGAAGATTTCTGGCTTTTAGG
CCTTTTCTATTTTGTTCATTTATTTTTGCAGGCAATCTTTTCCATGGAGGGCAGGGTATCCATTCTTTACCATG
GGTGTACCTGCTTAGGTTAAAAATCATACCAAGGCCTCATACTTCCAGGTTTCATGTTGCGTCTTGTGGAGGAG
GGAGAGCAGGTTACTTGGCAACCATATTGTACCTGTACCTGTACACATCTTGAAAAATAAAACGATAATAGAA
CTAGTGACTAATTTTCCCTTACAGTTCCTGCTTGGTCCCACCCACTGAAAGTAGCTCATCGTAGTGCGGGCCGTAT
TAGAAGCAGTGGGGTACGTTAGACTCAGATGGAAGTATTCTAGGTGCCAGTGTTAGGATGTCAGTTTTACAAA
ATAATGAAGCAATTAGCTATGTGATTGAGAGTTATTGTTTGGGGATGTGTGTTGTGGTTTTGCTTTTTTTTTTTT
AGACTGTATTAATAAACATACAACACAAGCTGGCCTTGTGTTGCTGGTTCCTATTAGTATTTTCTGGGGATTGT
TTGCTTTTTTAAGTAAAACACTTCTGACCCATAGCTCAGTATGTCTGAATTCAGAGGTCACATCAGCATCTTTCT
GCTTTGAAAACCTCTCACAGCTGTGGCTGCTTCACTTAGATGCAGTGAGACACATAGTTGGTGTTCGGATTTTTCAC
ATCCTTCCATGTATTTATCTTGAAGAGATAAGCACAGAAGAGAAGGTGCTCACTAACAGAGGTACATTACTGCAA
TGTTCTCTTAACAGTTAAACAAGCTGTTTACAGTTTAAACTGCTGAATATTATTTGAGCTATTTAAAGCTTATTA
TATTTTAGTATGAACTAAATGAAGGTTAAACATGCTTAAGAAAAATGCACTGATTTCTGCATTATGTGTACAGT
ATTGGACAAAGGATTTTATTCATTTTGTGCTTATTTTGAATATTGTCTTTTCATTTTAAATAAAGTTATAATAC
TTAAAAA

44/6881
FIGURE 42

GAATTCGGCACGAGATAAAAAATGGCTTCCAAAAGAGCTCTGGTCATCCTGGCTAAAGGAGCAGAGGAAATGGAGA
CGGTCATCCCTGTAGATGTCATGAGGCGAGCTGGGATTAAGGTCACCGTTGCAGGCCTGGCTGGAAAAGACCCAG
TACAGTGTAGCCGTGATGTGGTCATTTGTCCTGATGCCAGCCTTGAAGATGCAAAAAAAGAGGGACCATATGATG
TGGTGGTTCTACCAGGAGGTAATCTGGGCGCACAGAATTTATCTGAGTCTGCTGCTGTGAAGGAGATACTGAAGG
AGCAGGAAAACCGGAAGGGCCTGATAGCCGCCATCTGTGCAGGTCCTACTGCTCTGTTGGCTCATGAAATAGGTT
GTGGAAGTAAAGTTACAACACACCCCTCTTGCTAAAGACAAAATGATGAATGGAGGTCATTACACCTACTCTGAGA
ATCGTGTGAAAAAGACGGCCTGATTCTTACAAGCCGGGGGCCTGGGACCAGCTTCGAGTTTGCGCTTGCAATTG
TTGAAGCCCTGAATGGCAAGGAGGTGGCGGCTCAAGTGAAGGCTCCACTTGTTCTTAAAGACTTAGAGCAGCGAAC
TGCGACGATCACTTAGAGAAAACAGGCCGTTAGGAATCCATTCTCACTGTGTTTCGCTCTAAACAAAACAGTGGTAG
GTTAATGTGTTTCAAGATCGCTGTCCCTTACTACTTTTGCGGAAGTATGGAAGTCACAACACTACACAGAGATTTCTC
AGCCTACAAATTGTGTCTATACATTTCTAAGCCTTGTTTGCAGAATAAACAGGGCATTTAGCAAACATAAAAAAA
AAAAAAAAAACTCGAG

45/6881
FIGURE 43

MASKRALVILAKGAEEMETVIPVDVMRRAGIKVTVAGLAGKDPVQCSRDVVICPDASLED AKKEGPYDVVVLPGG
NLGAQNLSESAAVKEILKEQENRKGLIAAICAGPTALLAHEIGCGSKVTTHPLAKDKMMNGGHYTYSEN RVEKDG
LILTSRGPGTSFEFALAIVEALNGKEVAAQVKAPLV LKD

46/6881
FIGURE 44

CTCTAAAGCGCCGCAGCTGCCAAAATGCTCTACAGGTCCAACCTGCTGCCACTGGCAGTAATCGAAGACTTCAGCAG
ACACAAAATCAAGTAGATGAGGTGGTGGACATAATGCGAGTTAACGTGGACAAGGTTCTGGAAAGAGACCAGAAG
CTCTCTGAGTTAGACGACCGTGCAGACGCACTGCAGGCAGGCGCTTCTCAATTTGAAACGAGCGCAGCCAAGTTG
AAGAGGAAATATTGGTGGAGAATTGCAAGATGTGGGCAATCGGGATTACTGTTCTGGTTATCTTCATCATCATC
ATCATCGTGTGGGTTGTCTCTTCATGAAGAACCAGCGGAACTCAAAACTGCTGTTCAAGAAACCTCTTCAAGACT
TTTGACTTAGAACCTGCTATATTATCAAGCTTACCTACTGTTATCTCTAAAATTTTTTTTGTGTTAATGTAAAGT
TGAATTTCTAGGAAACGTGCCTTTGTTTTTTAATATGCACTCCAAATTAGAAGGCCGGCCCCGTCACATTTTGC
ACAGTGCCTTTACAGATTTACGTATGGGCTGATGAAGAGGCCTTCTTAAGTTCCAGAGTGCTATAATCTAGATGT
AATGTTGTCACTAATTAATTGCCATTACTCCCCTTTAG

47/6881
FIGURE 45

MSTGPTAATGSNRRRLQQTQNQVDEVVDIMRVNVDKVLERDQKLSELDDRADALQAGASQFETSAAKLKRKYWWKN
CKMWAIGITVLVIFIIIIIVWVSS

48/6881
FIGURE 46

GCTGCGGGTCTTTCCCTCACTCGTCCTCCGCGCGTCGCCGCTCTTCGGTTCTGCTCTGTCCGCCGCCATGGCCCA
AGCTGACATCGCGCTGATCGGATTGGCCGTCATGGGCCAGAACTTAATTCTGAACATGAATGACCACGGCTTTGT
GGTCTGTGCTTTTAATAGGACTGTCTCCAAAGTTGATGATTTCTTGGCCAATGAGGCAAAGGGAACCAAAGTGGT
GGGTGCCCAGTCCCTGAAAGAGATGGTCTCCAAGCTGAAGAAGCCCCGGCGGATCATCCTCCTGGTGAAGGCTGG
GCAAGCTGTGGATGATTTTCATCGAGAAATTGGTACCATTGTTGGATACTGGTGACATCATCATTGACGGAGGAAA
TTCTGAATATAGGGACACCACAAGACGGTGCCGAGACCTCAAGGCCAAGGGAATTTTATTTGTGGGGAGCGGAGT
CAGTGGTGGAGAGGAAGGGGCCCCGGTATGGCCCATCGCTCATGCCAGGAGGGAACAAAGAAGCGTGGCCCCACAT
CAAGACCATCTTCCAAGGCATTGCTGCAAAAGTGGGAAGTGGAGAACCCTGCTGTGACTGGGTGGGAGATGAGGG
AGCAGGCCACTTCGTGAAGATGGTGCACAACGGGATAGAGTATGGGGACATGCAGCTGATCTGTGAGGCATACCA
CCTGATGAAAGACGTGCTGGGCATGGCGCAGGACGAGATGGCCCAGGCCTTTGAGGATTGGAATAAGACAGAGCT
AGACTCATTTCCTGATTGAAATCACAGCCAATATTCTCAAGTTCCAAGACACCGATGGCAAACACCTGCTGCCAAA
GATCAGGGACAGCGCGGGGCGAGAAGGGCACAGGGAAGTGGACCGCCATCTCCGCCCTGGAATACGGCGTACCCGT
CACCTCATTTGGAGAAGCTGTCTTTGCTCGGTGCTTATCATCTCTGAAGGATGAGAGAATTCAAGCTAGCAAAAA
GCTGAAGGGTCCCCAGAAAGTTCCAGTTTGATGGTGATAAGAAATCATTCCTGGAGGACATTCGGAAGGCACTCTA
CGCTTCCAAGATCATCTCTTACGCTCAAGGCTTTATGCTGCTAAGGCAGGCAGCCACCGAGTTTGGCTGGACTCT
CAATTATGGTGGCATCGCCCTGATGTGGAGAGGGGGCTGCATCATTAGAAGTGTATTCTAGGAAAGATAAAGGA
TGCAATTTGATCGAAACCCGGAACCTCAGAACCTCCTACTGGACGACTTCTTTAAGTCAGCTGTTGAAAAGTGCCA
GGACTCCTGGCGGGCGGCAGTCAGCACTGGGGTCCAGGCTGGCATTCCCATGCCCTGTTTTACCACTGCCCTCTC
CTTCTATGACGGGTACAGACATGAGATGCTTCCAGCCAGCCTCATCCAGGCTCAGCGGGATTACTTCGGGGCTCA
CACCTATGAACCTCTTGCCAAACCAGGGCAGTTTATCCACACCAACTGGACAGGCCATGGTGGCACCGTGTCTATC
CTCGTCATACAATGCCTGATCATGCTGCTCCTGTACCCCTCCACGATTCCACAGACCAGGACATTCCATGTGCCT
CATGGCACTGCCACCTGGCCCTTTGCCCTATTTTCTGTTAGTTTTTTAAAGTGTGTGTAAGAGACTCCTGAGGA
AGACACACAGTTTATTTGTAAAGTAGCTCTGTGAGAGCCACCATGCCCTCTGCCCTTGCCCTCTTGGGACTGACCA
GGAGCTGCTCATGTGCGTGAGAGTGGGAACCATCTCCTTGCGGCAGTGGCTTCCGCGTGCCCCGTGTGCTGGTGC
GGTTCCCATCACGCAGACAGGAAGGGTGTTTGCGCACTCTGATCAACTGGAACCTCTGTATCATGCGGCTGAATT
CCCTTTTTCCTTTACTCAATAAAAAGCTACATCAGACTG

49/6881
FIGURE 47

MAQADIALIGLAVMGQNLIILNMNDHGFVVCAFNRVTSKVDDFLANEAKGTKVVGAQSLKEMVSKLKKPRRIILLV
KAGQAVDDFIEKLVPLLDTDGDIIDGGNSEYRDTTRRCRDLKAKGILFVGSGVSGGEEGARYGPSLMPGGNKEAW
PHIKTIFQGIAAKVGTGEPCCDWVGDEGAGHFVKMVHNGIEYGDMQLICEAYHLMKDVLGMAQDEMAQAFEDWNK
TELDSFLIEITANILKFQDTDGKHLLPKIRDSAGQKGTGKWTASALEYGVPTLIGEAVFARCLSSLKDERIQA
SKKLKGPQKFQFDGDKKSFLDIRKALYASKIISYAQGFMLLRQAATEFGWTLNYGGIALMWRGGCIIRSVFLGK
IKDAFDRNPQLNLLDDFFKSAVENCQDSWRRVSTGVQAGIPMPCFTTALSFYDGYRHEMLPASLIQAQRDYF
GAHTYELLAKPGQFIHTNWTGHGGTVSSSSYNA

50/6881
FIGURE 48

CGCCGCTCCGGCCTCCCGCGACTTCTCGAAGGTGGGCAGGTCCCACCTTGTGGAGG**ATGG**AGGTGACCGGGGACG
CCGGGGTACCAGAATCTGGCGAGATCCGGACTCTAAAGCCGTGTCTGCTGCGCCGCAACTACAGCCGCGAACAGC
ACGGCGTGGCCGCCTCCTGCCTCGAAGACCTGAGGAGCAAGGCCTGTGACATTCTGGCCATTGATAAGTCCCTGA
CACCAGTCACCCTTGTCTTGGCAGAGGATGGCACCATAGTGGATGATGACGATTACTTTCTGTGTCTACCTTCCA
ATACTAAGTTTGTGGCATTGGCTAGTAATGAGAAATGGGCATACAACAATTGAGATGGAGGTACAGCTTGGATTT
CCCAAGAGTCCTTTGATGTAGATGAAACAGACAGCGGGGCGAGGGTTGAAGTGGAAGAATGTGGCCAGGCAGCTGA
AAGAAGATCTGTCCAGCATCATCTCCTATCAGAGGAGGACCTCCAGATGCTTGTGACGCTCCCTGCTCAGACC
TGGCTCAGGAACACGTCAGAGTTGTGCCACCGTCCAGCGGCTGCAGCACACACTCCAACAGGTGCTTGACCAAA
GAGAGGAAGTGCGTCAGTCCAAGCAGCTCCTGCAGCTGTACCTCCAGGCTTTGGAGAAAAGAGGGCAGCCTCTTGT
CAAAGCAGGAAGAGTCCAAAGCTGCCTTTGGTGAGGAGGTGGATGCAGTAGACACGGGTATCAGCAGAGAGACCT
CCTCGGACGTTGCGCTGGCGAGCCACATCCTTACTGCACTGAGGGAGAAGCAGGCTCCAGAGCTGAGCTTATCTA
GTCAGGATTTGGAGTTGGTTACCAAGGAAGACCCCAAAGCACTGGCTGTTGCCTTGAACTGGGACATAAAGAAGA
CGGAGACTGTTTCAAGGAGGCTGTGAGCGGGAGCTCGCCCTGCGCCTGCAGCAGACGCAGAGCTTGCATTCTCTCC
GGAGCATCTCAGCAAGCAAGGCCTCACACCTGGTGACCTGCAGAATGCTAAGCGAGCCAGACAGGATCCACAT
AGCAGCAGCGGGAAGTGTGCCAAGGAAGCTCTGTGGCGTTGTGTTATTGGTAGACACCCCTCAGCCTCATCATTTG
ACTACCTATGTACTACTCTACCCCTGCCTTAGAGCACCTTCCAGAGAAGCTATTCCAGGTCTCAACATACGCCG
TTCCACCAATTTTTTTTTTTAGCCCCACCAGCTTCAGGACTTCTGCCAATTTTGAATGATATAGCTGCACCAACAA
TATCCCGCCTCCTCTAATTACATATGATGTTCTCTGTTCAAAAGTAATTGGCAGTGATTGGCCAGGCGCAGTGGC
TCACGCCTGTAATCCCAGCACTGGGAGGCCGAGGGGGGCGGATCGTGAAGTCAGGAGATCGAGACCATCCTGGCT
AACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAAAATTAGCCAGCCATGGTGGCGGGCGCCTGTAATCCC
AGCTACTTGGGAGGCTGAGGCAGGAGAATGGCATGAACCTGGGAGGCAGAGCTTGCAGTGAGCTGAGATTGCGCC
ACTGCACTCCAGCCTGGGCAACAGAGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAA

51/6881
FIGURE 49

MEVTGDAGVPESGEIRTLKPCLLRNYSREQHGVAASCLEDLRSKACDILAIKSLTPVTLVLAEDGTIVDDDDY
FLCLPSNTKFVALASNEKWAYNNSDGGTAWISQESFDVDETDGAGLKWKNNVARQLKEDLSSIIILLSEEDLQMLV
DAPCSDLAQELRQSCATVQRLQHTLQQVLDQREEVRQSKQLLQLYLQALEKEGSLLSKQEESKAAFGEVDAVDT
GISRETSSDVALASHILTALREKQAPELSLSSQDLELVTKEDPKALAVALNWDIKKTETVQEACERELALRLQQT
QSLHSLRSISASKASPPGDLQNPKRARQDPT

52/6881
FIGURE 50

CGGCGGAGCTGGTCCCGTTGTGCTGCGGGCGCCGCGCGGCCTGCAGTCCCAGGGCCCGCGCCCCGCGCCGCCCGCCC
GCCCCGCCATGGAGCCCCGGCCCCGACGGCCCCGCCGCTCCGGCCCCGCCGCCATCCGCGAGGGCTGGTTCCGCGA
GACCTGCAGCCTGTGGCCCCGGCCAGGCCCTGTCGCTGCAGGTGGAGCAGCTGCTCCACCACCGGCGCTCGCGCTA
CCAGGACATCCTCGTCTTCCGCGAGTAAGACCTATGGCAACGTGCTGGTGTGGACGGTGTATCCAGTGCACGGA
GAGAGACGAGTTCTCCTACCAGGAGATGATCGCCAACCTGCCTCTCTGCAGCCACCCCAACCCGCGAAAGGTGCT
GATCATCGGGGGCGGAGATGGAGGTGTCCTGCGGGAGGTGGTGAAGCACCCCTCCGTGGAGTCCGTGGTCCAGTG
TGAGATCGACGAGGATGTATCCAAGTCTCCAAGAAGTTCCTGCCAGGCATGGCCATTGGCTACTCTAGCTCGAA
GGTGACCCCTACATGTGGGTGACGGTTTTGAGTTCATGAAACAGAATCAGGATGCCTTCGACGTGATCATCACTGA
CTCCTCAGACCCCATGGGCCCCGCGGAAAGTCTCTTCAAGGAGTCTATTACCAGCTCATGAAGACAGCCCTCAA
GGAAGATGGTGTCTCTGCTGCCAGGGCGAGTGCAGTGGCTGCACCTGGACCTCATCAAGGAGATGCGGCAGTT
CTGCCAGTCCCTGTTCCTCGTGGTGGCCTATGCCTACTGCACCATCCCCACCTACCCAGCGGCCAGATCGGCTT
CATGCTGTGCAGCAAGAACCCGAGCACGAACCTCCAGGAGCCGGTGCAGCCGCTGACACAGCAGCAGGTGGCGCA
GATGCAGCTGAAGTACTACAACCTCCGACGTGCACCGCGCCGCTTTGTGCTGCCCAGTTTTGCCGCAAGGCCCT
GAATGATGTGAGCTGAGCCCAGGCGCCACCACTGATGCCACCCAGGACCTCGGACCTTGAGCCTGCGGGGTGCC
TCGGCCCCCTCCAGCCCCGGGCGGACCTCCTGCTGGCTCTCGCCCACCAACCAAGTGTTACAAGCCCCAGAATGC
TGCCCGGCCTGCCCTGCTGGGCGGACTGTCTGTGTGTCTGTCTCTTGGCGTTCCACCTCCAAGCCTATACCAGC
TGTGTACAGCGCCATCTCTCTGCCTTCTGTTGCCCCCG

53/6881
FIGURE 51

MEPGPDGPAASGPAAIREGWFRETCSLWPGQALSLQVEQLLHHRRSRYQDILVFRSKTYGNVLVLDGVIQCTERD
EFSYQEMIANLPLCSHPNPRKVLIIGGGDGGVLREVVKHPSVESVVQCEIDEDVIQVSKKFLPGMAIGYSSSKVT
LHVGDGFEFMKQNQDAFDVITDSSDPMGPAESLFKESYYQLMKTALKEDGVLCCQGECEWLHLDLIKEMRQFCQ
SLFPVVAYAYCTIPTYP SGQIGFMLCSKNPSTNFQEPVQPLTQQQVAQMLKYNSDVHRAAFVLPEFARKALND
VS

54/6881
FIGURE 52

AGGCGCAGGCGCAGGCGAGGGGCTGGGTGGCGGTTGAGACAGCGGCGGTACTGGGAGGCGTAGGTGAGGGTCGCG
AGGCTGCCCCGAGCTTCTGAGCGAGCGCGGTGCTTTTGGGAACGCGGGACGGGCGATCTGCGGCGCCAGGAGCTGG
GCCGAGGCGCGGCGGCGCGGCTGCCGGCTGCCCTGTGAATGGGAAGTTACGCGAAGTCCACCCAGCGTTTCTGAG
GCAATCTGAAGGCAAATCCTGTTTAGACCCAGGCGAAGGTTCCCGGTGACCCGGGCTCTCACCAGCCAATTGTCC
CTTGCCGTCTCTCCTGAGGGTGCCTGGAGCTTAAGCACTGTGTGCTCTTGGCCTCCACACTGGGGATGCCGCTGAC
TCCCACTGTCCAGGGCTTCCAGTGGATTCTCCGAGGCCCTGATGTAGAAACTTCCCCATTGGGTGCACCAAGAGC
AGCCTCACATGGTGTGGGCTTGACATCAAGAGCTGCCAGATCCAACAGGAAGATGGCCAATCTTTCCTAAGCTGCT
CACCTTACAAGAAAACGAATCGTACTGCTAAGAATTCAAACCTTCAGCAGTCATGGGGAGCCTTGGAAGGAGCCCG
AATCACTGATGGAATTGGACAGTGCATGGAGATGGTTCAGCAGGACAAGGGTAAGTGCAGGGGCAAGTCCAGGTC
ATACTGAGAGACAACGAGTGGCGCTGACAGAGACAGACAAAGATAAAATCAAAAGTTTGTGCTTCATCTTCAAAA
ACTCAAACATAATAACAAACTTGGCCTT

55/6881
FIGURE 53

MPLTPTVQGFQWILRGPDVETSPLGAPRAASHGVG

56/6881
FIGURE 54

CTGCGCCCGCGACGGAGGCGCGCTTCAAAGCGCAGGCGCGGGGAGGGGGTGGGGGAGGAGGGAAAGCGGCGAGTA
AGATGGAAGATGAGGAGGTCGCTGAGAGCTGGGAAGAGGCGGCAGACAGCGGGGAAATCCAAATCTCCTCCCAA
GTGCCCATTGTGATTGAGGACGATAGCCTTCCCGCGGGGCCCCCTCCACAGATCCGCATCCTCAAGAGGCCCCACC
AGCAACGGTGTGGTCAGCAGCCCCAACTCCACCAGCAGGCCCCACCCTTCCAGTCAAGTCCCTAGCACAGCGAGAG
GCCGAGTACGCCGAGGCCCCGGAAGCGGATCCTGGGCAGCGCCAGCCCCGAGGAGGAGCAGGAGAAACCCATCCTC
GACAGGCCAACCAGGATCTCCCAACCCGAAGACAGCAGGCAGGCCAATAATGTGATCAGACAGCCTTTGGGTCTT
GATGGGTCTCAAGGCTTCAAACAGCGCAGATAAATGCAGGCAAGAAAAGATGCCGCCGTTGCTGCCGTACCCGCC
TCTTGGGTCTGTCGCCACGGGTTGCACTGCCGTGGCAGACAGCTGGACTTGAGCAGAGGGAAACGACCTGACTTAC
TTGCACTGTGATCCCCCTTGCTCCGCCCCACTGTGACCTTGAACCCCATGCACTGTGACCTCCCCCTTCTCCCCC
TTCCCACTGTGATTGGCACATCGACAAGGGCTGTCCCAAGTCAATGGAAAGGGAAAGGGTGGGGGTTAGGGGAAG
GTTGGGGGGACCCAGCAAGGACTCAGAGAGTCAGACAGTGCCACTTGGCCACTTGGGGTAAAGCCAGTGCCAGCA
ATAACAGTTTATCATGCTCATTAAATTTGGGATTTCAAAACACAAATGAAAACCTCACACCCACCCACCCCAAGTG
CATGTCTCCATCACTTAAAAAGTAAGTTCCATTTGAAAATATCCTTTCTTTTTTTTTTCTTCCATTTTTTGTTG
TTTATACAAATATCTGATTTGCAAGAAAAAGTGCATGGGAGGGGTTTTAGTGGTTTAATGAATTTTTAATTAAGA
AAGGGTAGTTTGGTAGTCTACTTAAAAATGTTTCTGGGAAATTCACTAGAAACATTAACCAATAGGATTTTGGTG
AGCTTAGCTTCTGTATTCCTACTGCCGCCAGAAAAGGGCAGGGCTCTGCAGCCGCCAGGACAGACGAGCACCC
CATGCCTATACCTCCCTCCCCGAGCTAAGTCCCAGGGCATCTGGGCCTTGCCCTGGAGACTGGGCTAGCTCTGTAG
GCTCGGAGAGCCTGGGGAGGGTGCCAACCCACCTCTAGTATTTTGGGAGATAGGGAAAGTGAACCGACTTCCCC
TTCCCATACCCCTCAGGGTGGTTCCCTACCAGCCAGGCTTACTACTTCTAGAAGAAAGCAGAGTGCCAGGGAGTG
AGATTGCATCCCTGGGCTTAGAAGTGACGGAGAGAAGACTTGTTTTAGTATTTTGCCATCAGCACAAAGGAAAACCA
GGAGAGAGTCTGCCTCCAGGACTCTGAGCCTTCTGCCTCGTATGTTTCAAGAGGTGGATAGGTCTTCCCACTCCAG
CATGGCTTGAACCTTAGGGGTCTGCAGTGCTCCATCTCCATTGGTGGCCCCAGCTCA'GTAACCTATACCTGGTAC
ATTTCTGTGTGCAATCAGTACCTTGAAGGCAGAACATTCTGAATAAAGTTGGAAAAAGAACA

57/6881
FIGURE 55

CCACCTGGCACTGCCCACCACCCTGTAGCAGTGTGCCAGCAGGAGAGTCTGTCCTTTGCAGAGCTGCCCCGCCCTG
AAGCCCCGAGCCCAGTGTGTCTGGACCTTTTCCCTGTTGCCCCAGAGGAGCTTCGGGCTCCTGGCAGCCGCTGG
TCCCTGGGGACCCCTGCCCCCTCTCCAAGGGTTGCTATGGCCATTATCCCCAGGAGGCTCAGATACAGAGATCACC
AGCGGGGGGATGCGGCCAGCAGGGCTGGCAGCTGGCCACACTGTCCTGGTGCCAGCCCCAGCTCTGGAGGGA
CCCTGGAGTCCCCGACACACACAGCCACAGCGCCGGGCCAGCCACGGCTCGGAGAAGAAGTCTGCCTGGCGCAAG
ATGCGGGTGTACCAGCGTGAAGAGGTCCCCGGCTGCCCCGAGGCCACGCTGTCTTCTTAGAGCCTGGCCAGGTA
GTGCAAGAGCAGGCCCTGAGCACAGAGGAGCCAGGGTGGAGTTGTCTGGGTCCACCCGAGTGAGCCTCGAAGGT
CCTGAGCGGAGGCGCTTCTCGGCATCGGAGCTGATGACCCGGCTGCACTCTTCTCTGCGCCTGGGGCGGAATTCA
GCAGCCCCGGGCACTCATCTCTGGGTGAGGCACCGGAGCAGCCCGGGAAGGGAAGCATCTGGAATGGAGGCTCGA
AGTGTAGAGATGAGCGGGGACCGGGTGTGCGGGCCAGCCCTGGTGACTCACGAGAGGGCGATTGGTCCGAGCCC
AGGCTAGACACACAGGAAGAGCCGCCCTTTGGGGTCCAGGAGCACCAACGAGCGGCGCCAGTCTCGATTCTTCCTT
AACTCCGTCTCTATCAGGAATACAGCGACGTGGCCAGCGCCCGCGAACTGCGGCGGCAGCAGCGCGAGGAGGAG
GGCCCCGGGGACGAGGCCGAGGGCGCAGAGGAGGGGCCGGGGCCGCCGCGGGCCAACCTCTCCCCCAGCAGCTCC
TTCCGGGCGCAGCGCTCGGCGCGAGGCTCCACCTTCTCGCTGTGGCAGGATATCCCCGACGTACGCGGCAGCGGC
GTCCTGGCCACGCTGAGCCTGCGGGACTGCAAGCTGCAGGAGGCCAAGTTTGAGCTGATCACTCCGAGGCCTCC
TACATCCACAGCCTGTGCGTGGCTGTGGGCCACTTCTTAGGCTCTGCCGAGCTGAGCGAGTGTCTGGGGGCGCAG
GACAAGCAGTGGCTGTTTTCCAAACTGCCCCAGGTCAAGAGCACCAGCGAGAGGTTCTGTCAGGACCTGGAGCAG
CGGCTGGAGGCAGATGTGCTGCGCTTCAGCGTGTGCGACGTGGTGCTGGACCACTGCCCCGCCCTCCGCAGAGTC
TACCTGCCCTATGTACCAACCAGGCCTACCAGGAGCGCACCTACCAGCGCCTGCTCCTGGAGAACCCAGGTTTC
CCTGGCATCCTGGCTCGCCTGGAGGAGTCTCCTGTGTGCCAGCGTCTGCCCTTACCTCCTTCTTATCCTGCCC
TTCCAGAGGATCACCCGCCTCAAGATGTTGGTGGAGAACATCCTGAAGCGGACAGCACAGGGCTCTGAAGACGAA
GACATGGCCACCAAGGCCTTCAATGCGCTCAAGGAGCTGGTGCAGGAGTGAATGCTAGTGTACAGTCCATGAAG
AGGACAGAGGAACATCCACCTGAGCAAGAAGATCCACTTTGAGGGCAAGATTTTCCCGCTGATCTCTCAGGCC
CGCTGGCTGGTTTCGGCATGGAGAGTTGGTAGAGCTGGCACCCTGCCTGCAGCACCCCTGCCAAGCTGAAGCTG
TCCAGCAAGGCAGTCTACCTCCACCTCTTCAATGACTGCTTGCTGCTCTCTCGGCGGAAGGAGCTAGGGAAGTTT
GCCGTTTTCTGTCATGCCAAGATGGCTGAGCTGCAGGTGCGGGACCTGAGCCTGAAGCTGCAGGGCATCCCCGGC
CACGTGTTCTCTCCAGCTCCTCCACGGGCAGCACATGAAGCACCAGTTCTGCTGCGGGCCCGGACGGAAAGT
GAGAAGCAGCGATGGATCTCAGCCTTGTGCCCCCTCCAGCCCCCAGGAGGACAAGGAGGTCATCAGTGAGGGGGAA
GATTGCCCCCAGGTTTCACTGTGTTAGGACATACAAGGCACTGCACCCAGATGAGCTGACCTTGGAGAAGACTGAC
ATCCTGTGCTAGTGAGGACCTGGACCAGTGACGGCTGGCTGGAAGGGGTCCGCCTGGCAGATGGTGAGAAGGGGTGG
GTGCCCCAGGCCTATGTGGAAGAGATCAGCAGCCTCAGCGCCCGCCTCCGAAACCTCCGGGAGAATAAGCGAGTC
ACAAGTGCCACCAGCAAACCTGGGGGAGGCTCCTGTGTGATGGGCAGCCATGGCCTAGGACCCACCTCCATGCCT
GGCTCCTGGATGGTCTGAGGGGGCCTGCAGTGTCTCCATTCCCCAAGCTGCTCCTGCTGGCACTTCGTTCTGT
GGCCTTGGCATTGAGGGCACAGGCTGGACACAGGAATGGGGGCGCCTCCAGAGGGTCTCTCCGTCTCATGCTCC
TCAGTGTCCACACTTCAAGGCCAAGGATAGTTTCTTCTCTGACATGGGGACCATAACAGGTGATCACTGATACC
TGGCAAAGACTGGGGCCCTCTCCTTTCTATGTCCTCAATCCTGCCTGACTCTTGGTCCTTCTGGCAGGGACCTGG
CTGGGGAACGTTCTGGTGTGATGGTGTGCTGGGACCTATATGTATATTTATATATATCTGGGGTCTTGTCTACCAC
CTCC

58/6881
FIGURE 56

MDCGPPATLQPHLTGPPGTAHHPVAVCQQESLSFAELPALKPPSPVCLDLFPVAPEELRAPGSRWSLGTPAPLQG
LLWPLSPGGSDTEITSGGMRPSRAGSWPHCPGAQPPALEGPWSPRHTQPQRRASHGSEKKSAWRKMRVYQREEVP
GCPEAHAVFLEPGQVVQEALSTEEPRVELSGSTRVSLEGPERRRFSASELMTRLHSSRLGRNSAARALISGSG
TGAAREGKASGMEARSVEMSGDRVSRPAPGDSREGDWSEPRLDTQEEPPLGSRSTNERRQSRFLNSVLYQEYSD
VASARELRRQQREEEGPGDEAEGAEEGPGPPRANLSPSSSFRAQRSARGSTFSLWQDIPDVRGSGVLATLSLRDC
KLQEAKEFELITSEASYIHSLSVAVGHFLGSAELSECLGAQDKQWLFSKLPEVKSTSERFLQDLEQRLEADVLRFS
VCDVVLDHCPAFRRVYLPYVTNQAYQERTYQRLLENPRFPGILARLEESPVCQRLPLTSFLILPFQRITRLKML
VENILKRTAQGEDEDMATKAFNALKELVQECNASVQSMKRTEELIHLSSKKIHFEGKIFPLISQARWLVRHGELV
ELAPLPAAPPAKLKLSKAVYLHLFNDCLLLSRRKELGKFVAVFHAKMAELQVRDLSLKLQGIPIGHVFLQLLHG
QHMKHQFLLRARTSEKQRWISALCPSSPQEDKEVISEGEDCPVQVCVRTYKALHPDELTLKTDILSVRTWTSD
GWLEGVRLADGEKGWVPQAYVEEISSLSARLRNLRENKRVTSATSKLGEAPV

59/6881
FIGURE 57A

GAAGTTGCGCGCAGGCCGGCGGGCGGGAGCGGACACCGAGGCCGGCGTG CAGGCGTGCGGGTGTGCGGGAGCCGG
GCTCGGGGGGATCGGACCGAGAGCGAGAAGCGCGGCATGGAGCTCCAGGCAGCCCGCGCCTGCTTCGCCCTGCTG
TGGGGCTGTGCGCTGGCCCGGGCCGGCGGGCGGCAGGGCAAGGAAGTGGTACTGCTGGACTTTGCTGCAGCTGGA
GGGGAGCTCGGCTGGCTCACACACCCGTATGGCAAAGGTTGGGACCTGATGCAGAACATCATGAATGACATGCCG
ATCTACATGTACTCCGTGTGCAACGTGATGTCTGGCGACCAGGACAACCTGGCTCCGCACCAACTGGGTGTACCGA
GGAGAGGCTGAGCGTATCTTCATTGAGCTCAAAGTTTACTGTACGTGACTGCAACAGCTTCCCTGGTGGCGCCAGC
TCCTGCAAGGAGACTTTCAACCTCTACTATGCCGAGTCCGACCTGGACTACGGCACCAACTTCCAGAAGCGCCTG
TTCACCAAGATTGACACCATTTGCGCCCGATGAGATCACCGTCAGCAGCGACTTCGAGGCACGCCACGTGAAGCTG
AACGTGGAGGAGCGCTCCGTGGGGCCGCTCACCCGCAAAGGCTTCTACCTGGCCTTCCAGGATATCGGTGCCTGT
GTGGCGCTGCTCTCCGTCCGTGTCTACTACAAGAAGTGCCCCGAGCTGCTGCAGGGCCTGGCCCACTTCCCTGAG
ACCATCGCCGGCTCTGATGCACCTTCCCTGGCCACTGTGGCCGGCACCTGTGTGGACCATGCCGTGGTGCCACCG
GGGGGTGAAGAGCCCCGTATGCACTGTGCAGTGGATGGCGAGTGGCTGGTGCCATTGGGCAGTGCCTGTGCCAG
GCAGGCTACGAGAAGGTGGAGGATGCCTGCCAGGCCTGCTCGCCTGGATTTTTTAAGTTTGAGGCATCTGAGAGC
CCCTGCTTGGAGTGCCCTGAGCACACGCTGCCATCCCCTGAGGGTGCCACCTCCTGCGAGTGTGAGGAAGGCTTC
TTCCGGGCACCTCAGGACCCAGCGTCGATGCCTTGACACGACCCCCCTCCGCCCCACACTACCTCACAGCCGTG
GGCATGGGTGCCAAGGTGGAGCTGCGCTGGACGCCCCCTCAGGACAGCGGGGGCCGCGAGGACATTGTCTACAGC
GTCACCTGCGAACAGTGTGGCCCGAGTCTGGGGAATGCGGGCCGTGTGAGGCCAGTGTGCGCTACTCGGAGCCT
CCTCACGGACTGACCCGCACCAAGTGTGACAGTGAGCGACCTGGAGCCCCACATGAACCTACACCTTACCCTGGAG
GCCCCGAATGGCGTCTCAGGCCTGGTAACAGCCGCAGCTTCCGTACTGCCAGTGTGAGCATCAACCAGACAGAG
CCCCCAAGGTGAGGCTGGAGGGCCGAGCACCACCTCGCTTAGCGTCTCCTGGAGCATCCCCCGCCGAGCAG
AGCCGAGTGTGGAAGTACGAGGTCACTTACCGCAAGAAGGGAGACTCCAACAGCTACAATGTGCGCCGCACCGAG
GGTTTCTCCGTGACCCTGGACGACCTGGCCCCAGACACCACCTACCTGGTCCAGGTGCAGGCACTGACGCAGGAG
GGCCAGGGGGCCGGCAGCAAGGTGCACGAATTCAGACGCTGTCCCCGGAGGGATCTGGCAACTTGGCGGTGATT
GGCGGCGTGGCTGTGCGGTGTGGTCTGCTTCTGGTGCTGGCAGGAGTTGGCTTCTTTATCCACCGCAGGAGGAAG
AACCAGCGTGCCCGCCAGTCCCCGGAGGACGTTTACTTCTCCAAGTCAGAACAACCTGAAGCCCCCTGAAGACATAC
GTGGACCCCCACACATATGAGGACCCCAACCAGGCTGTGTTGAAGTTCACTACCGAGATCCATCCATCCTGTGTC
ACTCGGCAGAAGGTGATCGGAGCAGGAGAGTTTGGGGAGGTGTACAAGGGCATGCTGAAGACATCCTCGGGGAAG
AAGGAGGTGCCGGTGGCCATCAAGACGCTGAAAGCCGGCTACACAGAGAAGCAGCGAGTGGACTTCCCTCGGCGAG
GCCGGCATCATGGGCCAGTTCAGCCACCACAACATCATCCGCCTAGAGGGCGTCATCTCCAAATACAAGCCCATG
ATGATCATCACTGAGTACATGGAGAATGGGGCCCTGGACAAGTTCTTCCGGGAGAAGGATGGCGAGTTCAGCGTG
CTGCAGCTGGTGGGCATGCTGCGGGGCATCGCAGCTGGCATGAAGTACCTGGCCAACATGAACATATGTGCACCGT
GACCTGGCTGCCCCGAACATCCTCGTCAACAGCAACCTGGTCTGCAAGGTGTCTGACTTTGGCCTGTCCGCGTG
CTGGAGGACGACCCCGAGGCCACCTACACCACAGTGGCGGCAAGATCCCCATCCGCTGGACCGCCCCGGAGGCC
ATTTCTTACCGGAAGTTACCTCTGCCAGCGACGTGTGGAGCTTTGGCATTGTGATGTGGGAGGTGATGACCTAT
GGCGAGCGGCCCTACTGGGAGTTGTCCAACCACGAGGTGATGAAAGCCATCAATGATGGCTTCCGGCTCCCCACA
CCCATGGACTGCCCCCTCCGCCATCTACCAGCTCATGATGCAGTGTGGCAGCAGGAGCGTGCCCGCCGCCCAAG
TTCGCTGACATCGTCAGCATCCTGGACAAGCTCATTCTGCCCCCTGACTCCCTCAAGACCCCTGGCTGACTTTGAC
CCCCGCGTGTCTATCCGGCTCCCCAGCACGAGCGGCTCGAGGGGGTGCCCTTCCGCACGGTGTCCGAGTGGCTG
GAGTCCATCAAGATGCAGCAGTATACGGAGCACTTCATGGCGGGCCGGCTACACTGCCATCGAGAAGGTGGTGAG
ATGACCAACGACGACATCAAGAGGATTGGGGTGC GGCTGCCCCGCCACCAGAAGCGCATCGCCTACAGCCTGCTG
GGACTCAAGGACCAGGTGAACACTGTGGGGATCCCCATCTGAGCCTCGACAGGGCCTGGAGCCCCATCGGCCAAG
AATACTTGAAGAAACAGAGTGGCCTCCCTGCTGTGCCATGCTGGGCCACTGGGGACTTTATTTATTTCTAGTTCT
TTCCTCCCCCTGCAACTTCCGCTGAGGGGTCTCGGATGACACCCTGGCCTGAACTGAGGAGATGACCAGGGATGC
TGGGCTGGGCCCTCTTTCCCTGCGAGACGCACACAGCTGAGCACTTAGCAGGCACCGCCACGTCCCAGCATCCCT
GGAGCAGGAGCCCCGCCACAGCCTTCGGACAGACATATGGGATATTCCCAAGCCGACCTTCCCTCCGCCTTCTCC
CACATGAGGCCATCTCAGGAGATGGAGGGCTTGGCCCAGCGCCAAGTAAACAGGGTACCTCAAGCCCCATTTCTT
CACACTAAGAGGGCAGACTGTGAACCTGACTGGGTGAGACCCAAAGCGGTCCCTGTCCCTCTAGTGCCCTTCTTTA
GACCTCGGGCCCCATCCTCATCCCTGACTGGCCAAACCCTTGCTTCTCGGGCCTTTGCAAGATGCTTGGTTGT

60/6881
FIGURE 57B

GTTGAGGTTTTAAATATATATTTTGTACTTTGTGGAGAGAATGTGTGTGTGTGGCAGGGGGCCCCGCCAGGGCT
GGGGACAGAGGGTGTCAAACATTCGTGAGCTGGGGACTCAGGGACCGGTGCTGCAGGAGTGCCTGCCCATGCCC
CAGTCGGCCCCATCTCTCATCCTTTTGGATAAGTTTCTATTCTGTCAGTGTTAAAGATTTTGTGTTGTTGGACAT
TTTTTTCGAATCTTAATTTATTATTTTTTTTATATTTATTGTTAGAAAATGACTTATTTCTGCTCTGGAATAAAG
TTGCAGATGATCAAACCG

61/6881
FIGURE 58

GGTGGGCTGTAGGAATGAGGAGGAACTTAGGGAGAAACAGCTAGTGGGGAGGTAGGGCCTGGGGGAGCCGCCCCCT
TGCCCCAAGAGAAGGAGCCAGAACCCCCGGATCTGCATGCAAGGCCTGCTCCATGCCTCGCTCACAGCAGCCCAT
CCCACAGCCCGCCCCGGTGGGGCAGGCAACATCAAGACCCTAGGAGACGCCTATGAGTTTGCGGTGGACGTGAGA
GACTTCTCACCTGAAGACATCATTGTCACCACCTCCAACAACCACATCGAGGTGCGGGCTGAGAAGCTGGCGGCT
GACGGCACCGTCATGAACACCTTCGCTCACAAGTGCCAGCTGCCGGAGGACGTGGACCCGACGTCGGTGACCTCG
GCTCTGCGGGAGGACGGCAGCCTCACTATCCGGGCACGGCGTCACCCGCATACAGAACACGTCCAGCAGACCTTC
CGGACGGAGATCAAAATCTGAGTGCCCTCTCCCTTCCCTTTCCCTGTCCCCCGCCCCACGCCTGCCAGCAAAGCC
TCGCTAACCCTTACAACAGCTCCAGGACATCTCAGCCCAGGTTCTAGCCCCACGCACCCAGACCCAGGTG
GACCATCCTCCCAAACCTAGGGCCCTCCACTCTATCCAGGGCAGGCCAGGGACTCCCTGGCCTGACACATGATGCC
CAGATTTAGATTTGGCCTCCGTCACCTAATCCAGAGTACAGGGGCTGGGGTCAGGGAAGGAAGATCTAAAGAAC
CCACTGTGGGTGAGGGGAATGGGACCAGCAGGACATATGGGCAAGCTCTGCAGGACAGACAGGCAGACAAACCCT
CTGATCTATGA

62/6881
FIGURE 59

GCTCGTGTTAAATCTAGAACCGTAGCCAGACATGGGACTGGAGGACGAGCAAAAGATGCTTACCGAATCCGGAGA
TCCTGAGGAGGAGGAAGAGGAAGAGGAGGAATTAGTGGATCCCCTAACACAGTGAGAGAGCAATGCGAGCAGTT
GGAGAAATGTGTAAAGGCCCGGGAGCGGCTAGAGCTCTATGATGAGCATGTATCCTCTCGATCACATACAGAAGA
GGATTGCACGGAGGAGCTCTTTGACTTCTTGCATGCAAAGGACCATTGCGTGGCCACAACTCTTTAACAACCTT
GAAATAAATGTGTGGACTTAATTCACCCCAGCCTTCATCATCTGGGCATCAGAATATTCCTTATGGTTTCGGAT
GTACCAATTTGTTTCTTATTTGTGTAAGTTCACATGAACCTCGTGGGTTTTGGCTTAGGCTGGTAGCTTC
TATGTAATTCGCAGTGATTCCATCTAAATAAAAGTTCTGTGATCTGC

FIGURE 60

[illegible]

64/6881
FIGURE 61

MIRTL L L S T L V A G A L S C G D P T Y P P Y V T R V V G G E E A R P N S W P W Q V S L Q Y S S N G K W Y H T C G G S L I A N S W V L T A A H C I
S S S R T Y R V G L G R H N L Y V A E S G S L A V S V S K I V V H K D W N S N Q I S K G N D I A L L K L A N P V S L T D K I Q L A C L P P A G T I L P
N N Y P C Y V T G W G R L Q T N G A V P D V L Q Q G R L L V V D Y A T C S S S A W W G S S V K T S M I C A G G D G V I S S C N G D S G G P L N C Q A S
D G R W Q V H G I V S F G S R L G C N Y Y H K P S V F T R V S N Y I D W I N S V I A N N

65/6881
FIGURE 62

CGGACGCGTGGGCCCCGGCCAAGGCGAGTGCCGCGCGGGCCACCA**ATG**GCCACGGACGAGCTGGCCACCAAGCTGAG
CCGGCGGCTGCAGATGGAGGGCGAGGGCGGGCGGCGAGACCCCGGAGCAGCCCGGGCTGAACGGGGCAGCGGGCGGC
GGCGGGCGGGGACCCGACGAGGCGGCGGAGGCGCTGGGCAGCGCGGACTGCGAGCTGAGCGCCAAGCTGCTGCG
GCGCGCAGACCTCAACCAGGGCATCGGCGAGCCCCAGTCGCCCAGCCGCCGCTCTTCAACCCCTACACCGAGTT
CAAGGAGTTCTCCAGGAAGCAGATCAAGGACATGGAGAAGATGTTCAAGCAGTATGATGCCGGGCGGGACGGCTT
CATCGACCTGATGGAGCTAAACTCATGATGGAGAACTTGGGGCCCCCTCAGACCCACCTGGGCCTGAAAAACAT
GATCAAGGAGGTGGATGAGGACTTTGACAGCAAGCTGAGCTTCCGGGAGTTCTCCTGATCTTCCGCAAGGCGGC
GGCCGGGGAGCTTCAGGAGGACAGCGGGCTGTGCGTGCTGGCCCCGCTCTCTGAGATCGACGTCTCCAGTGAGGG
TGTCAGGGGGGCCAAGAGCTTCTTTGAGGCCAAGGTCCAGGCCATCAACGTGTCCAGCCGCTTCGAGGAGGAGAT
CAAGGCAGAGCAGGAGGAAAGGAAGAAGCAGGCGGAGGAGATGAAGCAGCGGAAAGCGGCCTTCAAGGAGCTGCA
GTCCACCTTTAAG**TAG**CGGGGGCTGCAGCCGACCGCCCTGCTCCGGCCCCAGTGTGGTGGGCGAGGGTGGCGCAT
GGGAGGCCGAGCCTGAATCCTTGCTGTGTCTGACGGGACCACTACTAAAAACCTAAAAATATCTGTGAATGGAG
CAAGTTCAAGGGTCTTATGGAGGTGGCCCGGGCCCCCTCCCCGCTCCCTTCCACTCTGCACGAGGCCGCCACACCGG
CGCTGGCTCCCTGCCCGGGCCGGCCCTCCCTGGCAATCCCTGGGCTCTCTTGACCCCTAACTGCCCCCTGCCTG
CTCCGGCACTGCCCCAGGCCAGCTCCTGGCCCTAGGTCCCTCCCAGCCCCATGTGCCTGCCGCTGCCCTCCAC
ACATCCCTGTCCCCCAACCCGGGAACCCCTGCCCTCCTCCAGCAGGCCGCACCGCCCCCTGGGGCCCCCTGCCAG
CCCCTTCCCAGGCTGGGAGACAGCAGAAGAGATAGAATCAGGGCTGCCCCCACAGAGTGGGACCCAAGGGGCTAA
TTGGAGGCACGAGGGGACCCCTCCCCAGGGCCTTTTCTCCTCTGCGTCTTCCATCTACTGAAATGGGAGAGGGG
GTGGGGAGCTTCTGTTCTGGTGAAGGGACCCGGGCAGGCCCCCAGCACCCCATGCTGACTTGGAGAACCCAGAT
CTCTGGGGCCCAGCCAGGCAGGGTGTGGGGGCAGCTGTGCCAATCTACCTCACAGGCCACCCCTGCCGGGCAT
GCCGTGGGATCATGGGCAGGGAAGGCTCTGGGGGTGCGAGACACCGCTGCTTAGCACCCCCAGCCAGAACACCCCT
GAGGGTCTCGGGGCTCTGGAGAGAGTGGGGCGGGAGGAAGAATTGGCACCTTCTAGGGAAGGAGACGAGCGCTT
CGCCTTGATTCTCCGAGAAGCCTCCGAGAAGTGCTTTAAGTGTGTTTGATGCGCCAGGCGGTGGGCAGCGGGGG
CCTGTCCAGCCCTCTCCCGCCATCCTTCCCCAAGTGACGTCCACTGCCTTGTACACGCGACCTGCCTGTCATGC
CCACCCCTGAGGAAGCATGGGGACCCTAACACCCTGGTGCCCTGCACCAGACAGGCCGTGGTCAGGCCCAGGCC
ACCGGCCGGGTCTGCCACAGCTTCCCACGTGCTTGCTGACATGCGTGTGCCTGTGTGTGGTGTCTGTTGCTGTG
TCGTGAAACTGTGACCATCACTCAGTCCAAACAAGTGAGTGCCCTCGAGGCCACAGTTATGCAACTTTCAGTGT
GTGTACATAACGACGTCACCTGCTTTTTTAACTCGATAACTCTTTATTTTAGTAAAATGCCAGGAGTCTTGGAAAGC
TACGCGGACTTGCAGAGGTTTTATTTTTTGGCCTTAGAATCTGCAGAAATTAGGAGGCACCGAGCCCAGCGCAGC
AGCCTCGGACCCGGATTGCGTTTGCCTTAGCGGATATGTTTATACAGATGAATATAAAATGTTTTTTTCTTTGGG
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

66/6881
FIGURE 63

MATDELATKLSRRLQMEGEGGGGETPEQPGLNGAAAAAAGAPDEAAEALGSADCELSAKLLRRADLNQGIGEPQSP
SRRVFNPYTEFKEFSRKQIKDMEKMFQYDAGR DGFIDLMELKLMMEKLGAPQTHLGLKNMIKEVDEDFDSKLSF
REFLLIFRKAAGELQEDSGLCVLARLSEIDVSSEGVKGAKSFFEAKVQAINVSSRFEEEIKAEQEERKKQAEEM
KQRKA AFKELQSTFK

67/6881
FIGURE 64

GCCTCCCACTTGGTTGCTCGTACGCGGCTAGTGGGTCCTCAGTGGATGTAGGCTGGGCGCCGCGATGTTTCGACGG
GACACCGGCGGAGAGCGACCTCGGGGTAAAGGGTGGGGCTGACGTCAGGAGCCAAGATGGCGGCGGTGGTCGCC
CTCTCCTTGAGGCGCCGGTTGCCGGCCACAACCCTTGCGGAGCCTGCCTGCAGGCCTCCCGAGGAGCCCAGACA
GCTGCAGCCACAGCTCCCCGTATCAAGAAATTTGCCATCTATCGATGGGACCCAGACAAGGCTGGAGACAAACCT
CATATGCAGACTTATGAAGTTGACCTTAATAAATGTGGCCCCATGGTATTGGATGCTTTAATCAAGATTAAGAAT
GAAGTTGACTCTACTTTGACCTTCCGAAGATCATGCAGAGAAGGCATCTGTGGCTCTTGTGCAATGAACATCAAT
GGAGGCAACACTCTAGCTTGCACCCGAAGGATTGACACCAACCTCAATAAGGTCTCAAAAATCTACCCTCTTCCA
CACATGTATGTGATAAAGGATCTTGTTCCTCGATTGAGCAACTTCTATGCACAGTACAAATCCATTGAGCCTTAT
TTGAAGAAGAAGGATGAATCTCAGGAAGGCAAGCAGCAGTATCTGCAGTCCATAGAAGAGCGTGAGAACTGGAC
GGGCTCTACGAGTGCATTCTCTGTGCCTGCTGTAGCACCAGCTGCCCCAGCTACTGGTGGAACGGAGACAAATAT
CTGGGGCCTGCAGTTCTTATGCAGGCCTATCGCTGGATGATTGACTCCAGAGATGACTTCACAGAGGAGCGCCTG
GCCAAGCTGCAGGACCCATTCTCTCTATACCGCTGCCACACCATCATGAACTGCACAAGGACCTGTCCTAAGGGT
CTGAATCCAGGGAAAGCTATTGCAGAGATCAAGAAAATGATGGCAACCTATAAGGAGAAGAAAGCTTCAGTTTAA
CTGTTTCCATGCTAAACATGATTTATAACCAGCTCAGAGCTGAACATAATTTATATCTAATTTGAGTTCCTTTAA
AGATCTTGGTTTTCCATGAATACAGCATGTATAATAAAAATTTTAAGAAATAAATGTTATTCTACTTTATTAAACA
AAAAA

68/6881
FIGURE 65

MAAVVALSLRRRLPATTLGGAQLQASRGAQTAAATAPRIKKFAIYRWDPDKAGDKPHMQTYEVDLNKCGPMVLDA
LIKIKNEVDSTLTFRSCREGICGSCAMNINGGNTLACTRRIDTNLNKVSKIYPLPHMYVIKDLVPDLSNFYAQY
KSIEPYLKKKDESQEGKQQYLQSIEREKLDGLYECILCACCSTSCPSYWWNGDKYLGPVLMQAYRWMIDSRDD
FTEERLAKLQDPFSLYRCHTIMNCTRTCPKGLNPGKAIAEIKMMATYKEKKASV

69/6881
FIGURE 66

AGTGTTGGGGTTGGCGGCCACAGCTAAGTCCAACACCAGCATGTCGCTGCAGAGAATCGTGCGTGTGTCCCTGGA
GCATCCCACCAGCGCGGTGTGTGTGGCTGGCGTGGAGACCCTCGTGACATTTATGGGTCAGTGCCTGAGGGCAC
AGAAATGTTTGAGGTCTATGGGACGCCTGGCGTGGACATCTACATCTCTCCCAACATGGAGAGGGGCGGGAGCG
TGCAGACACCAGGCGGTGGCGCTTTGACGCGACTTTGGAGATCATCGTGGTCATGAACTCCCCAGCAATGACCT
CAACGACAGCCATGTTTCAGATTTCCCTACCACTCCAGCCATGAGCCTCTGCCCCTGGCCTATGCGGTGCTCTACCT
CACCTGTGTTGACATCTCTCTGGATTGCGACCTGAACTGTGAGGGAAGGCAGGACAGGAACTTTGTAGACAAGCG
GCAGTGGGTCTGGGGGCCAGTGGGTATGGCGGCATCTTGCTGGTGAACCTGTGACCGTGATGATCCGAGCTGTGA
TGTCCAGGACAATTGTGACCAGCACGTGCACTGCCTGCAAGACCTGGAAGACATGTCTGTCATGGTCCTGCGGAC
GCAGGGCCCTGCAGCCCTCTTTGATGACCACAACTTGTCTCCATACCTCCAGCTATGATGCCAAACGGGGCACA
GGTCTTCCACATCTGCGGTCTGAGGATGTGTGTGAGGCCTATAGGCATGTGCTGGGCCAAGATAAGGTGTCTTA
TGAGGTACCCCGCTTGTCATGGGGATGAGGAGCGCTTCTTCGTGGAAGGCCCTGTCTTCCCTGATGCCGGCTTCAC
AGGACTCATCTCTCTTCCATGTCACTCTGCTGGACGACTCCAACGAGGATTTCTCGGCATCCCCTATCTTCACTGA
CACTGTGGTGTTCGAGTGGCACCCCTGGATCATGACGCCCAGCACTCTGCCACCCCTAGAGGTGTATGTGTGCCG
TGTGAGGAACAACACGTGTTTTGTGGATGCGGTGGCAGAGCTGGCCAGGAAGGCCGGCTGCAAGCTGACCATCTG
CCCACAGGCCGAGAACCACAACGACCGCTGGATCCAGGATGAGATGGAGCTGGGCTACGTTTCAGGCGCCGCACAA
GACCCTCCCGGTGGTCTTTGACTCCCCAAGGAATGGGGAAGTGCAGGATTTCCCTTACAAAAGAATCCTGGGTCC
AGATTTTGGTTACGTGACTCGGGAACCACGCGACAGGTCTGTGAGTGGCCTGGACTCCTTTGGGAACCTGGAGGT
CAGCCCTCCAGTGGTGGCCAATGGGAAAGAGTACCCCTGGGGAGGATCCTCATTGGGGGCAACCTGCCTGGGTC
AAGTGGCCGAGGGTCACCCAGGTGGTGCGGGACTTCTCCATGCCAGAAGGTGCAGCCCCCGTGGAGCTCTT
TGTGGACTGGTTGGCCGTGGGCCATGTGGATGAGTTTCTGAGCTTTGTCCCTGCCCCGATGGGAAGGGCTTCG
GATGCTCCTGGCCAGCCCTGGGGCCTGCTTCAAGCTCTTCCAGGAAAAGCAGAAGTGTGGCCACGGGAGGGCCCT
CCTGTTCCAGGGGGTTGTTGATGATGAGCAGGTCAAGACCATCTCCATCAACCAGGTGCTCTCCAATAAAGACCT
CATCAACTACAATAAGTTTGTGCAGAGCTGCATCGACTGGAACCGTGAGGTGCTGAAGCGGGAGCTGGGCCTGGC
AGAGTGTGACATCATTGACATCCCACAGCTCTTCAAGACCGAGAGGAAAAAAGCAACGGCCTTCTTCCCTGACTT
GGTGAACATGCTGGTGTGGGGAAGCACCTGGGCATCCCCAAGCCCTTGGGGCCATCATCAATGGCTGCTGCTG
CCTGGAGGAGAAGGTGCGGTCCCTGCTGGAGCCGCTGGGCCTCCACTGCACCTTCATTGATGACTTCACTCCATA
CCACATGCTGCATGGGAGGTGCACTGTGGCACCAATGTGTGCAGAAAAGCCCTTCTCTTTCAAGTGGTGGAACAT
GGTGCCCTGAGACAGCTCCCACCCACCATCTGTCCCCCTGGGGCGGGCATTGGCCCAGGTGGTGGAGACAGAGA
CAGGCCCTGAACGATAAGCACCAAGAGACCCCAAGGCTCCAGATGGAACACTGAGGGTGACCGTCCCTCTCAGA
AGCCTTTTCCCTGGAAGTGTCCATGCCTCACCTGCAACCCATGTGGTTCTCAGACTTGAATCTTCTCGGCCCCC
AAAAAGAAGGACCTCATTCTTATAGCCTCTCCTGTGATTCAACACAACCCATGGAGATGTCCCTTCTCACTCT
GAAATCATCCATTTGGGGACAAATCCACATTGGGGTCTAGAAACATCCACGTATCTCATCAGCCATCTTGTCTG
TGCATCCTAACAGAGGAAGGATCCATGATTCTGCTTTGGTCCAATTGCTTCCCTCTCTGCAGAGGAACAACCTAA
AACCAGACCACTCCACGCAGGACAGGCAGGAGAGATTCTTCTTAAAGCCTCCCCCATAAAAAGGGAGCTGTGGAT
CCACTTAGATCAGGGCGGAACCATCTTTACCCGGCCAAGCTCCTGCCAGATGTTGACCCTCACCCAGCGTGAG
CTGTCACATAGTAGGAGCTTCTAGATGCATGTGGAAGCAATGAGAGTTGTCCCTTÀGCCTTATAAACTCCCCATG
ATCTGACATGCAGAAATCCAGCCTTGTCAGAAATCCTCCTGGAATTTCTTGAGAGCGAAAGTATCTGGGGGATTG
TTGGGTACTAGGGAGACTGGGTACAAGGGTGAAGTAGTTCCCATATAACACATGGTTGACTATGGTGATCCAC
CTTGTGATGGTTAATATTAGGTGTCTGGAGAAGGTTGCTTCATTGGCCCTGGGACTTCTCTCTGCAGGAGGAGAG
AACGCTGCCTCTCCTCTGGATTGGTCTCAGGCTCTCTGTTGGCCTTTGGTCAGCGTTTCCACATCCTGCTCTGCT
GCAGGAGAGGGGGCTAAGGGGCTGGATCCACCAAGGCAGCTCACAGCGGGAAACTCTGGGAATGAACCACTGAA
TTCAGGGGATGGGGGTGGGGGGCGGTTCTCGAGGTGTGTGCCAGCTACACGTGTGTTCTGTATGGGTCCAGCTG
CGTTTCCATCACTCGCTAATAAATCAACAGAAACAC

70/6881
FIGURE 67

AGCCAGAGGGACGAGCTAGCCCGACGATGGCCCAGGGGACATTGATCCGTGTGACCCCAGAGCAGCCCACCCATG
CCGTGTGTGTGCTGGGCACCTTGACTCAGCTTGACATCTGCAGCTCTGCCCCTGAGGACTGCACGTCCCTTCAGCA
TCAACGCCTCCCCAGGGGTGGTCTGTGGATATTGCCACGGCCCTCCAGCCAAGAAGAAATCCACAGGTTCCCTCCA
CATGGCCCCCTGGACCCTGGGGTAGAGGTGACCCTGACGATGAAAGTGGCCAGTGGTAGCACAGGCGACCAGAAGG
TTCAGATTTTCATACTACGGACCCAAGACTCCACCAGTCAAAGCTCTACTCTACCTCACCGGGGTGGAAATCTCCC
TGTGCGCAGACATCACCCGCACCGGCAAAGTGAAGCCAACCAGAGCTGTGAAAGATCAGAGGACCTGGACCTGGG
GCCCTTGTGGACAGGGTGCCATCCTGCTGGTGAAGTGTGACAGAGACAATCTCGAATCTTCTGCCATGGACTGCG
AGGATGATGAAGTGCTTGACAGCGAAGACCTGCAGGACATGTGCTGATGACCCTGAGCACGAAGACCCCCAAGG
ACTTCTTCACAAACCATACTGCTGGTGTCCACGTGGCCAGGTCTGAGATGGACAAAGTGAGGGTGTTTCAGGCCA
CACGGGGCAAAGTGTCTCCAAAGTGCAGCGTAGTCTTGGGTCCCAAGTGGCCCTCTCACTACCTGATGGTCCCCG
GTGGAAAGCACAAACATGGACTTCTACGTGGAGGCCCTCGCTTTCCCGGACACCGACTTCCCGGGGCTCATTACCC
TCACCATCTCCCTGCTGGACACGTTCAACCTGGAGCTCCCCGAGGCTGTGGTGTTCGAAGACAGCGTGGTCTTCC
GCGTGGCGCCCTGGATCATGACCCCAACACCCAGCCCCCGCAGGAGGTGTACGCGTGCAGTATTTTTGAAAATG
AGGACTTCCTGAAGTCAGTGACTACTCTGGCCATGAAAGCCAAGTGAAGCTGACCATCTGCCCTGAGGAGGAGA
ACATGGATGACCAAGTGGATGCAGGATGAAATGGAGATCGGCTACATCCAAGCCCCACACAAAACGCTGCCCGTGG
TCTTCGACTCTCCAAGGAACAGAGGCCTGAAGGAGTTTCCCATCAAACGCGTGATGGGTCCAGATTTTGGCTATG
TAACTCGAGGGCCCCAAACAGGGGGTATCAGTGGACTGGACTCCTTTGGGAACCTGGAAGTGAGCCCCCAGTCA
CAGTCAGGGGCAAGGAATACCCGCTGGGCAGGATTCTCTTCGGGGACAGCTGTTATCCCAGCAATGACAGCCGGC
AGATGCACCAGGCCCTGCAGGACTTCCTCAGTGGCCAGCAGGTGCAGGCCCTGTGAAGCTCTATTCTGACTGGC
TGTCCGTGGGCCACGTGGACGAGTTCTTGAGCTTTGTGCCAGCACCCGACAGGAAGGGCTTCCGGCTGCTCCTGG
CCAGCCCCAGGTCTGTCTACAACTGTTCCAGGAGCAGCAGAATGAGGGCCACGGGGAGGCCCTGCTGTTCTGAAG
GGATCAAGAAAAAAAACAGCAGAAAATAAAGAACATTCTGTCAAACAAGACATTGAGAGAACATAATTCAATTG
TGGAGAGATGCATCGACTGGAACCGCGAGCTGCTGAAGCGGGAGCTGGGCCTGGCCGAGAGTGACATCATTGACA
TCCCGCAGCTCTTCAAGCTCAAAGAGTTCTCTAAGGCGGAAGCTTTTTTCCCCAACATGGTGAACATGCTGGTGC
TAGGGAAGCACCTGGGCATCCCCAAGCCCTTCGGGCCCGTCATCAACGGCCGCTGCTGCCTGGAGGAGAAGGTGT
GTTCCCTGCTGGAGCCACTGGGCCTCCAGTGCACCTTCATCAACGACTTCTTACCTACCACATCAGGCATGGGG
AGGTGCACTGCGGCACCAACGTGCGCAGAAAGCCCTTCTCCTTCAAGTGGTGGAAACATGGTGCCCTGAGCCCATC
TTCCCTGGCGTCTCTCCCTCCTGGCCAGATGTGCTGGGTCTCTGAGTGTGGCAAGCAAGAGCTCTTGTGAA
TATTGTGGCTCCCTGGGGGCGGCCAGCCCTCCAGCAGTGGCTTGCTTTCTTCTCCTGTGATGTCCAGTTTCCC
ACTCTGAAGATCCCAACATGGTCTTAGCACTGCACACTCAGTTCTGCTCTAAGAAGCTGCAATAAAGTTTTTTTA
AGTCACTTTGTAC

71/6881
FIGURE 68A

GGAAGCTCGTATTTACATTTTAAGTGTATCTGGTGAGTGGGCTGGAGCCCTCGTCTGGGCCGGAAGG
CCTCCGATCCGTCTTTTAGTTGCTTCTCTCCTTTTTTCTCTCCGGTTTCTCATCACTCCAACCAGCCGCGACCA
TGCCAGGAAGAAGGCGGGCGGGCGGCTGGGAGGAGCCGAGCTCGGGCAACGGCACTGCCCGCGCCGGGCCA
GGAAACGCGGGCGGGCCGGCGGGCAGGAAGCGCGAGCGGGCCGAGCGCTGCAGTAGCAGCAGCGGCGGGCAGCA
GCGGCGACGAGGACGGCCTGGAGCTCGACGGGGCCCCGGCGGGGGCAAGCGCGGGCGCGGCCGCGACAGCAG
GCAAGGCGGGCGGGCGGGCCGTGGTCATCACCGAACCAGACACCAAGGAGCGCGTCAAACCTGAAGGGTCAA
AGTGCAAAGGGCAGCTTTTGATTTTTGGGGCAACCAACTGGGACTTGATTGGTCGAAAAGAAGTGCCTAAACAGC
AAGCTGCTTACCGCAATCTCGGTGAGAATTTGTGGGGGCCCCACAGATATGGGTGCCTGGCGGGGGTCCGGGTGC
GGACAGTGGTCTCGGGCTCGTGTGCTGCACACAGCCTCCTCATCACACGGAAGGGAAGCTGTGGAGCTGGGGTC
GAAATGAGAAGGGGAGCTGGGACATGGTGACACCAAGAGAGTAGAAGCCCTAGACTCATCGAGGGTCTTAGCC
ACGAAGTGATTGTGTCTGCAGCATGTGGGCGGAACCACACCTTGGCCTTGACGGAACGGGCTCCGTGTTTGGCT
TTGGGGAAAACAAGATGGGGCAGCTGGGCCTTGGCAACCAGACAGACGCTGTTCCCAGCCCCGCGCAGATAATGT
ACAACGGCCAGCCAATTACCAAAATGGCCTGTGGGGCTGAATTCAGTATGATAATGGACTGCAAAGGAAACCTCT
ATTCTTTGGGTGCCCTGAATATGGTCAGCTGGGACACAACCTCAGATGGGAAGTTTCATCGCCCGGGCACAGCGGA
TAGAGTACGACTGTGAACTAGTTCCCCGGCGAGTGGCCATCTTCATTGAGAAGACGAAAGATGGACAGATTCTGC
CTGTACCAAACGTGGTTGTACGAGACGTGGCCTGTGGCGCTAACCACACGCTGGTCCTGGACTCCCAGAAGCGAG
TCTTCTCCTGGGGCTTTGGTGGCTATGGCCGGCTGGGCCACGCAGAGCAGAAGGATGAGATGGTCCCCCGCCTGG
TGAAGCTGTTTGACTTCCCTGGGCGTGGGGCTTCCAGATCTATGCTGGTTACACCTGCTCCTTTGCTGTGAGTG
AAGTGGGTGGTCTGTTTTTCTGGGGGGCCACCAACACCTCCCGTGAATCTACCATGTACCAAAAAGCAGTGCAGG
ACCTCTGCGGCTGGAGAATTCGGAGCCTGGCTTGTGGGAAGAGCAGCATCATTGTGGCCGCCGATGAGAGCAGCA
TCAGCTGGGGTCCGTACCGACCTTTGGGGAACCTGGGCTACGGGGACCACAAGCCCAAGTCTTCCACTGCAGCCC
AGGAGGTAAAGACTCTGGATGGCATTCTCTCAGAGCAGGTGCCATGGGCTACTCACACTCCTTGGTGATAGCAA
GAGATGAAAGTGAGACTGAGAAAGAGAAGATCAAGAACTGCCAGAATACAACCCCCGAACCCTCTGATGCTCCC
GGAGACTCCTCCGACTCCACACCTCTCGCGGCAGCTGTCAATTCATGTGCACTGGGACGGGAAGTCAAACGAGG
AATTTAAAAAAGCAAAAGTTGACCGAAGGTGCATTTTGTGTTAGACTCCCTGAGGTTCCGTTTTACACATGATCC
AACGTTAACTACCTTTTTTTCTGTATGCTTTCCAAAGTCCTTTTTTTTTCCCTTAATGTTGAATTAATACTTGC
TCATAGTTGATTTACCATTCCTACAAAAGAGGCAGAACTTTGAGCAATCTAGGTTTTTTTTTTTTTAAGTTTT
TTCTTTCTTCTTTCTGAATACACTCCCCAAAACACCCCTTTCCAGTTACAATTAGCATCGTGATCCAAGCAGA
TGCCACATGGAAGAGGAATCGCCATTTACTCAGAAAAAATGTCCCTTACAGGAACCGGCAGCAGCTAGGCAGTCA
CCGGCCCGCCTCCATCCAAATCACGCTCGCGTGCTTCGGAAGCATCCGGGTCACTCCTTCTCCGCTTTTTCTTG
CAGATGGGCCTAGGCCGGTGTGCGTTCTGTTTCTCCCTTGGCTGCCTGTACGCCACAGCCTTCTGGCTGCGAC
ATTATAGAATCGGCCGTGTCCCCCTGGTGGGGGATTGGGGATCTGTGTTTAGCCATTTATATCTACTTTAGCTG
TTAAAGAGGTCCAAATGAAAATCAGGTGATTGTGGAACCATGGGGACTTGGGGGTGGGGCAGAGGTGGGAACATT
TGTATCAGTTGAGTCAGCTTGGTGGCTCCCTGTGGAGCCAGGGCTGAGCCTTGTACGCGCACTCGCCAATTAAG
AGATGGACCAGCCAGCAGTCAAGTGCATTCTCCAGTCCTTGCAAGAAGGATCAGCCCTTTCTGTGCCAGCCTCGA
TCGCTTTGTGCTTTGGTCTCTTTTTCTCCCCCCCCGCTGGATCCTGCCTCGCGCGGGCCGTCTGTTGCTGAGAC
TCGGGGTACCGTTCTGCTGACCCAGCTCCCTTTAGTCACGTTTGCTTGGCTCTGGTACCAAATAGTTGGGATTAC
CGAAGAGTCCCCTTCTTGCCTGTCAGCACGGATGCTGTGACTGCCACCTGCGTCTCTGTCAGAGTCCCCGAGCTC
GCCGCCGTGTGTGCTGCGCTGAGTGAGTTATGAGGTGCCTTTCCCGGAACCTCCTCTCGCCTGGACCCAAGAGA
GGCGACAGCTGTGGCTGGGGCTCTTGCTTCCAGAGGGTCTGGACTGGTTTGGGTGCTTTAAAATAGATATTTAG
TTCAGTGGTGCTTATGGGGGAGATGGGACTAGAAGTTAAGTGTGAGACTTGGGTGGATGGGAAAGTTAAATATTG
GTCTCTTCAAGTTTTTTTTTCTTTTGTGTTTACCCTTGTCACTGTCTCCATGTTAAATGCCAAAATGAT
GTAGTTGTTGTTGCTTTTTTCCCTATTTTCCACCCAGTCGCTCCTTACCGTGACTCCTGCCCTTGGAGGGCATG
TAGCAGTGTCTGTCTGCCAGTCCCAAGGCCCTGTGGGAGGAGACTGGCCTGCATCTCTTAAGACTTAGTCTGA
CGCCACGCGCATCTCTTGTCTGTGTTCAATCAGTAGTCCAGGGGAGAAGCTTCTGCTACTTCAGAGCTTTGCTA
AACTAACCTAATTTGTCCAAATCACCCAAAACCACCATCTCTGACGTAAGCTTCCATGCGACAGCCTGATCCGT
TTCCCTGGACAGGTCTCTTTTCTGGAATGCAGCCCAGGCACCTGTGCTCCTGGCACCCCTTGAGGTCTCTTCTTTG
AGCCGTGGTCAACGAGAGGGTTGAGGACGCAGCACCCGAGGTCCCAGCCTTTGCAGGAGCCTCCCTGGGCTTAGC

72/6881
FIGURE 68B

TGGACTTAGATCTTCGGTGGCCTCATGTAAACGTGGCAGCCAGCCTCTTCTAGAACCCTAGCCCAGGGACTGGAG
CAGGAAAGGGACCTTCAAAGTGAAGACTGCCCTTGTCCCGCAGCTCCTTCTGGCTTAGATTGAAACATGGGCTTCC
TAATGGGTAAATCCTTTAAAACAAGGAGTTGTGGGGGAAGGGTGTGTCGACTCCTAGAGAAAGGTACACAGTT
GCCCCGTTGGGAATGTGCTTGGCGCTGACCCTGCGGGCATCTGACTGGTCTTCCAGCTCAGGAAAAAGAATTTGA
AAGAGGCTTAGCGTGAAGGGGAATCAAAGAGGAGGTTGTGATTTGGTCGAAGGTGCCTGGTTTAGTGCTGTAATT
GTCTTATTATTTTTTTTTATATATATATTTCTTGGAGTAAACATTTTAAAT

73/6881
FIGURE 69

ATGAGTGATCAGCAGCTGGACTGTGCCTTGGACCTAATGAGGCGCCTGCCTCCCCAGCAAATCGAGAAAAACCTC
AGCGACCTGATCGACCTGGTCCCCAGTCTATGTGAGGATCTCCTGTCTTCTGTTGACCAGCCACTGAAAATTGCC
AGAGACAAGGTGGTGGGAAAGGATTACCTTTTGTGTGACTACAACAGAGATGGGGACTCCTATAGGTCACCATGG
AGTAACAAGTATGACCCTCCCTTGGAGGATGGGGCCATGCCGTGAGCTCGGCTGAGAAAGCTGGAGGTGGAAGCC
AACAATGCCTTTGACCAGTATCGAGACCTGTATTTTGAAGGTGGCGTCTCATCTGTCTACCTCTGGGATCTGGAT
CATGGCTTTGCTGGAGTGATCCTCATAAAGAAGGCTGGAGATGGATCAAAGAAGATCAAAGGCTGCTGGGATTCC
ATCCACGTGGTAGAAGTGCAGGAGAAATCCAGCGGTGCGACCGCCATTACAAGTTGACCTCCACGGTGATGCTG
TGGCTGCAGACCAACAAATCTGGCTCTGGCACCATTGAACCTCGGAGGCAGCCTTACCAGACAGATGGAGAAGGAT
GAAACTGTGAGTGACTGCTCCCCACACATAGCCAACATCGGGCGCCTGGTAGAGGACATGGAAAATAAAATCAGA
AGTACGCTGAACGAGATCTACTTTGGAAAAACAAAGGATATCGTCAATGGGCTGAGGTCTGTGCAGACTTTTGCA
GACAAATCAAAACAAGAAGCTCTGAAGAATGACCTGGTGGAGGCTTTGAAGAGAAAGCAGCAATGCTTAAACCTCT
GTTTCATGCTAACCAGACACGCCGTGCACTCGTTAGATTCCCTTTCTTAGAAAACCTCGTTTTCTGCTCCCTTCCCT
CGTCCCTTCCCTCCCCGACAGGTCACATAACAGCTGCATCATTGACCGCACAGCGCCATCTCTCCCTGAGAATAA
AGCCGATAGCCACCTCCTCCGGCTCCGAGCCTGCTTCTGCCACACCTCGCTCTCAGTCTCTCCACATTTCCATAG
AGACCGTGTGGTTTTTTGTTTACCCGGG

74/6881
FIGURE 70

MSDQQLDCA~~LDLM~~RRLPPQQIEKNLS~~DLID~~LVPSLCEDLLSSVDQPLKIARDKVVGKDYL~~LLCD~~YNRDGDSYRSPW
SNKYDP~~P~~LEDGAMP~~SAR~~LRKLEVEANNAFDQYRDLYFEGGVSSVYLWDLDHGFAGVILIKKAGDGSKKIKGCWDS
IHVVEVQEKSSGRTAHYKLTSTV~~MLWL~~QTNKSGSGTMNLGGSLTRQMEKDETVSDCSPHIANIGRLVEDMENKIR
STLNEIYFGKTKDIVNGLRSVQTFADKSKQEALKNDLVEALKRKQQC

75/6881
FIGURE 71

CCGCGTCTCGCGTAGTCTCCCGCGCCGCGCTCCACTGCGCGCTTCGCTCTCCGCCGCCCGAGGCCCGCGCGCTCG
CCATGTCCCCGGCCACCGCCACCGCGGGTCGCCTCGGTGCTGGGCACCATGGAGATGGGGCGCCGCATGGACGCGC
CCGCCAGCGCCGCGGCCGTGCGCGCCTTTCTGGAGCGCGGCCACACCGAACTGGACACGGCCTTCATGTACAGCG
ACGGCCAGTCCGAGACCATCCTGGGCGGCCTGGGGCTCGGGCTGGGCGGTGGCGACTGCAGAGTGAAAATTGCCA
CCAAGGCCAACCCCTTGGGATGGAAAATCACTAAAGCCTGACAGTGTCCGGTCCCAGCTGGAGACGTCATTGAAGA
GGCTGCAGTGTCCCCAAGTGGACCTCTTCTACCTACACACACCTGACCACGGCACCCCGGTGGAAGAGACGCTGC
ATGCCTGCCAGCGGCTGCACCAGGAGGGCAAGTTCGTGGAGCTTGGCCTCTCCAATATGCTAGCTGGGAAGTGG
CCGAGATCTGTACCCTCTGCAAGAGCAATGGCTGGATCCTGCCCCTGTGTACCAGGGCATGTACAACGCCACCA
CCCGGCAGGTGGAAACGGAGCTCTTCCCCTGCCTCAGGCACTTTGGACTGAGGTTCTATGCCTACAACCCTCTGG
CTGGGGGCCTGCTGACTGGCAAGTACAAGTATGAGGACAAGGACGGGAAAACAGCCTGTGGGCCGCTTCTTTGGGA
ATAGCTGGGCTGAGACCTACAGGAATCGCTTCTGGAAGGAGCACCACTTCGAGGCCATTGCGTTGGTGGAGAAGG
CCCTGCAGGCCCGCATATGGCGCCAGCGCCCCCAGTGTGACCTCGGCTGCCCTCCGGTGGATGTACCACCACTCAC
AGCTGCAGGGTGCCACGGGGACGCGGTATCCTGGGCATGTCCAGCCTGGAGCAGCTGGAGCAGAACTTGGCAG
CAACAGAGGAAGGGCCCCCTGGAGCCGGCTGTCTGTGGATGCCTTTAATCAAGCCTGGCATTGTGGTTGCTCACGAAT
GTCCCAACTACTTCCGCTTAGGCCCCATCATGGCTCAGGCTGCCCAAGGCTTTTCTGTACCTCTTTTGTCTCTCA
CACTGACCAGTCTTGGCCTTAAGCTGACTTAGAAGGGTTTTTCTGAATTGTCTAGATCCATGCATTATTTTCTA
GCTTCCTGCCTTGCTCCCTATTCACTTTACACTGTGAAAGGTGGGGGGTGAGTCCCCTTGAGCGCTTCCTGTTG
AATAAAGCAGGCACTTGACCTGGCTGTAGCCTAGGTCTTGAGTGAACCCCAAAAAA

76/6881
FIGURE 72

MSRPPPPRVASVLGTMEMGRRMDAPASAAVRAFLERGHTELDTAFMYSDGQSETILGGLGLGLGGDCRVKIAT
KANPWDGKSLKPDSVRSQLETSKRLQCPQVDLFYLHTPDHGTPEETLHACQRLHQEGKFVELGLSNYASWEVA
EICTLCKSNGWILPTVYQGMYNATTRQVETELFPCLRHFGLRFYAYNPLAGGLLTGKYKYEDKDQKQPVGRFFGN
SWAETYRNRFWKEHHFEAIALVEKALQAAYGASAPSVTSAALRWMYHHSQHQGAHGDAVILGMSSEQLQNLAA
TEEGPLEPAVVDAFNQAWHLVAHECPNYFR

77/6881
FIGURE 73

ACCGTCTTCCGCCGCACGTGGATTTCAGCGCG**ATG**CCCCAAATCCAAGCGCGACAAGAAAGTCTCCTTAACCAAAAC
TGCCAAGAAAGGCTTGGAATTGAAACAAAACCTGATAGAAGAGCTTCGGAAATGTGTGGACACCTACAAGTACCT
TTTCATCTTCTCTGTGGCCAACATGAGGAACAGCAAGCTGAAGGACATCCGGAACGCCTGGAAGCACAGCCGGAT
GTTCTTTGGCAAAAACAAGGTGATGATGGTGGCCTTGGGTCTGGAGCCCATCTGATGAATACAAAGACAACCTGCA
CCAGGTTCAGCAAAAGGTTGAGGGGTGAGGTGGGTCTCCTGTTTACCAACCGCACAAAGGAAGAGGTGAATGAGTG
GTTACGAAATACACAGAAATGGACTACGCCCCGAGCTGGTAACAAAGCAGCTTTTACTGTGAGCCTGGATCCAGG
GCCCCCTGGAGCAGTTCCCCCACTCCATGGAGCCACAGCTCAGGCAGCTGGGCCTGCCCCACCGCCCTCAAGAGAGG
TGTGGTGACTCTGCTGTCTGACTACGAGGTGTGCAAGGAGGGCGATGTGCTGACCCCAGAGCAGGCTCGCGTCCT
GAAGCTTTTTGGGTATGAGATGGCTGAATTCAAGGTGACCATCAAATACATGTGGGATTACAGTCGGGAAGGTT
CCAGCAGATGGGAGACGACTTGCCAGAGAGCGCATCTGAGTCCACAGAAGAGTCAGACTCAGAAGATGATGAC**TG**
AAAGGGACTCGGGACTGAAGGTCTCCTGGAAGCTTCTGGGTCTCACTGGACCATCAGGACTGCTGCCGCCCTCT
GGAGAGAGCAGCTTTTTATTTGTCTGTAGACAGGGAACATGATGGGCACTGACCTCCTGTAAAGAATAAACTGT
GGGCCGGGCGCGGTGGCTCACGCCTGGAATCCCAGCACTTTGGGAAGCCGAGGTGGGCAGATCATAAGGTCAGGA
GATTAAGACCATCCTGGCTAACACGGTGAAACCCCGTCTCTACTAAAAATAGAAAAAAAAAACTAGTTGGGCATAG
TGGCATGTGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATCACTTGAACCCGGGAGGTGGAGGTTG
CCGTGAGTTGAGATTGGACCACTGCTCTCCAGCCTGGGCAACAGAGTAAAACTCTGTCCC

78/6881
FIGURE 74

MPKSKRDKKVSITKTAKKGLELKQNLIEELRKCVDTYKYLFI FSVANMRNSKLKDIRNAWKHSRMFFGKNKVMMV
ALGRSPSDEYKDNLHQVSKRLRGEVGLLFTNRTKEEVNEWFTKYTEM DYARAGNKAFTVSLDPGP LEQFP HSME
PQLRQLGLPTALKRGVVTLLSDYEVCKEGDVLTP EQARVLKLF GYEMAEFKVTIKYMWDSQSGRFQQMGDDL PES
ASESTEE SDEDD

79/6881
FIGURE 75

ATCGCTGGGCGACTGATTTTCGAGTTTCCGGTCAGGTTAGGCCGGGGGGGTGCGGTCTCTGGTCGGAAGGAGGTGGA
GAGTCGGGGGTCACCAGGCCTATCCTTGGCGCCACAGTCGGCCACCGGGGCTCGCCGCCGTGATGGAGAGCGGAG
GGCGGCCCTCGCTGTGCCAGTTTCATCCTCCTGGGCAACCACCTCTGTGGTCACCGCCGCCCTGTACTCCGTGTACC
GGCAGAAGGCCCGGGTCTCCCAAGAGCTCAAGGGAGCTAAAAAAGTTCAATTTGGGTGAAGATTTAAAGAGTATTC
TTTCAGAAGCTCCAGGAAAATGCGTGCCTTATGCTGTTATAGAAGGAGCTGTGCGGTCTGTTAAAGAAACGCTTA
ACAGCCAGTTTGTGGAAAACGCAAGGGGGTAATTCAGCGGCTGACACTTCAGGAGCACAAAGATGGTGTGGAATC
GAACCACCCACCTTTGGAATGATTGCTCAAAGATCATTCATCAGAGGACCAACACAGTGCCCTTTGACCTGGTGC
CCCACGAGGATGGCGTGGATGTGGCTGTGCGAGTGCTGAAGCCCCTGGACTCAGTGGATCTGGGTCTAGAGACTG
TGTATGAGAAGTTCCACCCCTCGATTTCAGTCCCTTACCGATGTTCATCGGCCACTACATCAGCGGTGAGCGGCCCA
AAGGCATCCAAGAGACCGAGGAGATGCTGAAGGTGGGGGCCACCTTCACAGGGGTTGGCGAACTGGTCTTGACA
ACAACCTCTGTCCGCCTGCAGCCGCCCAAACAAGGCATGCAGTACTATCTAAGCAGCCAGGACTTCGACAGCCTGC
TGCAGAGGCAGGAGTCGAGCGTCAGGCTCTGGAAGGTGCTGGCGCTGGTTTTTTGGCTTTGCCACATGTGCCACCC
TCTTCTTCATTCTCCGGAAGCAGTATCTGCAGCGGCAGGAGCGCCTGCGCCTCAAGCAGATGCAGGAGGAGTTCC
AGGAGCATGAGGCCAGCTGCTGAGCCGAGCCAAGCCTGAGGACAGGGAGAGTCTGAAGAGCGCCTGTGTAGTGT
GTCTGAGCAGCTTCAAGTCTGCGTCTTTCTGGAGTGTGGGCACGTTTGTTCCTGCACCGAGTGCTACCGCGCCT
TGCCAGAGCCCAAGAAGTGCCCTATCTGCAGACAGGCGATCACCCGGGTGATACCCCTGTACAACAGCTAATAGT
TTGGAAGCCGCACAGCTTGACCTGGAAGCACCCCTGCCCTTTTCAGGGATTTTTATCTCGAGGCCTTTGGAGG
AGCAGTGGTGGGGGTAGCTGTACCTCCAGGTATGATTGAGGGAGGAATTGGGTAGAACTCTCCAGACCCATGC
CTCCAATGGCAGGATGCTGCCTTTCCACCTGAGAGGGGACCCTGTCCATGTGCAGCCTCATCAGAGCCTCACCC
TGGGAGGATGCCGTGGCGTCTCCTCCCAGGAGCCAGATCAGTGCAGTGTGACTGAAAATGCCTCATCACTTAAG
CACCAAAGCCAGTGATCAGCAGCTCTTCTGTTCCTGTGTCTTCTGTTTTTTTTCTGGTGAATCGTTGCTTGCTGTG
GACTTGTTGGAGGACTCAGAGGGGAGGAAAAGGCTGGGCCCCGAGTACAACGGATGCCTTGGGTGCTGCCTCCGAA
GAGACTCTGCCGAGCTTTTTCTTCTTTTCTCCTCATGCCCCGGGAAACAGTCTTTCTTCAGAATTGTGAGGCTGGG
CAGGTCAACTTGTGTTCCCTTTCCCTCACCTGCTTGCCCTCCTTAACGCCTGCACGTGTGTGTAGAGGACAAAAGA
AAGTGAAGTCAGCACATCCGCTTCTGCCAGATGGTCGGGGCCCCGGGCAACAGATTGAAGAGAGATCATGTGAA
GGGCAGTTGGTCAGGCAGGCCTCCTGGTTTTCGCCACTGGCCCTGATTTGAACTCCTGCCACTTGGGAGAGCTCGG
GGTGGTCCCTGGTTTTTCCCTCCTGGAGAATGAGGCGCAGAGGCCTCGCCTCCTGAAGGACGCAGTGTGGATGCCA
CTGGCCTAGTGTCTGGCCTCACAGCTTCCTTGCAAGGCTGTACAAGGAAAAGCAGCCGGCTGGCACCCCTGAGC
ATATGCCCTCTTGGGGCTCCCTCATCCAGCCCGTCGCAGCTTTGACATCTTGGTGTACTCATGTGCTTCTCCTT
GTGTTACCCCTCCAGTATTACCATTTGCCCTCACCTGCCCTTGGTGAGCCTTTTAGTGCAAGACAGATGGGG
CTGTTTTCCCCACCTCTGAGTAGTTGGAGGTCACATACAGCTCTTTTTTTTATTGCCCTTTTCTGCCTCTGAA
TGTTTCATCTCTCGTCTCCTTTGTGTCAGGCGAGGAAGGGGTGCCCTCAGGGGCCGACACTAGTATGATGCAGTGT
CCAGTGTGAACAGCAGAAATTAAACATGTTGCAACC

[illegible]

81/6881
FIGURE 76B

TTTGTATTTGTTTTAGTATTGTGAAGTTGTGTTAAATAGTACTAGCTAGAAATACAAATTTCTGGTTATCATTTCTCTCCCTGTGGCACTTGACATTTTAATTGTCTTAAAGTTTTTGAAGTACATCTTCTGGCCCCCTTGAGTACTGCCAGAGGCAAAAGATGTTTGTTCCTTATTCATTCCACTTTTGTCTCCTGGGATCCCTTCTGTAGCCTAAAGTATGGCTGGGAAATGGACTTGAGAAGATTGGCTTGAATTAGATCATAATCATGTGTGATCCCATCATGAATTCATTGGAATTGTGTTGCATGTAAGGCAATCTTTCCTGTTGTAAATCTTCCTTTTTTAATGTACATATATTTTGAAAAATATGATAAACATGAAATTTT

82/6881
FIGURE 77

GGCGCCGAGTAGCCGGGCGGGCCGGAGCGCGGGCGGCGGAGGCAGCTGCGCCCGCGCCTCCTGCCCTCCCA
GGCCCCGCGCCCCGCGCCCGGGCCCCGGCGATGGTGACACATGCGGCGGCGCGCCAGCGGCAGGACCATGGT
TGAGCGCGCCAGCAAGTTCTGTGCTGGTGGTGGCGGGCCCGGTGTGCTTCATGCTCATCTTGTACCAGTACGCGGG
CCCAGGACTGAGCCTGGGCGCGCCCGGCGGCGGCGCGCCCGCCGACGACCTGGACCTGTTCCCCACGCCCGACCC
CCACTACGAGAAGAAGCACTACTTCCCGGTCCGCGAGCTGGAGCGCTCGCTGCGCTTCGACATGAAGGGCGACGA
CGTGATCGTCTTCCTGCACATCCAGAAGACGGGCGGCACACCTTCGGCCGCCACCTCGTGAGAACGTACGCCT
CGAGGTGCCGTGCGACTGCCGGCCCGGCCAGAAGAAGTGACCTGCTACCGGCCCAACCGCCGCGAGACTTGGCT
CTTCTCCCGCTTCTCCACCGGCTGGAGCTGCGGGCTGCACGCCGACTGGACCGAGCTCACCAACTGCGTGCCCGG
CGTGCTGGACCGCCGCGACTCCGCCGCGCTGCGCACGCCCAGGAAGTTCTACTACATCACCTGCTACGAGACCC
CGTGTCCCGCTACCTGAGCGAGTGCGGCATGTGCAGAGGGGTGCCACGTGGAAGACGTGCTTGCACATGTGTGA
TGGGCGCACGCCCACGCCTGAGGGGCTGCCGCCCTGCTACGAGGGCACGGACTGGTGGGGCTGCACGCTACAGGA
GTTTCATGGAAGTGCCTTACACCTGGCCAACAACCGCCAGGTGCGCATGCTGGCCGACCTGAGCCTGGTGGGGCTG
CTACAACCTGTCTTCATCCCCGAGGGCAAGCGGGGCCAGCTGCTGCTCGAGAGCGCCAAGAAGAACCTGCGGGG
CATGGCCTTCTTCGGCCTGACCGAGTTCCAGCGCAAGACGCGAGTACCTGTTTCGAGCGGACGTTCAACCTCAAGTT
CATCCGGCCCTTCATGCAGTACAACAGCACGCGGGCGGGCGGCGTGGAGGTGGATGAGGACACCATCCGGCGCAT
CGAGGAGCTCAACGACCTGGACATGCAGCTGTATGACTACGCCAAGGACCTCTTCAGCAGCACTACCAGTACAA
GCGGCAGCTGGAGCGCAGGGAGCAGCGCCTGAGGAGCCGCGAGGAGCGTCTGCTGCACCGGGCCAAGGAGGCGCT
GCCGCGGGAGGACGCCGACGAGCCGGGCCGCTGCCACCGAGGACTACATGAGCCACATCATTGAGAAGTGGA
GTGGCGGTGGTGGCCACGGGGAGGCCTCTTGGGGTGTGTGGGGGATAAAACAGGACAGACGACAGGTCCACCCAA
GACTGTCAAGGGATGAGCATCCCAAACCTGCTCCACAGAGGTAGCTGCGTCTTGAAAAAAACACAGCAGGGACA
TAGTGGGGCTGGGCAGGGATGGGGCTTGAGAAATCAACAGGTGCAGCCCAGTGGGTGAGAGGAAAGCGTGCTCGA
AGGATGCCATGGTCAGGGCAGAGCCTCCAGAGCAGGTGTTGTGCCTGGAGCTGCTCTCCTGGCCTCCTTGGAATTT
ATCGCAAAAAGTGAAGGTTTGCCTGAGAGACGAGGACAGCGGAAAGTGACCTGCCAGGCCGGGAGTGTGTCCCT
CACCAACTATGCACACAGCACTCGCTCTTAGCTCCTCTGTCCGGGCTACTAGGAGTGAGACCAGCTTCTGGCAAC
TGCCCCAGCTCCAGGCCATCCCATAGCTCCTCCTCTTCTGGCTGCCCCCAATGCCCCGAGGCCTGGGGAGCCCCC
AGCTCACCCATCTGTAGCTCCCTCAAAGTCAGGGCCACCCCATCTGAGGCAGAGAAGACTCGAGTCCAGCCCCC
AGGAAGCCTGCTCCCCTCTCTGGCCCATGGTCCTGCTTCATGCTTTGGGTCAGGAGGCCAAAGCTGATGTTCAGG
CCCCACCCACTCCCTACAGTCCTCAGACC

83/6881
FIGURE 78

AGAAACTCCCGGTGTGGCAGCTGAGATGGCCCAGGAAAGAACTATATTACCTTCAAAAAGAGAGGTACATGCGAT
GTTTGAGGTGGCATGAAGCTCAGTGGTGTATATTGGAATGAGTGAGTGACCATCCTGGAGCCTTCTGAAAGAG
GATTGGAACATCAGTTAACATCTGACCACTGCCAGCCCACCCCTCCCACCCACGTCGATTGCATCTCTGGGGCTC
CAGGGATAAAGCAGGTCTTGGGGTGCACCATGATTTACCAATTCTTAGTACTGGCCATTGGCACCTGCCTTACTA
ACTCCTTAGTGCCAGAGAAAGAGAAAGACCCCAAGTACTGGCGAGACCAAGCGCAAGAGACACTGAAATATGCCC
TGGAGCTTCAGAAGCTCAACACCAACGTGGCTAAGAATGTCATCATGTTCTTGGGAGATGGGATGGGTGTCTCCA
CAGTGACGGCTGCCCCGCATCCTCAAGGGTCAGTCCACCACAACCTGGGGAGGAGACCAGGCTGGAGATGGACA
AGTTCCCCTTCGTGGCCCTCTCCAAGACGTACAACACCAATGCCCAGGTCCCTGACAGTGCCGGCACCGCCACCG
CCTACCTGTGTGGGGTGAAGGCCAATGAGGGCACCGTGGGGGTAAAGCGCAGCCACTGAGCGTTCCCGGTGCAACA
CCACCCAGGGGAACGAGGTACCTCCATCCTGCGCTGGGCCAAGGACGCTGGGAAATCTGTGGGCATTGTGACCA
CCACGAGAGTGAACCATGCCACCCCAAGCGCCGCTACGCCCACTCGGCTGACCGGGACTGGTACTCAGACAACG
AGATGCCCCCTGAGGCCCTTGAGCCAGGGCTGTAAGGACATCGCCTACCAGCTCATGCATAACATCAGGGACATTG
ACGTGATCATGGGGGGTGGCCGGAATACATGTACCCCAAGAATAAACTGATGTGGAGTATGAGAGTGACGAGA
AAGCCAGGGGCACGAGGCTGGACGGCCTGGACCTCGTTGACACCTGGAAGAGCTTCAAACCGAGATACAAGCACT
CCCCTTTCATCTGGAACCGCACGGAACCTCTGACCCCTTGACCCCAACAATGTGGACTACCTATTGGGTCTCTTCG
AGCCAGGGGACATGCAGTACGAGCTGAACAGGAACAACGTGACGGACCCGTCACCTCTCCGAGATGGTGGTGGTGG
CCATCCAGATCCTGCGGAAGAACCCCAAAGGCTTCTTCTTGCTGGTGAAGGAGGCAGAATTGACCACGGGCACC
ATGAAGGAAAAGCCAAGCAGGCCCTGCATGAGGCGGTGGAGATGGACCGGGCCATCGGGCAGGCAGGCAGCTTGA
CCTCCTCGGAAGACACTCTGACCGTGGTCACTGCGGACCATTCCACGTCTTCACATTTGGTGGATACACCCCCC
GTGGCAACTCTATCTTTGGTCTGGCCCCCATGCTGAGTGACACAGACAAGAAGCCCTTCACTGCCATCCTGTATG
GCAATGGGCCTGGCTACAAGGTGGTGGGCGGTGAACGAGAGAATGTCTCCATGGTGGACTATGCTCACAACAAC
ACCAGGCGCAGTCTGCTGTGCCCCTGCGCCACGAGACCCACGGCGGGGAGGACGTGGCCGTCTTCTCCAAGGGCC
CCATGGCGCACCTGCTGCACGGCGTCCACGAGCAGAACTACGTCCCCCACGTGATGGCGTATGCAGCCTGCATCG
GGGCCAACCTCGGCCACTGTGCTCCTGCCAGCTCGGCAGGCAGCCTTGCTGCAGGCCCCCTGCTGCTCGCGCTGG
CCCTCTACCCCTGAGCGTCTGTCTGAGGGCCAGGGCCCCGGGCACCCACAAGCCCGTGACAGATGCCAACTT
CCCACACGGCAGCCCCCCCCCTCAAGGGGCAGGGAGGTGGGGGCCTCCTCAGCCTCTGCAACTGCAAGAAAGGGGA
CCCAAGAAACCAAAGTCTGCCGCCACCTCGCTCCCCTCTGGAATCTTCCCCAAGGGCCAAACCCACTTCTGGCC
TCCAGCCTTTGCTCCCTCCCCGCTGCCCTTTGGCCAACAGGGTAGATTTCTCTTGGGCAGGCAGAGAGTACAGAC
TGCAGACATTCTCAAAGCCTCTTATTTTTCTAGCGAACGTATTTCTCCAGACCCAGAGGCCCTGAAGCCTCCGTG
GAACATTCTGGATCTGACCCTCCAGTCTCATCTCCTGACCCTCCCACTCCCATCTCCTTACCTCTGGAACCCCC
CAGGCCCTACAATGCTCATGTCCCTGTCCCCAGGCCAGCCCTCCTTACGGGGAGTTGAGGTCTTTCTCCTCAGG
ACAAGGCCTTGCTCACTCACTCACTCCAAGACCACCAGGGTCCCAGGAAGCCGGTGCTGGGTGGCCATCCTACC
CAGCGTGGCCCAGGCCGGAAGAGCCACCTGGCAGGGCTCACACTCCTGGGCTCTGAACACACAGCCAGCTCCT
CTCTGAAGCGACTCTCCTGTTTGGAAACGGCAAAAAAATTTTTTTTTCTCTTTTGGTGGTGGTTAAAAGGGAA
CACAAAACATTTAAATAAACTTTCCAAATATTTCCGAGG

84/6881
FIGURE 79

GAACCGCCATCTTCCAGTAATTCGCCAAAATGAACGAACACAAAGGGAAAGAGGAGAGGCACCCAATAGATGTTCT
CCAGGCCTTTTAGAAAACATGGAGTTGTTCCCTTTGGCCACGTATATGCGAATCTATAAGAAAGGTGATATTGTAG
ACATCAAGGGAATGGGTACTGTTCAAAAAGGAACGCCCCACAAGTGTTACCATGGCAAACTGGAAGAGTCTACA
ATGTTATCCAGTATGCTGCTAGCATTGTTGTAAACAAACAAGTTAAGGGCAAGATTCTTGCCAAGAGAATTAATG
TGCGTATTGAGCACATTAAGCACTCTGAGAGCCGAGATAGCTTCCTGAAACGCGTGAAGGAGAATGATCAGAAAA
AGAGAGAAGCCAAAGAGAAAGGTACCTGGGTTCAACTAAAGCGCCAGCCTGCTCCACCCAGCAAAGCACACTTTG
TGAGAACCAATGGGAAGGAGCCTGAGCTGCTGGAACCTATTCTCTATGAATTCACGGCATAATAGGTATTTAAAA
AAAAAAAAAGACCTCTGGGCTGT

85/6881
FIGURE 80

DRTQREERGEAPNRMFSRPFRKHGVVPLATYMRIYKKGDIVDIKGMGTVQKGTPHKCYHGKTGRVYNVIQYAASIV
V NKQVKGKILAKRINVRIEHIKHSES RDSFLKRVKENDQKKREAKEKGTWVQLKRQPAPP SKAHFVRTNGKEPEL
LEPIIYEFTA

[illegible]

87/6881
FIGURE 82

MQTIKCVVVG DGAVGKTCLLISYTTNKFPS EYVPTVFDNYAVTVMIGGEPYTLGLFD TAGQEDYDRLRPLSYPQT
DVFLVCF SVVSPSSFENVKEKWVPEITHHCPKTPFLLVGTQIDLRDDPSTIEKLAKNKQKPITPETA EKLARDLK
AVKYVECSALTQKGLKNVFDEAILAALEPPEPKKSRRCVLL

88/6881
FIGURE 83

CGCGCGCGCCATTTCTAGTCGTTTTCAAAGCGCCTCGCGCTGATTCTCACGGGCCCGGCTGCCGGCCCCGCTCT
GCCCTGCATAATAAAATGGCTAATCAGGTGAATGGTAATGCGGTACAGTTAAAAGAAGAGGAAGAACCAATGGAT
ACTTCCAGTGTAACCTCACACAGAACTACAAGACACTGATAGAGGCAGGCCTCCCACAGAAGGTGGCAGAAAGA
CTTGATGAAATATTTTACAGACAGGATTGGTAGCTTATGTCGATCTTGATGAAAGAGCAATTGATGCTCTCAGGGAA
TTTAATGAAGAAGGAGCTCTGTCTGTACTACAGCAGTTCAAGGAAAGTGAAGTATCACATGTTTCAAGCAAAAGT
GCATTTTTATGTGGAGTTATGAAGACCTACAGGCAGAGAGAGAAACAGGGGAGCAAGGTGCAAGAGTCCACAAAG
GGACCTGATGAAGCGAAGATCAAGGCCTTGCTTGAGAGAACTGGTTATACTCTGGATGTAACACAGGACAGAGG
AAGTATGGTGGTCCCTCCACCAGACAGTGTGTACTCTGGCGTGCAACCTGGAATTGGAACGGAGGTATTTGTAGGC
AAAATACCAAGGGATTTATATGAGGATGAGTTGGTGCCCTTTTTGAGAAGGCCGGACCCATTTGGGATCTACGT
CTTATGATGGATCCACTGTCCGGTCAGAATAGAGGGTATGCATTTATCACCTTCTGTGGAAAGGAAGCTGCACAG
GAAGCCGTGAAACTGTGTGACAGCTATGAAATTCGCCCTGGTAAACACCTTGGAGTGTGCATTTCTGTGGCAAAC
AACAGACTTTTTGTTGGATCCATTCCGAAGAATAAGACTAAAGAAAACATTTTGGAAGAATTCAGTAAAGTCACA
GAGGGTTTGGTGGACGTTATTTCTCTATCATCAACCCGATGACAAAAAGAAGAATCGGGGGTTCTGCTTCCTTGAA
TATGAGGATCACAAGTCAGCAGCACAAGCCAGACGCCGGCTGATGAGTGGAAAAGTAAAAGTGTGGGGAAATGTA
GTTACAGTTGAATGGGCTGACCCTGTGGAAGAACCAGATCCAGAAGTCATGGCTAAGGTAAAAGTTTTGTTTGTG
AGAACTTGGCTACTACGGTGACAGAAGAAATATTGGAAGTCAATTTTCTGAATTTGGAAGTCTGAAAGAGTA
AAGAAGTTGAAAGATTATGCATTTGTTTCAATTTGAAGACAGAGGAGCAGCTGTTAAGGCTATGGATGAAATGAAT
GGCAAAGAAATAGAAGGGGAAGAAATTGAAATAGTCTTAGCCAAGCCACCAGACAAGAAAAGGAAAGAGCGCCAA
GCTGCTAGACAGGCCTCCAGAAGCACTGCGTATGAAGATTATTACTACCACCCTCCTCCTCGCATGCCACCTCCA
ATTAGAGGTCGGGGTCGTGGTGGGGGAGAGGTGGATATGGCTACCCTCCAGATTACTACGGCTATGAAGATTAC
TATGATGATTACTATGGTTATGATTATCACGACTATCGTGGAGGCTATGAAGATCCCTACTACGGCTATGATGAT
GGCTATGCAGTAAGAGGAAGAGGAGGAGGAAGGGGAGGGCGAGGTGCTCCACCACCACCAAGGGGGAGGGGAGCA
CCACCTCCAAGAGGTAGAGCTGGCTATTACAGAGGGGGGCACCTTTGGGACCACCAAGAGGCTCTAGGGGTGGC
AGAGGGGGTCTGCTCAACAGCAGAGAGGCCGTGGTTCCCGTGGATCTCGGGGCAATCGTGGGGGCAATGTAGGA
GGCAAGAGAAAGGCAGATGGGTACAACCAGCCTGATTCCAAGCGTCGTCAGACCAACAACCAACAGAACTGGGGT
TCCCAACCCATCGCTCAGCAGCCGCTTCAGCAAGGTGGTGACTATTCTGGTAACTATGGTTACAATAATGACAAC
CAGGAATTTTATCAGGATACTTATGGGCAACAGTGAAGTAGACAAGTAAGGGCTTGAAAATGATACTGGCAAGA
TACGATTGGCTCTAGATCTACATTCTTCAAAAAAAAAAATTGGCTTAACTGTTTCATCTTTAAGTAGCATTTTGC
TGCCATTTGTATTGGGCTGAAGAAATCACTATTGTGTATATACTCAAGTCTTTTTATTTTTCTCTTTTCATAAA
TGCTCTTGGACATTATTGGGCTTGCAAGATTCCCTTATTCTGGGGATTACAATGCTTTTTATCGTTTCAGGCTTCA
TTTTAGCTTCAAAAACAGCTGGGCACACTGTTAAATCATGATTTTGCAGAACCTTTGGTTTTGGACAGTTTTCATT
TTTTTGGATTTGGGATAGATTACATAGGAGTATGGAGTATGCTGTAAATAAAAAATACAAGCTAGTGCTTTGTCTT
AGTAGTTTTAAGAAATTAAAGCAAACAAATTTAAGTTTTCTTGATTGAAAATAACCTATGATTGTATGTTTTGC
ATTCCTAGAAGTAGGTTAACTGTGTTTTTAAATTGTTATAACTTCACACCTTTTTGAAATCTGCCCTACAAAATT
TGTTTTGGCTTAAACGTCAAAGCCGTGACAATTTGTTCTTTGATGTGATTGTATTTCCAATTTCTTGTTCATGTA
AGATTTCAATAAAACTAAAAATCTATTCAAAACATTA

89/6881
FIGURE 84

MANQVNGNAVQLKEEEEPMDSSTVHTTEHYKTLIEAGLPQKVAERLDEIFQTGLVAYVDLDERAIDALREFNEEG
ALSVLQQFKESDLSHVQNKSAFLCGVMKTYRQREKQGSKVQESTKGPDEAKIKALLERTGYTLDVTTGQRKYGGP
PPDSVYSGVQPGIGTEVFVGKIPRDLYEDELVPLFEKAGFIWDLRLMMDPLSGQNRGYAFITFCGKEAAQEAVKL
CDSYEIRPGKHLGVCISVANNRLFVGSIPKNKTENILEEFSKVTEGLVDVILYHQPDDKKKNRGFCFLEYEDHK
SAAQARRRLMSGKVWGNVVTVEWADPVEEPDPEVMAKVKVLFRNLATTVTEEILEKSFSEFGKLERVKKLKD
YAFVHFEDRGAAVKAMDEMNGKEIEGEEIEIVLAKPPDKKRKERQAARQASRSTAYEDYYYHPPPRMPPPIRGRG
RGGGRGGYGYPDDYYGYEDYYDDYYGYDYHDYRGGYEDFYGYDDGYAVRGRGGGRGGRGAPPPRGRGAPPPRG
RAGYSQRGAPLGPPRGSRGGRGPAQQQRGRGSRGSRGNRGGNVGGKRKADGYNQPD SKRRQTNNQQNWGSQPIA
QQPLQQGGDYSGNYGYNNNDNQEFYQDTYGQQWK

90/6881
FIGURE 85

CGGACTGGCAGGGGGCAGGGAAGCTCAAAGATCTGGGGTGCTGCCAGGAAAAAGCAAATTCTGGAAGTTAATGGT
TTTGAGTGATTTTAAATCCTTGCTGGCGGAGAGGCCCCCTCTCCCCGGTATCAGCGCTTCCTCATTCTTTGAA
TCCGCGGCTCCGCGGTCTTCGGCGTCAGACCAGCCGGAGGAAGCCTGTTTGCAATTTAAGCGGGCTGTGAACGCC
CAGGGCCGGCGGGGGCAGGGCCGAGGCGGGCCATTTTGAATAAAGAGGCGTGCCTTCAGGCAGGCTCTATAAGT
GACCGCCGCGGCGAGCGTGCGCGCGTTGCAGGTCACTGTAGCGGGACTTCTTTTGTTTTCTTTCTCTTTGGGGC
ACCTCTGGACTCACTCCCCAGCATGAAGGCGCTGAGCCCCGGTGCGCGGCTGCTACGAGGCGGTGTGCTGCCTGTC
GGAACGCAGTCTGGCCATCGCCCGGGGCCGAGGGAAGGGCCCCGGCAGCTGAGGAGCCGCTGAGCTTGCTGGACGA
CATGAACCACTGCTACTCCCGCCTGCGGGAAGTGGTACCCGGAGTCCCGAGAGGCACTCAGCTTAGCCAGGTGGA
AATCCTACAGCGCGTCATCGACTACATTCTCGACCTGCAGGTAGTCCTGGCCGAGCCAGCCCCCTGGACCCCCTGA
TGGCCCCCACCTTCCCATCCAGACAGCCGAGCTCACTCCGGAATTGTCTATCTCCAACGACAAAAGGAGCTTTTG
CCTGAGTCTCGGCCGTGTCCTGACACCTCCAGGTGAGTATCTCCTCTCTTGAGAGGGAGGTTTAAACGGCAAGT
CCTGGAGTTGGCAGACGTTTTGAAAAATTGCCACTCACTCGGTTTAGGGAACTGAGGCCAGAGAGGGACAAGTG
ACTTGCCCATGTTG

91/6881
FIGURE 86

MKALSPVRGCYEAVCCLSERSLAIARGRGKGPAAEEPLSLDDMNHCSRLRELVPGVPRGTQLSQVEILQRVID
YILD LQVVLAEPAPGPPDGPHLPIQTAE LTP ELVISNDKRSFCH

92/6881
FIGURE 87

TTCTCTTCCTGCTCTCCATCATGGCGCAGGATCAAGGTGAAAAGGAGAACCCCATGCGGGAACCTTCGCATCCGCA
AACTCTGTCTCAACATCTGTGTTGGGGAGAGTGGAGACAGACTGACGCGAGCAGCCAAGGTGTTGGAGCAGCTCA
CAGGGCAGACCCCTGTGTTTTCCAAAGCTAGATACACTGTCAGATCCTTTGGCATCCGGAGAAATGAAAAGATTG
CTGTCCACTGCACAGTTCGAGGGGCCAAGGCAGAAGAAATCTTGGAGAAGGGTCTAAAGGTGCGGGAGTATGAGT
TAAGAAAAACAACCTTCTCAGATACTGGAACTTTGGTTTTGGGATCCAGGAACACATCGATCTGGGTATCAAAT
ATGACCCAAGCATTGGTATCTACGGCCTGGACTTCTATGTGGTGCTGGGTAGGCCAGGTTTCAGCATCGCAGACA
AGAAGCGCAGGACAGGCTGCATTGGGGCCAAACACAGAATCAGCAAAGAGGAGGCCATGCGCTGGTTCCAGCAGA
AGTATGATGGGATCATCCTTCCTGGCAAATTAAATTCCCGTTTCTATCCAAAAGAGCAATAAAAAGTTTTCAGTGA
AATGTGCAA

93/6881
FIGURE 88

MAQDQGEKENPMRELRIKRLCLNICVGESGDRLTRAAKVLEQLTGQTPVFSKARYTVRSFGIRRNEKIAVHCTVR
GAKAEEILEKGLKVREYELRKNNFSDTGNFGFGIQEHIDLGIKYDPSIGIYGLDFYVVLGRPGFSIADKKRRTGC
IGAKHRISKEEAMRWFQQKYDGIILPGK

94/6881
FIGURE 89

GGAAGTTCCGGCGGGGGCGGCCGAGGGGGAAGAGTGTGTCTGCGGGAGAAAGAGGAGAATCGCCCAAGCGGCCTC
GGAAGTCCCAGGGAGTGGAGGCCCCGCGGTGGAGCCGTGTGGTGTATGTTGTGGTAACACCATGTCTGTGCCCCCT
GCTCACCGATGCTGCCACCGTGTCTGGAGCTGAGCGGGAAACGGCCGCGGTTATTTTTTTACATGGACTTGGAGA
CACAGGGCACAGCTGGGCTGACGCCCTCTCCACCATCCGGCTCCCTCACGTCAAGTACATCTGTCCCCATGCGCC
TAGGATCCCTGTGACCCTCAACATGAAGATGGTGATGCCCTCCTGGTTTGACCTGATGGGGCTGAGTCCAGATGC
CCCAGAGGACGAGGCTGGCATCAAGAAGGCAGCAGAGAACATCAAGGCCTTGATTGAGCATGAAATGAAGAACGG
GATCCCTGCCAATCGAATCGTCCTGGGAGGCTTTTACAGGGCGGGGCCCTGTCCCTCTACACGGCCCTCACCTG
CCCCCACCCTCTGGCTGGCATCGTGGCGTTGAGCTGCTGGCTGCCTCTGCACCGGGCCCTTCCCCCAGGCAGCTAA
TGGCAGTGCCAAGGACCTGGCCATACTCCAGTGCCATGGGGAGCTGGACCCCATGGTGCCCGTACGGTTTGGGGC
CCTGACGGCTGAGAAGCTCCGGTCTGTTGTACACCTGCCAGGGTCCAGTTCAAGACATAACCCGGGTGTCATGCA
CAGCTCCTGTCTCAGGAGATGGCAGCTGTGAAGGAATTTCTTGAGAAGCTGCTGCCTCCTGTCTAACTAGTCGC
TGGCCCCAGTGCAGTACCCACAGCTCATGGGGGACTCAGCAAGCAAGCGTGGCACCATCTTGATCTGAGCCGGTC
GAGCCCCCTGTCCCCACCCTTCTGACCTGTCTTTTCCCACAGGCCTCTGGGGGCAGGTGGCAAGGCCTGGCCGG
GCCTTCTCTCTGGCCTTAGCCACCTGGCTCTGTCTGCAGCAGGGGCAGGCTGCTTTCTTATCCATTTCCCTGGA
GGCGGGCCCCCTGGCAGCAGTATTGGAGGGGCTACAGGCAGCTGGAGAAAGGGGCCCAGCCGCTGACCCACTCA
CTCAGGACCTCACTCACTAGCCCCGCTTTGGGGCCCCCTCCTGTGACCTCAGGGTTTGGCCCATGGGGCCCCCCA
GGCCCCCTGCCCAACTGATTCTGCCAGATAATCGTGTCTCCTGCCTCCACTCAGCTGCTTCTCAGTCATGAATG
TGGCCATGGCCCCGGGGTCCCTTGCTGCTGTGGGCTCCCTGTCCCTGGGCAGGAGTGCTGGTGAGGAGGTGGAG
CCTTTTGAGGGGGGCCTTCCCTCAGCTGTTTCCCCACACTGGGGGGCTGGGCCCTGCCTCCCCGTTACCTCCTT
CCCTGCAGGCCTGGAGCCTGTAGGGCTGGACTGAGGTTTCAAGTCTCCCCCAGCTGTCTCACCCCCACTTTGTCC
CCTCTAGAGCAGGGAGGCAGTGGGGGAGGAGTTGTGTCTCGTCTTCTGTCTCCATGTGGTTTTTGGGTGTTTT
TCTTGTGTGTCTGATTCCGATAAAATTAAAGAAATTGCTTCCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

95/6881
FIGURE 90

MCGNTMSVPLLTDAA TVSGAERETA AVIFLHGLGDTGHSWADALSTIRLPHVKYICPHAPRIPVTLNMKMVMPSW
FDLMGLSPDAPED EAGIKKAAENIKALIEHEMKN GIPANRIVLGGFSQGGALS LYTALTCPHPLAGIVALSCWLP
LHRAFPQAANGSAKDLAILQCHGELDPMVPVRFGALTAEKLR SVVTPARVQFKTYPGVMHSSCPQEMAAVKEFLE
KLLPPV

96/6881
FIGURE 91

AGAAGGAGAAGGTCGGGTTGTAGAAGCTGGGGTGGCCGGCAGCTCGCTCATCGGTGTTTCGTGGGCTTTGTCGGTC
CGTGCCCTCGTCTCTCCCTGGAAAGGGAGGGAGGCTTCGACGTCGAGAGGGAGCCGCTGCCGCGTTAGTTCCGAGC
TTGAAGTCACTAGGACTTCTCTCAAACCTTGTGTGCTGAGGAGACTCAGATGTTGGCCTCAGCTCCTAGGCTGAAC
TCAGCAGATCGGCCCATGAAAACCTTCTGTATTGAGACAAAGGAAGGGATCTGTCAGAAAGCAACACTTGTTATCT
TGGGCTTGGCAGCAAGGAAGAGGACAGGTAGTGGAGATCCTGCAATCTGAAAAGCAGACTGAAAGGTGACAAAGA
AGCTGAAGATCGGGTGGTGGAGAGAGGTATAACATTCCAGCCCCTCAATCTAGAAATGTTAGTAAGAACCAACAAC
AGCTTAACAGACAGAAGACCAAGGAACAGAATTCCCAGATGAAGATTGTTTCATAAGAAAAAGAAAGAGGACATG
GTTATAACTCATCAGCAGCTGCCTGGCAGGCCATGCAAAATGGGGGAAGAACAAAAATTTTCCAAATAATCAAA
GTTGGAATTCTAGCTTATCAGGTCCCAGGTTACTTTTTAAATCTCAAGCTAATCAGAACTATGCTGGTGCCAAAT
TTAGTGAGCCGCCATCACCAAGTGTTCTTCCCAAACCACCAAGCCACTGGGTCCCTGTTTTCCTTTAATCCTTCAG
ATAAGGAAATAATGACATTTCAACTTAAACCTTACTTAAAGTACAGGTATAAAATAAGACAAATGTTTAAATTT
AGTTATGTTACGGATAGTTGTCAATTGGTCTGAAACAAATTCGCTAGGGAATCTATTTGTGTAGAATAATTAA
TGTAACAAAAACAGACCATCTCGTGTGTGTGCACTGTGATATAATGGTAGTATCAGTGCAACTTTAATGATTGT
ACTTGATATTAAGTGTTCTCAACTGAGTAACCTTTAAGTGGAACCAAGTTTAGATTTGGGGAGTGGTAAAGGAA
TCAGCTTTTTCTATTGTTAGGGGAAGACAGTAATTTATCATTATGACAGTAGATTGTTGAAAGTTGGTGAAT
CGGATTATAAGCTTCTAGCTAACACAAGGATTCAGAATTAGGTAAACATCTGAAGGTTTAGTATATTAGAAACAC
CCAAACCAGTAATATGCTAACCTGATGCACTGCTGAAAGAAATGTGAATTTTTTCGTAATAATTGCATTTTAGTG
AATTGTACAGTGGGTGGAAAGGGCATTGGAGCTCATTAGAATGAGACATAGTACACCCCAATGGCCCTGTTTAT
TAAATGTAGTGGATTAAGTGCTGTCAACAAATACACCAAAACCATTTTTTATAGAAACAGTATTTAATGGTCAC
TCAATAGCTTTCAAATAACATTTTTGTATTACAGCACTGCACAAGCTATTCTAATAGTGCTCTCGCCTCATCATT
CCTGCAAAGCTTGCTTTGGGGAGTTGGATAATGTGAAAATTTTAAGTACCTAGGGGAGAAAGAGCCATGTAAATA
TCTGTAATAAACTTGTTAGCATATGTAAAGTTTTCTTGCCCTTTATCTTACAAAAATGGAGTATTTTAGTATGAAT
TTGCTGAATGTAAGACCGTGGACTGTTTTTTATAATATGGCCTAATTTTAAAGGTCCAAAATAACTTGTTTTTAA
AGTTTGCCCTTGTGCTAAAGTGCCAGTGTATGTATGTTATACTTGATTTGGTTGTAACTATATTTCAAAGTAA
CCCTAGTGTAAATAAGTTTTATACTAAAAAGGTTTAAAGCTGCTAAACTATTTTTAAGAGATGFGAAATGCAGTA
TGGGACTATCTTTTTTTCCTCCTCTAAGCCCAAAGATTAACTAGAGTCCCTCCAACCTTATAGATTGTTGGCTTT
CACAATCTTATAACCTAGGATACAGGTAGTTTCGAGTATGGTGCCAGTGATGTTTTGTTTTGTTTGGTCAAGGG
GTAGGTGCAACCCAATGGACCACTTATGCAAAAAGATGTAAACTCTTGATAATACATTGATAACATGTTTTGCCA
ACTTTAAATGCTTAAACATAAGCGAAACCAGTAGCAAGTATGTGGTTCAGCTTAAAAATTTTGATTGTTAATGCC
CTATTTTCTAATTTGGCACCTCTTGATGCCTAAGCAGGTAAGCAGATGCCTAAGCTGTATTTCTCCAAATAAATC
AAGATGAAGTACTGCCAAGTTAAATATTGATAGCCTAAGACAAGTTTATGTAGTACTTAATGTACATGATATG
AATGTGAAGCATAAAATTAAATAAAATTTTTCCCCATTAAAAA

97/6881
FIGURE 92

MGGGERYNIPAPQSRNVSKNQQLNRQKTKEQNSQMKIVHKKKERGHGYNSSAAAWQAMQNGGKNKNFPNNQSWN
SSLSGPRLLEFKSQANQNYAGAKFSEPPSPSVLPKPPSHWVPVSFNPSPDKEIMTFQLKTLLKVQV

98/6881
FIGURE 93

GTCTGAGGCTCGGCCGCCTGAGCCGCGGACGGTTTGTCTGAGCCCGTTAGTGCGCCCGGCCGAGACACGCCGCCGC
CATGTCCCCGCTACCTGCGTCCCCCAACACGTCTCTGTTCGTTCAGGAACGTGGCCGACGACACCAGGTCTGAAGA
CTTGCGGCGTGAATTTGGTCGTTATGGTCCTATAGTTGATGTGTATGTTCCACTTGATTTCTACACTCGCCGTCC
AAGAGGATTTGCTTATGTTCAATTTGAGGATGTTTCGTGATGCTGAAGACGCTTTACATAATTTGGACAGAAAAGTG
GATTTGTGGACGGCAGATTGAAATACAGTTTGGCCAGGGGGATCGAAAGACACCAAATCAGATGAAAGCCAAGGA
AGGGAGGAATGTGTACAGTTCTTCACGCTATGATGATTATGACAGATACAGACGTTCTAGAAGCCGAAGTTATGA
AAGGAGGAGATCAAGAAGTCGGTCTTTTGATTACAACATATAGAAGATCGTATAGTCCTAGAAACAGTAGACCGAC
TGGAAGACCACGGCGTAGCAGAAGCCATTCCGACAATGATAGACCAAACCTGCAGCTGGAATACCCAGTACAGTTC
TGCTTACTACACTTCAAGAAAGATC**TGA**AAGCGGAAAAAGAACCAAAGAAGGGCAGTTCAAGCGACCAAAGGGTG
GGTGGAAGGTGCTGCAGTATGAATACTGTACGAATATTTGACTCTGGTCTGAAAAGATAAAAGAATGTTATCGA
AAACTACATGGAATAATTGAAGTCCCTTCAAGTTTGAAAGTAAGCATTTTAGGACAAATAAAAGGAAATTCAACT
TTGTACTTGTGGAAACTAATCCCTAAATATGAATAGGTTTATATTGATTTCATGGGTAACAGGTCCATAATAAATT
ATTGGAACTAGGATGTCTGAATATCAAGGAAGACAGCCATAGTCTCTTACAGTGCCTCTGTTGGTCTGTCTCAA
ACTGAATTGGGTGGGAAAAGGTATGGTCCAATATAAAAGTTCCATTTTTGCCATTATTGGCAAATCTTGCCTTTG
TTTATTTTGGTGCCAGTGTTTTCTGCTTAATCATTTGCTTTGTTGGCATCTGTGTTTATTTACTTGTACACCACA
TGCAGTTTACATCTGTCTTAATACTACTCCTTCCCAGGTAAATTCCAATTATATTGACATCCAGCTAAGAGGGCCC
ATCTCTTCTCACCTCTTTCCTAGTCAGTAATTCAGCAAATATTTATTGAGCCCTTACTGTGGGCAAATCATTGT
ACTGGATAATTGAGAAAAATAGATAATTCCCTTATTCAGTAAATGTCTACTGAGCACAATCTAGTGAATCATTAC
AGTATGGCCTCATTGTTTTGTTTGAGGTGTGTTATTCATAACAATATTTTACACCATTTCGTATCAATGTAATTAT
AGAACACAATATACGATCAAGGATAAGTAATTGTGTGGTTATCTGCCATTTAAAAGTATCCAGTATTTGATCACA
TTATTATAAATAATGAAAAAATGATTTAATCTGTAATAAACTGGTTTATTGTGCAGTGAAGTGAATATACTAGAG
TTATAATAAATTGTTTACTCTGCCTCACCAAACACATGCTAGGATATAACCCCCAAAATAAGTATTTAACTTTGC
ATTAGGTATAAAGGAGACTGGGTGCTATAATTAGATTATTTTGGAGGCAGACAGAGAGCTGTTATCCTAACTGATT
TAGTATGTTCTGTAATTGAGAAAATGTTACCAAATTATACTTTTTAGTGATTTACATGTACATTTTATAGGGGA
CATGTTCTGTGTATAGCGAATAAATAACTTTTATAGTATCAC

99/6881
FIGURE 94

MSRYLRPPNTSLFVRNVADDTRSEDLRREFGRYGPIVDVYVPLDFYTRRPRGFAYVQFEDVRDAEDALHNLDKRW
ICGRQIEIQFAQGDRKTPNQMKAKEGRNVYSSSRYYDDYDRYRRSRRSYERRRSRSRSFDYNYRRSYSPRNSRPT
GRPRRSRSHSDNDRPNCSWNTQYSSAYYTSRKI

100/6881
FIGURE 95

GTCTGAGGCTCGGCCGCCTGAGCCGCGGACGGTTTGCTGAGCCCGTTAGTGCGCCCGGCCGAGACACGCCGCCGC
CATGTCCCGCTACCTGCGTCCCCCAACACGTCTCTGTTTCGTACGGAACGTGGCCGACGACACCAGGTCTGAAGA
CTTGCGGCGTGAATTTGGTCGTTATGGTCCTATAGTTGATGTGTATGTTCCACTTGATTTCTACACTCGCCGTCC
AAGAGGATTTGCTTATGTTCAATTTGAGGATGTTTCGTGATGCTGAAGACGCTTTACATAATTTGGACAGAAAGTG
GATTTGTGGACGGCAGATTGAAATACAGTTTGCCAGGGGGATCGAAAGACACCAAATCAGATGAAAGCCAAGGA
AGGGAGGAATGTGTACAGTTCTTCACGCTATGATGATTATGACAGATACAGACGTTCTAGAAGCCGAAGTTATGA
AAGGAGGAGATCAAGAAGTCGGTCTTTTGATTACAACATATAGAAGATCGTATAGTCCTAGAAACAGTAGACCGAC
TGGAAGACCACGGCGTAGCAGAAGCCATTCCGACAATGATAGATTCAAACACCGAAATCGATCTTTTTCAAGATC
TAAATCCAATTCAGATCACGGTCCAAGTCCCAGCCCAAGAAAGAAATGAAGGCTAAATCACGTTCTAGGTCTGC
ATCTCACACCAAACTAGAGGCACTCTAAAACAGATTCCAAAACACATTATAAGTCTGGCTCAAGATATGAAAA
GGAATCAAGGAAAAAAGAACCCACTAGATCCAAATCTCAGTCAAGATCACAGTCTAGGTCTAGGTCAAAATCTAG
ATCAAGGTCTTGGACTAGTCCTAAGTCCAGTGGCCACTCGATAGTATAAACCATGGTCATTTTTAGGCATGTATCA
TTCATTTACTCATAGTTTGGTTTACTTAAATTATCAGGAATACAATGTTGCAATGATGCTTAAAAACACTTGTT
AGTTTTCCCTGTACCAGGCAATGGTTATAATTAAATGATATGCTGTTGAGAAGCCACTCTTAAGAGTCCAGTTT
GTTTAAATGTTATGGGCAGCTACCAATTTGTGGTGTCTCTGTATATTTTTGTAAAGATTCTCATTTTTTATGCTTG
AAGTATTTGGTGAAAAGATGTTGGTTGACCATAATTTGCAACATTGTCTCATTAAAAATAAACTTTTCATATTCAT
ATTTGGTAGAACTGTTAACCCTAGAAATGTAGCTTGCTAATAAGATAGAATGATACAAAAGTGAAGTAGTAGCCAC
AGTACAACACTGACTGCTCAGACACATTTAGGTTTCAGGGTGGACCTTTATGTCTTGTCAAGATGTCTAGGCCCGG
CTGGGCGTGGTGGCTCACACCTGTAATCCCAGCACCTTTGGGAGGCCGAGGCGGGCGGATCACGAGGTTCAGGAGTT
CGAGACCAGCCTGACCAACACGGTGAAACCCCGTCTCTACTAAAAATACAAAATTATCCGGGCATGGTGGCACA
TGCCTGTAATCTCAGCTACTCAGGAGGCTGAGGCAAGAGAATCGCTTGAACCTGGGAGGTAGAAGTTGCAGTGAG
CCAAAATCACGCCACTGCACTCCAGCCTGGGCAACAGAGTGAGACTCCGTCTCAAAAAAAAAAAAAACCGGATG
TCTAGGCCAATGATAATTATTTTTGATGCAGTGTGGATTAGTTCTTTTGTAAACCCCACTGTCTTGGGGAATGAT
GCCAGCTGGGAAATTGAGTTTTTACTGAAACATGGAGCCTTCACTGCTTTTTTTCTGGTTCCTATGAAGATTG
GAACATAGAAAACACAAAACTCACCTTAAATTTGAGCAGGTCGTTGATGGCAAAAATAATTTTAAGGAAAAAG
GAATATTCTTATGTAGTTATTCTAAAGTTTAAGGAGCGTTGTTGACCATAATATTGCTTAGTTTTCTTACTGCTG
TTAAGTAAGTAAATTGTTTCAAAGTAGGTTTTGTGTGTGTGTCCTAGTGTAAGAAGTGAATTTTGATGCTT
ACAGCACTTGGCTCGTGCATTTGTATCAAATTTGCCTGCCTCTTTATGAGGGAGGCCTGCTTTTCACACCTCAG
TTTATTTAATACGAGGCAAGTTGTAAGACAACACTCATTCTAGGTGATTCTGTGGTGCCATGAAATTTAAGGTAA
TTTGGGGAAAAGGATTAGTCAGTTTTAAGCAAGAGTCACATCTTTTGAGCTTTCGATTATCAGTGTAGTACCTGA
CTAAAAATGAAGTAATACCCTTAAACATTTATAATTTCTAGTATTTCTCTGAAAGATCGTTTTGGGGACAAAAG
TGACTTGACATGTCCAATTTCAATTCAGAATAAAAAGCTAGCATCTTTAAAAATCTCAGATTGCTTGCTTACAGA
TACAAGTACGAATTATGGACAAACGATTCCTTTTAGAGGATTACTTTTTTCAATTTTCGGTTTTAGTAATCTAGGC
TTTGCCTGTAAAGAATACAACGATGGATTTTAAATACTGTTTGTGGAATGTGTTTAAAGGATTGATTCTAGAACC
TTTGTATATTTGATAGTATTTCTAACTTTCAATTTCTTTACTGTTTGCAGTTAATGTTTCATGTTCTGCTATGCAAT
CGTTTATATGCACGTTTCTTTAATTTTTTTAGATTTTCTGGATGTATAGTTTAAACAACAAAAAGTCTATTTAA
AACTGTAGCAGTAGTTTACAGTTCTAGCAAAGAGGAAAGTTGTGGGGTTAACTTTGTATTTTCTTTCTTATAGA
GGCTTCTAAAAAGGTATTTTTATATGTTCTTTTTAACAATATTGTGTACAACCTTTAAACATCAATGTTTGGG
TCAAAACAAGACCCAGCTTATTTTCTGCTTGCTGTAAATTAAGCAAACATGCTATAATAAAACAAAAATGAAGG

101/6881
FIGURE 96

MSRYLRPPNTSLFVRNVADDTRSEDLRREFGRYGPIVDVYVPLDFYTRRPRGFAYVQFEDVRDAEDALHNLDRKW
ICGRQIEIQFAQGDRKTPNQMKAKEGRNVYSSRYDDYDRYRRSRRSYERRRSRSDYNYRRSYSPRNSRPT
GRPRRSRSHSDNDRFKHRNRSFSRSKSNRSRSKSKQPKKEMKAKSRSRASHTKTRGTSKTDKTHYKSGSRYEK
ESRKKEPPRSKSKSRSQSRSRSKSRSRSWTSPKSSGH

102/6881
FIGURE 97

AGGAACGAGATGGCGGTTCTCTGGAGGCTGAGTGCCGTTTTCGGGTGCCCCAAGGAGGCCGAGCTGGCTCCAAGGCT
GCATCTCTCCACTGGACTAGCGAGAGGGTTGTCAGTGTTTTGCTCCCGGGTCTGCTTCCGGCTGCTTATTTGAAT
CCTTGCTCTGCGACGGACTATTCCCTGGCTGCAGCCCTCACTCTTCATGGTCACTGGGGCCTTGGACAAGTTGTT
ACTGACTATGTTTCATGGGGATGCCTCGCAGAAAGCTGCCAAGGCAGGGCTTTTGGCATTTCAGCTTTAACCTTT
GCTGGGCTTTGCTATTTCAACTATCACGATGTGGGCATCTGCAAAGCTGTTGCCATGCTGTGGAAGCTCTGACCT
TTTTGACTTCCTACTTTGAAGAATTGATGTATGCCTCTTTGCCTCTGCTTTGTCATGCCATTAAGCTCACAATAA
GGAAGAAATAACAGATAAGTCCATTGGTGGACAGCCTTCTTCTCTTAATCACAAGATTATTTTCAGAATTTAACT
TTGAGGAAAAGGTTTGAGAGGAATTATATTTAAGTTGTGAGACTGAGTTCTGTATTCTGGTGAGTTAATGGGGTT
GCCTCCCAGCTTCTTATAAGACTCACAGTATAACTAAACATGATATATCAGCTTTTGCCTTTTAATTTCTCAATC
TCTTAAAGAGAATC

103/6881
FIGURE 98

CAGGAACGAGATGGCGGTTCCCTGGAGGCTGAGTGCCGTTTGCGGTGCCCAAGGAGGCCGAGCTCTGTTGCTGCG
AACTCCAGTGGTCAGACCTGCTCATATCTCAGCATTTCTTCAGGACCGACCTATCCCAGAATGGTGTGGAGTGCA
GCACATACACTTGTACCGAGCCACCATTCTGGCTCCAAGGCTGCATCTCTCCACTGGACTAGCGAGAGGGTTGT
CAGTGTTTTGCTCCCGGGTCTGCTTCCGGCTGCTTATTTGAATCCTTGCTCTGCGACGGACTATTCCCTGGCTGC
AGCCCTCACTCTTCATGGTCACTGGGGCCTTGGACAAGTTGTTACTGATTATGTTTCATGGGGATGCCTCGCAGAA
AGCTGCCAAGGCAGGGCTTTTGGCATTTCAGCTTTAACCTTTGCTGGGCTTTGCTATTTCAACTATCACGATGT
GGGCATCTGCAAAGCTGTTGCCATGCTGTGGAAGCTCTGACCTTTTTGACTTCCTACTTTGAAGAATTGATGTAT
GCCTCTTTGCCCTCTGCTTTGTTCATGCCATTAAGCTCACAATAAGGAAGAAATAACAGATAAGCCCATTTGGTGGAC
AGCCTTCTTCTCTTAATCACAAGATTATTTTCAGAAATTTAATCTTTGAGGAAAAGGTTTGAGAGGAATTATATCT
AAGTTGTGAGACTGAGTTCTGTATTCTGGTGAGTTAATGGGGTTGCCTCCCAGCTTCTTATAAGACTCACAATAT
AACTAAACATGATATATCAGCTTTTGCCTTTAAATTTCTCAATCTCTTAAAGAGAATCCAGCTTTATTATGATTA
GTACATGATCAAATTTCCATATTTGCCTTGGGAATAATGGACAAAGGGAAATACTCTTAATTCATGAATAAAAAAC
TTTGCAGAAAATTAGACAGTGTTTAAATTTTCAAAAACCTCCCTCTCTAGTCAGTAGATACCACCTACTGATGGTT
ACATATACTAGGGAAATTTTAAATTTAGGAAATGCTGCTATCTCATATTATAAATTTCTAAATCCTAGGAAGAAA
CGCTTGGAGTGCTTCTGAAGATACAGAAGTCCATTTAAGGGCAAGTTTCCCCAGAGACATATCAAATATTATC
CATTGTAAACTGAGATTTAATTCTCAAATGTATTCTACTTGTTCATAAACAATCTGTCCACAAATATAAACTAT
AAGTAATAAATTGTTATTTCCGCACAATGGGAATCTCTAATGTGAAAATGTATTCTATGAAAATAATTTTTTTAA
ATAAAATGTTGTATAAAAAAA

104/6881
FIGURE 99

AGAGAGAAAGGTTGTGATGGCGGCTATAGCTGCATCCGAGGTGCTGGTGGACAGCGCGGAGGAGGGGTCCCTCGC
TGC GGCGGGCGGAGCTGGCCGCTCAGAAGCGCGAACAGAGACTGCGCAAATTCCGGGAGCTGCACCTGATGCGGAA
TGAAGCTCGTAAATTAAATCACCAGGAAGTTGTGGAAGAAGATAAAAAGACTAAAATTACCTGCAAATTGGGAAGC
CAAAAAAGCTCGTTTGGAGTGGGAACTAAAGGAAGAGGAAAAAGAAAAGGAATGTGCGGCAAGAGGAGAAGACTA
TGAGAAAGTGAAGTTGCTGGAGATCAGTGCAGAAGATGCAGAAAGATGGGAGAGGAAAAAGAAGAGGAAAAACCC
TGATCTGGGATTTTCAGATTATGCTGCTGCCCAGTTACGCCAGTATCATCGGTTGACCAAGCAGATCAAACCTGA
CATGGAAACATATGAGAGACTGAGAGAAAAACATGGAGAAGAGTTTTTCCCAACATCCAATAGTCTTCTTCATGG
AACACATGTGCCTTCCACAGAGGAAATTGACAGGATGGTCATAGATCTGGAAAAACAGATTGAAAAACGAGACAA
ATATAGCCGGAGACGTCCTTATAATGATGATGCAGATATCGACTACATTAATGAAAGGAATGCCAAATTCAACAA
GAAAGCTGAAAGATTCTATGGGAAATACACAGCTGAAATTAAACAGAATTTGGAAAGAGGAACAGCTGTCTTAATC
CCTTCAAGAACTGTTTATAGAAGCTTGAGAATGGGGTAAAAATTTCTGCTAGCAAAATCAAGTTCTTTTTGAAAT
TTTATCAGTAATCCAGAATTTAGTAGTCCATGCCTTCTCACTCAGCATTTAGAAATAAAAAATGTGGTTTCTTAAA
CGTATATCCTTTTCATGTATATTTCCACATTTTTTGTGCTTGGATATAAGATGTATTTCTTGTAAGTGAAGTTGTTTT
GTAATCTACTTTGTATACATTCTAATTATATTATTTTTCTATGTATTTTAAATGTATATGGCTGTTTAAATCTTTG
AAGCATTTTGGGCTTAAGATTGCCAGCAGCACACATCAGATGCAGTCATTGTTGCTATCAGTGTGGAATTTGATA
GAGTCTAGACTCGGGCCACTTGGAGTTGTGTACTCCAAAGCTAAGGACAGTGATGAGGAAGATGGCAGTGGCCAC
CGGAGGACTGGAGCAGTCCCTCCTCATGGCGGCCTGTGACCAAGGTCGGGGAGGAGTGGAGCTATCCTTCCATGA
TCTGATCATGTACAGTTCCTTTTTTAAAAGCAATAAATGCTTGGGATTAGAATTTCTAAAAA

105/6881
FIGURE 100

MAAIAASEVLVDSAEEGSLAAAAELAAQKREQLRKFRFLHLMRNEARKLNHQEVVEEDKRLKLPANWEAKKARL
EWELKEEEKKKKECAARGEDYEKVKLLEISAEDAERWERKKKRKNPDLGFSDYAAAQLRQYHRLTKQIKPDMETYE
RLREKHGEEFFPTSNSLLHGTHVPSTEEIDRMVIDLEKQIEKRDKYSRRRPYNDADIDYINERNAKFNKKAERF
YGKYTAEIKQNLERGTAV

106/6881
FIGURE 101A

GGCGGCCCCACTCTGCTCTGTCTGTCAGCTTCGGAGCTCCTCCACCCTGGCTGCCGAAAGCCCCCTTCCCGCCATCTAATG
ATACACTCTGCATACGCTTCTGTTGAGAATTTGTGGCTAGACATTCTGTGGGACCGGGAATCCAAATTCCTTGGT
AGCTAGAGGAAAAAATAAAACAACAGCCAACCAAGTGAATCCCAACCCAACCCCTGAAGGGCTGAAAATTC
TCGCCTTCTTCAGAGCGGGGCATGGCATCGAACAGCATCTTCGACTCCTTCCCGACCTACTCGCCGACCTTCATC
CGCGACCCAAGCACCAGCCGCGCTTCACACCTCCCTCCCCGGCCTTCCCCTGCGGCGGCGGCGGCGGCAAGATG
GGCGAGAACAGCGGCGCGCTGAGCGCGCAGGCGGCCGTGGGGCCCCGAGGGCGCGCCCCGGCCCCGAGGTGCGCTCG
ATGGTGGACGTGCTGGCGGACCACGCAGGCGAGCTCGTGCGCACCAGACAGCCCCAACTTCTCTGCTCCGTGCTG
CCCTCGCACTGGCGCTGCAACAAGACGCTGCCCCGTGCGCTTCAAGGTGGTGGCATTGGGGGACGTGCCGGATGGT
ACGGTGGTGA CTGTGATGGCAGGCAATGACGAGAACTACTCCGCTGAGCTGCGCAATGCCTCGGCCGTGATGAAG
AACCAGGTGGCCAGGTTCAACGACCTTCGCTTCGTGGGCGCAGTGGGCGAGGGAAGAGTTTCACCCTGACCATC
ACTGTGTTTACCAACCCACCCAAGTGGCGACCTACCACCGAGCCATCAAGGTGACCGTGGACGGACCCCGGGAG
CCCAGACGGCACCGGCAGAAGCTGGAGGACCAGACCAAGCCGTTCCCTGACCGCTTTGGGGACCTGGAACGGCTG
CGCATGCGGGTGACACCGAGCACACCCAGCCCCCGAGGCTCACTCAGCACCACAAGCCACTTCAGCAGCCAGCCC
CAGACCCCAATCCAAGGCACCTCGGAACTGAACCCATTCTCCGACCCCGCCAGTTTGACCGCTCCTTCCCCACG
CTGCCAACCCCTACGGAGAGCCGCTTCCCAGACCCAGGATGCATTATCCCGGGGCCATGTCAGCTGCCTTCCCC
TACAGCGCCACGCCCTCGGGCAGCAGCATCAGCAGCCTCAGCGTGGCGGGCATGCCGGCCACCAGCCGCTTCCAC
CATACTACCTCCCGCCACCCTACCCGGGGGGCCCCGAGAACCAGAGCGGGGCCCTTCCAGGCCAACCCGTCCCCC
TACCACCTCTACTACGGGACATCCTCTGGCTCCTACCAGTTCTCCATGGTGGCCGGCAGCAGCAGTGGGGGCGAC
CGCTCACCTACCCGCATGCTGGCCTCTTGCAACAGCAGCGCTGCCTCTGTGCGCCGCCGGCAACCTCATGAACCCC
AGCCTGGGCGGCCAGAGTGATGGCGTGAGGCCGACGGCAGCCACAGCAACTCACCCACGGCCCTGAGCACGCCA
GGCCGCATGGATGAGGCCGTGTGGCGGCCCTACTGACCGCCCTGGTGGACTCCTCCCGCTGGAGGCGGGGACCCCT
AACAACCTTCAAGACCAGTGATGGGCGGCTCCGAGGCTCCGGGCGGGAATGGGACCTGCGCTCCAGGGTGGTCT
CGGTCCCAGGGTGGTCCCAGCTGGTGGGAGCCTCTGGCTGCATCTGTGAGCCACATCCTTGTACAGAGGCATAG
GTTACCACCCCCACCCCGGCCCGGATACTGCCCCCGGCCAGATCCTGGCCGTCTCATCCCATACTTCTGTGGG
GAATCAGCCTCCTGCCACCCCCCGGAAGGACCTCACTGTCTCCAGCTATGCCAGTGCTGCATGGGACCCATGT
CTCCTGGGACAGAGGCCATCTCTCTTCCAGAGAGAGGCAGCATTGGCCACAGGATAAGCCTCAGGCCCTGGGAA
ACCTCCCGACCCCTGCACCTTCGTTGGAGCCCCGTGCATCCCTGGGTCCAGCCCCCTCTGCATTTACACAGATTT
GAGTCAGAACTGGAAGTGTCACCCACCCACCACCTCGAGCGGGGTTCCTTCATTGTACAGATGGGGCAGG
ACCCAGCAGCTGCTGGCAGAGATGGTTTTGAGAACACATCCAAGCCAGTCCCCCAGCCAGCTTCCCTCCGTT
CCTAACTGTTGGCTTTCCCCCAGCCGCACGGGTCCCAGGCCCCAGAGAAGATGAGTCTATGGCATCAGGTTCTTA
AACCAGGAAAGCACCTACAGACCGGCTCCTCCATGCATTTTACCAGCTCAACGCATCCACTCTCTGTTCTCTTG
GCAGGGCGGGGGAGGGGGGATAGGAGTCCCTTTCCCTAGGTGGTCTCATAATTCCATTTGTGGAGAGAACAG
GAGGGCCAGATAGATAGGTCTTAGCAGAAGGCATTGAGGTGAGGGATCATTTTGGGTGAGACATCAATGTCCCTG
TCCCCCTGGGTCCAGCCAAGCTGTGCCCATCCCCAAGCCTCCTGGGAGGATCCAGCCAATCTTGCGACTCC
TGGCACACACCTGTCTGTAACTGTTTTGTGCTCTGAAAGCAAATAGTCTGAGCAAAAAAAAAAAAAAAAAACAAA
AAAACAAAAAAAAAAACAAAACAGTTTTTAAACTGATTTTAGAAAAAGAGCTTAATCTAACGTTTTCAAACACA
AGGTCTCTTACAGGTATAGTTCCGTGATTATGATAGCTCTGTGATTATAAGCAACATCCCCGCCCCCTCTCCCCC
CCGCGGACCCCCAGCTGCCTCCTGAGGGTGTGGGGTTATTAGGGTCTCAATACTTTCTCAAGGGGCTACACTCCC
CATCAGGCAGCATCCCACCAGCCTGCACCACAGGCTCCCCTGGGAGGACGAGGGAAACGCTGATGAGACGCTGGG
CATCTCTCCTCTGTGGCTCTAGGACATCTGTCCAGGAGGCTGGGCGGAGGTGGGCAGGATGTGAGAGGTGGGGAG
TACTGGCTGTGCGTGGCAGGACAGAAGCACTGTAAAGGGCTCTCCAGCCGCAGCTCAGCTGCACTGCGTTCCGAG
GTGAAGTCTTGCCCTGAATTTTGCAAAATGGGAAAGTGGGCGCTTGCCCAAGGGCCAGGCTGCATGGATTCTCA
CATCAGAGTTCTCTGGCCCTAGAAAGGCTTAGAAAAGGCGTAAGGGAACCTATAAAGGCTAGCAGCATGCGGTAT
TTTAACTTTCTGCCTCGGCCTCTGTGGATGCAGAAATCTGCCCTACAAAATGCTCTTCATTGGTTGTCTCTGTGA
GAGCACTGTCCCCACCCAACCTGTCACAACGGCCAGAACCATAACCCAGAGACACACTGGCAGGTTAGGCAGTCC
TTCTGGTGATCCTATTCCATTCCCTCCTGCTGCGGTTTCTCTTGGCCTGTCTCACTGGA AAAACAGTCTCCATC
TCCTCAAAATAGTTGCTGACTCCCTGCACCCAAGGGGCTCTCCATGCCTTCTTAGGAAGCAGCTATGAATCCAT
TGTCCTTG TAGTTTCTTCCCTCCTGTTCTCTGGTTATAGCTGGTCCCAGGTCAGCGTGGGAGGCACCTTTGGGTT

107/6881

FIGURE 101B

CCCAGTGCCCAGCACTTTGTAGTCTCATCCCAGATTACTAACCCTTCCTGATCCTGGAGAGGCAGGGATAGTAAA
TAAATTGCTCTTCCTACCCCATCCCCCATCCCCTGACAAAAAGTGACGGCAGCCGTACTGAGTCTGTAAGGCCCA
AAGTGGGTACAGACAGCCTGGGCTGGTAAAAAGTAGGTCCTTATTTACAAGGCTGCGTTAAAGTTGTACTAGGCAA
ACACACTGATGTAGGAAGCACGAGGAAAGGAAGACGTTTTGATATAGTGTTACTGTGAGCCTGTCAGTAGTGGGT
ACCAATCTTTTGTGACATATTGTCATGCTGAGGTGTGACACCTGCTGCACTCATCTGATGTAAAACCATCCCAGA
GCTGGCGAGAGGATGGAGCTGGGTGGAAACTGCTTTGCACATATCGTTTGCTTGGTGTTTGTTTTAAACGCACAAC
TTGCTTGTACAGTAAACTGTCTTCTGTACTATTTAACTGT

108/6881
FIGURE 102

CAGGAACGAGATGGCGGTTCTCTGGAGGCTGAGTGCCGTTTGC GGTGCCCAAGGAGGCCGAGCTCTGTTGCTGCG
AACTCCAGTGGTCAGACCTGCTCATATCTCAGCATTTCCTTCAGGACCGACCTATCCCAGAATGGTGTGGAGTGCA
GCACATACTTGTACCGAGCCACCATTCTGGCTCCAAGGCTGCATCTCTCCACTGGACTAGCGAGAGGGTTGT
CAGTGTTTTGCTCCCGGCTCTGCTTCCGGCTGCTTATTTGAATCCTTGCTCTGCGACGGACTATTCCCTGGCTGC
AGCCCTCACTCTTCATGGTCACTGGGGCCTTGGACAAGTTGTTACTGACTATGTTTCATGGGGATGCCTCGCAGAA
AGCTGCCAAGGCAGGGCTTTTGGCATTTCAGCTTTAACCTTTGCTGGGCTTTGCTATTTCAACTATCACGATGT
GGGCATCTGCAAAGCTGTTGCCATGCTGTGGAAGCTCTGACCTTTTTGACTTCCTACTTTGAAGAATTGATGTAT
GCCTCTTTGCCTCTGCTTTGTCATGCCATTAAAGCTCACAATAAGGAAGAAATAACAGATAAGTCCATTGGTGGAC
AGCCTTCTTCTCTTAATCACAAGATTATTTTCAGAAATTAACCTTTGAGGAAAAGGTTTGAGAGGAATTATATTTA
AGTTGTGAGACTGAGTTCTGTATTCTGGTGAGTTAATGGGGTTGCCTCCCAGCTTCTTATAAGACTCACAGTATA
ACTAAACATGATATATCAGCTTTTGCCTTTTAATTTCTCAATCTCTTAAAGAGAATCCAGCTTTAGTATGATTAG
CATATGATCAAACCTCCATATTTGCCTTTGGGAATAATGGACTAAGGGAAATACTCTTAATTCATGAATAAAACT
TTGCAGAAAATTAGACAGTGTTTAAATTTTCAAAAACCTCCCTCTCTAGTCGGTAGATACCACCTACCGATGGTTA
CATATACTAGGGAAAATTTTAAAATTAGGAAATGCTGATATCTCATATTATAAAATTTCTAAATCCTAGGAAGAAAC
GCTTGGAGTGCTTCTGAAGATACAGAAGTTCCATTTAAGGGCAAGTTTCCCATAGACGTATCAAAATATTACCC
ATTGTAAACTGAGATTTAATTCTCAAATGTATTCTACTTGTTCATAAACAATCTGTCCACAAATATAAACTATA
AGTAATAAATTGTTATTTTCGCACAATGGGAATCTCTAATGTGAAAATGTATTCTGTGAAAATAAATTTTTAAAT
AAAATGTTGTATAATAA

109/6881
FIGURE 103

AGGAACGAGATGGCGGTTCTCTGGAGGCTGAGTGCCGTTTGCGGTGCCCAAGGAGGCCGAGCTGGCTCCAAGGCT
GCATCTCTCCACTGGACTAGCGAGAGGGTTGTCAGTGTTTTGCTCCCGGTCTGCTTCCGGCTGCTTATTTGAAT
CCTTGCTCTGCGACGGACTATTCCCTGGCTGCAGCCCTCACTCTTCAIGGTCAGTGGGGCCTTGGACAAGTTGTT
ACTGACTATGTTTCATGGGGATGCCTCGCAGAAAAGCTGCCAAGGCAGGGCTTTTGGCATTTTCAGCTTTAACCTTT
GCTGGGCTTTGCTATTTCAACTATCACGATGTGGGCATCTGCAAAGCTGTTGCCATGCTGTGGAAGCTCTGACCT
TTTTGACTTCCTACTTTGAAGAATTGATGTATGCCTCTTTGCCTCTGCTTTGTCATGCCATTAAGCTCACAATAA
GGAAGAAATAACAGATAAGTCCATTGGTGGACAGCCTTCTTCTCTTAATCACAAGATTATTTTCAGAATTTAACT
TTGAGGAAAAGGTTTGAGAGGAATTATATTTAAGTTGTGAGACTGAGTTCTGTATTCTGGTGAGTTAATGGGGTT
GCCTCCCAGCTTCTTATAAGACTCACAGTATAACTAAACATGATATATCAGCTTTTGCCTTTTAATTTCTCAATC
TCTTAAAGAGAATC

110/6881
FIGURE 104

MAVLRRLSALYGAQGGRALLRTPVIRPAHISAFLODRPIPEWCGVQHLHLSPSHHPGSKAASLHWTSESVL
LLGLLPAAAYLNPCSAMDYSLAATLTLPGHWGLRQVVTMFMGMPRRKLPRQGFWHFQL

111/6881
FIGURE 105

AGTGTGGTCAGGCGGCTCGGACTGAGCAGGACTTTCCTTATCCCAGTTGATTGTGCAGAATACACTGCCTATCGC
TTGTCTTCTATTACCA**ATGG**CTTCTTCTGATATCCAGGTGAAAGAACTGGAGAAGCGTGCCTCAGGCCAGGCTTT
TGAGCTGATTCTCAGCCCTCGGTCAAAAGAATCTGTTCCAGAATTCCCCCTTTCCCCTCCAAAGAAGAAGGATCT
TTCCCTGGAGGAAATTCAGAAGAAATTAGAAGCTGCAGAAGAAAGACGCAAGTCCCATGAAGCTGAGGTCTTGAA
GCAGCTGGCTGAGAAACGAGAGCACGAGAAAGAAGTGCTTCAGAAGGCAATAGAAGAGAAACAACAACTTCAGTAA
AATGGCAGAAGAGAAACTGACCCACAAAATGGAAGCTAATAAAGAGAACCGAGAGGCACAAATGGCTGCCAACT
GGAACGTTTTCGAGAGAAGGATAAGCACATTGAAGAAGTGCGGAAGAACAAGAATCCAAAGACCCTGCTGACGA
GACTGAAGCTGAC**TAA**TTTGTCTGAGAACTGACTTTCTCCCCATCCCCTTCCTAAATATCCAAAGACTGTACTG
GCCAGTGTCATTTTATTTTTTCCCTCCTGACAAATATTTTAGAAGCTAATGTAGGACTGTATAGGTAGATCCAGA
TCCAGACTGTAAGATGTTGTTTTAGGGGCTAAAGGGGAGAACTGAAAGTGTTTTACTCTTTTTCTAAAGTGTTG
GTCTTTCTAATGTAGCTATTTTTCTTGTGTCATCTTTTCTACTTCAGTACACTTGGTGTACTGGGTTAATGGCTA
GTACTGTATTGGCTCTGTGAAAACATATTTGTGAAAAGAGTATGTAGTGGCTTCTTTTGAAGTGTTAGATGCTGA
ATATCTGTTCACTTTTCAATCCAATTCTGTCCCAATCTTACCAGATGCTACTGGACTTGAATGGTTAATAAAAC
TGCACAGTGCTGTTGGTGGCAGTGACTTCTTTTGAGTTAGGTAAATAAATCAAGCCATAGAGCCCCCTCCTGGTTG
ATACTTGTTCAGATGGGGCCTTTGGGGCTGGTAGAAATACCCAACGCACAAATGACCGCACGTTCTCTGCCCCG
TTTCTTGCCCCAGTGTGGTTTGCATTGTCTCCTTCCACAATGACTGCTTTGTTTGGATGCCTCAGCCCAGGTCAG
CTGTTACTTTCTTTAGATGTTTATTTGCAACAACCAATTTTTTGTCTGTGTCCCTTTTAAAAGGCAGATTAAA
AGCACAAAGCGTGTTCAGAGAACAGTTGAGAGAGAATCTCAAGATTCTACTTGGTGGTTTGCTTGCTCTACGTT
ACAGGTGGGGCATGTCCTCATCCTTTCTGCCATAAAAAGCTATGACACGAGAATCAGAATATTAATAAAACTTTA
TGTA

112/6881
FIGURE 106

MASSDIQVKELEKRASGQAFELILSPRSKESVPEFPLSPPKKKDLSEELIQKKLEAAEERRKSHEAEVLKQLAEK
REHEKEVLQKAIEENNNFSKMAEEKLTHKMEANKENREAQMAAKLERLREKDKHIEEVRKNKESKDFADETEAD

113/6881
FIGURE 107

GTGCAACGGCCGTTAGAGGAGCTGAGGGAGGGAACCCGCTCACCGCAGACGTAGTGGCTGCAGTCAGTCTTCC
CGAGTGAGGGATTTCGCCGCCCGCTTTCAGGCCCCGTTTGGCTTAAATAACTGTGATTGATGATGGCCATGCAGGAGAA
ATATCCAACCTGAGGGGATCTCTCACGTCACTTCACCGAGTTCGGATGTGATTGAGAAGGGCAGTTCCTTGGGGAC
TGAATGGCAGACCCAGTTATCTCGGAGCCCTTTCGGAGCCGCTTCAGCCGCTGTTCAAGTGTAGCCGACAGTGG
GGACACAGCCATTGGTACATCATGCTCAGATATTGCGGAGGATTTTTGTCAGCTCAAGTGGCAGTCCCTCTTTCCA
GCCCATCAAAAGCCACGTAACCATTTCCAACAGCCCATGTGATGCCTTCTACTTTAGGGACCTCTCCTGCCAAGCC
AAATTCTACACCTGTTGGACCTCTTCTCTAAACTCCCTTTGTGAGGGTTGGCTGAAAGTGTGGGAATGACAAG
AAATGGAGACCTCGGTGCAATGAAACATTCTCCAGGCCTATCTAGAGATCTCATGTATTTCTCTGGTGCTACTGG
AGAAAATGGAATTGAGCAGTCCTGGTTTCCAGCAGTGGGCCATGAAAGACAAGAAGAGGGCGAGGAAGTTTGATAT
TCCTAGCATGGAATCTACCTCAATCAGTCGGCAATGATGGAGACACTTTATTGAGATCCTCACCACCGAGTCCG
CTTCCACAACCCAAGAACCAGCACAAAGTAAGGAGTTGTACAGAGTGTTCCTGAGGCCAAGAAGGCACCGGGCAG
CGGGGCAGTGTGTTGAGCGGAATGGACCACATTCTAATAGCAGTGGGGTCCCTCCCTTTGGGACTCCAGCCTGCTCC
CGGGCACTCCAGCCAGCCTCTGCCCTCTCAGGTGTGGCAGCCGAGTCCCTGACACTTGGCATCCCCGAGAGCAATC
TTGTGAACCTCAGCACTTGTGCGCAGCAGCTGGAATTGATTGCTTTACAGATGGAGCAAATGCAGCTTCAGAATGG
AGCCATCTGCCACCATCTGTCTGCTTTTGGTCCCTTCACTGCCCATCTTAGAGCCAGCACAGTGGATCAGCATCTT
GAACAGTAATGAACACCTTCTGAAGGAAAAAGAGCTTCTCATTGACAAGCAGAGGAAACACATCTCTCAGCTGGA
GCAGAAAGTGCAGAGAGAGCGAACTGCAAGTCCACAGTGCCTCTTGGGCCGCCCTGCCCCCTTTGGTGATGTCTG
CTTGCTGAGGCTACAGGAATTGCAGCGAGAAAACACTTTCTTACGTGCACAGTTTGCACAGAAGACAGAAGCCTT
GAGCAGAGAAAAGATTGACCTTGAAAAGAACTCTCTGCTTCTGAAGTTGAAGTCCAGCTCATCAGAGAGTCGCT
CAAAGTGGCGTTGCAGAAGCATTCTGAGGAAGTGAAGAAACAGGAAGAAAGGGTCAAAGGTGCTGATAAACATAT
CAATAATTTGAAAAGAAATGCCAGAAGGAATCAGAGCAGAACCGGGAGAAGCAGCAGCGTATTGAGACCTTGGA
GCGCTACCTGGCTGACCTGCCCACACTGGAAGACCATCAGAAGCAGAGCCAGCAGCTTAAGGATTCTGAGTTGAA
GAGCACAGAGCTGCAGGAGAAAAGTGAAGTGAAGTGGAGAGTTTGGTGGAGGAGACCCAGGCAATCTGCAGAGAGAA
GGAGATTCAACTGGAAGCCTGAGGCAGAGAGAAGCAGAATTCTCCTCCGCTGGACATAGCCTGCAAGATAAACA
GTCTGTGGAGGAGACCAGTGGAGAAGGTCCAGAAGTGGAAATGGAGTCTTGGCAGAAGCGATACGATTGCTCCA
AAAGATTGTGGAGAAGCAGCAGCAGAGAAGATGGATCAGTTGCGCTCACAAGTACAGAGCCTAGAGCAGGAAGTGGC
TCAAGAAGAAGGAACAAGCCAGGCCCTGAGAGAGGAGGCCAGCGAAGGGATTGAGCCCTGCAGCAGCTGCGCAC
AGCCGTGAAGGAGCTTTCAGTGCAAAACCAGGACTTGATTGAGAAGAATCTGACACTCCAGGAACACCTGCGCCA
GGCCCAACCAGGGTCTCCACCTTACCAGACACGGCCAGCTGGCACTTGAGCTGCACCAGGAGTTGGCCAGTTG
CCTTCAAGATCTGCAGGCTGTCTGTAGCATTGTGACCCAGAGGGGCCAGGGCCATGACCCCAATCTCTCCCTGCT
CCTGGGCATTCACTCACAGCACCCAGAGACTCAGCTAGATTTGCAGAAGCCAGATGTGATCAAGAGGAAACTAGA
AGAGGTTCAACAGCTGCGTCGTGACATTGAGGACTTAAGGACCACCATGTGACAGAGATATGCCAGGACATGGG
AGAAAAGTGTGTACACAGTGAAGGAATTCTGGGGGATTCCCCAGGGAGGAGCTGGGCTGCTGAGAGCCTAGTCC
AGCAGGTTTCTGCCCTGACATTCTTGTCTGCTATTCCAGAGAGGTCTCAGAGGGGAGGGGAGAGCCTGCATC
TGGGGGCCAAGGGCTGATTAGGGAAGTGTGTCCTACCCACACTGGCATGTTGGATTACGTTTGTCTGTTAATTC
ACTCTCGACGGTGAGTTACTAATTAACCTTTTGGCAGGTACAACAGATAAGTCCCTACAAACTGTTCCCAGCCCTA
GGCTGACATGAGAGACGAACAGGCTGTCCACCTTTCTTCTCCATCCAATGGGATGGATCCATGTTTCAATCCCCT
TCACACCTTGGTCTCTGCTGATTAGAGAGCTCATCAGAGGGGCTGGAAAGGCTGAGCAAGTACCAGTGACAATGG
CCATTTAAGAATTCTCAGGCCCCATGTGCCAGCCTTCTTGGGAAGTGAAGTGGCTTTCTGGGTTTTCTCATGCCT
GGTCTTACTGCTTCTTCTCAGGGCTCTTGTCTCCCAGAAGCCTCAGGGTAATGTGTTGGTTAGCACGTAACCTA
CTAGGATTGGGGCCCTAGGGATTATAGCCAGGACTCTAATCTGCCTACCATGCCATTTAACAAGAGATCCCCTC
TCCAGCTGCCTTGTGTCCCTAGGGTCTTGGCCATGTGTTTAGTGTGCTAAACTTTCTCCTTTGTCTCAGGCCTT
CCAGGTAGTCCCCTTCTTGGACTTAAGAGTGCAAACTCTTCTGTGGTTCTAGCCTTGGGCAGAATTATATCCC
AGAGACCACAGAGCAACTGTCAAGCTGCTTACCCCTCAGGAGGCTACAGCCTGTGCCAGCCCTCTAATTTG
TGCTCTCTTGTGTTGGGGGTGGTGGGGGTATTCTCTTTCCCTTTCTGCTCTGGCCTCCTTGAAAGTTTCAAGT
ACCCAGTACAAGTCAGCCACCATGCTGACGGGTATTTTTCTCATAAAGTTTATAACCAGTTATTTATATGAATC
TTTGTATGTCCATTTGTTTGTATTGCGTATTTTGATTATAAAATAAAGTATCTTAACAG

114/6881
FIGURE 108

MAMQEKYPTEGISHVTSPSSDVIQKGSSSLGTEWQTPVISEPFRSRFSRCSSVADSGDTAIGTSCSDIAEDFCSSS
GSPPFQPIKSHVTIPTAHVMPSTLGTSPAKPNSTPVGPPSSSKLPLSGLAESVGMTRNGDLGAMKHSPGLSRDLMY
FSGATGENGIEQSWFFPAVGHERQEEARKFDIPSMESTLNQSAMMETLYSDPHHRVRFHNPRTSTSKELYRVLPEA
KKAPGSGAVFERNGPHSNSSGVLPLGLQPAPGHSSQPLPSQVWQPSPDTWHPREQSCELSTCRQQLELIRLQMEQ
MQLQNGAICHHPAAFGPSLPILPEPAQWISILNSNEHLLKEKELLIDKQRKHISQLEQKVRESELQVHSALLGRPA
PFGDVCLLRLOELQRENTFLRAQFAQKTEALSREKIDLEKKLSASEVEVQLIRESLKVALQKHSEEVKKQEERVK
GRDKHINNLLKKKCQKESEQNREKQQRIETLERYLADLPTLEDHQKQSQQKDSSELKSTELQEKVTELESLLLEETQ
AICREKEIQLESLRQREAEFSSAGHSLQDKQSVEETSGEGPEVEMESWQKRYDSLQKIVEKQQQKMDQLRSQVQS
LEQEVAQEEGTSQALREEAQRRDSALQQLR TAVKELSVQNQDLIEKNLTLQEH LRQAQPGSPSPD TAQLALELH
QELASCLQDLQAVCSI VTQRAQGHDPNLSLLLGIHSQHPETQLDLQKPDVIKRKLEEVQQLR RDIEDLRTTMSDR
YAQDMGENCVTQ

115/6881
FIGURE 109

GTAGCAGCTTCTTCTCCGAACCAACCCTTTGCTTCGGACTTCTCCGGGGCCAGCAGCCGCCGACCAGGGGGCCC
GGGGCCACGGGCTCAGCCGACGACCATGGGCTCCGTGTCCAACCAGCAGTTTGCAGGTGGCTGCGCCAAGGCGGC
AGAAGAGGCGCCCGAGGAGGCGCCGAGGACGCGGCCCCGGGCGGCGGACGAGCCTCAGCTGCTGCACGGTGCGGG
CATCTGTAAGTGGTTCAACGTGCGCATGGGGTTCGGCTTCTGTCCATGACCGCCCCGCGCGGGGTGCGGCTCGA
CCCCCAGTGGAATGCTTTTGTGCACCAGAGTAAGCTGCACATGGAAGGGTTCCGGAGCTTGAAGGAGGGTGAGGC
AGTGGAGTTACCTTTAAGAAGTCAGCCAAGGGTCTGGAATCCATCCGTGTACCGGACCTGGTGGAGTATTCTG
TATTGGGAGTGAGAGGCGGCCAAAAGGAAAGAGCATGCAGAAGCGCAGATCAAAAGGAGACAGGTGCTACAACCTG
TGGAGGICTAGATCATCATGCCAAGGAATGCAAGCTGCCACCCAGCCCAAGAAGTGCCACTTCTGCCAGAGCAT
CAGCCAIATGGTAGCCTCATGTCCGCTGAAGGCCAGCAGGGCCCTAGTGCACAGGGAAAGCCAACCTACTTTTCG
AGAGGAAGAAGAAGAAATCCACAGCCCTACCCTGCTCCCGAGGCACAGAATTGAGCCACAATGGGTGGGGGCTA
TTCTTTTGGCTATCAGGAAGTTTGGAGGAGCAGGCAGAGTGGAGAAAGTGGGAATAGGGTGCATTGGGGCTAGTTG
GCACTGCCATGTATCTCAGGCTTGGGTTACACCATCACCTTTCTTCCCTCTAGGTGGGGGGAAGGGTGAGTC
AAAGGAACCTCAACCATGCTCTGTCCAAATGCAAGTGAGGGTCTGGGGGCAACCAGGAGGGGGGAATCACCTA
CAACCTGCATACTTTGAGTCTCCATCCCAGAAATTTCCAGCTTTTGAAAGTGGCCTGGATAGGGAAGTTGTTTTT
CTTTTAAAGAAGGATATATAATAATTCCCATGCCAGAGTGAAATGATTAAAGTATAAGACCAGATTTCATGGAGCCA
AGCCACTACATTCTGTGGAAGGAGATCTCTCAGGAGTAAGCATTGTTTTTTTTTTCACATCTTGTATCCTCATACC
CACTTTTGGGATAGGGTGCTGGCAGCTGTCCCAAGCAATGGGTAATGATGATGGCAAAAAGGGTGTTTTGGGGGAA
CAGCTGCAGACCTGCTGCTCTATGCTCACCCCGCCCCATTCTGGGCCAATGTGATTTTATTTATTTGCTCCCTT
GGATACTGCACCTTGGGTCCCCTTTCTCCAGGATGCCAACTGCACTAGCTGTGTGCGAATGACGTATCTTGTGC
ATTTTAACTTTTTTTCCTTAATATAAATATTCTGGTTTTGTATTTTGTATATTTTAACTAAGGCCCTCATTTT
CTGCACTGTGTTCTCAGGTACATGAGCAATCTCAGGGATAGCCAGCAGCAGCTCCAGGTCTGCGCAGCAGGAATT
ACTTTTTGTGTTTTTGGCACCGTGGAGAGCAACTATTTGGAGTGCACAGCCTATTGAACCTACCTATTTTTTGGC
AATAAGAGCTGGCTTTTCTGCCATAGTGCTCTTGAACCCCCCTCTGCCTTGAAAATGTTTTATGGGAGACTAG
GTTTTAACTGGGTGGCCCCATGACTTGATTGCCTTCTACTGGAAGATTGGGAATTAGTCTAAACAGGAAATGGTG
GTACACAGAGGCTAGGAGAGGCTGGGCCCCGTGAAAAGGCCAGAGAGCAAGCCAAGATTAGGTGAGGGTTGTCTA
ATCCTATGGCACAGGACGTGCTTTACATCTCCAGATCTGTTCTTCACCAGATTAGGTTAGGCCTACCATGTGCCA
CAGGGTGTGTGTGTGTTTTGTAAACTAGAGTTGCTAAGGATAAGTTTAAAGACCAATACCCCTGTACTTAATCCT
GTGCTGTGCGAGGGATGGATATATGAAGTAAGGTGAGATCCTTAACCTTTCAAAATTTTCGGGTTCAGGGAGACA
CACAAGCGAGGGTTTTGTGGTGCCTGGAGCCTGTGTCTGCTGCTACAGTAGTGATTAATAGTGTATGGTAG
CTAAAGGAGAAAAAGGGGGTTTTCGTTTTACACGCTGTGAGATCACCGCAAACCTACCTTACTGTGTTGAAACGGGA
CAAATGCAATAGAACGCATTGGGTGGTGTGTGTCTGATCCTGGGTTCTGTCTCCCCTAAATGCTGCCCCCAAG
TTACTGTATTTGTCTGGGCTTTGTAGGACTTCACTACGTTGATTGCTAGGTGGCCTAGTTTGTGTAAATATAATG
TATTGGTCTTTCTCCGTGTTCTTTGGGGGTTTTGTTTACAACTTCTTTTGTATTGAGAGAAAAATAGCCAAAG
CATCTTTGACAGAAGGTTCTGCACCAGGCAAAAAGATCTGAAACATTAGTTTGGGGGGCCCTCTTCTTAAAGTGG
GGATCTTGAACCATCCTTTCTTTTGTATTCCCTTCCCTATTACCTATTAGACCAGATCTTCTGTCTAAAAAC
TTGTCTTCTACCTTGCCCTCTTTTCTGTTACCCCCAAAAGAAAACCTTACACACCCACACACATACACATTTTCT
GCTTGGAGTGTCTCCACAACCTTTAAATGATGTATGAAAAATACTGAAGCTAGGAAAACCTCCATCCCTTGT
CCCAACCTCCTAAGTCAAGACCATTACCATTTCTTTCTTTCTTTTTTTTTTTTTTTTAAATGGAGTCTCACTGT
GTCACCCAGGCAGAGGTTGCAGTGAGCTGAGATCGCACCCTGCACTCCAGCCTGGTTACAGAGCAAGACTCTGT
CTCAAACAAAACAAAACAAAACAAAACACACTACTGTATTTTGGATGGATCAAACCTCCTTAATTTTAAATTTCT
AATCCTAAAGTAAAGAGATGCAATTGGGGGCCTTCCATGTAGAAAGTGGGGTCAGGAGGCCAAGAAAGGGAATAT
GAATGTATATCCAAGTCACTCAGGAACCTTTTATGCAGGTGCTAGAACTTTATGTCAAAGTGGCCACAAGATTGT
TTAATAGGAGACGAACGAATGTAACCTCATGTTTACTGCTAAAAACCAAAGCTTTGTGTAAATCTTGAATTTAT
GGGGCGGGAGGGTAGGAAAGCCTGTACCTGTCTGTTTTTTTCTGATCCTTTTCCCTCATTCCTGAACTGCAGGA
GACTGAGCCCCCTTTGGGCTTTGGTGACCCCATCACTGGGGTGTGTTTTATTGATGGTTGATTTTGTGTACTGGG
TACTTCCTTTCCATTTTCTAATCATTTTTTAAACAAGCTGACTCTTCCCTTCCCTTCTCCTTTCCCTGGGAAA
ATACAATGAATAAATAAAGACTTATTGGTACGC

116/6881
FIGURE 110

GAGCAGTGTGAAGAAGAGGGCGAGAACGACCCCCGGACCGACCAAAGCCGCGCGCCGCTGCATCCCGCGTCCAGC
ACCTACGTCCCGCTGCCGTCGCCGCCGCCACCA**ATG**CCCAAGAGAAAAGGCTGAAGGGGATGCTAAGGGAGATAAAG
CAAAGGTGAAGGACGAACCACAGAGAAGATCCGCGAGGTTGTCTGCTAAACCTGCTCCTCCAAAGCCAGAGCCCA
AGCCTAAAAAGGCCCTGCAAAGAAGGGAGAGAAGGTACCCAAAGGGAAAAAGGGAAAAGCTGATGCTGGCAAGG
AGGGGAATAACCCCTGCAGAAAATGGAGATGCCAAAACAGACCAGGCACAGAAAGCTGAAGGTGCTGGAGATGCCA
AG**TGA**AGTGTGTGCATTTTTGATAACTGTGTACTTCTGGTGACTGTACAGTTTGAAATACTATTTTTTATCAAGT
TTTATAAAAATGCAGAATTTTGTCTTACTTTTTTTTTTTTTTTTAAAAGCTATGTTGTTAGCACACAGAACACTTC
ATTGTTGTTTTTGGGGGAAGGGGCATATGTCACATAATAGAATGTCTCCAAAGCTGGATTGATGTGGAGAAAACAC
CTTTCCCTTCTAGTTTTTGAAGACTTCCTCTTGGCTCCCAGGAGGAGGGATTCCCTGACTTTGACACACATGGCC
ACCTTGGCACAAAAGCCTTGTGGTATAGAAAAACAAATTTGTTTTTATGTCCTCTTCTCCCTTTCCATCTTTCAG
CATAGACTTAACTCCCTTAAGCCCAGACATCTGTTGAGACCTGACCCCTAGTCATTGGTTACCAGTGTGTCAGGC
AATCTGGACTTTCCAGTGATGCCACTGAGATGGCACCTGTCAAAAGAGCAGTGGTTCCATTTCTAGATTGTGGAT
CTTCAGATAAATTCTGCCATTTTCATTTCACTTCCTGAAAGTCAGGGTCGGCTTGTGAAAAGTTGTTAAACAACA
TGCTAAATGTGAAATGTCAACCCTCACTCTAAACTTTCCCTGTTTCAGAGCATCAGATGAAGACTTCATTGGGTTT
TATAGTGGCTTTCTGATTTTTGGTAGTCCATTGAAGAAGGGAGTTTGAAAGTTGTTGTATACTGTAAACGATTGT
CTGCCCATGTCCTGCCTGAAATACCATGATTGTTTATGGAAAGTATCTTTAATAAAGCTGGATACAGTTTGGC

117/6881
FIGURE 111

MPKRKAEGDAKGDKAKVKDEPQRRSARLSAKPAPPKPEPKPKKAPAKKGEKVPKGKKGKADAGKEGNNPAENGDA
KTDQAQKAEGAGDAK

118/6881
FIGURE 112A

GAAAGCGGAGAGTCACAGCGGGGCCAGGCCCTGGGGAGCGGAGCCTCCACCGCCCCCTCATTCCCAGGCAAGGG
CTTGGGGGGAATGAGCCGGGAGAGCCGGGTCCCGAGCCTACAGAGCCGGGAGCAGCTGAGCCGCCGGCGCCTCGG
CCGCCGCCGCCCTCCTCCTCCTCCGCCGCCAGCCCGGAGCCTGAGCCGGCGGGGCGGGGGGAGAGGAGC
GAGCGCAGCGCAGCAGCGGAGCCCCGCGAGGCCCGCCCGGGCGGGTGGGGAGGGCAGCCCGGGGGACTGGGCCCC
GGGGCGGGGTGGGAGGGGGGGAGAAXXX
XXTCGAGGCGGCGGCTGCGGCAGCGGC
CGAGCGCGGTGGAATGAAGGCAGCCGCCGGGCAGGAAAGCGAGGGCCCCGCCGTGGGGCCGCCGCATCCGCTGG
GAAAGGAGCTGCTGGACGGGGCCGAGAGCAATGGGGGTGGCGGCGGCGGCGGAGCCGGCAGCGGCGGCGGGCCCCG
GCGCGGAGCCGGACCTGAAGAACTCGAACGGGAACGCGGGCCCTAGGCCCGCCCTGAACAATAACCTCACGGAGC
CGCCCCGGCGGCGGCGGTGGCGGCAGCAGCGATGGGGTGGGGGCGCCTCCTCACTCAGCCGCGGCGCCTTGCCGC
CCCCAGCCTACGGCTTCGGGCAACCCTACGGCCGGAGCCCGTCTGCCGTGCCCGCCCGCGGCGGCGCGCTCTTCC
ACCAACAACATGGCGGACAACAAAGCCCTGGCCTGGCAGCGCTGCAGAGCGGCGGCGGGGCGCTGGAGCCCT
ACGCGGGGGCCCCAGCAGAACTCTCACGACCAGGCTTCCCCAACACCAGTACAACCTCTACTACCCCAACCGCA
GCGCCTACCCCCCGCCCGCCCGGCCACGCGCTGAGCTCCCCGAGAGGTGGCACTCCGGGCTCCGGCGCGGCGG
CGGCTGCCGGCTCCAAGCCGCTCCTCCTCCAGCGCCTCCGCCTCCTCGTCGCTCTCGTCTCTCGCTCAGCAGC
GCTTCGGGGCCATGGGGGAGGCGGCCCTCCGCGGCCGGCGGGGGAACCTCCAGCCACCGCCACCCCCACCC
TCAACCAACTGCTCACGTCGCCAGCTCGGCCCGGGGCTACCAGGGCTACCCCGGGGGCGACTACAGTGGCGGGC
CCCAGGACGGGGGCGCCGCAAGGGCCCGGCGGACATGGCCTCGCAGTGTGGGGGGCTGCGGCGGCGGCAGCTG
CGGCGGCGGCGCCTCGGGAGGGGGCCCAACAAAGGAGCCACCACGCGCCATGAGCCCCGGGAGCAGCGGCGGCG
GGGGGACCGCTCGCCCCGACCCCTCAGCCATCCAGTCCAATGGATCAGATGGGCAAGATGAGACCTCAGCCAT
ATGGCGGGACTAACCCTACTCGCAGCAACAGGGACCTCCGTACGAGACCGCAGCAAGGACATGGGTACCCAGGGC
AGCCATACGGGTCCAGACCCCGCAGCGGTACCCGATGACCATGACGGGCGGGCGCAGAGTGCCATGGGCGGCC
TCTCTTATACACAGCAGATTCTCCTTATGGACAACAAGGCCAGCGGGTATGGTCAACAGGGCCAGACTCCAT
ATTACAACCAGCAAAGTCTCACCCTCAGCAGCAGCAGCCACCCTACTCCCAGCAACCACCGTCCCAGACCCCTC
ATGCCCAACCTTCGTATCAGCAGCAGCCACAGTCTCAACCACCACAGCTCCAGTCTCTCAGCCTCCATACTCCC
AGCAGCCATCCCAGCCTCCACATCAGCAGTCCCCGGCTCCATACCCCTCCCAGCAGTCGACGACACAGCAGCACC
CCCAGAGCCAGCCCCCTACTCACAGCCACAGGCTCAGTCTCCTTACCAGCAGCAGCAACCTCAGCAGCCAGCAC
CCTCGACGCTCTCCAGCAGGCTGCGTATCCTCAGCCCCAGTCTCAGCAGTCCCAGCAAACCTGCCTATTCCCAGC
AGCGCTTCCCTCCACCGCAGGAGCTATCTCAAGATTCAATTTGGGTCTCAGGCATCCTCAGCCCCCTCAATGACCT
CCAGTAAGGGAGGGCAAGAAGATATGAACCTGAGCCTTCACTCAAGACCCTCCAGCTTGCCGTATCTATCTGGTT
CAATAGATGACCTCCCCATGGGGACAGAAGGAGCTCTGAGTCTGGAGTGAGCACATCAGGGATTTCAGCAGCC
AAGGAGAGCAGAGTAATCCAGCTCAGTCTCCTTCTCTCCTACCTCCCTCACCTGCCTGGCATCCGAGGCC
CTTCCCCGTCCCCTGTTGGCTCTCCCGCCAGTGTGCTCAGTCTCGCTCAGGACCACTCTCGCCTGCTGCAGTGC
CAGGCAACCAGATGCCACCTCGGCCACCCAGTGGCCAGTCGGACAGCATCATGCATCCTTCCATGAACCAATCAA
GCATTGCCCAAGATCGAGGTTATATGCAGAGGAACCCCGAGATGCCCCAGTACAGTTCCCCCGAGCCGGCTCAG
CCTTATCTCCGCGTCAGCCTTCCGGAGGACAGATACACACAGGCATGGGCTCCTACCAGCAGAACTCCATGGGGA
GCTATGGTCCCCAGGGGGGTGAGTATGGCCACAAGGTGGCTACCCAGGCAGCCAACTATAATGCCTTGCCCA
ATGCCAACTACCCAGTGCAGGCATGGCTGGAGGCATAAACCCTATGGGTGCCGGAGGTCAAATGCATGGACAGC
CTGGCATCCACCTTATGGCACACTCCCTCCAGGGAGGATGAGTCACGCCTCCATGGGCAACCGGCCCTTATGGCC
CTAACATGGCCAATATGCCACCTCAGGTTGGGTGAGGGATGTGTCCCCCACCAGGGGGCATGAACCGGAAAACCC
AAGAAACTGCTGTGCGCATGCATGTTGCTGCCAACTCTATCCAAAACAGGCCGCCAGGCTACCCCAATATGAATC
AAGGGGGCATGATGGGAACCTGGACCTCCTTATGGACAAGGGATTAATAGTATGGCTGGCATGATCAACCCTCAGG
GACCCCATATTCCATGGGTGGAACCATGGCCAACAATTCTGCAGGGATGGCAGCCAGCCAGAGATGATGGGCC
TTGGGGATGTAAAGTTAACTCCAGCCACCAAAATGAACAACAAGGCAGATGGGACACCCAAGACAGAATCCAAAT
CCAAGAAATCCAGTTCTTCTACTACAACCAATGAGAAGATCACCAAGTTGTATGAGCTGGGTGGTGAGCCTGAGA
GGAAGATGTGGGTGGACGTTATCTGGCCTTCACTGAGGAGAAGGCCATGGGCATGACAAATCTGCCTGCTGTGG
GTAGGAAACCTCTGGACCTCTATCGCCTCTATGTGTCTGTGAAGGAGATTGGTGGATTGACTCAGGTCAACAAGA
ACAAAAAATGGCGGGAACCTTGAACCAACCTCAATGTGGGCACATCAAGCAGTGTGCCAGCTCCTTGAAAAAGC

119/6881
FIGURE 112B

AGTATATCCAGTGTCTCTATGCCTTTGAATGCAAGATTGAACGGGGAGAAGACCCTCCCCCAGACATCTTTGCAG
CTGCTGATTCCAAGAAGTCCCAGCCCCAAGATCCAGCCTCCCTCTCCTGCGGGATCAGGATCTATGCAGGGGCCCC
AGACTCCCCAGTCAACCAGCAGTTCCATGGCAGGATGAGCAGGAGCAATTACAGTTGGGATCCAGGATGCCTTTAATGATGGAA
ACAGTCAGATCCCCCATTGCCAGGCATGAGCAGGAGCAATTACAGTTGGGATCCAGGATGCCTTTAATGATGGAA
GTGACTCCACATTCCAGAAGCGGAATTCCATGACTCCAAACCCTGGGTATCAGCCCAGTATGAATACCTCTGACA
TGATGGGGCGCATGTCTATGAGCCAAATAAGGATCCTTATGGCAGCATGAGGAAAGCTCCAGGGAGTGATCCCT
TCATGTCTCAGGGCAGGGCCCCAACGGCGGGATGGGTGACCCCTACAGTCGTGCTGCCGGCCCTGGGCTAGGAA
ATGTGGCGATGGGACCACGACAGCACTATCCCTATGGAGGTCTTATGACAGAGTGAGGACGGAGCCTGGAATAG
GGCCTGAGGGAAACATGAGCACTGGGGCCCCACAGCCGAATCTCATGCCTTCCAACCCAGACTCGGGGATGTATT
CTCCTAGCCGCTACCCCCCGCAGCAGCAGCAGCAGCAGCAGCAACGACATGATTCTTATGGCAATCAGTTCTCCA
CCCAAGGCACCCCTTCTGGCAGCCCTTCCCCAGCCAGCAGACTACAATGTATCAACAGCAACAGCAGAATTACA
AGCGGCCAATGGATGGCACATATGGCCCTCCTGCCAAGCGGCACGAAGGGGAGATGTACAGCGTGCCATACAGCA
CTGGGCAGGGGCAGCCTCAGCAGCAGCAGTTGCCCCAGCCAGCCCGAGCCTGCCAGCCAGCAACAAGCTGCCC
AGCCTTCCCCTCAGCAAGATGTATACAACAGTATGGCAATGCCTATCCTGCCACTGCCACAGCTGCTACTGAGC
GCCGACCAGCAGGCGGGCCCCAGAACCAATTTCCATTCCAGTTTGGCCGAGACCGTGTCTCTGCACCCCTGGCA
CCAATGCCCAGCAAAACATGCCACCACAAATGATGGGCGGGCCCATACAGGCATCAGCTGAGGTTGCTCAGCAAG
GCACCATGTGGCAGGGGCGTAATGACATGACCTATAATTATGCCAACAGGCAGAGCACGGGCTCTGCCCCCAGG
GCCCCGCTATCATGGCGTGAACCGAACAGATGAAATGCTGCACACAGATCAGAGGGCCAACCACGAAGGCTCGT
GGCCTTCCCATGGCACACGCCAGCCCCCATATGGTCCCTCTGCCCCCTGTGCCCCCATGACAAGGCCCCCTCCAT
CTAACTACCAGCCCCACCAAGCATGCAGAATCACATTCCCTCAGGTATCCAGCCCTGCTCCCTGCCCCGGCCAA
TGGAGAACCGCACCTCTCCTAGCAAGTCTCCATTCTGCACTCTGGGATGAAAATGCAGAAGGCAGGTCCCCCAG
TACCTGCCTCGCACATAGCACCTGCCCCGTGTGCAGCCCCCATGATTGCGCGGGATATCACCTTCCACCTGGCT
CTGTTGAAGCCACACAGCCTGTGTTGAAGCAGAGGAGGCGGCTCACAAATGAAAGACATTGGAACCCCGGAGGCAT
GGCGGGTAATGATGTCCCTCAAGTCTGGTCTCCTGGCAGAGAGCACATGGGCATTAGATAACCATCAACATCCTGC
TGTATGATGACAACAGCATCATGACCTTCAACCTCAGTCAGCTCCAGGGTTGCTAGAGCTCCTTGTAGAATATT
TCCGACGATGCCTGATTGAGATCTTTGGCATTTTAAAGGAGTATGAGGTGGGTGACCCAGGACAGAGAACGCTAC
TGGATCCTGGGAGGTTTCAGCAAGGTGTCTAGTCCAGCTCCCATGGAGGGTGGGGAAGAAGAAGAAGAACTTCTAG
GTCCTAAACTAGAAGAGGAAGAAGAAGAGGAAGTAGTTGAAAATGATGAGGAGATAGCCTTTTTCAGGCAAGGACA
AGCCAGCTTCAGAGAATAGTGAGGAGAAGCTGATCAGTAAGTTTGACAAGCTTCCAGTAAAGATCGTACAGAAGA
ATGATCCATTTGTGGTGGACTGCTCAGATAAGCTTGGGCGTGTGCAGGAGTTTGACAGTGGCCTGCTGCACTGGC
GGATTGGTGGGGGGGACACCACTGAGCATATCCAGACCCACTTCGAGAGCAAGACAGAGCTGCTGCCTTCCCGGC
CTCACGCACCCCTGCCACCAGCCCCCTCGGAAGCATGTGACAACAGCAGAGGGTACACCAGGGACAACAGACCAGG
AGGGGCCCCCACCTGATGGACCTCCAGAAAAACGGATCACAGCCACTATGGATGACATGTTGTCTACTCGGTCTA
GCACCTTGACCGAGGATGGAGCTAAGAGTTCAGAGGCCATCAAGGAGAGCAGCAAGTTTCCATTGTGCATTAGCC
CAGCACAGAGCCACCGGAACATCAAGATCCTAGAGGACGAACCCACAGTAAGGATGAGACCCCACTGTGTACCC
TTCTGGACTGGCAGGATTCTCTTGCCAAGCGCTGCGTCTGTGTGTCCAATACCATTGCAAGCCTGTCAATTTGTGC
CAGGCAATGACTTTGAGATGTCCAACACCCAGGGCTGCTGCTCATCCTGGGCAAGCTGATCCTGCTGCACCACA
AGCACCCAGAACGGAAGCAGGCACCACTAATTTATGAAAAGGAGGAGGAACAGGACCAAGGGGTGAGCTGCAACA
AAGTGGAGTGGTGGTGGGACTGCTTGGAGATGCTCCGGGAAAACACCTTGGTTACACTCGCCAACATCTCGGGGC
AGTTGGACCTATCTCCATACCCCGAGAGCATTTGCCTGCCTGTCTGGACGGACTCCTACACTGGGCAGTTTGCC
CTTCAGCTGAAGCCCAGGACCCCTTTTCCACCCTGGGCCCAATGCCGTCTTTCCCCGCAGAGACTGGTCTTGG
AAACCCTCAGCAAACTCAGCATCCAGGACAACAATGTGGACCTGATTCTGGCCACACCCCCCTTCAGCCGCTGG
AGAAGTTGTATAGCACTATGGTGCCTTCTCAGTGACCGAAAGAACCCTGTGCGGGGAGATGGCTGTGGTAC
TGCTGGCCAACCTGGCTCAGGGGGACAGCCTGGCAGCTCGTGCCATTGCAGTGCAGAAGGGCAGTATCGGCAACC
TCCTGGGCTTCTAGAGGACAGCCTTGCCGCCACACAGTTCCAGCAGAGCCAGGCCAGCCTCCTCCACATGCAGA
ACCCACCCTTTGAGCCAACCTAGTGTGGACATGATGCGGGCGGGCTGCCCGCGCGTGTGCTTGCCTTGGCCAAGGTGG
ACGAGAACCCTCAGAGTTTACTCTGTACGAATCACGGCTGTTGGACATCTCGGTATCACCGTTGATGAACTCAT
TGGTTTCAAGTCATTTGTGATGTACTGTTTTTATTGATTGGCCAGTCATGACAGCCGTGGGACACCTCCCCCCCC

120/6881
FIGURE 112C

GTGTGTGTGTGCGTGTGTGGAGAACTTAGAAACTGACTGTTGCCCTTTATTTATGCAAAACCACCTCAGAATCCA
GTTTACCCTGTGCTGTCCAGCTTCTCCCTTGGGAAAAAGTCTCTCCTGTTTCTCTCTCCTCCTTCCACCTCCCCCT
CCCTCCATCACCTCACGCCTTTCTGTTCCCTTGTCTCACCTTACTCCCCTCAGGACCCTACCCACCCCTCTTTGA
AAAGACAAAGCTCTGCCTACATAGAAGACTTTTTTTATTTTAACCAAAGTTACTGTTGTTTACAGTGAGTTTGGG
GAAAAAAAATAAAATAAAATGGCTTTCCAGTCCTTGCATCAACGGGATGCCACATTTCATAACTGTTTTTAAT
GGTAAAAAAAAAAAAA

121/6881
FIGURE 113

CAACAATGTGGACCTGATTCTGGCCACACCCCCCTTCAGCCGCCTGGAGAAGTTGTATAGCACTATGGTGCGCTT
CCTCAGTGACCGAAAGAACCCGGTGTGCCGGGAGATGGCTGTGGTACTGCTGGCCAACCTGGCTCAGGGGGACAG
CCTGGCAGCTCGTGCCATTGCAGTGCAGAAGGGCAGTATCGGCAACCTCCTGGGCTTCCTAGAGGACAGCCTTGC
CGCCACACAGTTCCAGCAGAGCCAGGCCAGCCTCCTCCACATGCAGAACCCACCCTTTGAGCCAAGTGTGGA
CATGATGCGGCGGGCTGCCCGCGCGCTGCTTGCCTTGGCCAAGGTGGACGAGAACCCTCAGAGTTTACTCTGTGA
CGAATCACGGCTGTTGGACATCTCGGTATCACCGTTGATGAACCTATTGGTTTCACAAGTCATTTGTGATGTACT
GTTTTTGGATTGGCCAGTCATGACAGCCGTGGGACACCTCCCCCCCCCGTGTGTGTGTGCGTGTGTGGAGAACTTA
GAAACTGACTGTTGCCCTTTATTTATGCAAAACCACCTCAGAATCCAGTTTACCCTGTGCTGTCCAGCTTCTCCC
TTGGGAAAAAGTCTCTCCTGTTTCTCTCTCCTCCTTCCACCTCCCCTCCCTCCATCACCTCACGCCCTTCTGTTC
CTTGTCCTCACCTTACTCCCCTCAGGACCTACCCCCACCTCCTTTGAAAAGACAAAGCTCTGCCTACATAGAAGA
CTTTTTTTATTTTAAACCAAAGTTACTGTTGTTTACAGTGAGTTTGGGGAAAAAATAAAAAATAAAATGGCTTTC
CCAGTCCTTGCATCAACGGGATGCCACATTTTATAACTGTTTTTAAATGGTAAAAAAAAAAAAAAAAAATACAAAA
AAAAATTCTGAAGGACAAAAAGGTGACTGCTGAACTGTGTGTGGTTTATTGTTGTACATTACAAATCTTGCAGG
AGCCAAGAAGTTCGCAGTTGTGAACAGACCCTGTTCACTGGAGAGGCCTGTGCAGTAGAGTGTAGACCCTTTCAT
GTACTGTACTGTACACCTGATACTGTAAACATACTGTAATAATAATGTCTCACATGGAAACAGAAAACGCTGGGT
CAGCAGCAAGCTGTAGTTTTTAAAAATGTTTTTAGTTAAACGTTGAGGAGAAAAAAAAAAAAAGGCTTTTCCCCCA
AAGTATCATGTGTGAACCTACAACACCCTGACCTCTTCTCTCCTCCTTGATTGTATGAATAACCCTGAGATCAC
CTCTTAGAACTGGTTTTTAACCTTTAGCTGCAGCGGCTACGCTGCCACGTGTGTATATATATGACGTTGTACATTG
CACATAACCCTTGGATCCCCACAGTTTGGTCCTCCTCCCAGCTACCCCTTTATAGTATGACGAGTTAACAAGTTGG
TGACCTGCACAAAGCGAGACACAGCTATTTAATCTCTTGCCAGATATCGCCCCTCTTGGTGCGATGCTGTACAGG
TCTCTGTAAAAAGTCCTTGCTGTCTCAGCAGCCAATCAACTTATAGTTTATTTTTTTCTGGGTTTTTGTGTTTGT
TTGTTTTCTTTCTAATCGAGGTGTGAAAAAGTTCTAGGTTTCAAGTTCTGATGAAGAAACACAATTGAGAT
TTTTTCAGTGATAAAATCTGCATATTTGTATTTCAACAATGTAGCTAAAACCTTGATGTAAATTCCTCCTTTTTT
CCTTTTTTGGCTTAATGAATATCATTTATTCAGTATGAAATCTTTATACTATATGTTCCACGTGTTAAGAATAAA
TGTACATTAAATCTTGGT

122/6881
FIGURE 114

[illegible]

123/6881
FIGURE 115

MERASLIQKAKLAEQAERYEDMAAFMKGAVEKGEELSCEERNLLSVAYKNVVGQRAAWRVLSSIEQKSNEEGSE
EKGPEVREYREKVETELQGVCDTVLGLLDSHLIKEAGDAESRVFYLMKMGDYYRYLAEVATGDDKKRIIDSARSA
YQEAMDISKKEMPPPTNP IRLGLALNFSVFHYEIANSPEEAISLAKTTFDEAMADLHTLSEDSYKDSTLIMQLLRD
NLTLWTADNAGEEGGEAPQEPQS

124/6881
FIGURE 116

CCGGAAGTCGAGTTAGTCTAGTTAGTATCGGCCTGTTATCTCCTTTTGCGCGACACGGTCTCAGCTGTTCCGCCT
GAGGCGAGTGACGCTGGCCGCCAACGAGGTATACGTACTGGGACCCTCGCCCTCAGTCTCGTCTCCGGCGCGGCT
ACCTGCCCCGTTTTCCCTGTGAGTTGACCTGCTCCGGGGCCGCGGGCCGCCA**ATGG**CAGGGGGCCGCTCCGACCACG
GCCTTCGGGCAGGCGGTGACCGGCCCGCGGGCTCAGGGAAGACCACGTACTGCCTGGGCATGAGTGAGTTCCTG
CGCGCGCTGGGCCGGCGCGTGGCGGTGGTGAACCTGGACCCGGCCAACGAGGGGCTGCCGTACGAGTGCGCGTG
GACGTGGGCGAGCTGGTGGGGCTGGGCGACGTGATGGACGCGCTGCGCCTGGGGCCCAACGGCGGCCTGCTCTAC
TGCATGGAGTACCTGGAAGCCAACCTGGACTGGCTGCGTGCCAAGCTCGACCCCTCCGCGGCCACTACTTCCTC
TTCGACTGCCCAGGCCAGGTGGAGCTCTGCACGCATCACGGCGCCTTGCGCAGCATCTTCTCCCAAATGGCGCAG
TGGGACCTCAGGCTGACTGCCGTCCACCTCGTGGATTCTCACTACTGCACAGACCCTGCCAAGTTCATTTTCAGTA
CTGTGTACCTCCCTGGCCACCATGCTGCACGTGGAACCTGCCCCACATCAACCTCCTTTCCAAGATGGACCTCATT
GAGCATTATGGGAAGCTGGCCTTCAACCTGGACTACTACACAGAGGTTCTGGACCTCTCCTACCTGCTTGACCAC
CTGGCTTCTGACCCTTTCTTCCGCCACTACCGCCAGCTCAATGAGAAGCTAGTGCAGCTCATCGAAGACTATAGC
CTTGTCTCCTTTATCCCTCTCAACATCCAGGACAAGGAGAGCATCCAGCGAGTCCTGCAGGCTGTGGATAAAGCC
AATGGATACTGTTTCAGAGCCCAAGAGCAGCGAAGCTTGGAAGCCATGATGTCTGCCGCAATGGGAGCCGACTTC
CATTTCTCTTCCACACTGGGCATCCAGGAGAAGTACCTGGCACCCCTCGAACCAGTCAGTGGAGCAGGAAGCCATG
CAGCTG**TAG**CAACAAGGTGGACCCTGGAGAGCAGGATGCATAATCCAGCACTGGGGAAAGTGGAGGCTCCTGATG
CAGGCTGCAGACCCAAGAGCAAGTCCTCCCAGCCAGAGCTGGCGGGCTGGCAAGGGGATATTCAGCTCTGCAAAG
GACTTCTGGCCAAAAAGCCAGACATGGTGCCAAGCAGAACACCCCCCATACTGTGAGTGGTGTCCGTGAGCTCTG
GGCCCTGCCACCAGAAAGTCGAGCACTGGTCCTAGTCAGGCTGTGATGAAATGTGCTACAATACAAGAGTTTATT
TTCT

125/6881
FIGURE 117

MAGAAPTAFGQAVTGPPGSGKTTYCLGMSEFLRALGRRVAVVNLDPANEGLPYECADVGVGLGDVMDALRL
GPNGGLLYCMEYLEANLDWLRAKLDPLRGHYFLFDCPGQVELCTHHGALRSIFSQMAQWDLRLTAVHLVDSHYCT
DPAKFISVLCTSLATMLHVLPINLLSKMDLIEHYGKLAFNLDYYTEVLDSL YLLDHLASDPFFRHYRQLNEKL
VQLIEDYSLVSFIPLNIQDKESIQRVLQAVDKANGYCFRAQEQRSLEAMMSAAMGADFHFSSSTLGIQEKYLAPSN
QSVEQEAMQL

126/6881
FIGURE 118

TAGAGTCGTTGGGCCCCGGCGCGACCCGCAGGAGCGTAGAGAGCGCGGGACTAGAGTGCAGAGCTCCGGGACGTGG
ATCGGAGCCGGCGCGATGGGCGGAGAGCAGGAGGAGGAGCGGTTTCGACGGCATGTTGCTGGCCATGGCTCAGCAG
CACGAGGGCGGCGTGCAGGAGCTTGTGAACACCTTCTTCAGCTTCCTTCGACGCAAAACAGACTTTTTTCATTGGA
GGAGAAGAAGGGATGGCAGAGAAGCTTATCACACAGACTTTTCAGCCACCACAATCAGCTGGCACAGAAGACCCGG
CGGGAGAAGAGAGCCCCGGCAGGAGGCGGAGCGGCGGGAGAAGGCGGAGCGGGCGGCCAGACTGGCCAAGGAAGCC
AAGTCAGAGACCTCAGGGCCCCAGATCAAGGAGCTAACTGATGAAGAGGCAGAGAGGCTGCAGCTAGAGATTGAC
CAGAAAAAGGATGCAGAGAATCATGAGGCCCAGCTCAAGAACGGCAGCCTTGACTCCCCAGGGAAGCAGGATACT
GAGGAAGATGAGGAGGAAGATGAGAAGGACAAAGGAAAACTGAAGCCCAACCTAGGCAACGGGGCAGACCTGCCC
AATTACCGCTGGACCCAGACCCCTGTCGGAGCTGGACCTGGCGGTCCCTTTCTGTGTGAACTTCCGGCTGAAAGGG
AAGGACATGGTGGTGGACATCCAGCGGCGGCACCTCCGGGTGGGGCTCAAGGGGCAGCCAGCGATCATTGATGGG
GAGCTCTACAATGAAGTGAAAGTGGAGGAGAGCTCGTGGCTCATTGAGGACGGCAAGGTGGTGAAGTGTGCATCTG
GAGAAGATCAATAAGATGGAGTGGTGGAGCCGCTTGGTGTCCAGTGACCCTGAGATCAACACCAAGAAGATTAAC
CCTGAGAATTCCAAGCTGTCAGACCTGGACAGTGAGACTCGCAGCATGGTGGAAAAGATGATGTATGACCAGCGA
CAGAAGTCCATGGGGCTGCCAACTTCAGACGAACAGAAGAAACAGGAGATTCTGAAGAAGTTCATGGATCAACAT
CCGGAGATGGATTTTTTCCAAGGCTAAATTCAACTAGCCCCCTGTTTTTTTCTCCCTGAACTCTTGGGGCTGAGCTG
CAACCACCCAACCTTTCTTTCCCACTCTTCTCTGGGACTTGTGGGCCTCAGGGCTTGGGGCAGGCATGGGACTGGC
CCAGGCACACAGGTCCCGGGGCATCAGGAGAAAGGCTGGGTCTTGGGACCTTGTCTCCCCAGTTGGCCTACTGT
TACACATTAAAACGATTTGCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

127/6881
FIGURE 119

MGGEQEEERFDGMLLAMAQQHEGGVQELVNTFFSFLRRKTDFFIGGEEGMAEKLITQTFSHHNQLAQKTRREKRA
RQEAERREKAERAARLAKEAKSETSGPQIKELTDEEAERLQLEIDQKKDAENHEAQLKNGSLDSPGKQDTEEDEE
EDEKDKGKCLKPNLGNLADLPNYRWTQTLSELDLAVPFCVNFRLKGKDMVVDIQRRLRVGLKGQPAIIDGELYNE
VKVEESSWLIEDGKVVTVHLEKINKMEWWSRLVSSDPEINTKKINPENSCLSDLDSETRSMVEKMMYDQRQKSMG
LPTSDEQKKQEILKKFMDQHPMDFSKAKFN

128/6881
FIGURE 120

CCTGGTATGATTCCATCCTGAGCGGCTGTTCTCTTGAGCAGCGTTCATTTATCTCCGTCTGCCTTCTGTCCCACC
TAAGTGTGTGCCGCCACCCAATAGAAGATTCGATGGACATGGACATGAGCCCCCTGAGGCCCCAGAACTATCTTT
TCGGTTGTGAATAAAGGCTGACAAAGATGATCACTTTAAGGTGGATAATGATGAAAATGAGCACCAGTTATCTT
TAAGAACGGTCAGTTTAGGGGCTGGTACAAAGGATGAATTGCACATTGTTGAAGCAGAGGCAATGAATTACAAAG
GCAGTCCAATTAAAGTAACACTGGCAACTTTGAAAATGTCTGCACAGCCAACAGTTTCCCTTGGGGGCTTTGAAA
TAACACCACCAGTGGTCTTAAGATTTAAGTGTGGTTCAGGGCCAGTGCATATTAGTGGACAGCACTTAGTAGCTG
TGGAGGAAGATGCAGAGTCAGAAGATGAAGAGGAGGAGGATGTGAACTCTTAAGTATATCTGGAAAGCGGTCTG
CCCCTGGAGGTGGTAGCAAGGTTCACAGAAAAAAGTAAAACTTGCTGTTGATGAAGATGATGATGATGATGATG
ATGATGATGATGATGATTTTGATGATGAGGAAGCTGAAGAAAAAGTGCCAGTGAAGAAAGGACAAGAATCCTTCA
AAACACAGGAAAAAACTCCTAAAACACCAAAAGGATCTAGTTCTGTAGAAGACATTAAAGCAAAAATGCAAGCAA
GTATAGAAAAAGGGGGTTCTCTTCCCAAAGTGGAAGCCGAGTTCATCAATTTTGTGAAGAATTGCTTCTGGATGA
CTGACCAAGAGGCTATTCAAGATCTCTGGCAGTGGAGGAAGTCTCCTTAAGAAAAATAGTTTCAACAATTTGTTAA
AAATTTTCCATCATATTTCAATTTCTGTAACAGTTGATATCTGGCIGTCCTTTTTATAATGCAGAGTGAGAACTTT
CCCTACCGTGTTTGATAAATGTTGTCCAGGTTCCATTGCCAAGAATGTGTTGTCCAAAATGCCTGTTTAGTTTTT
AAAGATGGAACACCCCTTTGCTTGGTTTTAAATATGTATGGAATGTTATGATAGGACATAGTAGTAGCGGTGGT
CAGACATGGAAATTGTGGGAAGACAAAAATATGCCTGTGAAATAAACTCAATATTTTAATAAAGTAAAAAAA
AAAAAA

129/6881
FIGURE 121

MDMDMSPLRPQNYLFGCELKADKDDHFKVDNDENEHQLSLRTVSLGAGTKDELHIVEAEAMNYKGSPIKVTLATL
KMSAQPTVSLGGFEITPPVVLRFKCGSGPVHISGQHLVAVEEDAEESEDEEEEDVKLLSISGKRSAPGGGSKVPQK
KVKLAVDEDDDDDDDDDDDDDFDDEEAEEKVPVKKGQESFKTQEKTPKTPKGSSSVEDIKAKMQASIEKGGSLPKV
EAEF INFVKNCFWMTDQEAIQDLWQWRKSP

130/6881
FIGURE 122

AGCTGCTGGCTGGGCTGCCTGTTGAGTCAGCCTTCTTCCCTCACGGCTCTTCTCCCGGTCCCTGAAACTCGGCTG
CCAGGGGAGCTGGAGCCACCTGCGAAGGTGTCCTCCCATACTGGACCCCTACAGGAAGCTCCGTGTGCCCAGCTG
GGGCACAGCCCCAGCTGATGCCCCAGAGGGGCCACCCATCGCAAGAGGGGGCTTTGGGCTCTGCCCTCCCTCCCCA
TGGCGCATGGGCCAAAGCCTGAGACTGAAGGACTGTTGGACCTCAGCTTCCTGACAGAGGAGGAGCAGGAGGGCCA
TTGCTGGCGTCCCTCCAACGAGATGCCCGCCTGCGCCAGCTGGAGGAGGGGCGGGTCAGCAAGCTCCGGGGCCTCAG
TGGCAGACCCTGGGCAGCTGAAGATCCTGACAGGGGACTGGTTCCAGGAAGCACGCTCCCAGCGGCACCAACAATG
CCCCTTCGGCTCTGACCTTGTCCGAGCGTCTATGCGCAGGAAGAAGAGCACCAGGGGAGACCAGGCTCCAGGGCC
ACGACAGGGAGGCTGAGGCTGCTGTGAAAGAGAAGGAAGAGGGGGCCAGAGCCCAGGCTCACCATTGATGAGGGCC
CTCAGGAGAGGCTCAGGGAGACTGAGGCTTCAGATCCTGAGGAGGCGTCCCAGGGCCAGGAAGATCCTGGCCAAG
GAGACCAACAGGTCTGTGCCGAGGAGGCTGACCCGGAGCTGGAGCCCGCGTCGGGGGGAGAGCAGGAGCCGCGGC
CCCAGCAAGCCCAGACCAAGGCCGCGTCCCAGATCCTGGAGAATGGGGAGGAGGGCCCCGGGGCCCCGACCCCTCTC
TCGACCGCATGCTCAGCAGCAGCTCCTCGGTGTCCAGCCTTAACTCCTCCACGCTGAGCGGCAGCCAGATGAGCC
TGTCAGGCGACGCGGAGGCGGTGCAGGTCCGCGGCTCCGTGCACCTTCGCGCTGCACTACGAGCCGGGCGCCGCCG
AGCTGCGCGTGACGTGATCCAGTGCCAGGGCCTGGCCGCCGCCCGCGCGCCGCTCGGACCCCTACGTCAAAA
GCTACCTCCTCCCGGATAAGCAGAGCAAGCGCAAGACGGCGGTGAAGAAACGGAATCTGAATCCGGTTTTCAACG
AGACTCTCCGGTACTCCGTCCCGCAGGCCGAGCTTCAGGGCCGCGTGCTGAGCCTGTCTGTGTGGCACCGCGAAA
GCCTGGGTGCGAACATCTTTCTGGGCGAAGTTGAAGTGCCCTGGACACGTGGGACTGGGGCTCTGAGCCACCT
GGCTCCCCCTGCAGCCCCGGGTCCACCCCTCTCCGACGACCTTCCGAGCCGCGGGTTACTCGCCCTGTCCCTCA
AGTACGTCCCCGCCGGCTCCGAGGGCGCAGGACTGCCCCCGAGCGGGGAGCTGCACTTCTGGGTGAAGGAGGCTC
GGGACCTCCTGCCGCTGCGGGCAGGATCCCTGGACACTTACGTACAATGCTTCGTGCTGCCTGATGACAGCCAGG
CCAGCCGCCAGCGTACAAGGGTTGTGCGACGCAGCCTCAGCCCTGTGTTCAATCACACCATGGTGTACGATGGCT
TTGGGCCTGCTGACCTGCGCCAGGCTTGTGCCGAGCTCTCCCTCTGGGACCATGGGGCCCTGGCCAACCGCCAGC
TGGGGGGCACACGCCTCAGCCTGGGCACCGGCAGCAGCTATGGGCTGCAGGTGCCCTGGATGGATTCCACACCTG
AGGAGAAGCAGCTGTGGCAAGCCCTCCTGGAGCAGCCGTGCGAATGGGTGGATGGCCTTCTACCCCTCAGAACCA
ACCTGGCCCCCAGGACGTAGCCCCACCAAGCCTCTCTCTTGGACCCCCATCTCAGGGCCTGCCCTTGGCTAAAG
TCAATAAAGTCTATTCTAAGAGC

131/6881
FIGURE 123

MPQRGHPSQEGWLWALPSLPMAHGPKPETEGLLDLSFLTEEEQEAIAGVLQRDARLRQLEEGRVSKLRASVADPGQ
LKILITGDWFQEARSQRHHNAHFGSDLVRASMRRKKSTRGDQAPGHDREAEAAVKEKEEGPEPRLTIDEAPQERLR
ETEASDPPEASQAQEDPGQGDQQVCAEEADPELEPASGGEQEPRPQQAQTKAASQILENGEEAPGPDPSLDRMLS
SSSSVSSLNSSTLSGSQMSLSGDAEAVQVRGSVHFALHYEPGAAELRVHVIQCQGLAAARRRRSDPYVKSyllPD
KQSKRKTAVKKRNLPVFNETLRYSVPAELQGRVLSLSVWHRESLGRNIFLGEVEVPLDTWDWGSEPTWLPLQP
RVFPSPDDLPSRGLLALSLKYVPAGSEGAGLPPSGELHFWVKEARDLLPLRAGSLDTYVQCFVLPDDSQASRQRT
RVVRRSLSPVFNHTMVYDGFPGADLRQACAELSLWDHGALANRQLGGTRLSSLGTGSSYGLQVPWMDSTPEEKQLW
QALLEQPCEWVDGLLPLRTNLAPRT

132/6881
FIGURE 124

ATGCCGTTAGTAACGAGGAACATCGAGCCAAGGCACCTGTGCCGTCAGACGTTGCCTAGCGTTAGAAGCGAGCTG
GAATGCGTGACCAACATCACCTGGCAAATGTCATCCGACAGCTGGGCAGCCTGAGTAAATATGCAGAGGACATT
TTTGAGAGCTCTTTACTCAGGCAAATACCTTTGCCTCTCGGGTAAGCTCCCTTGCTGAGAGGGTCGACCGACTA
CAGGTTAAAGTCACTCAGCTGGATCCCAAGGAAGAAGAAGTGTCACTGCAAGGAATCAACACCCGAAAAGCCTTC
AGAAGTTCCACCATTCAAGACCAGAAGCTTTTTGACAGAACTCTCTCCAGTGCCTGTCTTAGAAACATACAAT
ACCTGTGATACTCCTCCCCCTCTCAACAATCTTACCCCTTACAGGGACGATGGAAAAGAGGCACTCAAATTCTAC
ACAGACCTTCATACTTCTTTGATCTTTGGAAGGAGAAGATGCTGCAGGACACCAAGGATATCATGAAAGAGAAG
AGAAAGCACAGGAAAGAAAAGAAAGATAATCCAAATCGAGGGAATGTAAACCCACGTAAAATCAAGACACGTAAG
GAAGAGTGGGAGAAAATGAAGATGGGGCAAGAATTTGTGGAGTCCAAAGAAAAGCTGGGGACTTCTGGGTATCCA
CCCACTTTGGTGTACCAGAATGGCAGCATTGGCTGTGTTGAAAACGTGGATGCAAGTAGCTATCCGCCACCACCA
CAGTCAGACTCTGCTTCTTCACCTTCTCCTTCCTTCTCCGAGGACAACTTGCTCCTCCACCAGCAGAATTCAGT
TACCCAGTGGACAACCAAAGAGGATCTGGTTTGGCTGGACCCAAAAGATCCAGTGTGGTCAGCCCAAGCCATCCA
CCACCAGCTCCTCCTCTAGGCTCTCCACCAGGCCCTAAACCCGGGTTTGCTCCACCACCTGCCCCCTCCGCCACCT
CCGCCCTCCAATGATAGGCATCCACCTCCACCACCGCCTGTAGGATTTGGGTCTCCAGGGACGCCTCCACCACCC
TCACCCCATCTTTCCACCTCACCTGATTTTGCTGCCCCCTCCACCTCCTCCTCCACCACCAGCAGCTGACTAC
CCAATCTGCCACCACCTCCCTTGTCCCAGCCAACAGGAGGAGCACCTCCTCCTCCCCCTCCTCCTCCTCCTCCG
GGGCCCCCTCCTCCCCCTTTCACTGGTGCAGATGGCCAGCCTGCTATACCACCACCGCTTTCTGATACCACCAAG
CCCAAGTCCTCCTTGCTGCGTGAGCGATGCGCGTAGCGACCTGCTTTTCAAGCATCCGTCAAGGTTTTAGCTG
CGCAGGGTTGAGGAGCAGCGGAACAAGAGAAGCGGGATGTTGTGGGCAATGACGTGGCCACCATCTTGTCTCGT
CGCATTGCTGTTGAGTACAGTGACTCAGAAGATGACTCCTCTGAATTTGATGAGGACGACTGGTCCGATTAA

133/6881
FIGURE 125

MPLVTRNIEPRHLCRQTLPSVRSELECVTNITLANVIRQLGSLSKYAEDIFGELFTQANTFASRVSSLAERVDRL
QVKVTQLDPKEEEVSLQGINTRKAFRSSTIQDQKLFDNRSLPVPVLETYNTCDTPPPLNNLTPYRDDGKEALKFY
TDP SYFFDLWKEKMLQDTKDIMKEKRKHRKEKKDNPNRGVNP RKIKTRKEEWEKMKMGQEFVESKEKLGTS GYP
PTLVYQNGSIGCVENV DASSYPPPPQSDSASSPSPSFSEDNLPPPPAEFSYPVDNQRGSGLAGPKRSSVVS PSH P
PPAPPLGSPPGPKPGFA PPPAPPPPPPPMIGIPPPPPFVGFGSPGTPPPPSPPSFPPHPDFAAPPPPPPPAADY
PTLPPPLSQPTGGAPPPPPPPPPGPPPPFTGADGQFAIPPLSDTTKPKSSLP AVSDARS DLLSAIRQGFQL
RRVEEQREQEKRDVVGNDVATILSRRIAVEYSDSEDDSSFEDEDDWSD

134/6881
FIGURE 126

GCAGCACCCCAGTTCTCCCCGCACGCCGGCACTCGCGGCTGCTGGAGCCCCGGCTGGCTCACCCCCGGGGCCGGGC
AGAATTGGGCTCCAGGTCTCTGACCCCTCCCAAGGATCATGCCGCAGCCCCACTGACCCAGGAGTAGGGGCCTAA
GGGCAGGGAACCTGGAATGGGCTGTGTGTTCTGCAAGAAATTGGAGCCGGTGGCCACGGCCAAGGAGGATGCTGG
CCTGGAAGGGGACTTCAGAAGCTACGGGGCAGCAGACCACTATGGGCCTGACCCCACTAAGGCCCGGCTGCATC
CTCATTGCCCCACATCCCCAACTACAGCAACTTCTCCTCTCAGGCCATCAACCCTGGCTTCCTTGATAGTGGCAC
CATCAGGGGTGTGTCAGGGATTGGGGTGACCCTGTTCAATTGCCCTGTATGACTATGAGGCTCGAACTGAGGATGA
CCTCACCTTCACCAAGGGCGAGAAGTTCCACATCCTGAACAATACTGAAGGTGACTGGTGGGAGGCTCGGTCTCT
CAGCTCCGGAAAAAAGTGGCTGCATTCCCAGCAACTACGTGGCCCCCTGTTGACTCAATCCAAGCTGAAGAGTGGTA
CTTTGGAAAAGATTGGGAGAAAGGATGCAGAGAGGCAGCTGCTTTCACCAGGCAACCCCCAGGGGGCCTTTCTCAT
TCGGGAAAAGCGAGACCACCAAGGTGCCTACTCCCTGTCCATCCGGGACTGGGATCAGACCAGAGGCGATCATGT
GAAGCATTACAAGATCCGCAAAGTGGACATGGGCGGCTACTACATCACCACACGGGTTCAAGTTCAACTCGGTGCA
GGAGCTGGTGCAGCACTACATGGAGGTGAATGACGGGCTGTGCAACCTGCTCATCGCGCCCTGCACCATCATGAA
GCCGCAGACGCTGGGCTTGGCCAAGGACGCCTGGGAGATCAGCCGCAGCTCCATCACGCTGGAGCGCCGGCTGGG
CACCGGCTGCTTCGGGGATGTGTGGCTGGGCACGTGGAACGGCAGCACTAAGGTGGCGGTGAAGACGCTGAAGCC
GGGCACCATGTCCCCGAAGGCCTTCTGGAGGAGGCGCAGGTCATGAAGCTGCTGCGGCACGACAAGCTGGTGA
GCTGTACGCCGTGGTGTGCGAGGAGCCCATCTACATCGTGACCGAGTTTATGTGTACGGCAGCTTGTGGAATTT
TCTCAAGAACCCAGAGGGCCAGGATTTGAGGCTGCCCCAATTGGTGGACATGGCAGCCCAGGTAGCTGAGGGCAT
GGCCTACATGGAACGCATGAACTACATTACCGCGACCTGAGGGCAGCCAACATCCTGGTTGGGAGCGGCTGGC
GTGCAAGATCGCAGACTTTGGCTTGGCGCGTCTCATCAAGGACGATGAGTACAACCCCTGCCAAGGTTCCAAGTT
CCCCATCAAGTGGACAGCCCCAGAAGCTGCCCTCTTTGGCAGATTACCATCAAGTCAGACGTGTGGTCTTTGG
GATCCTGCTCACTGAGCTCATCACCAGGGCCGAATCCCCTACCCAGGCATGAATAAACGGGAAGTGTGGAACA
GGTGGAGCAGGGCTACCACATGCCGTGCCCTCCAGGCTGCCAGCATCCCTGTACGAGGCCATGGAACAGACCTG
GCGTCTGGACCCGGAGGAGAGGCCTACCTTCGAGTACCTGCAGTCCTTCTGGAGGACTACTTCACCTCCGCTGA
ACCACAGTACCAGCCCCGGGATCAGACATAGCCTGTCCGGGCATCAACCCTCTCTGGCGGTGGCCACCAGTCCTT
GCCAATCCCCAGAGCTGTTCTTCCAAAGCCCCAGGCTGGCTTAGAACCCCATAGAGTCTTAGCATCACCGAGGA
CGTGGCTGCTCTGACACCACCTAGGGCAACCTACTTGTTTTACAGATGGGGCAAAAGGAGGCCAGAGCTGATCT
CTCATCCGCTCTGGCCCCAAGCACTATTTCTTCCCTTTTCCACTTAGGCCCCTACATGCCTGTAGCCTTTCTCACT
CCATCCCCACCCAAAGTGCTCAGACCTTGTCTAGTTATTTATAAACTGTATGTACCTCCCTCACTTCTCTCCTA
TCACTGCTTTTCTACTCTCTCTTTTATCTCACTCTAGTCCAGGTGCCAAGAATTTCCCTTCTACCCCTCTATTCTCT
TGTGTCTGTAAAGTTACAAAGTCAGGAAAAGTCTTGGCTGGACCCCTTTCTGCTGGGTGGATGCAGTGGTCCAGG
ACTGGGGTCTGGGCCCAGGTTTGGAGGAGAAGGTTGCAGAGCACTTCCACCTCTCTGAATAGTGTGTATGTGTT
GGTTTATTGATTCTGTAAATAAGTAAATGACAATATGAATCCTC

135/6881
FIGURE 127

GGCACGAGGCTTCGTAAAGATGGCCGCGGAGGCTTTTGGAGCCAACTGGGAGCGCAGTACGCGTTTTCTGGAGCA
TGGGCAGAGGAGACAGGAACAAGCGTAGCATCCGTGAGCACCGATTGGCTGAAGCGAGCACCCCGGGAGCTGACT
GGCTCCGCCATTTCGCGGGAAGGCGTTTGTGGTGCCAGAGAAAAGTAGCCAGAGCGGCGCAGTGGCGGCCGCGTTC
TGTGGTTTTCCGCTATTCCCCCAGACCCGCACCTTCTCGGCCTCTTTGCGGAGAATCGTGACCAAG**ATGT**TGGAAC
AGTGGATTGAAAAGCTATGGCAGCTCCTCATACGGGGGAGCCGGCGGCTACACGCAGTCCCCGGGGGGCTTTGGA
TCGCCCCGACCTTCTCAAGCCGAAAAGAAATCAAGAGCCCCGAGCCCAGCACATTGTGCCCTGTACTATATCTCAG
CTGCTTTCTGCCACTTTGGTTGATGAAGTGTTTGAAGTTGGGAATGTTGAGATTTACAGGTCCTACTATTGTGGGG
ATCATCAGACATGCAGAGAAGGCTCCAACCAACATTGTTTACAAAATAGATGACATGACAGCTGCACCCATGGAC
GTTCCGCCAGTGGGTTGACACAGATGACACCAGCAGTGAAAACACTGTGGTTCCTCCAGAAACATATGTGAAAGTG
GCAGGCCACCTGAGATCTTTTCAGAACAAAAAGAGCCTGGTAGCCTTTAAGATCATGCCCTGGAGGATATGAAT
GAGTTCACCACACATATTCTGGAAGTGATCAATGCACACATGGTACTAAGCAAAGCCAACAGCCAGCCCTCAGCA
GGGAGAGCACCTATCAGCAATCCAGGAATGAGTGAAGCAGGGAACCTTTGGTGGGAATAGCTTCATGCCAGCAAAT
GGCCTCACTGTGGCCCCAAAACCAGGTGTTGAATTTGATTAAGGCTTGTCCAAGACCTGAAGGGTTGAACTTTCAG
GATCTCAAGAACCAGCTGAAACACATGTCTGTATCCTCAATCAAGCAAGCTGTGGATTTTCTGAGCAATGAGGGG
CACATCTATTCTACTGTGGATGATGACCATTTTAAATCCACAGATGCAGAA**TAA**CTGGATCTAACTGGGTACCTG
AGATATTTTACAGCTGGACCTAGTTTCACAATCTGTTGTCTCCAGCTCTGCATATGTCTGGCCAGGGGGCTTCTA
GGAAGTAGGTTTCATCTATCAAATGTCTCCTCTGACTTCCTTTTGAACTTACTGCTCTTCTGTTTTATTTTGT
TTGTTTGAAGCTCAGAGGGAGATGGGCAATTGACAGGGATGCAATCCAGGGTGGGATTTCTTGAGGAAGTTACAA
ATAAGCTTGTTACAACATCAAGATAGATGGAATTGGAAGGATGCTACCAGGAGAGTACTTACATAGTGCTCAGGA
GTTTCTCTTCTTAAAATGTTTACTGCTGAAAGATGAGCAGGACCAGGGCGTTATAGGCAGAGCCCTAGCCGAGAA
ACCTGCTGGCCTCTGCCTGTTTTCAATTTCCCACTTTGGTTGTGTGGCATTACTTTCAGAATTGCACTTTCTGCT
TGTCATGACTTTTTGACACACTTGCCATGACGTGTGTTTCTGTGAACATGAAGTTCTGCGGTAGTGCCTCCAGGG
GCAGAGGAAAAGAAGAAGTGTTACTGCGTTTTGTACAAAATAAATACAGTCATATGTTTAATAAAACAGTTCTAT
TGTAACAAAAAAAAAAAAAAAAAAAAA

136/6881
FIGURE 128

MWNSGFESYGSSSYGGAGGYTQSPGGFGSPAPSQAEEKSRARAQHIVPCTISQLLSATLVDEVFRIGNVEISQVT
IVGIIRHAEKAPTNIIVYKIDDMTAAPMDVRQWVDTDDTSSSENTVVPPEYVKVAGHLRSFQNKKSIVAFKIMPLE
DMNEFTTHILEVINAHMVLSKANSQPSAGRAPISNPGMSEAGNFGGNSFMPANGLTVAQNQVLNLIKACPRPEGL
NFQDLKNQLKHMSVSSIKQAVDFLSNEGHIYSTVDDDHFKSTDAE

137/6881
FIGURE 129

GGAGGGAGACGCAGAGGCGGACAAGATGGCGGCGGCAGCTGTACAGGGCGAGAGAAGCGGTGGTAGCGGAGGCTG
TAGTGGGGCTGGTGGTGCTTCCAAGTGCAGGACAGGGAGTGGCCGTAGCGGCTTGTTGGATAAGTGGAAGATAGA
TGATAAGCCTGTAAAAATTGACAAGTGGGATGGATCAGCTGTGAAAACTCTTTGGATGATTCTGCCAAAAAGGA
GAAGAGCATCTTTCTCGTGGCCACAGGAAAGATCCTACAGGAATGGATCCTGATGATATTTGGCAGCTGTCCTC
CAGTCTTAAAGGGTTTGATGACAAATACACCTTGAAGCTGACCTTCATCAGTGGGAGAACAAAGCAGCAGCGGGA
AGCCGAGTTCACAAAGTCCATTGCTAAGTTTTTTGACCACAGTGGGACACTGGTCATGGATGCATATGAGCCTGA
AATATCCAGGCTCCATGACAGTCTTGCCATAGAAAGAAAAATAAAGTAGCCAATTCTAAAAGTAGCCCTCTTTCT
CCTGGATCTTGCTGAATTAGTGGCTTGGGGGGTGGGGGAGATAAAAAGAACTTAAAATGGGTAAAGTAAGAAATG
TTAAAAAG

138/6881
FIGURE 130

CTGGGCCCGGGGAAATGGCGGCTTCAGGAGAGAGCGGGACTTCAGGCGGCGGAGGCAGCACCGAGGAAGCATTAT
GACCTTCTACAGTGAGGTGAAACAAATAGAGAAGAGAGACTCGGTTCTAACTTCGAAAAATCAGATTGAAAGACT
GACCCGTCCTGGTTCCTCTTACTTCAATTTGAACCCATTTGAGGTTCTTCAGATAGATCCTGAAGTTACAGATGA
AGAAATAAAAAAGAGGTTTCGGCAGTTATCCATCTTGGTGCATCCTGACAAAAATCAAGATGATGCTGACAGAGC
ACAAAAGGCTTTTGAAGCTGTGGACAAAGCTTACAAGTTGCTACTGGATCAGGAGCAAAGAAGAGGGCCCTGGA
TGTAATTCAGGCAGGAAAAGAATACGTGGAACACACTGTGAAAGAGCGAAAAACAATTAAAGAAGGAAGGAAA
ACCTACAATTGTAGAGGAGGATGATCCTGAGCTGGAAACGACAAAGGGAAGAAGAGATTGAAGCTCAAGAAAAAG
CCAAACGGGAAAGAGAGTGGCAGAAAACTTTGAGG

139/6881
FIGURE 131

TCCAGCACCAAAGCGGCCGTTCTCGGATTCCGGAGCGTTCTGGAGCCCCGAGAGACGCCCCGGGGTTCTAGAAGC
TCCCCGGCGGGCGCCAGTCCCGGCTTCATTTCGGGCGTCCCTCCGAAACCCACTCGGGTGCACGGGTTCGTGGCGA
GCCGCGACCGGGTCTTGGCGCGCACC**ATGAT**CGTGGCGGACTCCGAGTGCCGCGCAGAGCTCAAGGACTACCTGC
GGTTTCGCCCCGGGCGGCGTTCGGCGACTCGGGCCCCGGAGAGGAGCAGAGGGAGAGCCGGGCTCGGCGAGGCCCTC
GAGGGCCCAGCGCCTTCATCCCCGTGGAGGAGGTCCTTCGGGAGGGGGCTGAGAGCCTCGAGCAGCACCTGGGGC
TGGAGGCACTGATGTCTCTGGGCGAGTAGACAACCTGGCAGTGGTGATGGGCCTGCACCCTGACTACTTTACCA
GCTTCTGGCGCCTGCACTACCTGCTGCTGCACACGGATGGTCCCTTGGCCAGCTCCTGGCGCCACTACATTGCCA
TCATGGCTGCCGCGCCCATCAGTGTTCTTACCTGGTAGGCTCCACATGGCCGAGTTTCTGCAGACTGGTGGTG
ACCCTGAGTGGCTGCTGGGCCTCCACCGGGCCCCGAGAAGCTGCGCAAACCTCAGCGAGATCAACAAGTTGCTGG
CGCATCGGCCATGGCTCATCACCAAGGAACACATCCAGGCCTTGCTGAAGACCGGCGAGCACACTTGGTCCCTGG
CCGAGCTCATTAGGCTCTGGTCTGCTCACCCACTGCCACTCGCTCTCCTCCTTCGTGTTTGGCTGTGGCATCC
TCCCTGAGGGGGATGCAGATGGCAGCCCTGCCCCCAGGCACCTACACCCCTAGTGAACAGAGCAGCCCCCAA
GCAGGGACCCGTTGAACAACCTCTGGGGGCTTTGAGTCTGCCCGCAGCTGGAGGCGCTGATGGAGCGCATGCAGC
AGCTGCAGGAGAGCCTGCTGCGGGATGAGGGGACGTCCCAGGAGGAGATGGAGAGCCGCTTTGAGCTGGAGAAGT
CAGAGAGCCTGCTGGTGACCCCCCTCAGCTGACATCCTGGAGCCCTCTCCACACCCAGACATGCTGTGCTTTGTGG
AAGACCCTACTTTTCGGATATGAGGACTTCACTCGGAGAGGGGCTCAGGCACCCCTACCTTCCGGGGCCAGGATT
ATACCTGGGAAGACCATGGCTACTCGCTGATCCAGCGCTTTACCCTGAGGGTGGGCAGCTGCTGGATGAGAAGT
TCCAGGCAGCCTATAGCCTCACCTACAATACCATCGCCATGCACAGTGGTGTGGACACCTCCGTGCTCCGCAGGG
CCATCTGGAACCTATATCCACTGCGTCTTTGGCATCAGATATGATGACTATGATTATGGGGAGGTGAACCAGCTCC
TGGAGCGGAACCTCAAGGTCTATATCAAGACAGTGGCCTGCTACCCAGAGAAGACCACCCGAAGAATGTACAACC
TCTTCTGGAGGCACTTCCGCCACTCAGAGAAGGTCCACGTGAACCTTGCTGCTCCTGGAGGCGCGCATGCAAGCCG
CTCTGCTGTACGCCCTCCGTGCCATCACCCGCTACATGACCT**TGACT**CCTGAGCAGGACCTGGGCCCCGGTTACGT
CCCCACAAGGACTTCTCTGTCTGGAGACAGCCCCAGACCCTTTTGTGTCCCATGCCACCCCTCCCCACGCTGCAG
TGGGCTTGTGTGTGATGTGCAGTCCCAGGCCACACCCTCCCTTTTCTCACTGGAATGGACAGTTCATTGCACT
GACTCTGGGATCTCAGCCCTGCTCCTGGGAGCTGGAAGAGCACTTGGAGATCCTAAGGGACCACACCCTTCTCTC
TTCCCTGCCCACAGAGGCAGAGGGCACAGGAAAGAAGCCGGGCCAAGCTCGGAATTAATGTGCCACAAGTGTTG
TGGCCTTCTGAACTGGGAAGTCCCTGGCTGGCCCCCGGGGGAGAGGGGCAAATGCCTCCGGGACTGACACTCCA
GGCAGCTTTGCCTTCTCTCCCTGTCACTTCCAGATTTTATTACCTCCTACTTGCCATTACCCATCAATGTGAA
AGTCAGGGTCACAGCTGGTCTGTGTGCCAGTTCCCTAAAAGCCTGTTCTGTTGGGCAGCCTGAGGCTGTTGCC
GAATCCTAGTTTCACTTTTTTGAATTTTCCCTTTTCCCTTTTCTCCATGCTTAATGGTGTGAGGCGTCAGG
AGAGAGGCCAAGTACATAAAAAAAAAAAAAAGCAGATTATCTCTAGAGAGTTTGAGCCTTTGCTGGTCACATTGC
CTTCTGAAGAGGAGGAGTATTAGATTATAAATCCTCTTTATTTTGGTCCTTTATGCTTGAGGTTCCAACCTGGA
GCCACAGTGTGTGAGAGGAGGAGGAGAGGGAGAATTCTGTTCTCCAGAGCTGCACCTGCCTCGCAGAGGCCAGC
ACCCCACTCTCCTGCCTCCAGTGGCCCTGCCGCAGATGTCTCCAAAAAGTTGAGCCTTTCTAGATGGCTTAGGT
GGCACCATGGCTACATTGCCAAACCTCTGACTGCCACAGCTGCAGACTGAGAGGGTGGGTCTGAGTCCCCACAATG
TCTGAAGCTGCCCCTGGGATTCTCAGGCCAACCTGCCAACAGCAAGCGGATTTCTTGCAAGATCAGGGACCCCA
TTTCTGCAGCCAGTGTCTCCTGGGTGCCCTTCTGAGGACTCCACCCCCATCCAGTATCTCATCTGTCCCCTCTC
CTGGGGCTTAAGTGGGTGCTTCCAGGCAGAAGCAGCCAAGGACCGATTCCAGGCACCTTCTGTAGCAAATGACT
GTGAATTACGACTTCTCTTGCCCTTCTTCTAGCAGTCTGTGCCTCCTCTCTGACCAGTTTGGAGGGCACTGAAGA
AAGGCAAGGGCCGTGCTGCTGCTGGGCGGGGAGGAGAGGAGCCTGGCCAGTGTGCCACATTAAATACCCGTGCA
GGCGCGGAGAAGCAACCGGCACCCCTTCCGGCCTGAAAGCCCTCCCTGCAAGAAGGTGTGCAGGAGAGAAGAGG
CCCCGGCATGGGGATCTGGGTTCTAGAGGGCATGTGATGACTGTAAATGTTCACTGGGTGGGTAGGGAGTGGTAT
CCAGTGTTCAAGTGCAGAAATCTTTGGCTTTGCTACCAGTTCATATGATGAGAAATAAACGTTGCTGAGGTTT
TGTTTCATAAAAAAAAAAAAAAAAAAAAAA

140/6881
FIGURE 132

MIVADSECRAELKDYLRFAPGGVGDSGPGEEQRESRARRGPRGPSAFIPVEEVLREGAESLEQHLGLEALMSSGR
VDNLAVVMGLHPDYFTSFWRHLHYLLLHTDGPLASSWRHYIAIMAAARHQCSYLVGSHMAEFLQTGGDPEWLLGLH
RAPEKLRKLSEINKLLAHRPWLITKEHIQALLKTGEHTWSLAELIQALVLLTHCHSLSSFVFGCGILPEGDADGS
PAPQAPTPPSEQSSPPSRDPLNNSGGFESARDVEALMERMQQLQESLLRDEGTSQEEMESRFELEKSESLLVTPS
ADILEPSPHPDMLCFVEDPTFGYEDFTRRGAQAPPTFRAQDYTWEDHGYSLIQRLYPEGGQLLDEKFQAAYSITY
NTIAMHSGVDTSVLRRAIWNYIHCVFGIRYDDYDYGEVQNQLLERNLKVYIKTVACYPEKTTTRMYNLFWRHFRHS
EKVHVNLLLLLEARMQAALLYALRAITRYMT

141/6881
FIGURE 133

GAGACGTCGGCTTCCGACCGGAAGTGAGAAGAGGAGGAAAGTTGGCTGGTTGCACCGATCTGGGGGCTTCCCGGGC
TCGGGTAAACGGAGTGCTGGTATCTAATCGTCGCTCAAAAAGCTCCTAGGTATATCCCGTGCCCTTACCTGACTGGG
GGCTCTGAGTCCAGTTGTGTTGTCTTCAACTTAGACACCATGGAGGCACCTCCAGTCAACATGATGCCTGTCACT
GGGGGCACCATTAACATGATGGAGTACCTGTTGCAGGGAAGTGTTTTAGATCACAGTTTGGAAAGCCTCATCCAC
CGCCTTCGTGGTTTTGTGTGACAACATGGAACCTGAGACTTTCCCTTGACCATGAGATGGTATTCCCTCCTTAAGGGC
CAGCAAGCCAGCCCATTTGTTCTCAGGGCCCGACGCTCTATGGACAGGGCAGGGGCACCTGGCATCTGCGCTAC
CTGGGACAGCCAGAAATGGGAGACAAGAACCGCCATGCCCTGGTGCGAAACTGCGTGGACATTGCCACATCTGAG
AACCTCACCGACTTCTTGATGGAAATGGGCTTCCGCATGGACCATGAGTTTGTGCTAAGGGACATTGTTCGGT
AAGGGCATCATGAAGATTATGGTGTACAAGATTTCCGCATCCTGGTGCCAGGGAACACAGACAGCACTGAGGCC
TTGTCACTCTCCTATCTCGTGGAATTAAGTGTGGTAGCACCCGCTGGGCAGGACATGGTCTCTGATGACATGAAG
AATTTCGCAGAACAGCTAAAACCTCTGGTTCACCTAGAGAAAATAGACCCCAAGAGGCTCATGTGACTAAGAGGA
TCTGTCCACATTTGGGGCCTATCCTTACTTGTGTTTTGAAAAAATATGTTTGCTTTTTTTGGTTTTTGTGTTTTG
TTTTTGAGACAGAGTCTCGCTTTGTTTCCCAGGCTGGAGTGCAGTGGCACGATCTCGGCTCACTGCAACCTCTGC
CTCCTGGGTTCAAGCAATTCTCCACCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACATGCCACCATGCTCAG
CTAATTTTTGTATTTTTAGTAGAAATGGGGATTACCATGTTGGTCAGGCTATTCTCGAACTCCTGACCTCGTGA
TCCACCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCACGCCTGGCCAAAAAATATGTTTT
AAATGTCCCATTTACCATTTGCCAGGCAGGCATTCTTCCTTCAGGGAGAGGATGGTGAGAATTAATTGGTTCTTT
GCACTGTTCTCCTCATGTGGCGATTTCACTTTTCATGACAGCCTTTCTATATTAAAGGCTCAGGATGTCACGGAGA
ATCTATCTAATCCCACCTGTATTAAGAGGGGAAACCGGGCCAAGCGCAGTGGCTCACACCTCTAATCCCAGCACTT
TGGGAGGCTGAGGTAGGTGGATCACCCAAGGTCAGGAGTTTGAGACCAGCCTGGCCAAATGGTGAAACCCCATCT
CTACGAAAAATACAAAATTTAGCCGGGCATGGTAGCAGGCGCTTGTAATCCCAGCTACTTTGGGAGGCTGAGGCTG
GAGAATCGCTTGAACCCAGGAGGTGAAGGTTGCAGTGACCAGAGATGACGCCATTGCACTCCAGCCTGGGTGAGA
AGAGCGAAACTCCGTCTCAAAAAAATAAAAATGAAGAGGGGAAACCAGAATAAATTATCTTTTGAAAGGACA
ATTTCTTGTTTGGCCATTTGTGTATAAGGTTGGTAACATTAGAGGCTGTGAGCTTGTGTTACATGGTAATAAAGC
CAATGAAGAG

142/6881
FIGURE 134

GGCCGGCCTCTCCCTTCCCGGGGTTCTTCGCGCCGGGCCCTTCCGCGTGGGTGAGTGAATGTGAGAGTCAGCGC
TCGCGCCGCGCGCGCCGCCCTCCGCTGTTCCGCGCTCTGCTTTAGGCGGTGGGGGGCGGGCGCGCGCTAAA
AGCATAGAGACGGGCATTGAGCTCTTGGGCTAGAGCGTCGCCGAGTCGGAGCCGGAGCCTGAGCCGCGCGCTGTG
TCTCCGCTGCGTCCGCCGAGGCCCGGAGTGTACAGGACAAAAGCCTCCGCCTGCTCCCGCAGACGGGGCTCATC
TGCCGCCGCCGCCGCGCTGAGGAGAGTTCGCCGCCGTCGCCGCCCGTGAGGATCTGAGAGCCATGTCCGGCCAGCA
GCCTCTTGAGCAGAGACCAAAGGTCAAGGAAACAAAGTACAAAATGGATCTGTACATCAAAAAGGATGGATTAA
ACGATGATGATTTTGAACCTTACTTGAGTCCACAGGCAAGGCCCAATAATGCATATACTGCCATGTGAGATTCCCT
ACTTACCCAGTTACTACAGTCCCTCCATTGGCTTCTCCTATTCTTTGGGTGAAGCTGCTTGGTCTACGGGGGGTG
ACACAGCCATGCCCTACTTAACCTTCTTATGGACAGCTGAGCAACGGAGAGCCCCACTTCCCTACCAGATGCAATGT
TTGGGCAACCAGGAGCCCTAGGTAGCACTCCATTTCTTGGTCAGCATGGTTTTTAATTTCTTTCCAGTGGGATTG
ACTTCTCAGCATGGGGAATAACAGTTCTCAGGGACAGTCTACTCAGAGCTCTGGATATAGTAGCAATTATGCTT
ATGCACCTAGCTCCTTAGGTGGAGCCATGATTGATGGACAGTCAGCTTTTGCCAATGAGACCCTCAATAAGGCTC
CTGGCATGAATACTATAGACCAAGGGATGGCAGCACTGAAGTTGGGTAGCACAGAAGTTGCAAGCAATGTTCCAA
AAGTTGTAGGTTCTGCTGTTGGTAGCGGGTCCATTACTAGTAACATCGTGGCTTCCAATAGTTTGCCTCCAGCCA
CCATTGCTCCTCCAAAACCAGCATCTTGGGCTGATATTGCTAGCAAGCCTGCAAAACAGCAACCTAACTGAAGA
CCAAGAATGGCATTGCAGGGTCAAGTCTTCCGCCACCCCCGATAAAGCATAACATGGATATTGGAACCTGGGATA
ACAAGGGTCCCGTTGCAAAAGCCCCCTCACAGGCTTTGGTTCAGAATATAGGTGAGCCAACCCAGGGGTCTCCTC
AGCCTGTAGGTGAGCAGGCTAACAATAGCCCACCAGTGGCTCAGGCATCAGTAGGGCAACAGACACAGCCATTGC
CTCCACCTCCACCACAGCCTGCCAGCTTTCAGTCCAGCAACAGGCAGCTCAGCCAACCCGCTGGGTAGCACCTC
GGAACCGTGGCAGTGGGTTTCGGTCATAATGGGGTGGATGGTAATGGAGTAGGACAGTCTCAGGCTGGTTCTGGAT
CTACTCCTTCAGAACCCACCCAGTGTGAGAGAAGCTTCGGTCCATTAATAACTATAACCCCAAAGATTTTGACT
GGAATCTGAAACATGGCCGGGTTTTTCATCATTAAAGAGCTACTCTGAGGACGATATTCACCGTTCCATTAAGTATA
ATATTTGGTGCAGCACAGAGCATGGTAACAAGAGACTGGATGCTGCTTATCGTTCCATGAACGGGAAAGGCCCGG
TTTACTTACTTTTTAGTGTCAACGGCAGTGGACACTTCTGTGGCGTGGCAGAAATGAAATCTGCTGTGGACTACA
ACACATGTGCAGGTGTGTGGTCCCAGGACAAATGGAAGGGTCGTTTTGATGTGAGGTGGATTTTTGTGAAGGACG
TTCCCAATAGCCAACCTGCGACACATTGCGCTAGAGAACAACGAGAATAAACCAGTGACCAACTCTAGGGACACTC
AGGAAGTGCCTCTGGAAAAGGCTAAGCAGGTGTTGAAAATTATAGCCAGCTACAAGCACACCACTTCCATTTTTG
ATGACTTCTCACACTATGAGAAACGCCAAGAGGAAGAAGAAAGTGTAAAAAGGAACGTCAAGGTGCTGGGAAAT
AAAAGGCAGTTCTACACAGACTGCAGCAACGGTTGCATCTGCATATCCTAAGAGGAAAAAATGACCTTCAAGAGA
ATTAGGACTTTTTTCTTAATTTCACTGACTTCAGAGACGATTGCAGACTTGCAGTTTAAGTATTGGAATTTTACA
AAAGACATAGGACTTAACTGGAAAATGAAAAAAGAAAAAGAAAAAAGAAAAAAGAAAAAATCCCTCTAGGTAG
TTTAGGTGAAAAATGTCCCTTTTATTTTGGCTTTGGTTGTGATTTTCAAGCATAATGCTATGTTTTTTTGTCTTT
TTACTATGTTTTTTCGATTTTTTAAGTCCGTAAGTGCATACAGTTTTCTCTAATTTTTAAACCTTTCTCCTCCC
ATTTTGACATTTGCACTTGGAGAACACTTGAGTTGTGAAGGTTTTGGGCATCCACCCAGAAAGTGGGAATTTGA
TTTTATCCTTCCGAACCTGGAAGAACATTTTTATGAAGAATTTTTGTCTAGGAGAATATAACAGTGTTACCCAAGG
TTGTGTCTTTAAGGGTGGTTCAATTTCTCTGACCTTTTGTTACTCAAAGTAAAGTACTAGGAGTCTAAGAAATG
TTCTGTTCTTGTACATTATACTGATTAAGTCAGGATTAATTTGATTTCAAAGCTGAGAACAGTGGTAAAAACTCG
TTTACAGAAATGCATTTTGGAGAGAAAAATACTGTAAACGTGTGCTGAATGTTTCTCAGTTTCTTGTTCAGC
CAATGAGGAAAGGCATTGCCTTTCTTTTTACCATTAACTCACTTCTCAATAAACGTGAGATCCTGTTGAGCATC

143/6881
FIGURE 135

GTACGTCGCCGGGGTTTCGGCTGCGTCCGTCCCGCCGCCCGCCCGTTGCCGCCGCCGCCGCTGCCGCCGTGCTCTC
GCTTTGCCCGCCGCCCTAAGGGGGGCTGGGGCCGGGGCCAGCCATCACTGCCGTTGCCGGGATGCCGCGGGTG
TACATCGGCCGCTGAGCTACCAGGCCCGGGAGCGCGATGTGGAGCGCTTCTTTAAGGGCTACGGGAAGATCCTG
GAGGTGGATCTGAAGAACGGATATGGTTTTGTGGAGTTTGATGATCTGCGTGATGCAGATGATGCTGTTTATGAA
CTGAATGGCAAAGACCTTTGTGGTGAGCGAGTAATTGTTGAGCATGCCCGCGGCCCACGGCGAGATGGCAGTTAC
GGTTCGGACGCGAGTGGATATGGTTATAGAAGAAGTGGCCGAGATAAATATGGCCCTCCTACTCGCACAGAGTAC
AGACTTATTGTGGAGAATTTGTCAAGTCGGTGCGAGCTGGCAAGACCTAAAGGATTATATGCGTCAGGCAGGAGAA
GTGACTTATGCAGATGCTCACAAGGGACGCAAAAATGAAGGGGTGATTGAATTTGTATCTTATTCTGATATGAAA
AGAGCTTTGGAAAAGTTGGATGGAAGTGAAGTCAATGGGAGAAAAATCAGATTAGTTGAAGACAAGCCAGGTTCC
AGACGACGCCGGTCTACTCCAGAAGCCGGAGTCATTCAAGGTCTCGCTCTCGAAGCAGACATTCCTCGTAAGAGC
AGAAGCCGAAGTGGCAGCAGCAAAAGCAGTCATTCTAAGAGTAGATCTCGGTCCAGGTTCGGGCTCCCGCTCCCGG
AGCAAGAGCCGGAGCCGGAGCCAGAGTCGGAGCCGGAGCAAGAAAGAGAAAAAGCAGGAGCCCCAGCAAGGAAAAG
AGCCGCAGCCGCAGCCATAGCGCTGGCAAGAGCCGCAGCAAGAGCAAAGACCAAGCTGAAGAGAAGATCCAAAAC
AATGACAATGTCGGGAAACCCAAGAGCCGGAGTCCTAGCAGGCATAAAAGTAAGAGCAAAAGTCCGAGCAGGAGT
CAGGAGAGGAGAGTGGAGGAGGAGAAGCGAGGGAGTGTGAGCAGGGGCAGGAGCCAGGAGAAGAGCCTCCGCCAG
AGTCGGAGCCGGAGCAGGAGCAAAGGGGGCAGCAGGAGCCGGAGCAGGAGCCGCAGCAAGAGCAAGGACAAGAGG
AAGGGCAGGAAGAGAAGCAGAGAGGAGAGCCGCAGTCGCAGTCGCAGCCGCAGCAAGAGTGAGAGGAGCAGAAAG
CGAGGCAGCAAGCGAGACAGCAAGGCGGGCAGCAGCAAGAAGAAGAAGAAGGAAGACACTGACCGCTCCCAGTCC
AGATCTCCATCCCGCTCCGTGTCAAAGGAGCGGGAACATGCCAAGTCTGAATCCAGCCAGAGGGAAGGTGAGGA
GAGAGTGAGAATGCTGGCACCAATCAGGAGACCCGGTCCAGGTGAGATCCAATTCCAAATCGAAACCAAACCTT
CCATCAGAATCACGCTCCAGATCAAAGTCAGCTTCAAAAACCCGATCTCGGTCCAAGTCTAGATCCAGGTCTGCT
TCCAGATCGCCCTCCCGATCTAGATCTAGGTCCCACTCAAGGTCTTAAGTGGCTATGGCCACAGCTGGAAGTACC
CGAGAAGTCTTTTGTACATGTTTGGTAGCCGTAGCACAAAGTGAATTGGAGTAGAACATGTCACTGCTGTACATTTT
TAACTCCCCTAATGGTGTGTCTATAATTGTTAAATCTAAGTGCTTCCTCTCAGTAAAGCCTCCTGGCACCAGGCC
TTCTTGCTCGACTGAAAAAAATTTTCTCTTTGAAAATCCCTTTTACTCATGGCCCACAGTAGAATATCCAAAAC
GCCTTGGCTTTTACGGCCTGGCCTTTCTTACAGGGAGCTCAGTAACCTGGACGGCTCTAAGGCTGGAATGACCACA
TAGGTAGGTATGGTGAGTTCAACCATTTTTGCTCTTGAATTGATGCCCTTCGATGTATGCCATTTAGTGAAAGTG
CTAAGTCTTAAGTTTCTTACCCTTTGGTTTTCATATTTTTGGACTTAACAAAGTTGTGAATAGCACAGTCGAGGA
AAATTGATACCTGCAGTAACCCATAGGAAATAAACTGTAGAGTTCCATATTCTGGTATTGTGATTATATTGTTTT
ATATT

144/6881
FIGURE 136

AGGGTTCTCTCCCCTTGCCACCATGAGCGAGTCATTTGACTGTGCAAAATGCAACGAGTCCCTGTATGGACGCAA
GTACATCCAGACAGACAGCGGCCCCCTACTGTGTGCCCTGCTATGACAATACCTTTGCCAACACCTGTGCTGAGTG
CCAGCAGCTTATCGGGCATGACTCGAGGGAGCTGTTCTATGAAGACCGCCATTTCCACGAGGGCTGCTTCCGCTG
CTGCCGCTGCCAGCGCTCACTAGCCGATGAACCCCTTCACTGCCAGGACAGTGAGCTGCTCTGCAATGACTGCTA
CTGCAGTGCCTTTTCTCGCAGTGCTCCGCTTGTGGGGAGACTGTCTATGCCCTGGGTCCCGGAAGCTGGAATATGG
AGGCCAGACATGGCATGAGCACTGCTTCCTGTGCACTGGCTGTGAACAGCCACTGGGCTCCCGTTCTTTTGTGCC
CGACAAGGGTGCTCACTACTGCGTGCCCTGCTATGAGAACAAGTTTGCTCCTCGCTGCGCCCGCTGCAGCAAGAC
GCTGACACAGGGTGGAGTGACATACCGTGATCAGCCGTGGCATCGAGAATGTCTGGTCTGTACCGGATGCCAGAC
GCCCCCTGGCAGGGCAGCAGTTCACCTCCCGGGATGAAGATCCCTACTGTGTGGCCTGTTTTGGAGAACTCTTTGC
ACCTAAGTGCAAGCAGCTGCAAGCGCCCCATCGTAGGACTCGGTGGAGGCAAGTATGTGTCCCTTTGAAGACCGACA
CTGGCACCACAAGTCTTCTCCTGCGCCCGCTGCTCTACCTCCCTGGTGGGCCAGGGCTTCGTACCGGATGGAGA
CCAAGTGCTCTGCCAGGGCTGTAGCCAGGCAGGGCCCTAAGCCAGGGCTCCTGGACCCAGGGCTTTCCCATACCAC
GGGCCCAGGACTGTGGCTCCTTTTCTAAACCACCTCTGGGACTCAGCTCCCCCGCCAAAAAAATGGGTCTCCT
TCTGGGCTCCAGGATTGTCTCCCCACTCCAGCATCCCCAACTGGTACTCCCTGACCCAGGGCCCCAAACCTGGG
CTCTTACAGAGCCTCCATGAGTCAAGCCCCCTCCCCACACCTGGACTCCAGAATTCACCTCTCCCTGCAGTCT
GGGTTCCCAGACTGAGTCTCTCCCCAAATCAGGGCTCTAGACCCGAGCCCTCCAAACCTGGACTCTGGGACTTA
GGCCCCCTTAAATCTAGACTTCTCTTTATAGGTTTCAGGTCTCCTATGGGTGCCTGGGAAGTCTTGAAAGTGGA
CTGTTCTCAGGCTTGACCTGCCCCACCCATCCCCGCGGTTGAGGCTGTGGGGCAGCAGATCAGGAGCCCACTG
ATAAGGGGCCCTAGGGTACAGGGTGCTGCCAGCAGGTGCCACCGAGTGTCTTCTCATTTTATTTTCTCAGCTCCAT
TTTGCCCATAGATGGGCAGAGGGGTGAGATTGGCTCATCCCCCTTCCAGATTCTGCAATAAAGCGGTGTGAGG

145/6881
FIGURE 137

CTACAGATACTGCCGTGTGAGAGTACCTGAGGGGCTCCTGAAAGACCTACTGCCAGGACCAGTGACCCTGGTGAT
GGAACGCTCGGAGGAGCTCAACAAGGACCTAAACCCCTTTACGCCTCTTGTAGGCATTTCGGATTCCCTGATCATGC
TTTTATGCAAGACTTGGCTCAGATGTTTGAGGGTCCGCTTGCTCTCACTAGTGCCAACCTCAGCTCCCAGGCCAG
TTCTCTGAATGTCGAGGAGTTCCAGGATCTCTGGCCTCAGTTGTCCTTGGTTATTGATGGGGGACAAATTGGGGA
TGGCCAGAGCCCCGAGTGTGCGCTTGGCTCAACTGTGGTTGATTTGTCTGTGCCCCGAAAAGTTTGGCATCATTTCG
TCCAGGCTGTGCCCTGGAAAGTACTACAGCCATCCTCCAACAGAAGTACGGACTGCTCCCCTCACATGCGTCCTA
CCTGTGAAACTCTGGGAAGCAGGAAGGCCCAAGACCTGGTGCTGGATACTATGTGTCTGTCCACTGACGACTGTC
AAGGCCTCATTTCAGAGGCCACCGGAGCTAGGGCACTAGCCTGACTTTTAAGGCAGTGTGCTTTTCTGAGCACT
GTAGACCAAGCCCTTGGAGCTGCTGGTTTAGCCTTGACCTGGGGAAAGGATGTATTTATTTGTATTTTCATATA
TCAGCCAAAAGCTGAATGGAAAAGTTAAGAACATTCCTAGGTGGCCTTATTCTAATAAGTTTCTTCTGTCTGTTT
TGTTTTTCAATTGAAAAGTAATTAATAACAGATTTAGAATCTAGTGAGAGCCTCCTCTCTGGTGGGTGGTGGCA
TTTAAGGTTCAAACCAGCCAGAAGTGCTGGTGCTGTTTAAAAAGTCTCAGGTGGCTGCGTGTGGTGGCTCATGCC
TGTAATCCCAACATTCTGGGAGGCCCAGGCGGGAGAACTGCTTGAGCCCAGGAGTTCAGAATCAGCCTGGGCAAC
ATAGCAATACTCCGTCTCATAAAAAATTAATAAAATAAAAAGTCTCAGGTGACCAAAGGCTCCTGAAGCTAGAACCA
GGTTTGGATAAAGATTGAAGAGCCACAGGCCACTCTTCCCTCTGAGCCATTGGGCCTAGTGGTGTGATGTATTGT
AATTGCTCGCAGGGAGAGCAGTCTTTTGGTGTAATAGTGGGATGTCTGCTTAGTTGGCAGGGGTTTCAGTCCAAA
TGGAAGAATATTGGGAAATAAACCTCCACTATCCTTTATAGCCAGGGACTTTTTTCTTATTTATTCATAAAATAA
ATTATAGTTAATTATACCCATAACACCTTTATTTAAATCCAGTGTTCTCCGCAGCCTTTTGTCTATTTATATGTG
TACCAAGTGTTAAACATAATTATTATTGGGCATTTGAACCTTTGTTTTTCTTTAAAGAAATGCTGCTATTAAACAT
ATTTGTAAATGGA

146/6881
FIGURE 138

MERSEELNKDLNPFTPLVGIRIPDHAFMQDLAQMFEGPLALTSANLSSQASSLNVEEFQDLWPQLSLVIDGGQIG
DGQSPECLRGSTVVDLSVPGKFGIIRPGCALESTTAILQQKYGLLP SHASYL

147/6881
FIGURE 139A

AGGCCCAGCGCTGGCGCAGTGAGAACTTCGAGAGACCCGTGGACCTGGAGGGCTCTGGGGATGATGACTCCTTTTC
CCGATGATGAACCTGGATGACCTCTACTCGGGGTCGGGCTCGGGCTGTAAGTACCCCCCTCCCTACCTCTGCCTGG
GGGCAGTGACCAGTCTGTATCCAGCCTCAACTCTGAGAAGCCCACGGGGGGCTTGCTTCAGTGAGGCAGGGGGCA
TTCAGTGCCTGGGTGAGGCAAGTTCTTCTTGCTCTGGATCCCCAGAACAAGAAGGGCAGAACATCCTTCTGGGGA
TAGAACAAGACCTGGGAGGACCTCAGGGCCCAGAATGTCCAGGTCTCCAGGGTCCCACGTCTGCATCTTTGTGTG
TGCTATGTGGCTTTCTCTGCAGACCTTGCTTGGTTCCGGTGGTCCCGTCAGGTGCAATAAGCTGTGGCCAATGGT
GGGGTTAGGGCAGTGATGACACAGGGCAGGTGCTTCAAGTGGTGCCTGGGATGGCCCCGCCCTGGGGGAAGGGGAG
CCAGGTGAGCTGGGTCTAGCAGAATCTCGGGAGAGAAGGGCACC GCGAACCCCACTCTGCCATGTAGCAACTGTG
TGCCCCCTCGGTGCTCCCCCTCCCTGAATCCCTGTATTTTACCTGTGGATGGTGAGAAATACGACTTCTTCTCAG
TGCTCTAGGAGGGTTTGGGATAGGAAGCTGGGGTCTGGCACAGAGGAGGAGCTCTCAAAATGGTAGCAAAAAGA
AGGCAGCTGAGACTGGGCCCAGTGAGGGCACGGGCTGGCATCTGAGGAGATGGTACGGGGTCTGCACGCCACAGA
GCTGGCTCCCCACAGCCCTCGCCTCTGGTCTCCCCCTCCTTAGCCAAGTCCTTTGAGCCTCTTTCAAATTAATCTT
TGTA AAAACCCGTTTATATTGGGTACATCTCTATTTCGCAAAGTTCCTGGCTCCCCCTCCCTCCTGCCTGGTTCCG
AGCCCAGGAGCTGGCTGTGGCTTCTCCCTCCCCCATCCCCTACTCCCCATCTCATTTTCCCTCCCAAGTTCCTTAC
TGTCGGGCTTTTGCCTCAGCCAGATTGCTCAAGCAGTTCCCTGCCTCAAGGGCTTCTTTTCCCTTTTACCCTCC
GCCTCTGCCTCTGGGGGAAGCCCTTAGTGTACCACCCCTGCCTTGAGCTTGTGGTAGGGGTGCCTTTGGGGTCTG
ACTCTTCCCGAGAATGCCACTCCTGTGTTCCTTGCAGCCCCAGCAAGTTTGCAGCCAGTAGCGCCTCAGTTGC
TGCTGCCTGGATTCAACCTCATAGAACTGTAGGCTGGGTGGGCAGGAATAGTCAAGGAAGGCTTCCCGGGAGAG
GCGGCCCCCAGAATTTTGTACTTGGCAGAGAGAAGTTGGGGAACATCAGCAACTGACCACCTTTAGCTGGGCTGT
GCCTTCCCTCCTTTCTCTCATCTTTTCTGGGAAAATTGGGTAAAGAGAGGGGGTTGGGAGACCTAATCTTGATGGC
CATTGCTTACCTGGGATCCTCATGCCCCCTCACAACACCCAGCTCCCTAGCTCTCTCCCTCTCCCCACCCCCCTC
AGACTTCGAGCAGGAGTCGGGCATTGAGACAGCCATGCGCTTCAGCCCAGATGTAGCCCTGGCGGTGTCCACCAC
ACCTGCGGTGCTGCCACACCACGAACATCCAGCCTGTGGGCACACCATTTGAAGAGCTCCCCTCTGAGCGCCCCAC
CCTGGAGCCAGCCACCAGCCCCCTGGTGGTGACAGAAGTCCCGGAAGAGCCCAGCCAGAGAGCCACCACCGTCTC
CACTACCATGGCTACCACTGCTGCCACAAGCACAGGGGACCCGACTGTGGCCACAGTGCCTGCCACAGTGGCCAC
CGCCACCCCCAGCACCCCTGCAGCACCCCTTTTACGGCCACCACTGCTGTTATAAGGACCACTGGCGTACGGAG
GCTTCTGCCTCTCCCACTGACCACAGTGGCTACGGCACGGGCCACTACCCCCGAGGCGCCCTCCCCGCCACCAC
GGCGGTGTCTTGGACACCGAGGCCCAACACCCAGGCTGGTCAGCACAGCTACCTCCCGCCAAGAGCCCTTCC
CAGGCCGGCCACCACCCAGGAGCCTGACATCCCTGAGAGGAGCACCCCTGCCCTGGGGACCACTGCCCCCTGGACC
CACAGAGGTGGCTCAGACCCCAACTCCAGAGACCTTCTGACCACAATCCGGGATGAGCCAGAGGTTCCGGTGAG
TGGGGGGCCCAGTGAGAGACTTCGAGCTGCCAGAAGAAGAGACCACACAACCAGACACAGCCAATGAGGTGGTAGC
TGTGGGAGGGGCTGCGGCCAAGGCATCATCTCCACCTGGGACACTGCCCAAGGGTGCCCGCCGGGCCCCCTGGCCT
CCTGGACAATGCCATCGACTCGGGCAGCTCAGCTGCTCAGCTGCCTCAGAAGAGTATCCTGGAGCGGAAGGAGGT
GCTCGTAGCTGTGATTGTGGGCGGGGTGGTGGGCGCCCTCTTTGCTGCCTTCTTGGTACACTGCTCATCTATCG
TATGAAGAAAAAGGATGAGGGCAGCTACACGCTGGAGGAACCCAAGCAGGCGAGCGTCACATACCAGAAGCCTGA
CAAGCAGGAGGAGTTCTATGCCCTAGTGGAGCCACAGTGCCTCCCTGCAGCCTCAACACCACCCTGCTGTCCAGTC
CCCAGCCTGGCCCCACCAGCCCAAGCCTGGGACTGGGCCTGGAACCTGGCCCCAGTTCTTCTCTGCCCTCTCTCC
CAAGGTCTGCCCAGGCTGCCAGCCTCACACAGATCTTCCCCGAGGAAGAGGGGCTGCTGCCATCTGCCCCAGACT
GTGCCCTTACGAGCTCATCTCTTGTTCCTCATCCCTGCCACCAGTCTGGGGCTTCAGGACCTCATGTGAGATG
GATGGGAGGAAGAAAGCTCCTGATTGGCTGGTGGTGGGAAGAAAGGGTGGGGCTTGAGATGAGCCTGAGCCCTGAC
TTGGCACCCACAGTGCTCACTGAGATCTCCTTTTGGGGCAGAGAGGCACCTCAGGCTGGTTTCCAGGACAAACAT
TTGGTAAACACAGCCCTTGAAATCATCTAGACACTGCAACCTCTTGCTCGTATCCCAGGGCCTCTCTCTAGCTGG
GTGAGAGGGTGTCCCTTGTACCCAGCCTGTTTTGTCTGGTCTCTCTGGGGTGTGTAATCTCTCTCTTGCCTG
CCAAGTACACATGTACCCAGACTTCATTTCTTCTGTCATCTTCCCCCAAGAAACAGCTTCCTGAGGGTGTGGGG
CAGCCACTGGTGAGGAGGGGCTGCTCTGATGTCCCTCCTATGAGGGGACTCTGCACAGACACCATTGCCACACT
ATCACCATATTTTCACTCAGTCACACACAAGACAAAAGCATGCAATGACAAAACCATACGCAATCCTGACCGCCC
AGCCAATCAAGACATATCACAGAACACACGCGTCCTTCCAAGAATGTTTATCCTCATGCATCACTTACACACCCC
CAGACACGTACTGCAATGCAAGTCACTAGTCATGGTCACATGACAGTGACAGTGTGGCCTCCTCCTACCCCAAT

148/6881
FIGURE 139B

ACACCCACACTCTGGCACCACACACATTGTCTCCAGCTTTCAGGCTTACTGGGGAGGGTGAATCGAGCCAGAAC
AATCAGCCCATAATTGGGTCCCCCTAAGTTGCCCCGTCATACTCAGTCCCATGCCATGGTGCCACACCAACCATG
CAGCCGCCAACCCAGCCAGTGTGAGACACAATCCCATGTGGATGCACAGTCTCACTCCACATGACCTGCTCTCA
ATGCTGGAGGGGAAAACAGGCAGGCCCTTGCCCTTTCTCGGAAAAAGTGTGGGGCCACAGCCCTTTTAGGGCATTGCA
TGCAGGTGGGCCTGGCTTCACCCCTACCTGCTTCCCTCCCCACCGCAGCTGGCAGAGGGGGAGGTTTGGGGCCAGA
CCCCCACTAGCTGGGAGCCTGGGGGCTCCTCTAAGGCTGAGGAAGGAAATTTGGCCCCAGGTTGTTGGGGGGTCT
TGGGTCTCCCAGGACGGAAGGCCAGGGCAGGGAGGGGGCATGTGTTGGGCTCCTTTATCTCCCTGTGTCCCT
TCCTGCTTTGAGCTAGGGGGCTGACTCTGCCTCCCAGGACACAAGTCTCCAAAGTGCCTGTGAGGGCGGGCCCTC
CGCACCCCTCTGCCCTCTGCCTGGCAGGCCAACCTCAGCCCACCTGCCAGAGGCCCTCCCTGTGGACACCCCTC
ACCTATTTGGCCAAACAATTCTGGCTGCAGCTTCAGGGGCCATGGCTGGAAGCAGCCCCTGCAGATCCCTCAGGC
CCCGAGGTGAGGTTTGGAGGATGAGACCAGGTGATAGTGGGGGAGGGGTACTTCCTTTGTTACCTAGCAAGTA
GGGCTATTTCCATCGGTATTTTAAATGTGGGGTCACAGATCTTTTGGGGAGGGTGTGCTTGGCAGGGGGCCTCTT
GGAGCCAAAGGGATGTGTTGTGAGTTGCGATTGGCTGGCACTCACACCCCCACCCCTCACCCACATCCAGATTC
AAGTCAGGAAGGCAGGTTTATTTAGGGCCCTTTTCAAGATGCCCTGGCAGCAGATTTCTGCAGGATGAGGGGT
AGCGGTGTGTAGGCAGTGAGGGGGAGGTTCCAGGGGCTGTCCACAGCCTGTCTTTTCCAGGCTGGGCTCCATCT
TCCAGTCCCAAACCCCTCCTTCACAGGGCCCAGAGGCTTGTGAGGAAGCCAGGTGGACCCAGCCTTAGAAGAGTG
GGCATGGGGGGCCCTGATATCTGGAGGGGGCGGGTTGGCCTCAGTCATCTTTGGAGCAGAAGGGCTGGGTCCCTG
GGGCCACAGACCACAAGGCTCAGCCTCCCTACCCTGCTCCCTGGGGTGTGCTGTCTTGGAGAGCACAGCTCTGG
TGAGACGGCCTGGGCAGGCCGAGGCTGAGAAACCAGGGAGGATAGAGGAGAAAAGGGCTTGGGCCCCCAGCCCCA
GAAGATGCTGGACCCCAGGTGGGAGACCCAACAGTGGGTGCAGTTTCTCAGTAGGGCTGGAGCCAATGGTGGGGG
TGGCCCCCGCAGGCCTGGCTCCTCACATCCCAGGGGTGGCTTCTGATTGGGGCTTGGGCTCCAGGCACTGGCT
TCTCTTCTCTGTGTCTTAGCATTTGAGAGAAGAGGCCAGGGGCCCTTGTTCATGGATCCCTGGACCCAAGGCAGA
TGTCCAGGCTTTATCTCCTGAGGATGAGGAGTCTGACCAGCCCAAATCTGCCCTGGCCGGCCTGACCGGGGCAA
GGCAGTCCAAGAGAGTTTCTGAGGAGCAGCTAGGCTCTCCAGGTGCAATGTGGGTGCAGGGCCCTCATGTCCC
CCTACCCCTGCCTGTGATGGAGTGTCTGAGGGGCTTTGGCATTGTGCTGGAAGCACAGGGAGTTCCAAATGAGAG
GGAGCTTCTGTGGCTTGAGAGCCTCTGGGGCCTTGGCTGCCAGAGCACGAGGCAGGCCAGGACCTGGAGAGCCCA
GACCCTGTCTCCAGGAGGCCAGGAGGCCAGATGGGGGCTTGCCTGAAAGACTGGTCCCTTGATCGCTGGAGGC
ATGTGGGTGGCAACCAGGGCTGGGCAGGGCTTAGGGTGTGTGGGCCAAACCCCCCTGGGGTTGGCAAAGCCGCCT
GTCAGGCCTCCTGGTGGGGGGCCCCCTGGACACAGGGAGCAGACCCTCTGCCTCATGGGGTAGGAGTGGCTGCCTCC
TGTGTTCTCTGGATTTCTTCTCCCAACAATAACCCCTGGACTTGCCTCCCCAGGCCTCTTGCCTGTAAATAGA
AGCCCGCAAACCTGTACAGATTTACAGAGGCATCGAGACTGGGCCCTGGGAGTTGCCATCTGAGAGCCGATGGCCC
CAGCATCCCCAGGTGCCTGCCTGGCACCACAGTGACCCTGGCCTCAGCGTGGCAAATGCATGTAAATATTTTTC
GTAGGCAGCGTGGCTCCAGAGAGCCCCCTGAAGACAGTGTCCCTCCCTCCTGTGAGTCCCTTCTCCTGTACAGAA
CCTGCCTGGGGTGGGTGGGGGTCTGCCATTCCCTCCCCAGGCCTTCCCTGCCCTTCTCTCCCTGTAACTGT
TTATTAACCATACTGTCTGTGAGTTTATGGCCAAAACCTTAAATAAGAAAAACAAAAGAAAAAGACAGTGAAAA
AAGAGACCAAGGCGCCTGCCCCACTGCGGGTACTCTCCTGTTCCAGCCTTGTGAAGGAACTGGTTTTGTTTTGT
TTTAACTTCTGTGCTGTGCCATTTATAAGAGGAA
ATAAAATTAAGCTGAAATG

149/6881
FIGURE 140

AGCCATGCCTTTCTTGGACATCCAGAAAAGGTTCGGCCTTAACATAGATCGATGGTTGACAATCCAGAGTGGTGA
ACAGCCCTACAAGATGGCTGGTCGATGCCATGCTTTTGAAAAAGAATGGATAGAATGTGCACATGGAATCGGTTA
TACTCGGGCAGAGAAAGAGTGCAAGATAGAATATGATGATTTTCGTAGAGTGTTTGCTTCGGCAGAAAACGATGAG
ACGTGCAGGTACCATCAGGAAGCAGCGGGATAAGCTGATAAAGGAAGGAAAGTACACCCCTCCACCTCACCACAT
TGGCAAGGGGGAGCCTCGGCCCTGAACAGAGCAGCTGCTGATGCTGGAGGCTGATTTTCCTGTTCTCTGTTCTC
CACTGGAAAGGTTGTTTACGACAAACCTCCTTGTCAAAGTGTGTAAAAATAAAGGATTGCTCCATCCT

150/6881
FIGURE 141

GCTGAGCGGGCTTTGGACACCATGAACTTTGATGTGATTAAGGGAAAGCCAATCCGCATCATGTGGTCTCAGAGG
GATCCCTCTTTGAGAAAATCTGGTGTGGGAAACGTCTTCATCAAGAACCCTGGACAAATCTATAGATAACAAGGCA
CTTTATGATACTTTTCTGCTTTTGGAAACATACTGTCTGCAAGGTGGTGTGTGATGAGAACGGCTCTAAGGST
TATGCCTTTGTCCACTTCGAGACCCAAGAGGCTGCCGACAAGGCCATCGAGAAGATGAATGGCATGCTCCTCAAT
GACCGCAAAGTATTTGTGGGCAGATTCAAGTCTCGCAAAGAGCGGGAAGCTGAGCTTGGAGCCAAAGCCAAGGAA
TTCACCAATGTTTATATCAAAAACCTTTGGGGAAGAGGTGGATGATGAGAGTCTGAAAGAGCTATTCAGTCAGTTT
GGTAAGACCCTAAGTGTCAAGGTGATGAGAGATCCCAATGGGAAATCCAAAGGCTTTGGCTTTGTGAGTTACGAA
AAACACGAGGATGCCAATAAGGCTGTGGAAGAGATGAATGGAAGAAATAAGTGGTAAAATCATATTTGTAGGC
CGTGACAAAAGAAAAGTAGAACGGCAGGCAGAGTTAAACGGAAATTTGAACAGTTGAAACAGGAGAGAATTAGT
CGATATCAGGGGGTGAATCTCTACATTAAGAACTTGGATGACACTATTGATGATGAGAAATTAAGGAAAGAATTT
TCTCCTTTTGGATCAATTACCACTGCTAAGGTAATGCTGGAGGATGGAAGAAGCAAAGGGTTTGGCTTCGTCTGC
TTCTCATCTCCTGAAGAAGCAACCAAGCAGTCACTGAGATGAATGGACGCATTGTGGGCTCCAAGCCACTATAT
GTTGCCCTGGCCAGAGGAAGGAAGAGAGAAAGGCTCACCTGACCAACCAGTATATGCAACGAGTGGCTGGAATG
AGAGCACTTCCTGCCAATGCCATCTTAAATCAGTTCCAGCCTGCAGCGGGTGGCTACTTTGTGCCAGCAGTCCCA
CAGGCTCAGGGAAGGCCTCCATATTATACACCTAACCAAGTTAGCACAGATGAGGCCTAATCCACGCTGGCAGCAA
GGTGGGAGACCTCAAGGCTTCCAAGGAATGCCAAGTGCTATACGCCAGTCTGGGCCTCGTCCAACCTCTTCGCCAT
CTGGCTCCAACCTGGTAATGCTCCGGCCTCTCGTGGCCTCCCTACTACCACTCAGAGAGTCGGGTCTGAGTGCCCC
GACCGCTTGGCTATGGACTTTGGTGGGGCTGGTGCCGCCAGCAAGGGCTGACTGACAGCTGCCAGTCTGGAGGC
GTTCCACAGCTGTGCAGAACTTAGCGCCACGCGCTGCTGTTGCTGCTGCTGCTCCCCGGGCTGTTGCCCCCTAC
AAATACGCCTCCAGTGTCGCGCAGCCCTCATCCTGCCATACAGCCTCTGCAGGCACCCCAGCCTGCGGTCCATGTG
CAGGGGCAGGAGCCACTGACTGCCTCCATGCTGGCTGCAGCACCCCCCAGGAACAGAAGCAGATGCTGGGAGAA
CGCTTGTTCCCACTCATCCAAACAATGCATTCAAATCTGGCTGGGAAGATCACGGGAATGCTGCTGGAGATAGAC
AACTCTGAGCTGCTGCACATGTTAGAGTCCCCGAGTCTCTCCGCTCCAAGGTGGATGAAGCTGTAGCAGTTCTA
CAGGCTCATCATGCCAAGAAAGAAGCTGCCCAGAAGGATTCAAAGCCAAATAACCCCTTATGGAATTCAACTCA
AGGTTTGAAGACTTCCTAGCTTGTCTATGGACCTCAACACCAAGGATTACAAATTGCAAATTTAATAGGTCATT
TTGTATCAAAGGTCAATTATGAAGCACCTAGAATTTTTCAATTATACGAATATGTTCTTTGGGTTCTGCTGTGG
CCCAGACAGTGTTAACTTTTTTTTTTATTGTGGGTTTTGATTTTTTCCCCCAGAAATTGGTTTTATTTGATGTACC
CAAGTCTTACGTTTCCAATAAAGAAAAAAAATCTCCAT

151/6881
FIGURE 142

ACCAGGCAGCCTGCGTTTCGCCATGAAGCGACCCAAGGAGCCGAGCGGCTCCGACGGGGAGTCCGACGGACCCATC
GACGTGGGCCAAGAGGGCCAGCTGAGCCAGATGGCCAGGCCGTGTCCACCCCCAGCTCTTCGAGATGCAAGCC
AGGAAGAAAACGCAGAGGGATCATAGAGAAACGGCGTCGAGACCGCATCAACAGTAGCCTTTCTGAATTGCGACGC
TTGGTCCCCACTGCCTTTGAGAAACAGGGCTCTTCCAAGCTGGAGAAAGCCGAGGTCTTGACAGATGACGGTGGAT
CACTTGAAAATGCTCCATGCCACTGGTGGGACAGGATTCTTTGATGCCCCGAGCCCTGGCAGTTGACTTCCGGAGC
ATTGTTTTTCGGGAGTGCCTCACTGAGGTCATCAGGTACCTGGGGGTCTTGAAGGGCCAGCAGCCGTGCAGAC
CCCGTCCGGATTTCGCTTCTCTCCACCTCAACAGCTACGCAGCCGAGATGGAGCCTTCGCCCCACGCCCCTGGC
CCTTTGGCCTTCCCTGCCTGGCCCTGGTCTTTCTTCCATAGCTGTCCAGGGCTGCCAGCCCTGAGCAACCAGCTC
GCCATCCTGGGAAGAGTGGCCAGCCCTGTCTCCCCGGTGTCTCTCTCTGCTTACCCCATCCAGCCCTCCGA
ACCGTCCCCCTTCGAGAGCCACAGGCATCATCCTGCCAGCCCGGAGGAATGTGCTGCCAGTCGAGGGGCATCT
TCCACCCGGAGGGCCCGCCCCCTAGAGAGGCCAGCGACCCCTGTGCCTGTGCCCCCAGCAGCAGGGCTGCCAGG
AGCAGCCACATCGCTCCCCTCCTGCAGTCTTCTCCCCAACACCCCTGGTCTACAGGGTGGCTGCTTACGTG
GCTGTTCCACCCCCAACTCATCTCCCAGGGCCAGCTGGGAGGCCAGCGGGAGCCATGCTCTACCACTCCTGG
GTCTCTGAAATCACTGAAATCGGGGCTTTCTGAGCTGCCCTTACCACCCCGCCCCAAGGAATAAGGAAGGTTT
TTTTACCAGGAGCCCAAAAAGGGCACTGCCTTTTCTGCTTTGCTTCGTGGACTGGCTCATATGTGAAGGCACGT
TCTCCAGCCATCAGAGGCCCCCTCCTCCTCCAACCCATCTCTCCTTCTCACTGTTATCCCAGCTTATCCACCCAG
CTCTCCTGGAGCTGTTCTGGTCTCAGAGGCTTGGTTCCATTTCTCACCTGAACAGATGAGTCTGGGAGAGACCC
TCAGAGATCCGCCCAGACCCCTCTCCTGCCCTCTGCACACCAGCAGCAGGCATGAACCTTGGGTCTGGGAAAAAG
CTTTAACCTGCAGGGCACCAGGACCCAAGGCAGGCTGTTCTTGGGGCGGTCAGACCCAGTCAGGAGCAATGAC
TGACTGGCTGCAGCCTTCCCACGCCAAGAGGCTGGAACATAGTGTCTGCCTCGCTTCTGGAGATAGTAACTGAG
CAGGGGCTACAAAGAGGTCTCCTGGGAACCCTGTCTGCCCTTCCCACCTGTCTTGGGCCACACCATCACACTG
AACCACAGGACAGACCCCTTTCTCCACCACAGCCAAGGCCTGGAGACTGGGGGCCCAGCAGAGCCTGCTCCCACCC
TCTCCAGCAGCAGACACCCACCCCTCTCACTGACTAACAGGTCCCTGCACACAGCTGGCCTGGTAAACCCAGCT
GGGAGGTTTTCTAGGCAGCAGCAAACTCTGTGACAGGGTGTCTCACACCAGGCCTTGGACAGCTCTCCCAGACA
GGAGCCAGGGTTGAGCAATGGAGAGCCAGCCCCACGTCTTACAGTCGCCATCCTCCAGGCGTGTGGTCCCTCC
CCATTGGGTGCACAGTGCAGAGGGGCCGTGGCCCCATGTGATGGTGGCAGAGAGGAACCTCTTGGGATTTCAGCA
CCAGACGTCTGTGCTGCCTGGTTTGCATCCGGCTCACAGAGCCAGACTGCTGGAACAGCCAAGGACTGTAGGC
TGGACAAAAATAACTGCAAGGAGGGGCAAGAGAAAGGATGATTGAGGCACCTTGGCCCTTCAAGGTCATGCAGT
GGGTCGAGCGCCTGAGATCCTGTTACCAGGACTCCACAGAGCTGGCTCTGCTCAGAAGCCATTTTATTCCCCGG
CTCCACCCTAGGCCACTTTTTCTAACAGAGGAACAATGGTCCAGCAGTCGTTCCAGCAGAACAGCGGAGCCT
GGACTGACACCCAGTGGGACCACTGTTGCCACACCAGTTGATAAAATGCAGAAACCCTTCTGTACTCGTTGGTAA
ATATCTACTCCCCAAGTGACTCCAGGTGCCCCCACCGCCTGGCACTTCCCCAGGACTCCTACGATCTGGTTA
CTGCCCTGGCCGATCCAAGGCTGTGGAGTCCCAGAGCCAGCAGTTCACTGGTGTCTATTCCACACTGGTTAGATAC
TTCAGTTGTACCCCTGGGAAGATTCTCCACCTCCTCCCTTTGATGGAACCACCCTCCCCAGAGGCTGCATTGA
GGAGACTCCACAGACTGAAAAGTGAGTTTGCAGAAACCTTGGGGAAAAGGGCCCTTTCAAAGAAGTGGATAAGAG
GGAGGAGATCATTGAGTGACCCAGAAAGCTCTTTTGAAAAGACAGACTCCTCAAGGAGAGATAAAGAGGAAAGCA
CCTCTTTTCATTTTTTAGTGTGAGCTAATTCCATCAGACTGCTGTCTCCTGGACCCATCTGAGATGTGCAGTAGC
AAGGAGAGGGGGGATCATTTTAGAGAGTGGGTCAATTGGCAGGGAGTGCTCCGGAGGGAGGCAGAGGGGAGACTGT
GGTAGAAGGAAGACAGAACTCACACATGCTCCCAGGATTGGGGACAGGGACAGAGGAGGTAACAGAAGGCAAAGG
CCAGTTTTCCCCGTTATCATGAAGGGGCCACTCAGGACAGGAACAAGGACAACCTCCTCCTCCTCCTCCTCCTC
CTGCTGCTCCTGGGATAACCAGGTCAGTGATGTAGTCTTGCACTTTGGCAACTTCCTAGCCTGAGAATCCCTAGTG
GGGCTGTGGGAAACACATTTCCACGTTGCAAGCATGCAACTCCAAAGAATCTGTGATGCCACTGAAATGAGATGG
GAATGATCCAGCTCTTTCAGCATCTTGGTTGAACTTGCTTTTCAATTGTCCCTGGGATATTGTGGAAGGAAAGGTGA
CTGTGTGATCTGATTCTGTGGTCAAGGACTTGCATCTTGTGTTTCTATCCCCAAGCCTTCTGGTGTCTCCAAC
CCTACCCCATTCATGGGTTGTTGCGGACATCCAATAAAGATTTTTTTTAGTGCTTCTGGAAAAAAAAAAAAAAAA
AACC

152/6881
FIGURE 143

MKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQMQARKKRRGIIEKRRRDRINSSLSELRRLVPTAFE
KQGSSKLEKAEVLQMTVDHLKMLHATGGTGFFDARALAVDFRSIGFRECLTEVIRYLGVLGPGSSRADPVRI RLL
SHLNSYAAEMEPSPTPTGPLAFPAPWPSFFHSCPLPALS NQLAILGRVPSPVLPGVSSPAYPIPALRTAPLRRA
TGIILPARRNVLP SRGASSTRRARPLERPATPVFVAPSSRAARSSHIAPLLQSSSPTPPGPTGSAAYVAVPTPNS
SSPGPAGRPAGAMLYHSWVSEITEIGAF

153/6881
FIGURE 144

GATCCTAAATTGCAGCAAGGCTACAATGCTATGGGATTCTCCCAGGGAGGCCAATTTCTGAGGGCAGTGGCTCAG
AGATGCCCTTCACCTCCCATGATCAATCTGATCTCGGTTGGGGGACAACATCAAGGTGTTTTTGGACTCCCTCGA
TGCCCAGGAGAGAGCTCTCACATCTGTGACTTCATCCGAAAAACACTGAATGCTGGGGCGTACTCCAAAGTTGTT
CAGGAACGCCTCGTGCAAGCCGAATACTGGCATGACCCCATAAAGGAGGATGTGTATCGCAACCACAGCATCTTC
TTGGCAGATATAAATCAGGAGCGGGGTATCAATGAGTCTTACAAGAAAAACCTGATGGCCCTGAAGAAGTTTGTTG
ATGGTGAAATTCCTCAATGATTCCATTGTGGACCCTGTAGATTTCGGAGTGGTTTGGATTTTACAGAAGTGGCCAA
GCCAAGGAAACCATTCCCTTACAGGAGACCTCCCTGTACACACAGGACCGCCTGGGGCTAAAGGAAATGGACAAT
GCAGGACAGCTAGTGTCTTGGCTACAGAAGGGGACCATCTTCAGTTGTCTGAAGAATGGTTTTATGCCACATC
ATACCATTCCCTTGGATGAAACCCGTATAGTTTACAATAGAGCTCAGGGAGCCCCCTAACTCTTCCAAACCACATGG
GAGACAGTTTCCCTTCATGCCCAAGCCTGAGCTCAGATCCAGCTTGCAACTAATCCTTCTATCATCTAACATGCCC
TACTTGGAAGATCTAAGATCTGAATCTTATCCTTTGCCATCTTCTGTTACCATATGGTGTGAATGCAAGTTTA
ATTACCATGGAGATTGTTTTACAACTTTTGATGTGGTCAAGTTTCAGTTTTAGAAAAGGGAGTCTGTTCCAGATC
AGTGCCAGAAGTGTGCCCAGGCCCAAAGGAGACAATACTAAAGTAGTGAGATAGATTCTAAGGGCAAACATTT
TTCCAAGTCTTGCCATATTTCAAGCAAAGAGGTGCCCAGGCCTGAGGTACTCACATAAATGCTTTGTTTTGCTGG
TGATTTAACCAAGTGCTTGAAAAATCTTGCTTGGCTATTTCTGCATCATTTCTTAAGGCTGCCTTCCTCTCTCAG
TACGTTGCCCTCTGTGCTATCATCTTATCATCAATTATTAGACAAATCCCACTGGCCTACAGTCTTGCTTCTGCA
GCACCCACTTTGTCTCCTCAGGTAGTGATGAATTAGTTGCTGTACAAAAGGAGGGAAGTAGCACCCAAATTAAG
TTGCTTAAGAGAGGAAATGTACATCTTGTATAACTTAGGGAGCGAAGAAAAATGTAGGCGCGAAAGTGAAAAGTGA
GGCAGCTAGTTCTTCTTATTCCATTCTCGACCAACCTGCCCTTTCTTAATATGACTAGTGGTCTTGATGCTAGAG
TCAACTTACTCTGTTGCTGGCTTTAGCAGAGAATAGGAGGAACCATATGAAAAAGATCAGGCTTTCTGACTTCCA
TCCCCAAAACACATTTACCAGCATACTCCAAACTGTTTCTGATGTGTTCCATGAGAAAAGGATTGTTTGCTCAAA
AAGCTTGGAATACTACACACTCCCTTTCTCCTTCTGGAGATCAACCCACATTAGAGTGTCTAAGGACTCCTGA
GAATTCCTGTTACAGTAAACAAACTAACGTAATCTACCATTTCTTACACTATTTGAGCATGGAAATCATAGTCC
CCACTCTGTGAAAACCTAACGCTTTTTGGAAGACATTTCTGTAGCATGTCAGTTTGGAGAAATGATGAGCTACGC
CTTGATGAAAGAACCGTGTTGGTGCTGCTAAGTTTAGCCATTATGGTTTTTCCTTTCTCTCTTAAAGCCTTATT
CTTCAACTAAAAGATGAGGATTAAGAGCAAGAAGTTGGGGGGGATGTGAAAATAATTTTATGAGGTTGTCTAAAA

T

154/6881
FIGURE 145

GGGTCGCGCGGAGATTGCTGGGCGGTTCTTGCCGGAAGCGGAGAGCGGCTGATCGCAGTCCGGAGGTGAGGCGGA
ACTCTGAGGCAGATATCCTCCCTTTCTCCTCGGCTGCTGCTCTTACTTTGACAAGCCAGGCTAACATTGAAGGT
GGTCCATTATGGCTGACATGCAAAATCTGGTAGAAAGATTGGAGAGGGCAGTGGGCCCGCCTGGAGGCAGTATCTC
ATACCTCTGACATGCACCGTGGGTATGCAGACAGTCCTTCAAAAGCAGGAGCAGCTCCATATGTGCAGGCATTG
ACTCGCTGCTTGCTGGTCCTGTGGCAGAGTACTTGAAGATCAGTAAAGAGATTGGGGGAGACGTGCAGAAACATG
CGGAGATGGTCCACACAGGTTTGAAGTTGGAGCGAGCTCTGTTGGTTACAGCTTCTCAGTGTCAACAGCCAGCAG
AAAATAAGCTTTCCGATTTGTTGGCACCCATCTCAGAGCAGATCAAAGAAGTGATAACCTTTTCGGGAGAAGAACC
GAGGCAGCAAGTTGTTTAATCACCTGTGAGCTGTGAGCGAAAGTATCCAGGCCCTGGGCTGGGTGGCTATGGCTC
CCAAGCCTGGCCCTTATGTGAAAGAAATGAATGATGCCGCCATGTTTTATACAAACCGAGTCTTCAAAGAGTACA
AAGATGTGGATAAGAAGCATGTAGACTGGGTCAAAGCTTATTTAAGTATATGGACAGAGCTGCAGGCTTACATTA
AGGAGTTCCATACCACCGACTGGCCTGGAGCAAAACGGGGCCTGTGGCAAAAGAACTGAGCGGACTGCCATCTG
GACCCTCTGCCGGATCAGGTCTCTCCCTCCCTCCACCATGCCCTCCCTCTCCCTCCCTCAGTCTCTACCACTTCACTGCT
CATATGAGTCTGCTTCCCGCTCAGCACTGTTTCGCGCAGATTAATCAGGGGGAGAGCATTACACATGCCCTGAAAC
ATGTATCTGATGACATGAAGACTCACAAGAACCCTGCCCTGAAGGCTCAGAGTGGTCCAGTACGCAGTGGCCCCA
AACCATTCTCTGCACCTAAACCCCAAACCAGCCCATCCCCCAAACGAGCCACAAAGAAGGAGCCAGCTGTACTTG
AACTGGAGGGCAAGAAGTGGAGAGTGGAAAATCAGGAAAATGTTTCCAACCTGGTGATTGAGGACACAGAGCTGA
AACAGGTGGCTTACATATACAAGTGTGTCAACACGACATTGCAAATCAAGGGCAAAATTAAGTCCATTACAGTAG
ATAACTGTAAGAACTTGGCCTGGTATTTCGATGACGTGGTGGGCATTGTGGAGATAATCAACAGTAAGGATGTCA
AAGTTCAGGTAATGGGTAAAGTGCCAACCATATCCATCAACAAAACAGATGGCTGCCATGCTTACCTGAGCAAGA
ATTCCTGGATTGTGAAATAGTCAGTGCCAAATCTTCCGAGATGAATGTCCTCATTCTACAGAAGGCGGTGACT
TTAATGAATTCCCAGTTCTGAGCAGTTCAAGACCCTATGGAACGGGCAGAAGTTGGTCACCACAGTGACAGAAA
TTGCTGGATAAGCGAAGTGCCACTGGGTTCTTTGCCCTCCCTTCACACCATGGGATAAATCTGTATCAAGACGGT
TCTTTTCTAGATTTCTCTACCTTTTTTGCTCTTAAAACTGCTTCTCTGCTCTGAGAAGCACAGCTACCTGCCTTC
ACTGAAATATACCTCAGGCTGAAATTTGGGGTGGGATAGCAGGTCAGTTGATCTTCTGCAGGAAGGTGCAGCTTT
TCCATATCAGCTCAACCACGCCGCCAGTCCATTCTTAAGGAACTGCCGACTAGGACTGATGATGCATTTTAGCTT
TGAGCTTTTGGGGGTTATTCTACCAACAAACAGTCCATTGGAAAAGAAAACAGTCCCTGGAATTAACAGATCAGAA
TGTTACACTGGTTAATCTTTTTTTAACAATGAGCATGAAGGTAGCAGAAGCTGGTGTGTTTCCAGATGGTTCTT
CTAACCAAATAATTTTTTCACTGTTGACAAGCGAGGCAAGGGTTGCACTGGACCAAAGGCTGAGGCTTGGCCATC
TAGCATTCCATACAAAATTGTTTCTTATAAGCATTCCTTTTATTCTCTATTCTATCCTGGGTCTGCCTCAACCGT
GAGATAGGAGAGTCTCTGGTACTAGCTGCTGTAGCAGTGCCCTTCATCCAGGGCAGTTAATGGAGTCTTGGACCC
TTTCTTTCTCTGGGATCCCTGCCAGCACCTTCTTATAGAGATGACTTTTAAAGGAAAAAAAAAAAAAAAAAAC
CCACATGATTTCAAGGAGTCTGGCATTCTGAATCCTTCTTCCCTGCCAGGTGCCTGTACCTGTCTTCACTGCC
TCCTTTTCCCTGTGATGCTCATCAGCTTATGGCTTCTGTCTAAGCACCTGAACAGAGGACTGAAACCTCCACTGC
AGGCTGGTTTTAGGTCTTGAATTATGTAAGAATCTTGACACAGCACTGCTAATGTAAATTTTCACTTGTTTTTCCCT
CTAGGACAAACACTTACCAAAATATGCAACTTTTTTTTTTGGTGGGAAGAGAGATTGTCCTGTGATTCTACCCATT
TCCTGAGGCCTGTGGAAATAAACCTTTATGTACTTAAAGTTATACAGAAAATAGAATAAAGTTAATACCAAACCTT
G

155/6881
FIGURE 146

GGCTTCGGTCGCTACCGCTCCCGCTCTGCCACCCCGCCAACCGCCGCTCGGGCCTCCGTCGCTGCCGCGTCGCT
TTCTCGCTCCTTGGATCGCACATCCTCCCAGATGCAGCGCCGGGACGACCCCGCCGCGCATGAGCCGGTCTTC
GGGCCGTAGCGGCTCCATGGACCCCTCCGGTGCCACCCCTCGGTGCGTCAGACGCCGTCTCGGCAGCCGCCGCT
GCCTCACCGGTCCCAGGGAGGCGGAGGGGGATCCCGCGGGGGCGCCCGGGCCTCGCCCGCCACGCAGCCGCCACC
GCTGCTGCCGCCCTCGGCCACGGGTCCCGACGCGACAGTGGGCGGGCCAGCGCCGACCCCGCTGCTGCCCCCTC
GGCCACAGCCTCGGTCAAGATGGAGCCAGAGAACAAGTACCTGCCGAACCTCATGGCCGAGAAGGACTCGCTCGA
CCCGTCCTTCACTCACGCCATGCAGCTGCTGACGGCAGAAATTGAGAAGATTGAGAAAGGAGACTCAAAAAGGA
TGATGAGGAGAATTACTTGGATTTATTTCTCATAAGAACATGAACTGAAAGAGCGAGTGCTGATACCTGTCAA
GCAGTATCCCAAGTTCAATTTTGTGGGGAAGATTCTTGGACCACAAGGGAATACAATCAAAAGACTGCAGGAAGA
GACTGGTGCAAAGATCTCTGTATTGGGAAAGGGCTCAATGAGAGACAAAGCCAAGGAGGAAGAGCTGCGCAAAGG
TGGAGACCCCAAATATGCCCACTTGAATATGGATCTGCATGTCTTCATTGAAGTCTTTGGACCCCATGTGAGGC
TTATGCTCTTATGGCCCATGCCATGGAGGAAGTCAAGAAATTTCTAGTACCGGATATGATGGATGATATCTGTCA
GGAGCAATTTCTAGAGCTGTCTACTTGAATGGAGTACCTGAACCTCTCGTGAGCTGGGGTGCCAGTGAGAGG
CCGGGGAGCTGCACCTCCTCCACCACCTGTTCCAGGGGCCGTGGTGTGGACCACCTCGGGGGGCTTTGGTACG
TGGTACACCAGTAAGGGGAGCCATCACCAGAGGTGCCACTGTGACTCGAGGCGTGCCACCCACCTACTGTGAG
GGGTGCTCCAGCACCAAGAGCACGGACAGCGGGCATCCAGAGGATACCTTTGCCTCCACCTCCTGCACCAGAAAC
ATATGAAGAATATGGATATGATGATACATACGCAGAACAAAGTTACGAAGGCTACGAAGGCTATTACAGCCAGAG
TCAAGGGGACTCAGAATATTATGACTATGGACATGGGGAGGTTCAAGATTCTTATGAAGCTTATGGCCAGGACGA
CTGGAATGGGACCAGGCCGCTCGCTGAAGGCCCTCCTGCTAGGCCAGTGAAGGGAGCATACAGAGAGCACCCATA
TGGACGTTATTAAACAAACATGAGGGGAAAATATCAGTTATGAGCAAAAGTTGTTACTGATTTCTTGTATCTCC
CAGGATTCTGTTGCTTTACCCACAACAGACAAGTAATTGTCTAAGTGTTTTCTTCGTGGTCCCTTCTTCTCC
CCACCTTATTCCATTCTTAACCTCTGCATTCTGGCTTCTGTATGTAGTATTTTAAATGAGTTAAATAGATTTAG
GAATATTGAATTAATTTTTTAAGTGTGTAGATGCTTTTTTCTTTGTTGTTTAAATATAAACAGAAGTGACCTTT
TATAATAAAAAAAGAAGTTGAGTAAAAAACAACACACAAACCTGTTAGTTTCAAAAATGACATTGCTTGCT
TAAAGGTTCTGAAGTAAAGGCTTGTTAAGTTTCTCTTAGTTTTGATTTGAGGCATCCCGTAAAGTTGTAGTTGCA
GAATCCCAAACCTAGGCTACATTTCAAATTCAGGGCTGTTTAAAGATTTAAATCACAACATTAACGGCAGTAGG
CACCACCATGTAAAAGTGAGCTCAGACGTCTCTAAAAATGTTTCCTTTATAAAAGCACATGGCGGTTGAATCTT
AAGGTTAAATTTAATATGAAAGATCCTCATGAATTAATAGTTGATGCAATTTTTAACGTTAATTGATATAAAA
AAAAAACAACAAAATTAGGCTTGTAACACTGACTTTTTTCATTACGTGGGTTTTGAAATCTAGCCCCAGACATAC
TGTGTTGAGAGATACTTAGAGGGAGGAGTAGGTTTTGAAGAGGTTGATGGTGGTGGGGAGGGAAGGCCTCCTGA
ATTGAGTTTGATGCAGAGCTTTTTAGCATGAAGAATCTTTCAGTCATAGTACTAATAATTAATTTTCAGTATT
TAAAAAGACAAAGTATTTGTCCATTTGAGATTCTGCACTCCATGAAAAGTTCACCTGGACGCTGGGGCCAAAAG
CTGTTGATTTTCTTAAGTTGACGGTTGTCAATATATCGAACTGTTCCCAAGTTAGTCAAGTATGTCTCAACACTA
GCATGATATAAAAAGGGACACTGCAGCTGAATGAAAAGGAATCAAAATCCACTTTGTACATAAGTTAAAGTCCT
AATTGGATTTGTACCGTCCTCCCATTTTGTCTCGGAAGATTAAATGCTACATGTGTAAGTCTGCCTAAATAGGT
AGCTTAACTTATGTCAAAATGTCTGCAGCAGTTTGTCAATAAAGTTTAGTCCTTTTTTA

156/6881
FIGURE 147

MQRRDDPAARMSRSSGRSGSMDPSGAHPSVRQTPSRQPPLPHRSRGGGGSRGGARASPATQPPFLLPPSATGPD
ATVGGPAPTPLLPPSATASVKMEPENKYLPELMAEKDSLDPSTHAMQLLTAEIEKIQKGDSKKDDEENYLDLFS
HKNMKLKERVLIPVKQYPKFNFVGKILGPQGNTIKRLQEETGAKISVLGKGSMRDKAKEEELRKGGDPKYAHLNM
DLHVFIEVFGPPCEAYALMAHAMEEVKKFLVPDMMDDICQEQFLELSYLNQVPEPSRGRGVFVRGRGAAPPPPV
PRGRGVGPPRGALVRGTPVRGATVRGATVTRGVPPPTVRGAPAPRARTAGIQRIPLPPPPAPETYEEYGYDDTY
AEQSYEGYEGYYSQSQGDSEYYDYGHGEVQDSYEAYGQDDWNGTRPSLKAPPARPVKGAYREHPYGRY

157/6881
FIGURE 148

CTCGCGTCACAGCCGGG**ATGA**AGCCGATCCTACTGCAGGGCCATGAGCGGTCCATTACGCAGATTAAGTATAACC
GCGAAGGAGACCTCCTCTTTACTGTGGCCAAGGACCCTATCGTCAATGTATGGTACTCTGTGAATGGTGAGAGGC
TGGGCACCTACATGGGCCATACCGGAGCTGTGTGGTGTGTGGACGCTGACTGGGACACCAAGCATGTCCTCACTG
GCTCAGCTGACAACAGCTGTCTGTCTCTGGGACTGTGAAACAGGAAAGCAGCTGGCCCTTCTCAAGACCAATTCGG
CTGTCCGGACCTGCGGTTTTGACCTTTGGGGGCAACATCATCATGTTCTCCACGGACAAGCAGATGGGCTACCAGT
GCTTTGTGAGCTTTTTTGAACCTGCGGGATCCGAGCCAGATTGACAACAATGAGCCCTACATGAAGATCCCTTGCA
ATGACTCTAAAATCACCAGTGCTGTTTGGGGACCCCTGGGGGAGTGCAATCATCGCTGGCCATGAGAGTGGAGAGC
TCAACCAGTATAGTGCCAAGTCTGGAGAGGTGTTGGTGAATGTTAAGGAGCACTCCCGGCAGATCAACGACATCC
AGTTATCCAGGGACATGACCATGTTTGTGACCGCGTCCAAGGACAACACAGCCAAGCTTTTTGACTCCACAACCTC
TTGAACATCAGAAGACTTTCGGACAGAACGTCCTGTCAACTCAGCTGCCCTCTCCCCCAACTATGACCATGTGG
TCCTGGGCGGTGGTCAGGAAGCCATGGATGTAACCACAACCTCCACCAGGATTGGCAAGTTTGAGGCCAGGTTCT
TCCATTTGGCCTTTGAAGAAGAGTTTGGGAAGAGTCAAGGGTCACTTTGGACCTATCAACAGTGTTGCCTTCCATC
CTGATGGCAAGAGCTACAGCAGCGGCGGCGAAGATGGTTACGTCCGTATCCATTACTTCGACCCACAGTACTTTG
AATTTGAGTTTGAGGCT**TAA**GAAGCTGGATCTCCTGCCGGGCGTGGTTGGCTCATGCCTGTAATCCCACCACTTT
TTTTTTAAGGCAGGCGGATCACCTGAGGTCAGGAGTTTAAGACCAGCCTGACCAACATGGAGAAACCTCGTCTCT
ACTAAAAATACAAAATTAGCCAGGCATGGTGGCACACGCCTATAGTCCCAGCTACTCAGGAGGCTGAGGCAGGA
GAATCACTTGAACCCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCACGTCATTGCACTCCATCCTGAGCCACAAG
AGCAAACTCCGTCTCAAAAAAAAAAAGAAGAAGGTGGATCTCCAACCAGGCCAGAGAAGATTCTCACAGAAGG
TTTTGAACTCTAAGAAATAAATTGGTTTGGTAATAAATGGCTTCTGGTCAGA

158/6881
FIGURE 149

MKPILLQGHERSITQIKYNREGDLLFTVAKDPIVNVWYSVNGERLGTIMGHTGAVWCVDADWDTKHVLTGSADNS
CRLWDCETGKQLALLKTNSAVRTC GFDFGGNIIMFSTDKQMGYQCFVSFFDLRDP SQIDNNEPYMKIPCND SKIT
SAVWGPLGECIIAGHESGELNQYSAKS GEVLNVKEHSRQINDIQLSRDMTMFVTASKDNTAKLFDSTTLEHQKT
FRTERPVNSAALSPNYDHVVLGGGQEAMDVTTTSTRIGKF EARFFHLA FEEEFGRVKGHFGPINSVAFHPDGKSY
SSGGEDGYVRIHYFDPQYFEFEFEA

159/6881
FIGURE 150

GAGCGGAGCCGCGGGCGGGAGGGCGGACGGACCGACTGACGGTAGGGACGGGAGGCGAGCAAG**ATG**GCGCAGACG
CAGGGCACC CGGAGGAAAGTCTGTTACTACTACGACGGGGATGTTGGAAATTACTATTATGGACAAGGCCACCCA
ATGAAGCCTCACC GAATCCGCATGACTCATAATTTGCTGCTCAACTATGGTCTCTACCGAAAAATGGAAATCTAT
CGCCCTCACAAAGCCAATGCTGAGGAGATGACCAAGTACCACAGCGATGACTACATTAAATTCTTGCGCTCCATC
CGTCCAGATAACATGTCGGAGTACAGCAAGCAGATGCAGAGATTCAACGTTGGTGAGGACTGTCCAGTATTTCGAT
GGCCTGTTTGAGTTCTGTGCTAGTTGTCTACTGGTGGTTCTGTGGCAAGTGCTGTGAACTTAATAAGCAGCAGACG
GACATCGCTGTGAATTGGGCTGGGGGCCTGCACCATGCAAAGAAGTCCGAGGCATCTGGCTTCTGTTACGTCAAT
GATATCGTCTTGGCCATCCTGGAACTGCTAAAGTATCACCAGAGGGTGCTGTACATTGACATTGATATTACCAT
GGTGACGGCGTGGAAGAGGCCTTCTACACCACGGACCGGGTCATGACTGTGTCTTTTCATAAGTATGGAGAGTAC
TTCCAGGAACTGGGGACCTACGGGATATCGGGGCTGGCAAAGGCAAGTATTATGCTGTAACTACCCGCTCCGA
GACGGGATTGATGACGAGTCCTATGAGGCCATTTTCAAGCCGGTCATGTCCAAAGTAATGGAGATGTTCCAGCCT
AGTGCGGTGGTCTTACAGTGTGGCTCAGACTCCCTATCTGGGGATCGGTTAGGTTGCTTCAATCTAACTATCAAA
GGACACGCCAAGTGTGTGGAATTTGTCAAGAGCTTTAACCTGCCTATGCTGATGCTGGGAGGCGGTGGTTACACC
ATTTCGTAACGTTGCCCCGTGCTGGACATATGAGACAGCTGTGGCCCTGGATACGGAGATCCCTAATGAGCTTCCA
TACAATGACTACTTTGAATACTTTGGACCAGATTTCAAGCTCCACATCAGTCCTTCCAATATGACTAACCAGAAC
ACGAATGAGTACCTGGAGAAGATCAAACAGCGACTGTTTGAGAACCTTAGAATGCTGCCGCACGCACCTGGGGTC
CAAATGCAGGCGATTCTTGAGGACGCCATCCCTGAGGAGAGTGCGGATGAGGACGAAGACGACCCTGACAAGCGC
ATCTCGATCTGCTCCTCTGACAAACGAATTGCCTGTGAGGAAGAGTTCTCCGATTCTGAAGAGGAGGGAGAGGGG
GGCCGCAAGA ACTCTTCCA ACTTCAAAAAAGCCAAGAGAGTCAAAACAGAGGATGAAAAAGAGAAAGACCCAGAG
GAGAAGAAAGAAGTCACCGAAGAGGAGAAAACCAAGGAGGAGAAGCCAGAAGCCAAAGGGGTCAAGGAGGAGGTC
AAGTTGGCCT**TGA**ATGGACCTCTCCAGCTCTGGCTTCTGCTGAGTCCCTCACGTTTCTTCCCCAACCCCTCAGAT
TTTATATTTTCTATTTCTCTGTGTATTTATATAAAATTTATTAAATATAAATATCCCCAGGGACAGAAACCAAG
GCCCCGAGCTCAGGGCAGCTGTGCTGGGTGAGCTCTTCCAGGAGCCACCTTGCCACCCATTCTTCCGTTCTTAA
CTTTGAACCATAAAGGGTGCCAGGTCTGGGTGAAAGGGATACTTTTATGCAACCATAAGACAAACTCCTGAAATG
CCAAGTGCCTGCTTAGTAGCTTTGGAAAGGTGCCCTTATTGAACATTCTAGAAGGGGTGGCTGGGTCTTCAAGGA
TCTCCTGTTTTTTTTCAGGCTCCTAAAGTAACATCAGCCATTTTTAGATTGGTTCTGTTTTCGTACCTTCCCACTG
GCCTCAAGTGAGCCAAGAAACACTGCCTGCCCTCTGTCTGTCTTCTCCTAATTCTGCAGGTGGAGGTTGCTAGTC
TAGTTTCCTTTTTGAGATACTATTTTCATTTTTGTGAGCCTCTTTGTAATAAAATGGTACATTTCT

160/6881
FIGURE 151

MAQTQGTRRKVCYYYDGDVGNYYYGQGHMPKPHRIRMTHNLLLNYGLYRKMEIYRPHKANAEEMTKYHSDDYIKF
LRSIRPDNMSEYSKQMQRFNVGEDCPVFDGLFEFCQLSTGGSVASAVKLNKQQTDI AVNWAGGLHHAKKSEASGF
CYVNDIVLAILELLKYHQRVLYIDIDIHHGDGVEEAFYTTDRVMTVSFHKYGEYFPGTGDLRDIGAGKGKYYAVN
YPLRDGIDDESIEAIFKPVMSKVMEMFQPSAVVLQCGSDSLSGDRLGCFNLTIKGHAKCVEFVKSFNLPMLMLGG
GGYTIRNVARCWTYETAVALDTEIPNELPYNDYFEYFGPDFKLHISPSNMTNQNTNEYLEKIKQRLFENLRMLPH
APGVQMQAIPEDAIPESGDEDEDDEDPDKRISICSSDKRIACEEEFSDSEEEGEGGRKNSSNFKKAKRVKTEDEKE
KDPEEKKEVTEEEKTKEEKPEAKGVKEEVKLA

161/6881
FIGURE 152

GGCACGAGGGCGCGGAGCGGAGCGGCGGGCGCGAGCTAGCGGGTCGGCCGCGGAGCGGAGGTGCAGCTCGGCT
TCCCCGGGCACCCCTCCCCCTCGGGCGCCAGCCCCACCCCTCCGCCGGCCGGGCGGACCCCGCCGTACTATCCCC
TGCGGCGCGAGCCCGGGGCGGCTCCAAGCGCCCCCAGCAGACCCCATCATCGGCCAGCCAGAGCTCCAAGGCTC
CCCGGGGCGACGTGACCGCCGAGGAGGCAGCAGGCGCTTCCCCCGGAAGGCCAACGGCCAGGAGAATGGCCACG
TGAAAAGCAATGGAGACTTATCCCCCAAGGGTGAAGGGGAGTCGCCCCCTGTGAACGGAACAGATGAGGCAGCCG
GGGCCACTGGCGATGCCATCGAGCCAGCACCCCTAGCCAGGGTGCTGAGGCCAAGGGGGAGGTCCCCCCAAGG
AGACCCCAAGAAGAAGAAGAAATTCTCTTTCAAGAAGCCTTTCAAATTGAGCGGCCTGTCCCTTCAAGAGAAATC
GGAAGGAGGGTGGGGTGATTCTTCTGCCTCCTCACCCACAGAGGAAGAGCAGGAGCAGGGGGAGATCGGTGCCT
GCAGCGACGAGGGCACTGCTCAGGAAGGGAAGGCCGAGCCACCCCTGAGAGCCAGGAACCCCAAGGCCAAGGGG
CAGAGGCTAGTGCAGCCTCAGAAGAAGAGGCAGGGCCCCAGGCTACAGAGCCATCCACTCCCTCGGGGCCGAGA
GTGGCCCTACACCAGCCAGCGCTGAGCAGAAATGAGTAGCTAGGTAGGGGCAGGTGGGTGATCTCTAAGCTGCAA
AACTGTGCTGTCTTGTGAGGTCACTGCCTGGACCTGGTGCCCTGGCTGCCTTCCTGTGCCCAGAAAGGAAGGGG
CTATTGCCTCCTCCAGCCACGTTCCCTTTCTCCTCTCCCTCCTGTGGATTCTCCCATCAGCCATCTGGTTCTC
CTCTTAAGGCCAGTTGAAGATGGTCCCTTACAGCTTCCCAAGTTAGGTTAGTGATGTGAAATGCTCCTGTCCCTG
GCCCTACCTCCTTCCCTGTCCCCACCCCTGCATAAGGCAGTTGTTGGTTTTCTTCCCCAATTCTTTTCCAAGTAG
GTTTTGTTTACCCTACTCCCCAAATCCCTGAGCCAGAAGTGGGGTGCTTATACTCCCAAACCTTGAGTGTCCAGC
CTTCCCTGTGTGTTTTTAGTCTCTTGTGCTGTGCCTAGTGGCACCTGGGCTGGGGAGGACACTGCCCCGTCTAGG
TTTTTATAAATGTCTTACTCAAGTTCAAACCTCCAGCCTGTGAATCAACTGTGTCTCTTTTTTGAAGTTGGTAAGC
AAGTATTAGGCTTTGGGGTGGGGGGAGGTCTGTAATGTGAAACAACCTTCTGTCTTTTTTCTCCCACTGTTGTA
AATAACTTTTAATGGCCAAACCCAGATTGTACTTTTTTTTTTTCTAACTGCTAAACCATCTCTTCCACCT
GGTTTACTGTAACATTTGGAAGGAATAAATGTCGTCCCTTTTTAAAAAAAAAAAAAAAAAAAAAAAAA

162/6881
FIGURE 153

MGSQSSKAPRGDVTAEAAAGASPAKANGQENGHVKSNGDLSPKGEGESPPVNGTDEAAGATGDAIEPAPPSQGAE
AKGEVPPKETPKKKKKFSFKKPKLSGLSFKRNRKEGGDSSASSPTEEEQEQQGEIGACSDGTAQEGKAAATPE
SQEPQAKGAEASAASEEEAGPQATEPSTPSGPESGPTPASAEQNE

163/6881
FIGURE 154

GCTCCCATTTGGCTGATGTTGGCGCGAAGGTGCGCGAGTCAGCCCTCGCGCTGGGGGCGCAGGAAACAATAGAGGC
CGCGCGCACAGAGCGAGCTCTTGACGCCTCCCCGCCCCCTCCCGCAACGCTCGACCCCAGGATTCCCCCGGCTCGC
CTGCCCCGCCATGGCCGACAAGGAAGCAGCCTTCGACGACGCAGTGGAAGAACGAGTGATCAACGAGGAATACAAA
ATATGGAAAAAGAACACCCCTTTTCTTTATGATTTGGTGATGACCCATGCTCTGGAGTGGCCAGCCTAACTGCC
CAGTGGCTTCCAGATGTAACCAGAATTTGGAGGTTTTGGTTTCACTTAGTGGAATAATTGAAATAGAAATCAAGAT
CAACCATGAAGGAGAAGTAAACAGGGCCCGTTATATGCCCCAGAACCCTTGTATCATCGCAACAAAGACTCCTTC
CAGTGATGTTCTTGTTTTTGACTATACAAAACATCCTTCTAAACCAGATCCTTCTGGAGAGTGCAACCCAGACTT
GCGTCTCCGTGGACATCAGAAGGAAGGCTATGGGCTTTCTTGGAACCCAAATCTCAGTGGGCACTTACTTAGTGC
TTCAGATGACCATAACCATCTGCCTGTGGGACATCAGTGCCGTTCCAAAGGAGGGAAAAGTGGTAGATGCGAAGAC
CATCTTTACAGGGCATAACGGCAGTAGTAGAAGATGTTTCTTGGCATCTACTCCATGAGTCTCTGTTTGGGTCAGT
TGCTGATGATCAGAACTTATGATTTGGGATACTCGTTCAAACAATACTTCCAAACCAAGCCACTCAGTTGATGC
TCACACTGCTGAAGTGAAGTGCCTTTCTTTCAATCCTTATAGTGAGTTTCACTTCTTGCCACAGGATCAGCTGACAA
GACTGTTGCCTTGTGGGATCTGAGAAATCTGAACTTAAAGTTGCATTCTTTGAGTCACATAAGGATGAAATATT
CCAGGTTTCACTGGTACCTCACAATGAGACTATTTTAGCTTCCAGTGGTACTGATCGCAGACTGAATGTCTGGGA
TTTAAGTAAAATTGGAGAGGAACAATCCCCAGAAGATGCAGAAGACGGGGCCACCAGAGTTGTTGTTTATTTCATGG
TGGTCATACTGCCAAGATATCTGATTTCTCCTGGAATCCCAATGAACCTTGGGTGATTTGTTCTGTATCAGAAGA
CAATATCATGCAAGTGTGGCAAATGGAGTTAGTCCTTGACCACTAGTTTGATGCCATCTCCATTTTGGGTGACCT
GTTTCACCAGCAGGCCTGTTACTCTCCATGACTAACTGTGTAAGTGCTTAAAAATGGAATAAATTGCTTTTCTACA
TAA

164/6881
FIGURE 155A

GGCTCGCATCCCCATAGTGCTGGGTTACAGTGAAGGTACGCCCCGCGCTCTGCTCTGGAGAGGCAGGGTGGGATA
GGGAACGTCTCGAGTGGCGCCCGCAGTCA**ATG**GTGGTGTTCGTTGGCCCGCCCTCCCGGCGCTCCTAGGGCTGTT
TAAGAAGAAGGGCTCTGCCAAGGCTGAGAATGACAAACATCTAAGTGTAGGGCCTGGCCAGGGGCCAGGGTCTGC
AGTGGATGAGCACCAGGACAACGTCTTCTTTCCAGTGGGCGACCCCCCACCTGGAAGAGCTGCACACTCAGGC
CCAGGAGGGGCTCCGCTCCCTACAACACCAAGAGAAACAGAACTGAACAAGGTGGCTGGGACCATGGAGACAC
CCAGAGTATCCAGTCCCTCCCGACGGGGCCGGATGAAGACAACATCTCCTTCTGCAGTCAGACCACATCCTACGT
GGCTGAGAGCTCCACAGCAGAGGACGCGCTCTCCATCCGCTCGGAGATGATCCAGCGCAAAGGCTCCACCTTCCG
ACCCCATGACTCATTTCCCAAATCTGGAAAGTCAGGGCGGCGTGGCGGGAGCGGCGGAGCACTGTGCTGGGACT
CCCGCAGCATGTGCAGAAGGAGCTTGGCCTGAGGAATGAGCGTGAGGCACCAGGCACGCCCCGGGCTCCTGGTGC
ACGGGATGCCGTACGCATCCCCACAGTGGACGGCCGCCCCGAGGCACCTCAGGGATGGGGGGCCCGGGTGTCCCT
GCAGGCGCTGGAGGCGGAGGCGGAGGCTGGCGCTGAGACAGAGGCCATGCTGCAGCGCCACATTGACCGTGTCTA
CCGGGATGACACCTTTGTTGGCCGGTCCACGGGTACCCGGGCCCCACCATTGACCCGGCCCATGTCCCTAGCAGT
GCCTGGATTGACAGGAGGGGAGGGCCTGCAGAGCCCCCTGAGCCCGCCATGTCCATCTCCCCCAGGCCACCTA
CCTGTGCAAGTTGATTCCACATGCTGTGCTGCCGCTACAGTGGACGTGGTGGCCCTAGGCCGCTGCAGCCTGCG
CACACTAAGCCGCTGCAGCCTGCACTCGGCCAGCCAGCCTCAGTCCGCTCGCTGGGGCGCTTCTCCTCCGTCTC
CAGCCACAGCCCCGAGCCGCCACCCATCCTCCTCCAGTGACACCTGGAGCCACTCTCAATCCTCCGACACCAT
TGTGTCTGACGGTTCACCTCTCCTCTAAGGGTGGCTCTGAGGGCCAGCCGAGAGCTCTACGGCTAGCAATAG
CGTGGTACCCCTCCCGAGGAGGCAGTGGGAGGGGCTCTCCAGTGGGGGAGCACTGCTGAGGCCTCAGACAC
ACTCAGCATTCGGAGCAGTGGGCAGTTGTCTGGCCGGAGTGTGTCCCTGCGTAAGCTGAAGCGGCCTCCACCCCC
TCCCCGCGGACCCACTCCCTCCATCAGCGGGGCTTAGCAGTGCCATGAGGCCATTAGGGTTGCCCCCTAAGCC
TGAGCGTAAGCAGCAGCCCCAGCTGCCTCGGCCACCCACCACTGGTGGCTCAGAAGGGGCGGGGGCAGCACCTG
TCCACCCAACCCAGCCAACAGCTGGGTACCTGGCTTGTCTCCGGGTGGTTCCCGGCGCCCCCACGGTCCCCAGA
ACGGACACTTTGCCCCCTCAGTGGATACTCGAGCCAAAGTGGTACTCCACCCCTCCCTCCCAAGGGCCTGGCAGG
TCCCCCTGCTTCCCCAGGCAAGGCCCAGCCCCCTAAACCAGAGCGTGTACGTCTCTTCGCTCCCTGGGGCCTC
CGTCTCCTCTTCCCTCACGTCTTTATGTTCTCTCCTCTGACCCAGCCCCCTCAGACCGCTCTGGGCCACAGAT
ATTGACCCCCCTGGGTGACAGTTTGTCTATACCTCCTCACCCCAAGGTGCCTGCCCCCTTCTCCCCACCTCCCTC
CAAGCCCAGGAGCCCTAACCAGCTGCCCCCTGCTCTAGCCGCCCCCTGCTGTGGTTCTGGGCCTGTTTCTACCAC
TGACGCCAGTCTCAGTCCCCTCCCCTCAGACAAACCTTGACTCCACTGCAGGAGTCTCCTGTCTATCTCCAA
AGACCAGTCACCCCACCTTCCCCACCCCCATCTTATCATCCACCCCCACCACCCACTAAGAAGCCAGAGGTGGT
TGTGGAGGCACCATCTGCCTCAGAGACTGCTGAGGAGCCCCCTCCAAGATCCCAACTGGCCCCCTCCCCACCCCC
TGCCCCCTGAGGAGCAGGACCTGTCCATGGCTGACTTCCCCCACCAGAGGAGGCTTTTTTCTCTGTGGCCAGCCC
TGAGCCTGCAGGCCCTTACGGCTCCCCAGAGCTTGTGAGCTCCCCGGCTGCTTCGTCTCCTCAGCTACTGCTTT
GCAGATTACGCCCCGGGTAGCCCAGACCCTCCTCCAGCTCCGCCAGCCCCAGCTCCTGCTAGTTCCGCCCCAGG
GCATGTGGCCAAGCTCCCTCAGAAGGAACCGGTGGGCTGTAGCAAGGGTGGTGGGCTCCAGGGAGGACGTAGG
TGCGCCCTGGTACGCCCCCTGCTCCTGCAGATGGTGCAGCTCGCTCCGTGGGTGCTCCAGGAGGGGCTCCAC
CCCAGCACTGGGGCCATCGGCCCCCAGAAACCACTGCGAAGGGCCCTGTGAGGGCGGGCCAGCCAGTGCCTGC
CCCCCTCCTCAGGGCTCCATGCTGCGGTCCGACTCAAGGCCTGCAGCCTGGCCGCCAGTGAAGGCCTCTCAAGTGC
TCAGCCCAACGGACCGCTGAGGCAGAGCCACGGCCTCCCAGTCCCCTGCCTCAACGGCCAGTTTCTATCTTCTC
CAAGGGCTCTAGGAAGCTGCAGCTGGAGCGGCCCGTGTCCCCTGAGACCCAGGCTGACCTCCAGCGGAATCTGGT
GGCAGAACTCCGGAGCATCTCAGAGCAGCGGCCACCCAGGCCCAAAGAAGTCACCTAAGGCTCCCCACCTGT
GGCCCGCAAGCGTCTGTGGGAGTCCCCCACCAGCCTCCCCAGTTACCTCGAGCTGAGCCCCCTTACTGCTCC
TCCACCAATGGGCTCCCTCACACCCAGGACAGGACTAAGAGGGAGCTGGCGGAGAATGGAGGTGTCTGCAGCT
GGTGGGCCCAGAGGAGAAGATGGGCTCCCGGGCTCAGACTCACAGAAAGAGCTGGCC**TG**ACCACCAGGCACCTC
ACTGGCACTGCTGACCCATCCCAGAAACACAATCTCAGGGACCCGAGCAGCTCCAAGGACGAGAGGATACAGCAG
ACACAACCTAATAGAGAGGGCGCCTGCAGCCTTAACCTCCACGGCCTTCGATACTTATGCAAGCCTGGTGTGCT
CCTGTCTCAGAGTCATCCTGCGCTCATGCCTTTTTCCGAATGGGTTCACCTCTGGCAGTTGCCGCTTCAGTCTT
GGCCTTAGCCTCATCTTGAAGTGGGTAGCTGGCGGGAGAGGGTGGCTGCGCCCCCTGCTGGCCCTGAGGCTGCAG
AGTTGGGAGCAGGACACCTCACCTGAGTTTCATTTTTTTTTTCATGTCCAAACCATGCACATACTATAGTCCAGAAT

165/6881
FIGURE 155B

CAAAGCACTTTTGAAGAGTGGCTGCATGGCCATCCTCCAGGGCCCAGGAAGTTGCATTCCAAGGGCCTGTTTACA
TGGCAGCAGAATCCATCCCCGGCAGTCAGCCCATAGCTTGGGACCAGTCTGTGCCCTCCTGCCCAGTCCAGTTTA
CTCCTCTTGGTTCTGAAGGTGGCCAAGTCATTGTGTTCCACAGGCTTCTCTAGGCTGGGGGCAGGTGTGGGGC
TGTGGAATTCCAAAGCACAAAAGGTGCAGAGGGGATTGGCCTTCTGTGCCTCAACTACCAACCACCTCCTGC
CTTCCAGTTCTGCCAGGTGCTCCATGCTGGGGACAAGTAGGAGACTGCCAGGGCCCAAAGAAATGGGTGAGCAGT
AGAGTCATCTCGGGGCACTTGGCAGTGTCAAGCACCTGCCCTTGCCTCCTTGACCACACTGGGGTGGGTGGGCC
CCCAGCACTTCAGAGGCAGGAGCCTTTGGGCTGAGCAAGCACTGAGGAGGTGGATGGAAGGGAGCATCTGGAGGG
GGGGAGCTTCTTTGAGCAGTGGGCCCAGGCCTGGCCCTCCACACTTCATTCTCTGACCTTTCTCTCTCCTCATTT
CGGTGCATGTCCTTTCTGCAGCTGCCTTTCAGCACAGGTGGTTCCACTGGGGGCAGCTAACGCTGAGTGACAAGG
ATGGGAAGCCACAGGTGCATTTTACTCAAGTCTTCTCTAGTCAATGAGGGGCACCCAGTGCTTCTAGGGCAGGCT
GGGTGGTGGTCCCCTAGGTATCAGCCTCTCTTACTGTACTCTCCGGGAATGTTAACCTTTCTATTTTCAGCCTGT
GCCACCTGTCTAGGCAAGCTGGCTTCCCCATTGGCCCCCTGTGGGTCCACAGCAGCGTGGCTGCCCCCAGGGCCA
CQGCTTCTTTCTTGATCCTCTTTCTTAAACAGTGACTTGGGCTTGAGTCTGGCAAGGAACCTTGCTTTTAGCTTC
ACCACCAAGGAGAGAGGTTGACATGACCTCCCCGCCCCCTCACCAAGGCTGGGAACAGAGGGGATGTGGTGAGAG
CCAGGTTCCTCTGGCCCTCTCCAGGGTGTTCCTCACTAGTCACTACTGTCTTCTCCTTGTAAGTCAATCAAT
ATTCTTCCCTTGCTGTGGGCAGTGGAGAGTGCTGCTGGGTGTACGCTGCACCTGCCCACTGAGTTGGGGAAAGA
GGATAATCAGTGAGCACTGTTCTGCTCAGAGCTCCTGATCTACCCACCCCTAGGATCCAGGACTGGGTCAAAG
CTGCATGAAACCAGGCCCTGGCAGCAACCTGGGAATGGCTGGAGGTGGGAGAGAACCTGACTTCTCTTTCCCTCT
CCCTCCTCCAACATTACTGGAACCTCTATCCTGTTAGGATCTTCTGAGCTTGTTTCCCTGCTGGGTGGGACAGAGG
ACAAAGGAGAAGGGAGGGTCTAGAAGAGGCAGCCCTTCTTTGTCTCTGGGGTAAATGAGCTTGACCTAGAGTAA
ATGGAGAGACCAAAAGCCTCTGATTTTTAATTTCCATAAAATGTTAGAAGTATATATATACATATATATATTTCT
TTAAATTTTTGAGTCTTTGATATGTCTAAAAATCCATTCCCTCTGCCCTGAAGCCTGAGTGAGACACATGAAGAA
AACTGTGTTTCATTTAAAGATGTTAATTAAATGATTGAAACTTG

166/6881
FIGURE 156

MVVFVGRRLPALLGLFKKKGSAKAENDKHL SVGPGQGPGSAVDEHQDNVFFPSGRPPHLEELHTQAQEGLRSLQH
QEKQKLNKGGWDHGDTSIQSSRTGPDENISFCSQTTSYVAESSTAEDALSIRSEMIQRKGSTFRPHDSFPKSG
KSGRRRRERRRSTVLGLPQHVKELGLRNEREAPGTPRAPGARDAVRIPTVDGRPRGTSGMGARVSLQALEAEAEA
GAETEAMLQRHIDRVYRDDTFVGRSTGTRAPPLTRPMSLAVPGLTGGAGPAEPLSPAMSI SPQATYLSKLIPHAV
LPPTVDVVALGRCSLRTL SRC SLHSASPASVRSLGRFSSVSSPQPRSRHPSSSSDTWSHSQSSDTIVSDGSTLSS
KGGSEGQPESSSTASNSVPPPPQGGSGRGSPSGGSTAEASDTLSIRSSGQLSGRSVSLRKLKRPPPPPRRTHSLHQ
RGLAVPDGPLGLPPKPERKQQPQLPRPPTTGGSEGAGAAPCPNPANSWVPGLSPGGSRRPPRSPERTLSPSSGY
SSQSGTPTLPPKGLAGPPASPGKAQPPKPERVTSLRSPGASVSSSLTSLCSSSSDPAPSDRSGPQILTPLGDRFV
IPPHPKVPAPFSPPPSKPRSPNPAAPALAAPAVVPGFVSTTDASPQSPPTPQTTLTPLQESPVISKDQSPPPSP
PSYHPPPPPTKKPEVVVEAPSASETAEELQDPNWPPPPPPAPEEQDLSMADFPPPEEAFFSVASPEPAGPSGSP
ELVSSPAASSSSATALQIQPPGSPDPPPPAPPAPAPASSAPGHVAKLPQKEPVGCSKGGGPPREDVGAPLVTPSL
QMVRLRSVGAPGGAPTPALGPSAPQKPLRRALSGRASVPAPSSGLHAAVRLKACSLAASEGLSSAQPNGPPEAE
PRPPQSPASTASFIFSKGSRKLQLERPVS PETQADLQRNLVAELRSISEQRPPQAPKKSPKAPPPVARKPSVGVP
PPASPSYPRAEPLTAPPTNGLPHTQDRTKRELAENGGVLQLVGPEEKMGLPGSDSQKELA

167/6881
FIGURE 157

ATGGGGGACGCTCCCAGCCCTGAAGAGAACTGCACCTTATCACCCGGAACCTGCAGGAGGTTCTGGGGGAAGAG
AAGCTGAAGGAGATACTGAAGGAGCGGGAACCTTAAATTTACTGGGGAACGGCAACCACGGGCAAACCATGTG
GCTTACTTTGTGCCCATGTCAAAGATTGCAGACTTCTTAAAGGCAGGGTGTGAGGTAACAATTCTGTTTGGCGAC
CTCCACGCATACCTGGATAACATGAAAGCCCCATGGGAACCTCTAGAACTCCGAGTCAGTTACTATGAGAATGTG
ATCAAAGCAATGCTGGAGAGCATTGGTGTGCCCTTGGAGAAGCTCAAGTTCATCAAAGGCACTGATTACCAGCTC
AGCAAAGAGTACACACTAGATGTGTACAGACTCTCTCCGTGGTTCACACAGCACGATTCCAAGAAGGCTGGAGCT
GAGGTGGTAAAGCAGGTGGAGCACCCCTTTGCTGAGTGGCTCTTATACCCCGGACTGCAGGCTTTGGATGAAGAG
TATTTAAAGTAGATGCCCAATTTGGAGGCATTGATCAGAGAAAAGATTTTCACCTTTGCAGAGAAGTACCTCCCT
GCACTTGGCTATTCAAAACGGGTCCATCTGATGAATCCTATGGTTCCAGGATTAACAGGCAGCAAAATGAGCTCT
TCAGAAGAGGAGTCCAAGATTGATCTCCTTGATCGGAAGGAGGATGTGAAGAAAAAACTGAAGAAGGCCTTCTGT
GAGCCAGGAAATGTGGAGAACAAATGGGGTTCTGTCTTCATCAAGCATGTCTTTTTTCCCCTTAAGTCCGAGTTT
GTGATCCTACGAGATGAGAAATGGGGTGGAAACAAAACCTACACAGCTTACGTGGACCTGGAAAAGGACTTTGCT
GCTGAGGTTGTACATCCTGGAGACCTGAAGAATTCTGTTGAAGTCGCACTGAACAAGTTGCTGGATCCAATCCGG
GAAAAGTTTAATACCCCTGCCCTGAAAAAACTGGCCAGCGCTGCCTACCCAGATCCCTCAAAGCAGAAGCCAATG
GCCAAAGGCCCTGCCAAGAATTCAGAACCAGAGGAGGTCATCCCATCCCGGCTGGATATCCGTGTGGGGAAAATC
ATCACTGTGGAGAAGCACCCAGATGCAGACAGCCTGTATGTAGAGAAGATTGACGTGGGGGAAGCTGAACCACGG
ACTGTGGTGAGCGGCCTGGTACAGTTCGTGCCCAAGGAGGAAGTGCAGGACAGGCTGGTAGTGGTGTGTGCAAC
CTGAAACCCGAGAAGATGAGAGGAGTCGAGTCCCAAGGCATGCTTCTGTGTGCTTCTATAGAAGGGATAAACCGC
CAGGTTGAACCTCTGGACCCCTCCGGCAGGCTCTGCTCCTGGTGAGCACGTGTTTGTGAAGGGCTATGAAAAGGGC
CAACCAGATGAGGAGCTCAAGCCCAAGAAGAAAGTCTTCGAGAAGTTGCAGGCTGACTTCAAATTTCTGAGGAG
TGCATCGCACAGTGGAAGCAAACCAACTTCATGACCAAGCTGGGCTCCATTCCTGTAAATCGCTGAAAGGGGGG
AACATTAGCTTAGCCAGCCCAGCATCTTCCCCCTTCTTCCACCACTGAGTCATCTGCTGTCTCTTCAGTCTGCTC
CATCCATCACCCATTTACCCATCTCTCAGGACA

168/6881
FIGURE 158

MGDAPSPEEKLHLITRNLQEVLGEEKLKEILKERELKIYWGTTGKPHVAYFVPMSKIADFLKAGCEVTILFAD
LHAYLDNMKAPWELLELRVSYENVIKAMLESIGVPLEKLKFIKGTDYQLSKEYTLDVYRLSSVVTQHDSKKAGA
EVVKQVEHPLLSGLLYPGLQALDEEYLVKVD AQFGGIDQRKIFTFAEKYLPALGYSKRVHLMNPMVPGLTGSKMSS
SEEESKIDLLDRKEDVKKKLKKAFCPEPGNVENNGVLSFIKHVLFPLKSEFVILRDEKWGGNKITYTAYVDLEKDFA
AEVVHPGDLKNSVEVALNKLLDPIREKFNTPALKKLASAAYPDPSKQKPMAGPAKNSEPEEVIPSRLDIRVGKI
ITVEKHDPDADSLYVEKIDVGEAEPRTVVSGLVQFVPKEELQDRLVVVL CNLKPQKMRGVESQGMLLCASIEGINR
QVEPLDPPAGSAPGEHV FVKGYEKGQPDEELKPKKKVFEKLQADFKISEECIAQWKQT NFMTKLGSISCKSLKGG
NIS

169/6881
FIGURE 159

GCGCGAGCAAGATGGCCACCACCAAGCGCTCTTGTACGTGGGTGGACTGGCAGAGGAAGTGGACGACAAAGTTC
TTCATGCTGCGTTCATTCCCTTTTGGAGACATCACAGATATTCAGATTCCCTCTGGATTATGAAACAGAAAAGCACC
GAGGATTTGCTTTTGTGAATTTGAGTTGGCAGAGGATGCTGCAGCAGCTATCGACAACATGAATGAATCTGAGC
TTTTTGGACGTACAATTCGTGTCAATTTGGCCAAACCAATGAGAATTAAGGAAGGCTCTTCCAGGCCAGTTTGGT
CAGATGATGACTGGTTGAAGAAGTTTTCTGGGAAGACGCTTGAAGAGAATAAAGAGGAAGAAGGGTCAGAGCCTC
CCAAAGCAGAGACCCAGGAGGGAGAGCCCATTTGCTAAAAAGGCCCGCTCAAATCCTCAGGTGTACATGGACATCA
AGATTGGGAACAAGCCGGCTGGCCGCATCCAGATGCTCCTGCGTTCTGATGTCGTGCCCATGACAGCAGAGAATT
TCCGCTGCCTGTGCACTCATGAAAAGGGCTTTGGCTTTAAGGGAAGCAGCTTCCACCGCATCATCCCCCAGTTCA
TGTGCCAGGGCGGTGATTTACAAAACCACAATGGCACTGGGGGCAAGTCCATCTATGGGAAGAAGTTCGATGATG
AAAACTTTATCCTCAAGCATACGGGACCAGGTCTACTATCCATGGCCAACCTCTGGCCCAAACACCAATGGCTCTC
AGTTCTTCCTGACATGTGACAAGACAGACTGGCTGGATGGCAAGCATGTGGTGTGTTGGAGAGGTCACCGAAGGCC
TAGATGTCTTGCGGCAAATTGAGGCCCAGGGCAGCAAGGACGGGAAGCCAAAGCAGAAGGTGATCATCGCCGACT
GTGGGGAGTACGTGTGAGGCGGCACTCTCTCTGCTTCCCCCTCCGCTCTTGACCCTGCATATCCAGGAAGGAAC
GCCAGCCTCAGAGGAGGCAGCACCGAGGGTGCCTGTTTGAAGCAAGCAGCATTTGGGATATGTGCCCTTCCTCAG
GGTCTGCTTGGAGCAGCTCCTCTGCAGGCACAGCCTGGACTATTCCCAGGCACAGCTGTGGGCCCAGGAGCCAGC
TCAGGTGCTCCCCCTCCACCATGGGCAGGCTGTGCAAAAAGCCACTGGCTTTTCTCAGCATTTGCTGCTGGGCCT
CTCCTGGGACTACCAGTGTGGCTCTTACGTGTTTTCTTTGCTAAAATAAACCTAGTTCTTATATTAATAAAAAA
AAAAA

170/6881
FIGURE 160

MATTKRVLYVGGLAEEVDDKVLHAAFIPFGDITDIQIPLDYETEKHRGFAFVEFELAEDAAAAIDNMNESELFGR
TIRVNLAKPMRIKEGSSRPVWSDDDWLKKFSGKTLEENKEEEGSEPPKAETQEGEPIAKKARSNPQVYMDIKIGN
KPAGRIQMLLRSDVVPMTAENFRCLCTHEKGF GFKGSSFHRIIPQFMCQGGDFTNHNGTGGKSIYGKKFDDENFI
LKHTGPGLLSMANS GPNTNGSQFFLTCDKTDWLDGKHVVFGEVTEGLDVLRQIEAQGSKDGKPKQKVI IADCGEY
V

171/6881
FIGURE 161

TCAAAGCACCTGCAGCCCCAATTTGTGATCCAGCAGCAGCCACAGCCACAACAGCAGCAGCCGCCGCCCCAGCAG
TCACGGCCTGTGCTCCAAGCTGAGCCCCACCCCAGCTCGCCTCAGTCTCTCCAAGCGTGGCCCTCCAGCCCAGC
TCAGAGGCCCATGCC**ATG**CCACTAGGCCCGGTTACACCCGCCCTGCCACTCCAGTGTCCCACTGCCAACCTGCAC
AAGCCTGGCGGCAGTCAGCAGTGTACCCCTCCACACCTGATACTGGGCCTCAGAATGGACATCCCAGGGCGTG
CCCCACACCCCTCAACGCAGGTTCCAGCACACTTCAGCTGTCTATTACAACCTGCAGCCTGCTTCACCACTGCCC
CAGCAGTGTGTCCCTGATGACTGGAAAGAGTGGCACCAGGGGAGAAAAGTGTGCCTGAGACGCGGTCTGGCCCA
TCACCACATCAGCAGGCTATTGTCACTGCCATGCCCTGGTGGCCTGCCTGTACCCACGAGCCCTAACATCCAGCCG
TCCCCAGCTCACGAGACAGGGCAGGGCATTGTTTCATGCACTGACCGACCTCAGCAGCCCCGGCATGACCTCAGGG
AACGGAACTCTGCCTCCAGCATCGCCGGCACTGCCCCCCAGAATGGTGAGAATAAACACCACAGGCCATTGTG
AAACCCCAAATCCTGACGCATGTTATCGAAGGGTTTGTGATCCAGGAGGGGGCGGAGCCTTTCCCGGTGGGACGC
TCGTCCCTGCTGGTGGGGAATCTCAAGAAGAAGTATGCACAGGGGTTCTGCCTGAGAACTTCCACAGCAGGAT
CACACCACCACCACTGACTCGGAGATGGAGGAGCCCTATCTGCAAGAATCCAAAGAGGAGGGTGTCTCCCTCAA
CTCAAGTGTGAGCTCTGTGGCCGGGTGGACTTTGCCTATAAGTTCAAGCGTTCCAAGCGCTTCTGTTCCATGGCT
TGTGCAAAGAGGTACAACGTGGGATGCACCAAACGGGTGGGACTTTTCCACTCAGACCGGAGCAAGCTGCAGAAG
GCAGGAGCTGCGACCCACAACCGCCGTCGGGCCAGCAAAGCCAGTCTGCCACCACTTACCAAGGATACCAAGAAG
CAGCCAACAGGCACTGTGCCCCCTTTCGGTTACTGCTGCTTTGCAGCTAACACACAGCCAGGAAGACTCCAGCCGT
TGCTCAGATAACTCAAGCTATGAGGAACCTTGTACCCATCTCAGCCAGCTCATCTACTTCCCGCCGGCGACAA
GGCCAGCGGGACCTGGAGCTCCCCGACATGCATATGCGGGACCTGGTGGGCATGGGACACCATTCTGCCAAGT
GAGCCCACCAAGTGAATGTAGAAGACGTCTACGAATTCATCCGCTCTCTGCCAGGCTGCCAGGAGATAGCAGAG
GAATTCCGTGCCCAGGAAATCGACGGGCAAGCCCTGCTGCTGCTCAAGGAGGACCACCTGATGAGCGCCATGAAC
ATCAAGCTGGGGCCCGCCCTGAAGATCTACGCCCGCATCAGCATGCTCAAGGACTCC**TAG**GGCTGGTGGCAGCCA
GGATTCTGGCCCAGGGCGCCTCCTCCCGACTGAGCAGAGCCAGACAGACATTCTGAGGGGCCAGAAATGGGGC
CGGTTGGAGGGCAGGGGCTCTCCCTAGGGGCATAGCTGGTGAGGAGGTCTGGGCACCTCCTCCATGGCTCTCAGG
CGCCTTTCATTTCTGTGGGAGGGGCAGAGAGGTAGGTGGCACAGAAGATGGGGCTTTATGCTTGTAATATTGAT
AGCACTGGCTTCCTCCAAAGTCCCAATACTCTAGCCCCGCTCTCTTCCCCTCTTCTGTCCCCCATTTTCCAGGG
GGTATATGGTCAGGGCTCCCCAACCTGAGTTGGGTTACTTCAAGGGCAGCCAGCAGGCCTGGATGGAGGCCTAGA
AAGCCCTTGCCTTCCTTCCCTCCCACTTCTTTCTCCAGGCCTGGTTAACTCTTCCGTTGTCAGCTTCTCCCCCTT
AGCCTGTTTCTGCAGCAGCCAGGGTTCTCCCCCTACACCCTCTGCAGGTGGAGAGAGAGAAGCTGGGGCCAGCC
GGGCCGTGCCTGCTGGCACAGACGCCCTTAACGCTGTGTGATGACTGTGTGACTGTGTGGGAGCCTGGACTGACA
GATAGGCCAAGGGCTACTCTCTGGCATCTCCAGGTGTTTTGTAGCAAACAGCCACTTAGTGCTTTGTCTGGACT
CCACTCAGCCTCAGGATGGGGAATAGCCAAGAATGGCAGCCTCAGCGCAGAGGCAAGGTGAGAAAGAGACGGCGC
TTCAGAGTTTCTTTCCAGACACCCCTCCCGCACTGTGAAGTTCCCCTGACCGCCCTCCTGGTTACAAAGAGC
ATTAAGAAAGCTGCGGTGGTCTGAGCAACATAGCCCAAAGGGCTGAGCCTCTGGCCTGCCTGCCCGCCACCCCT
GGGAGTCCCAGTGGTGAGGCTCAGAGAACTGCTAAGGGGAAAGAACAGCTGGAGTTTCTGTTGATGTGAAGAAGG
CAGCTCTTGGCCTCCCACTCCACACTTCTTTGCCTATAAATCTTCTAGCAGCAATTTGAGCTACCTGAGGAGG
AGGCAGGGCAGAAAGGGCGAGGGCCTGCCTCTGACCTGCCGTGTCTTTGCAGGAAGGAGGTAGGCACCTTTCTG
AGCTTATTCTATTCCCCACCCACACCCCCAGGCAGGGTTGGAAATGAAGGACTTTTTTAACCTTTGTTTTGTTTT
TTAAAAATAAATCTGTAAATCTG

172/6881
FIGURE 162

MPLGPVTPALPLQCPTANLHKPGGSQQCHPPTPDTGPNQGHPEGVPHTPQRRFQHTSAVILQLQPASPVPQQCVF
DDWKEVAPGEKSVPETRSGPSPHQQAIVTAMPGGLPVPTSPNIQPSPAHEGTGGIVHALTDLSSPGMTSGNGNSA
SSIAGTAPQNGENKPPQAIVKPQILTHVIEGFVIEGAEPFPVGRSSLLVGNLKKKYAQGFLEKLPQQDHTTTT
DSEMEEPYLQESKEEGAPLKLKCELCGRVDFAYKFKRSKRFCSMACAKRYNVGCTKRVGLFHSDRSKLQKAGAAAT
HNRRRASKASLPPLTKDTKKQPTGTVPLSVTAALQLTHSQEDSSRCSNDSYEEPLSPISASSSTSRRRQGGQDRL
ELPDMHMRDLVGMGHHFLPSEPTKWNVEDVYEFIRSLPGCQEIAEEFRAQEIDGQALLLLKEDHLMSAMNIKLGP
ALKIYARISMLKDS

173/6881
FIGURE 163

AGACAAGGCAAATTTAAGTAGGCTCATGGGCTTTTCCAGTTGGGTTGGAAAGTTCCTCTCCGATGACTGTTATATT
CTCAAAGAAATATGAGGAGAGGGGCAGGGCATGGTGGCTCACATCCGTAATCCTAGCAAATCATAGTGGCCTACA
GCCAACGCCTTCTTCGCTCACTGGCCAACCTGGAACTTCAGTCCCCCATGCCTCCCGCCTCTCACCCAGGGGCC
AATAGGAATGATCAGAGGTTTCGCAACTTAGTGTTCATCAAGCATAGTAATTGCAATTGGCTATTGGAGCTGTCGAT
CGTGGAGTAGGCGGGGCCGTGCCAGCTGGCCTATATAAGACGAGGACAAAGGCGGCGCGCCGCCTGTGTTCATCCG
CCATTTTGTGAGAAGCAAGGTGGCCTCCACGTTTCTGAGCGTCTTCTTCGCTTTTGCCTCGACCGCCCTTGAC
CACAGACATGTCTCGGGATCGGTTCCGGAGTCGTGGCGGTGGCGGTGGTGGCTTCCACAGGCGTGGAGGAGGCGG
CGGCCGCGGCGGCCTCCACGACTTCCGTTCTCCGCCGCCCGGCATGGGCCTCAATCAGAATCGCGGCCAGGCCCG
ACTCCGACCCCGCCGCCTGCAGTCACCTCGGCCCCCTCCCGGGGCGCCGCCACCCACCCCGCCAAGCAGCGGGGTC
CCTACCACACCTCCTCAGGCCGGAGGCCCGCCGCCTCCGCCCGCGGCAGTCCCGGGCCCGGGTCCAGGGCCTAAG
CAGGGCCCAAGTCCGGGTGGTCCCAAAGGCGGCAAAATGCCTGGCGGGCCGAAGCCAGGTGGCGGCCCGGGCCTA
AGTACGCTTGGCGGCCACCCCAAGCCGCCGCATCGAGGCGGCGGGGAGCCCCGCGGGGGCCGCCAGCACCACCCG
CCCTACCACCAGCAGCATCACCAGGGGCCCCCGCCCGGCGGGCCCGGCGGCCGAGCGAGGAGAAGATCTCGGAC
TCGGAG

174/6881
FIGURE 164

MAFPVGLESSSPMTVIFSKKYEERGRAWWLTSVILANHSGLOPTPSSLTGQLETSPVPCLPPLTQGPIMGIRGSQ
LSVIKHSNCNWLLELSIVE

175/6881
FIGURE 165

GGCGAGCAGTCTGCGCGCGGATGGCCGCAGCGGCGATGGCGGCAGCGGCAGGTGGAGGGGCTGGCGCGGCCCGCT
CCCTCTCGCGCTTCCGAGGCTGCCTGGCTGGTGCGCTGCTCGGGGACTGCGTGGGCTCCTTCTACGAGGCCACG
ACACCGTCGACCTGACGTCAGTCCTGCGTCATGTCCAGAGTCTGGAGCCGGACCCCGGCACGCCCGGGAGTGAGC
GGACAGAAAGCCTTGTACTACACAGATGACACAGCCATGGCCAGGGCCCTGGTGCACTCCCTGCTAGCCAAGGAGG
CCTTTGACGAGGTGGACATGGCTCACAGATTTGCTCAGGAGTACAAGAAAGACCCTGACAGGGGCTATGGTGCTG
GAGTAGTCACTGTCTTCAAGAAGCTCCTGAACCCCAAATGTCGCGATGTCTTTGAGCCTGCCCGGGCCAGTTTA
ACGGGAAAGGCTCCTATGGCAATGGAGGTGCCATGCGGGTGGCTGGCATCTCCCTGGCCTATAGCAGTGTCCAGG
ATGTGCAGAAAGTTTGCCCGGCTCTCGGCCAGCTGACACACGCCTCCTCCCTGGGTTACAATGGCGCCATCCTGC
AGGCCCTGGCTGTGCACCTGGCCTTGAGGGCGAGTCTTCCAGCGAGCACTTTCTCAAGCAACTCCTGGGCCACA
TGGAGGATCTGGAGGGTGATGCCAGTCCGTCTTGATGCCAGGGAGTTGGGCATGGAGGAGCGTCCATACTCCA
GCCGCCTGAAGAAGATTGGAGAGCTTCTAGACCAGGCATCGGTGACCAGGGAGGAAGTGGTGTCTGAGCTAGGGA
ATGGCATTGCTGCCTTTGAGTCGGTACCCACCGCCATCTACTGCTTCCTACGCTGCATGGAGCCAGACCCTGAGA
TCCCTTCTGCCTTCAATAGCCTCAAAGGACTCTCATTTATTCCATCTCACTTGGTGGGGACACAGACACCATTG
CCACCATGGCTGGGGCCATTGCTGGTGCCTACTATGGGATGGATCAGGTGCCAGAGAGCTGGCAGCAAAGCTGTG
AAGGCTACGAGGAGACAGACATCCTGGCCCAAAGCCTGCACCGTGTCTTCCAGAAGAGTTGATGAGGGCTACAGC
TGTTGGGGCTCTGCCAGGTCCCCTGGGACCAACTACAGCTCCAATCAGAAACCCTGCGCTTCCTTGAGTGTGGCT
TCCCACTTTTCTGCAATTGTGGAGCTGACTGAGTACACCGGTGAGGCTGGGGTCTCTGCAGGGGAGGTCAGTGA
ACAGCGAGCAAGGGACTGGTGCCTCGCTGGTGCTGGGTCTCTGGTTTGCTGCAGAGCCGTAGGACACTCCTGGCT
CCTCAGTAGGACAGACAGACGCAGGCGGGTTTATTTGGAGGGGTACTTGTGGCATTTTCTGTATTGTCTTGGA
CATGGGATGTGGGGAGGTGGAAATGATGAGCAGTAGCATCATTTCTCCCTGTTGGGTTTTAGCCAGTTTGCCAGC
AAGCGCATCCTAGCAGGGTCCCCGAGCAGCAGGTTGTGTGGATGAAGGGACAGGCACTTGCATCCAGCTGATCTA
GGTCACACCTGGCTCTTGGCTGCCATGTGGCTTATTAACAGCTTCCAGTGGAAGTCGCAATAAACAGTTTTTGGT
AAATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

176/6881
FIGURE 166

MAAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDTVDLTSVLRHVQSLEPDPGTPGSERTEALYY
TDDTAMARALVQSLLAKEAFDEVDMHRFAQEYKKDPDRGYGAGVTVFKKLLNPKCRDVFEPARAQFNGKGSYG
NGGAMRVAGISLAYSSVQDVQKFARLSAQLTHASSLGYNAILQALAVHLALQGESSSEHFLKQLLGHMEDLEGD
AQSVLDARELGMEERPYSRLKKIGELLDQASVTREEVVSELGNGIAAFESVPTAIYCFLRCMEPDPEIPSAFNS
LQRTLIYSISLGGDDTDIATMAGAIAGAYYGMDQVPESWQQSCEGYEETDILAQSLHRVFQKS

177/6881
FIGURE 167

CCGTGGCTAGGCGAGTGGGGCGGGCGGCCGGCACCATGTCGAGGCAGGCGAACCGTGGCACCGAGAGCAAGAAA
ATGAGCTCTGAGCTCTTCACCCTGACCTATGGTGCCCTGGTCACCCAGCTATGTAAGGACTATGAAAAATGATGAA
GATGTGAATAAACAGCTGGACAAAATGGGCTTTAACATTGGAGTCCGGCTGATTGAAGATTTCCTTGGCTCGGTCA
AATGTTGGGAGGTGCCATGACTTTTCGGGAAACTGCGGATGTCATTGCCAAGGTGGCGTTCAAGATGTACTTGGGC
ATCACTCCAAGCATTACTAATTGGAGCCCAGCTGGTGATGAATTCTCCCTCATTTTGGAAAATAACCCCTTGGTG
GACTTTGTGGAACCTTCCTGATAACCACTCATCCCTTATTTATTCCAATCTCTTGTGTGGGGTGTTCGCGGGAGCT
TTGGAGATGGTCCAGATGGCTGTGGAGGCCAAGTTTGTCCAGGACACCCTGAAAGGAGACGGTGTGACAGAAATC
CGGATGAGATTTCATCAGGCGGATTGAGGACAATCTTCAGCTGGAGAGGAATTAACCATCCCTACAACCTCGAGGAT
AGCCATCAGGAGCACTGTTGGAATCAGCAGGCCTCTGTGCTCCCTCTGCCCTCCAGAACTCAGTGACTCTTGAAC
ATGGATGTTATATATTCTTATAACCTGTTTCCATTCTCCATTCAAATAAAGAGCAGACTGCGATATAGTCCATTT
ACCCCATGTGTGCACATTGAGGAGCGACAGTCTCTGCCCCCATTCCCTTGAGAGGGGGCTGGATGTAATCACCTTT
GGTTGGACTAGAAAGAGCTCAAACCATTTTACATTCCCTGTTTGAATTTTCCAAAGCAAACTCACTTTGACCCCA
TTAAGAGGCAAGCCTGGCACATCTATCCCTGGGCCTTTAGAAAGCCATTTGCCTCAAATGGCTATAGGGTTGTGG
GGTGGAGGGAGGAAGGGCTGGGAGGGAGTGGGGAGGAATTGCTAGCTGTAGTGTGACACATTGTAGTGTGTTGCCA
GGAAAGGAGCCAGTCATGCCGGAACACTGACTTCTGGGAAGCCACCCAGGTCTCATTCCCTCCCTGCTGTTGGAG
GCAACATCTCCTCTTTTTTACAGAGGGTACATCCTTTTTTCTTACAAATTCTTCAATAAAGACACATTCTTGAGTG
AAATCCCTAAAAA

178/6881
FIGURE 168

MSRQANRGTESKKMSSELFTLTYGALVTQLCKDYENDEDVNKQLDKMGFNIGVRLIEDFLARSNVGRCHDFRETA
DVIKVAFKMYLGITPSITNWSPAGDEFSLILENNPLVDFVELPDNHSSLIYSNLLCGVLRGALEMVQMAVEAKF
VQDTLKGDGVTEIRMRFIRRIEDNLPAGEE

179/6881
FIGURE 169A

ACTTACTATTGGAGGCAGTGGGCAGCGCAGGACAGGCCAGGGCCGCCGACCCTGGCAATGACTGTCACCAGCTG
GAGGGAAGAGCTGAGAATGAAGCGGAGAGCATCAGACAGAGGAGCTGGGGAACGTCGGCCAGGGCCAAGGCTCT
AGGAAGTGGGATTTCTGGAAATAATGCAAAGAGAGCTGGACCATTTCATCCTTGGTCCCCGTCTGGGCAACTCACC
GGTGCCAAGCATAGTGCAGTGTGTTGGCGAGGAAAGATGGCACGGATGACTTCTATCAGCTGAAGATCCTGACCCT
GGAGGAGAGGGGGGACCAAGGCATAGAGAGCCAGGAAGAGCGGCAGGGCAAGATGCTGCTGCACACCCAGTACTC
ACTGCTGTCTCTCCTGCACACGCAGGATGGCGTGGTGCACCACCACGGCCTCTTCCAGGACCGCACCTGTGAAAT
CGTTGAGGACACAGAATCCAGCCGGATGGTTAAGAAGATGAAGAAGCGCATCTGCCTCGTCTGGACTGCCTCTG
TGCTCATGACTTCAGCGATAAGACCGCTGACCTCATCAACCTGCAGCACTACGTTCATCAAGGAGAAGAGGCTCAG
CGAGAGGGGAGACTGTGGTAATCTTCTACGACGTGGTCCGCGTGGTGGAGGCCCTGCACCAGAAAAATATCGTGCA
CAGAGACCTGAAGCTGGGGAACATGGTGCTCAACAAGAGGACACATCGGATAACCATCACCAACTTCTGCCTCGG
GAAGCATCTGGTGAGCGAGGGGGACCTGCTGAAGGACCAGAGAGGGAGCCCTGCCTACATCAGTCCCGACGTGCT
CAGCGGCCGGCCGTACCGTGGCAAGCCCAGTGACATGTGGGCCCTGGGCGTGGTGTCTTTCACCATGCTGTATGG
CCAGTTCCCCTTCTACGACAGCATCCCGCAGGAGCTCTTCCGCAAGATCAAGGCTGCCGAGTATACCATTCCTGA
GGATGGACGGGTTTCTGAGAACACCGTGTGTCTCATCCGGAAGCTGCTGGTCTTTGACCCCCAGCAGCGCCTGGC
CGCCGCCGACGTCTGGAGGCCCTCAGTGCCATCATTGCATCATGGCAGTCCCTGTCTCTGAGTGGGCCCTTT
GCAAGTGGTTCTTGACATTGATGACCAAATGAGCAATGCGGATAGCTCCCAGGAGGTGAGTTGGGGAGGGCAGAT
GGGCCATTACCCAGCCCCAAGGGACAGGCTTCTGGGGGCAGGCAGGGCAAGGGCAGAGGTGGCAGCTACCCGCAG
GCCACAGAGTTTCTTGGTCTTCTTCCCCAGCCTTGGGGTGGGAAAGGGAGACTTCAGTCTCAGCCTGAGCTGC
CTGGGGCCTGCCTTGGGCTTGGTGTAGCTGGAGATCTTTGGCCAGAGAGACCTGTGAGACAGCCGAGCTGGAGCC
AGTGCCCCAAGTGGCCCAGGCCAGCCCTCTCAGCTTCCCTCCTGCTGCCCAAGTCACATTTCTCTGCCCCCTGACTC
AGAGTTCTCTCTCACCTTTCCTGCTTTTTTCAATTTTTCAGATGATTCAATTTCTCCCTATTTCTTTCTCCCCATTCC
CTGCACTGGAGAAAGTGTTGGGCCTAGGGTGGGGGCAGAGACTTGGGCACCAGGCAGCAGAGGGCAGGTGATCTT
AGGGTGGCCCCCTGGAGGGCAGGGCTTGGCCGAGCAACAGCATTGCTGGGCCCTGGATATTGGAAGGACCTTCCCT
CCCTGGCCCCACCTTGGAGCTCCACAGTGAGCAGTGTGCAGGTAGGACCAGGAGGGGCGTGCCTGGGAGAGCCTC
CCAGAGCCTCCTGGCCCCCGAGGAAAGAGAGTTCCAATCCCTACCCACCTCCAGCTTCCACCCCTTtagctgtttg
GCTAAATCATCATCACTAGCCCGCAGTGAGTGCCTACCCGAGGGCACCTCATTAGCCCTCACTGCGGGCCTG
CGTGGCCTGTGTTCTTAGCCCCATGTTACAGAAGAGGAAACAGGGTTAGAGAGGACTTTCCCAAAGCCACACAGC
TTAGAAGTAGTGGAGCTAAGCCTTGAACCCAAGTCTCATCCGGAAGCCCTGCTGTCTCCTGTGGTGAAGTGCACG
GGGACACCACTTCAGCTTCTGTTACCATCTGCCTAGACCATCCAGGGAGCTCAGCATGGGGCCCTGCGTATGTG
GCTCCTCCAGGTGCTGCGCCCCCAGCCCAGGGCTTGTCTGTACCTCTTGACGTGCATTAGCCGCTCAGGGCTCA
GAGAACCTTTGCGAGGGGCCAGACAGCTAAGGCTTCTGAGGTAAAGTGACCTCTCACGCAGCCAGTGAGTTAGGA
AGCATGAGTCTGCGTCAGTCCCGGGTCCGCAGGGCGGCCTGCAAGGGGAGTTGAGGTTGGCTGGAGGGGGTCAGG
GACCCACCTCAGCGCCACTCCACCCCCGGCCTTGAGGCCTGAGGGTGTGGTGCCTGGAAGGGTGAAGTGCAGGA
GCCAGGCTGCCAGCACTCTTGCTGCTGCTGCTGCGCTGCCTTCATCTGGGTTTATCTTTGTCTCCTTC
CCACCTCCCCGCCTCAAAGGCGAAGGTGACGGAGGAGTGCTCCAGTACGAGTTTGAAGTACATGCGTCAGC
AGCTGCTGCTGGCCGAGGAGAAGAGCTCCATCCATGACGCCCCGAGCTGGGTACCCAAGCGGCAGTTTCGGCAGCG
CACCACCGGTGCGACGGCTGGGCCACGACGCACAGCCCATGACCTCCTTGGACACGGCCATCCTGGCGCAGCGCT
ACCTGCGGAAATAACAGCCTCAGCCGGGGCCACCAGCACTGCTGCCACTTCTTCCAGCCCCAGCCAAAGGCGTG
CTGTACGGGCTGGGCCCTGTAGTGTGCTGACTCTCCCGGGCCACAATAGGGACAGGGCAGGGACAGGGACAGCCCA
GGTCACACGTGGGGTCAGCAGAGGTACCACGAAGCTACCTTTTGGGATGATTGCTCGATTGTTTGGTTTTTAAAT
CTGAGAAGCCTAGATAACTAATCTGCTTTTAAATCACGATGTTTTAATCTACCTCTGTCTCTTTAACCATGCTGTC
TCTGGACTGAGCAAGAGGGAGGAGGGAGCCTGCTCACCCTCCTCAGGGCCTTCCCCAGCGGCCACCACTGACC
TGGGGCGCTGCTCCCCACAGTCCAAATAAGCTGAAAGTGCAGCTCGCTGCAGGCCCCAGAGCGAGCTTCCCCTCC
TCCCTGCTCTCCAGGCCCTGCCACAGCCTCTTCCGTCCCTCTCTTCTGATCCAGGCCCTCAGTCCAAGCT
TTGGAAAACCTTACCTCATCTTAAACCGAACTCAAATATATTTATTTTTTACCATACCAACTTCTCTCCCATC
TCTAGGTGGCTCAGTCCATGGCCACTCCCTGCCCCCAGCCTGGCTGGACAGCAAGGAATCCACAGCCCACACGTG
AGCTCCCTCCTCAGCCCCAGGCAGGGAAGCCCCCTCTGCCAGTCCCTGTCCCCTTTTACGCCCACAGTCCCTCTC
TGCTGCCGGTGATGGGAGGCCCTTCTAGACCTGGCTCTTCTCTCCCGTCTCAGTGGCTTCTCTGAGGTGCTGTA

180/6881

FIGURE 169B

CACGCGCGTTAACCTGTTCCCTTCTCTATCCTTCCCCGTGGTACTGAGCTCACGTGGACTCCCAGTGCGAAGGGG
CCCATGGGTTGGGCTGCAGGCCTGGCCGTGAGCGGGGGCTGCCTGCACGCTCCCCTAGCCTACTCTTGTGTTTAG
GGGATGGTGGGAACATATCCCAGTGCCCTTGCCCTATAATAGATGTGGTGACTCTCCCGGTAGACCCTAGCAAGG
GTCCTCCATGGTGGTGAGGGACTCAGGAGAATTGTAGGGATTGGGGGACCCTGCCTGCCTGGCTTGAGAACAGCC
CTGCTGCCCTTTTGAGCCGAGATTTTGAAGTGGATGCCCCGTCTTGCCAGAAATGCTGTTCTCACCAGAATGCCCC
CTCCCCCTTGCCCTTACTGGACTTGGCCCTGCCTGATGCCAAGCAAAGACCCTTCCCCAGAGGCCTACCCCCATA
TGTCTCAGAGAGGCTGAGTGTCCCCTCCAGGCAGTCATGGGCCCTGAGGCCCTCCTGCCTGGCCCTGCTCCCC
AGTGGGGAGGTGACTGTGTTTCCAGAGTGTGAGCCGCTCTCCTCCCCCTAAAAAGCTGACTCACTGTGAGTGAC
CTTGGGCAAGTTCCCAAACCTCCTTGTGCCTCAGTTTCCCCATCTGGAAAAAATGGGGCCACCTCTTGCCAGCAG
TAGCAGGGCTGCCCACGCCCCTTTCTCCCCATGCCCCATCCAGCACTTGGGCGACTCATGCCTCTGCCTCAGTGG
GCCTGTGGGAGCCTACTGGAGCCCAGCACTTACTCCCCCTGAGCAGCGAGCCTGCGTCTGTCTCAGCTGTCCAGC
GCTGAGGGCCAGGGTCTTGTGCTGTGGGGCTGGGGGATGCCCTCTTTTCTATATTTATTTCATAGAAAGTCTCCT
GCGGGAGCGGAAATGCAGTCCGGCCCTAGGGCTCCCAGCCCTTGACTGTCTCCTGTGAGGGCCTGAAGCTGGGCC
AGGGCCCGTCGCAGCGGAGCCCCCTCTCAGCAGCCCACCGGTCCCTCCAGGCTGCTGCCCCGTGCGTGGTCTTTC
TCCTCCTTTTCAAAGCAATAGCCGCCGGGTCTGCAAAGCCCTGTCAGACAGACTGGGCCCTTCCAAGGTCAAGCC
ATGTGTCTGATGACATTCTTGGTGAAGCAAAGGAGAGGAGGATGGGTGAGCCCTCACTGGGTGTCACACACTGAG
AGAAGTCCTATTGTAAAGAAACGGAAAAAGTCACAAAAAAGTTTGTATAAAGACATATTTTTGTACTACATGGGG
ACTCTTCCTGCATGTCAGCAATAAACTTCTGATCTGG

181/6881
FIGURE 170

MKRRASDRGAGETSARAKALGSGISGNNAKRAGPFILGPRLGNSPVPSIVQCLARKDGTDDFYQLKILTLLEERGD
QGIESQEERQGGKMLLHTEYSLLSLLHTQDGVVHHHGLFQDRTCEIVEDTESSRMVKKMKKRICLVLDCLCAHDFS
DKTADLINLQHYVIKEKRLSERETVVIFYDVVRVVEALHQKNIVHRDLKLGNMVLNKRTHRITITNFC LGKHLVS
EGDLLKDQRGSPAYISPDVLSGRPYRGKPSDMWALGVVLF TMLYGQFPFYDSIPQELFRKIKAAEYTIPEDGRVS
ENTVCLIRKLLVLDPPQRLAAADVLEALSATIASWQSLSSLSGFLQVVPDIDDQMSNADSSQEVSWGGQM GHYPA
PRDRLLGAGRARA EVAATTRPQSFLGLLPQPWGGKGRLQSSA

182/6881
FIGURE 171

ATTGGGACGCTGCGGCCTGGCCTTCAGGCCACTGGCTACCGAACCCCGGGGCTCTTCACCAGTCCAGCTCGTTTC
CAGCACCATGTCGGTGCGGACGCTACCGCTGCTCTTCTTGAACCTTGGGCGGGGAGATGCTTTACATCCTCGACCA
ACGGCTGCGGGCCCAGAACATCCCGGGAGACAAGGCCCGCAAAGTTCTGAATGACATCATCTCCACCATGTTCAA
TAGAAAGTTTATGGAGGAATTATTCAAGCCTCAAGAGCTCTACTCCAAGAAGGCCCTGAGGACTGTCTATGAGCG
CCTGGCTCATGCCTCCATTATGAACTGAACCAGGCCAGCATGGATAAGCTCTATGACCTGATGACCATGGCTTT
CAAATATCAAGTATTGCTGTGTCCCCGACCCAAGGATGTGCTGCTGGTCACTTTCAATCACTTGGATACCATCAA
GGGATTCATCCGAGACTCCCCAACCATCCTGCAGCAAGTGGACGAGACTTTGCGGCAGCTGACAGAAATATATGG
TGGTCTCTCTGCAGGGGAGTTCCAGCTGATCCGGCAGACACTCCTCATCTTCTTCCAAGACCTGCACATCCGAGT
ATCCATGTTTCTAAAGGACAAAGTTTCAAGATAATAACGGTCGCTTTGTGTTGCCGGTGTCCGGGCCTGTTCTTG
GGAACTGAAGTTCCAGGACTCATCAGAATGTTCAACAACAAAGGTGAAGAAGTGAAGAGGATAGAATTCAAGCA
TGGTGGAACTATGTCCCTGCACCCAAAGAAGGTTCTTTTGAACCTTATGGAGACCGAGTCTGAACTGGGAAC
TAACATGTACAGCGTGAATCAGCCTGTGGAACTCATGTGTCTGGATCATCAAAGAACTTAGCCTCATGGACCCA
GGAAAGCATTGCTCCAAACCCTCTTGCTAAAGAAGAGCTGAATTTCTTGGCCAGGCTGATGGGAGGGATGGAGAT
TAAGAAACCCAGTGGCCCTGAGCCCAGATTCCGGTTGAATCTCTTTACCACCGATGAAGAAGAGGAACAAGCAGC
GCTAACCAGGCCAGAAGAGTTATCCTATGAAGTTATCAACATACAAGCCACCCAGTCTCTTTTCAGCAATCTGGC
CACCATTGAGGGGGCCTGACTGGGTGACAGATGAATGGGAAGGTTCTGACCTGTTTTGAGTCCGGCTCCACCT
TGCTGTACATATCAGAATGTCACTGCTCTGAGTGTGTCCCAGGGCCTTGGAGGTGGGCCGTGAGGTGCCGAGAA
GCAGCCGCAGCCTCCTCCCTCCACCTATCCAGAGCGATGCTGGTGATTTCAAACGTATCTGTCTATCAGTAAA
TAAACAAGATGCAGATCTCTGGT

183/6881
FIGURE 172

MSVRTLP LLFLNLGGEMLYILDQRLRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALRTVYERLA
HASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVLLVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGL
SAGEFQLIRQTLLIFFQDLHIRVSMFLKDKVQNNNGREFVLPVSGPVPWGTEVPGLIRMFNNKGEEVKRIEFKHGG
NYVPAPKEGSFELYGDRVLKLGTMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNFLARLMGGMEIKK
PSGPEPGFRLNLFTTDEEEEAALTRPEELSYEVINIQTQSLFSNLATIQQGLTG

184/6881
FIGURE 173

GAAGCTGGACTGCAGCTGGTTTTCAGGAACTTCTCTTGACGAGAAGAGAGACCAAGGAGGCCAAGCAGGGGCTGGG
CCAGAGGTGCCAACATGGGGAACTGAGGCTCGGCTCGGAAAGGTGAAGTAACTTGTCCAAGATCACAAAGCTGG
TGAACATCAAGTTGGTGCT**ATG**GCAAGGCTGGGAACTGCAGCCTGACTTGGGCTGCCCTGATCATCCTGCTGCT
CCCCGGAAGTCTGGAGGAGTGCGGGCACATCAGTGTCTCAGCCCCATCGTCCACCTGGGGGATCCCATCACAGC
CTCCTGCATCATCAAGCAGAACTGCAGCCATCTGGACCCGGAGCCACAGATTCTGTGGAGACTGGGAGCAGAGCT
TCAGCCCCGGGGCAGGCAGCAGCGTCTGTCTGATGGGACCCAGGAATCTATCATCACCTGCCCCACCTCAACCA
CACTCAGGCCTTTCTCTCCTGCTGCCTGAACTGGGGCAACAGCCTGCAGATCCTGGACCAGGTTGAGCTGCGCGC
AGGCTACCCCTCCAGCCATACCCCACAACCTCTCCTGCCTCATGAACCTCACAACCAGCAGCCTCATCTGCCAGTG
GGAGCCAGGACCTGAGACCCACCTACCCACCAGCTTCACTCTGAAGAGTTTCAAGAGCCGGGGCAACTGTCTAGAC
CCAAGGGGACTCCATCCTGGACTGCGTGCCCAAGGACGGGCAGAGCCACTGCTGCATCCACGCAAACACCTGCT
GTTGTACCAGAATATGGGCATCTGGGTGCAGGCAGAGAATGCGCTGGGGACCAAGCATGTCCCCACAACCTGTGTCT
TGATCCCATGGATGTTGTGAAACTGGAGCCCCCATGCTGCGGACCATGGACCCAGCCCTGAAGCGGGCCCTCC
CCAGGCAGGCTGCCTACAGCTGTGCTGGGAGCCATGGCAGCCAGGCCTGCACATAAATCAGAAGTGTGAGCTGCG
CCACAAGCCGCAGCGTGGAGAAGCCAGCTGGGCACTGGTGGGCCCCCTCCCCCTTGGAGGGCCCTTCAGTATGAGCT
CTGCGGGCTCCTCCAGCCACGGCCTACACCTGCAGATACGCTGCATCCGCTGGCCCCCTGCCTGGCCACTGGAG
CGACTGGAGCCCCAGCCTGGAGCTGAGAACTACCGAACGGGCCCCCACTGTCTAGACTGGACACATGGTGGCGGCA
GAGGCAGCTGGACCCAGGACAGTGCAGCTGTTCTGGAAGCCAGTGCCCTGGAGGAAGACAGCGGACGGATCCA
AGGTTATGTGGTTTTCTTGGAGACCCTCAGGCCAGGCTGGGGCCATCCTGCCCCCTCTGCAACACCACAGAGCTCAG
CTGCACCTTCCACCTGCCTTCAGAAGCCAGGAGGTGGCCCTTGTGGCCTATAACTCAGCCGGGACCTCTCGCCC
CACCCCGGTGGTCTTCTCAGAAAGCAGAGGGCCAGCTCTGACCAGACTCCATGCCATGGCCCGAGACCCTCACAG
CCTCTGGGTAGGCTGGGAGCCCCCAATCCATGGCCTCAGGGCTATGTGATTGAGTGGGGCCTGGGGCCCCCAG
CGCGAGCAATAGCAACAAGACCTGGAGGATGGAACAGAATGGGAGAGCCACGGGGTTTCTGCTGAAGGAGAACAT
CAGGCCCTTTTCTAGCTCTATGAGATCATCGTACTCCCTTGTACCAGGACACCATGGGACCCTCCAGCATGTCTA
TGCCTACTCTCAAGAAATGGCTCCCTCCCATGCCCCAGAGCTGCATCTAAAGCACATTGGCAAGACCTGGGCACA
GCTGGAGTGGGTGCCTGAGCCCCCTGAGCTGGGGAAGAGCCCCCTTACCCACTACACCATCTTCTGGACCAACGC
TCAGAACCAGTCTTCTCCGCCATCCTGAATGCCTCCTCCCGTGGCTTTGTCTCCATGGCCTGGAGCCCGCCAG
TCTGTATCACATCCACCTCATGGCTGCCAGCCAGGCTGGGGCCACCAACAGTACAGTCCCTCACCTGATGACCTT
GACCCAGAGGGGTGCGAGCTACACATCATCCTGGGCCTGTTTGGCCTCCTGCTGTTGCTCACCTGCCTCTGTGG
AACTGCCTGGCTCTGTTGCAGCCCCAACAGGAAGAATCCCTCTGGCCAAGTGTCCAGACCCAGCTCACAGCAG
CCTGGGCTCCTGGGTGCCACAATCATGGAGGAGGATGCCTTCCAGCTGCCCCGCCCTTGGCACGCCACCCATCAC
CAAGCTCACAGTGCTGGAGGAGGATGAAAAGAAGCCGGTGCCCTGGGAGTCCCATAACAGCTCAGAGACCTGTGG
CCTCCCCACTCTGGTCCAGACCTATGTGCTCCAGGGGGACCCAAGAGCAGTTTCCACCCAGCCCCAATCCAGTC
TGGCACCAGCGATCAGGTCCCTTATGGGCAGCTGCTGGGCAGCCCCACAAGCCCAGGGCCAGGGCACTATCTCCG
CTGTGACTCCACTCAGCCCCCTTGGCGGGCCTCACCCAGCCCCAAGTCCATGAGAACCTCTGGTTCCAGGC
CAGCCCCCTGGGGACCTGGTAACCCAGCCCCAAGCCAGGAGGACGACTGTGTCTTTGGGCCACTGCTCAACTT
CCCCCTCCTGCAGGGGATCCGGGTCCATGGGATGGAGGCGCTGGGGAGCTTCT**TAG**GGCTTCTGGGGTTCCCTTC
TTGGGCTGCCTCTTAAAGGCCTGAGCTAGCTGGAGAAGAGGGGAGGGTCCATAAGCCCATGACTAAAACTACC
CCAGCCCAGGCTCTCACCATCTCCAGTCACCAGCATCTCCCTCTCCTCCCAATCTCCATAGGCTGGGCCTCCAG
GCGATCTGCATACTTTAAGGACCAGATCATGCTCCATCCAGCCCCACCAATGGCCTTTTGTGCTTGTTCCTAT
AACTTCAGTATTGTAAAC

185/6881
FIGURE 174

MARLGNCSLTWAALIILLLLPGSLEECGHISVSAPIVHLGDPITASCI IKQNC SHLDPEPQILWRLGAELQPGGRQ
QRLSDGTQESIITLPHLNHTQAF LSCCLNWGNSLQILDQVELRAGYPPAIPHNLSCLMNLT TSSLICQWEPGPET
HLPTSFTLKSFKSRGNCQTQGDSILDCVPKDGQSHCCIPRKHLLLYQNMGIWVQAENALGTSMSPQLCLDPM DVV
KLEPPMLRTMDPSPEAAP PQAGCLQLCWEFWQPGLHINQKCEL RHK PQRGEASWALVGPLPLEALQYELCGLLPA
TAYTLQIRCIRWPLPGHWS DWSPSLELR TTERAPT VR LDTWWRQ RQLDPR TVQLFWKPVPLEEDSGRIQGYV VSW
RPSGQAGAILPLCNTTEL SCTFHLPSEAQEVALVAYNSAGTSRPTPVVFSESRGPALTRLHAMARDPHSLWVGWE
PPNPWPQGYVIEWGLGPPSASNSNKTWRMEQNGRATGFLLKENIRPFQLYEII VTPLYQDTMGPSQH VYAYSQEM
APSHAPELHLKHIGKTWAQLEWVPEPPELGKSPLTHYTIFWTNAQNQSFSAILNASSRGFVLHGLEPASLYHIHL
MAASQAGATNSTVLTLMTLTPEGSELHIILGLFGLLLLLLTCLCGTAWLCCSPNRKNPLWPSVPDPAHSSLG SWVP
TIMEEDAFQLPGLGTPPI TKLTVLEEDEKKPVPWESHNSSETCGLPTLVQTYVLQGDPRAVSTQPQS QSGTSDQV
LYGQLLGSP TSPGPGHYLRCDSTQPLL AGLTPSPKSYENLWFQASPLGTLVTPAPSQEDDCVFGPLLNFPLLQGI
RVHGMEALGSF

186/6881
FIGURE 175

GGGTCGCGCGGAGATTGCTGGGCGGTTCTTGCCGGAAGCGGAGAGCGGCTGATCGCAGTCCGGAGGTGAGGCGGA
ACTCTGAGGCAGATATCCTCCCTTTCTCCTCGGCTGCTGCTCTTACTTTGACAAGCCAGGCTAACATTGAAGGT
GGTCCATTATGGCTGACATGCAAAATCTGGTAGAAAGATTGGAGAGGGCAGTGGGCCCGCTGGAGGCAGTATCTC
ATACCTCTGACATGCACCGTGGGTATGCAGACAGTCCTTCAAAAGCAGGAGCAGCTCCATATGTGCAGGCATTG
ACTCGCTGCTTGCTGGTCCGTGTGGCAGAGTACTTGAAGATCAGTAAAGAGATTGGGGGAGACGTGCAGAAACATG
CGGAGATGGTCCACACAGGTTTGAAGTTGGAGCGAGCTCTGTTGGTTACAGCTTCTCAGTGTCAACAGCCAGCAG
AAAATAAGCTTTCCGATTTGTTGGCACCCATCTCAGAGCAGATCAAAGAAGTGATAACCTTTTCGGGAGAAGAACC
GAGGCAGCAAGTTGTTAATCACCTGTCTCAGCTGTCTCAGCGAAAGTATCCAGGCCCTGGGCTGGGTGGCTATGGCTC
CCAAGCCTGGCCCTTATGTGAAAGAAATGAATGATGCCGCCATGTTTTATACAAACCGAGTCTCTCAAAGAGTACA
AAGATGTGGATAAGAAGCATGTAGACTGGGTCAAAGCTTATTTAAGTATATGGACAGAGCTGCAGGCTTACATTA
AGGAGTTCCATACCACCGGACTGGCCTGGAGCAAAACGGGGCCTGTGGCAAAAGAACTGAGCGGACTGCCATCTG
GACCCTCTGCCGGATCATGTCTCTCTCCCTCCACCATGCCCCCTCTCTCCCCAGTCTCTACCATTTTCATGCT
CATATGAGTCTGCTTCCCGCTCATCACTGTTTCGCGCAGATTAATCAGGGGGAGAGCATTACACATGCCCTGAAAC
ATGTATCTGATGACATGAAGACTCACAAGAACCCTGCCCTGAAGGCTCAGAGTGGTCCAGTACGCAGTGGCCCCA
AACCATTCTCTGCACCTAAACCCCAAACAGCCCATCCCCCAAACGAGCCACAAAGAAGGAGCCAGCTGTACTTG
AACTGGAGGGCAAGAAGTGGAGAGTGGAAAATCAGGAAAATGTTTCCAACCTGGTGATTGAGGACACAGAGCTGA
AACAGGTGGCTTACATATACAAGTGTGTCAACACGACATTGCAAAATCAAGGGCAAAATTAAGTCCATTACAGTAG
ATAACTGTAAGAAACTTGGCCTGGTATTTCGATGACGTGGTGGGCATTGTGGAGATAATCAACAGTAAGGATGTCA
AAGTTTCAGGTAATGGGTAAAGTGCCAACCATATCCATCAACAAAACAGATGGCTGCCATGCTTACCTGAGCAAGA
ATTCCCTGGATTGTGAAATAGTCAAGTGCCAAATCTTCCGAGATGAATGTCTCTATTCTACAGAAGGCGGTGACT
TTAATGAATTCCCAGTTCTTGAGCAGTTCAAGACCCTATGGAACGGGCAGAAGTTGGTCAACACAGTGACAGAAA
TTGCTGGATAAGCGAAGTGCCACTGGGTCTTTTGCCCTCCCTTCACACCATGGGATAAATCTGTATCAAGACGGT
TCTTTTCTAGATTTCTCTACCTTTTTTGCTCTTAAACTGCTTCTCTGCTCTGAGAAGCACAGCTACCTGCCTTC
ACTGAAATATACCTCAGGCTGAAATTTGGGGTGGGATAGCAGGTGAGTTGATCTTCTGCAGGAAGGTGCAGCTTT
TCCATATCAGCTCAACCACGCCGCCAGTCCATTCTTAAGGAAGTCCGACTAGGACTGATGATGCATTTTAGCTT
TGAGCTTTTGGGGGTATTCTACCAACAAACAGTCCATTGGAAAGAAAACAGTCCCTGGAATTAACAGATCAGAA
TGTTCACTGGTTAATCTTTTTTTAACAATGAGCATGAAGGTAGCAGAAGCTGGTGTGTTTCCAGATGGTTCTT
CTAACCAAACTAATTTTTTCACTGTTGACAAGCGAGGCAAGGGTTGCACTGGACCAAAGGCTGAGGCTTGGCCATC
TAGCATTCCATACAAAATTGTTTCTATAAGCATTCCTTTTATTCTCTATTCTATCTCTGGGTCTGCCTCAACCGT
GAGATAGGAGAGTCTCTGGTACTAGCTGCTGTAGCAGTGGCCTTCATCCAGGGCAGTTAATGGAGTCTTGGACCC
TTTCTTTCTCTGGGATCCCTGCCCAGCACCTTCCTATAGAGATGACTTTAAAAGGAAAAAAAAAAAAAAAAAAAC
CCACATGATTTCAAGGAGTCTGGCATTCTGAATCCTTCTTCCCTGCCAGGTGCCCTGTCACCTGTCTTCACTGCC
TCCTTTTCCCTGTCTGCTCATCAGCTTATGGCTTCTGTCTAAGCACCTGAACAGAGGACTGAAACCTCCACTGC
AGGCTGGTTTTAGGTCTTGAATTATGTAAGAATCTTGACAGCACTGCTAATGTAAATTTAGTTGTTTTTCCCT
CTAGGACAAACACTTACCAAAATATGCAACTTTTTTTTTGGTGGGAAGAGAGATTGTCCTGTGATTCTACCCATT
TCCTGAGGCCTGTGGAAATAAACCTTTATGTACTTAAAGTTATACAGAAAATAGAATAAAGTTAATACCAAACTT
G

187/6881
FIGURE 176

CCGGAGTCTCGCGCCCGCGGTCAITGTGACACAGCGAAGATGCGTTCGCCCCGGCTGCCTGTGGCTCTTGGCTGTGG
CTCTCCTGCCATGGACCTGCGCTTCTCGGGCGCTGCAGCATCTGGACCCGCCGGCGCCGCTGCCGTTGGTGATCT
GGCATGGGATGGGAGACAGCTGTTGCAATCCCTTAAGCATGGGTGCTATTAAAAAATGGTGGAGAAGAAAATAC
CTGGAATTTACGTCTTATCTTTAGAGATTGGGAAGACCCTGATGGAGGACGTGGAGAACAGCTTCTTCTTGAATG
TCAATTCCCAAGTAACAACAGTGTGTGTCAGGCACCTTGCTAAGGATCCTAAATTGCAGCAAGGCTACAATGCTATGG
GATTCTCCCAGGGAGGCCAATTTCTGAGGGCAGTGGCTCAGAGATGCCCTTCACCTCCCATGATCAATCTGATCT
CGGTTGGGGGACAACATCAAGGTGTTTTTGGACTCCCTCGATGCCAGGAGAGAGCTCTCACATCTGTGACTTCA
TCCGAAAAAACACTGAATGCTGGGGCGTACTCCAAAGTTGTTTCAGGAACGCCTCGTGCAAGCCGAATACTGGCATG
ACCCCATAAAGGAGGATGTGTATCGCAACCACAGCATCTTCTTGGCAGATATAAATCAGGAGCGGGGTATCAATG
AGTCTTACAAGAAAAACCTGATGGCCCTGAAGAAGTTTGTGATGGTGAAATTCCTCAATGATTCCATTGTGGACC
CTGTAGATTTCGGAGTGGTTTTGGATTTTACAGAAGTGGCCAAGCCAAGGAAACCATTCCCTTACAGGAGACCTCCC
TGTACACACAGGACCGCTGGGGCTAAAGGAAATGGACAATGCAGGACAGCTAGTGTCTTGGCTACAGAAGGGG
ACCATCTTCAGTTGTCTGAAGAATGGTTTTATGCCACATCATACCATTCCCTTGGATGAAACCCGTATAGTTCAC
AATAGAGCTCAGGAGCCCTAACTCTTCCAAACCACATGGGAGACAGTTTCCTTCATGCCCAAGCCTGAGCTCA
GATCCAGCTTGCAACTAATCCTTCTATCATCTAACATGCCCTACTTGGAAGATCTAAGATCTGAATCTTATCCT
TTGCCATCTTCTGTTACCATATGGTGTGTAATGCAAGTTTAATTACCATGGAGATTGTTTTACAACTTTTGATG
TGGTCAAGTTCAGTTTTAGAAAAGGGAGTCTGTTCCAGATCAGTGCCAGAACTGTGCCAGGCCCAAAGGAGACA
ACTAACTAAAGTAGTGAGATAGATTCTAAGGGCAAACATTTTTCCAAGTCTTGCCATATTTCAAGCAAAGAGGTG
CCCAGGCCTGAGGTACTCACATAAATGCTTTGTTTTGCTGGTGATTTAACAGTGCTTGAAAAATCTTGCTTGG
CTATTTCTGCATCATTTCTTAAGGCTGCCTTCCTCTCTCAGTACGTTGCCCTCTGTGCTATCATCTTATCATCAA
TTATTAGACAAATCCCACTGGCCTACAGTCTTGCTTCTGCAGCACCCACTTTGTCTCCTCAGGTAGTGATGAATT
AGTTGCTGTCACAAAAGGAGGGAAGTAGCACCCAAATTAAGTTGCTTAAGAGAGGAAATGTACATCTTGTATAAC
TTAGGGAGCGAAGAAAATGTAGGCGCGAAAAGTGAAAAGTGAGGCAGCTAGTTCTTCTTATCCATTCTCGACCAA
CCTGCCCTTTCTTAATATGACTAGTGGTCTTGATGCTAGAGTCAACTTACTCTGTTGCTGGCTTTAGCAGAGAAT
AGGAGGAACCATATGAAAAAGATCAGGCTTTCTGACTTCCATCCCCAAAACACATTTACCAGCATACTCCAACT
GTTTCTGATGTGTTCCATGAGAAAAGGATTGTTTGCTCAAAAAGCTTGGAATACTACACACTCCCTTTCTCCT
TCTGGAGATCAACCCACATTAGAGTGTCTAAGGACTCCTGAGAATTCCTGTTACAGTAAACAAAACCTAACGTAAT
CTACCATTTCTTACACTATTTGAGCATGGAAATCATAGTCCCCACTCTGTGAAAACCTTAACGCTTTTTGGAAGAC
ATTTCTGTAGCATGTCAGTTTGGAGAAATGATGAGCTACGCCTTGATGAAAGAACCGTGTGGTGCTGCTAAGTT
TAGCCATTATGGTTTTTCTCTCTCTCTTAAGCCTTATTCTTCAACTAAAAGATGAGGATTAAGAGCAAGAAG
TTGGGGGGGATGTGAAAATAATTTTATGAGGTTGTCTAAAAT

188/6881
FIGURE 177

MASPGCLWLLAVALLPWTCASRALQHLDPPAPLPPLVIWHGMGDSCCNPLSMGAIKKMVEKKIPGIYVLSLEIGKT
LMEDVENSFFLNVNSQVTTVCQALAKDPKLQQGYNAMGFSQGGQFLRAVAQRCPSPPMINLISVGGQHQG VFGLP
RCPGESSHICDFIRKTLNAGAYSKVVQERLVQAEYWHDP IKEDVYRNHSIFLADINQERGINESYKKNLMALKKF
VMVKFLNDSIVDPVDSEWFGFYRSGQAKETIPLQETS LYTQDRLGLKEMDNAGQLVFLATEGDHLQLSEEFYAH
IIPFLG

189/6881
FIGURE 178

CCTTACGGCCAGAAACGCCACCTTCCAGTAATTCGCCAAAATGACAAACACAAAGGGAAAGAGGAGAGGCACCCG
ATACATGTTCTCTAGGCCTTTTAGAAAACATGGAGTTGTTCCCTTTGGCCATGTATATGCGAATCTATAAGAAAGG
TGATATTGTAGACATCAAGGGAATGGGTACTGTTCAAAAAGGAATGTCCACAAGTGTTACCATGGCAAAACTGG
AAGAGTCTACAATGTTCCCCAGCATGCTGTTGGCATTGTTGTAAACAAACAAGTTAAGGGCAAGATTCTTGCCAA
GAGAATTAATGTGTGTATTGAGCACATTAAGCACTCTAAAAGCCGAGATAGCTTCCTGAAACGTGTGAAGGAAAA
TGATCCTCCACCCAGAGAAGCACAGTGTGTGAGAACCAATGGGAAGGAGCCTGAGCTGCTGGAACTATTCCCTA
TGAATTCATGGCATAAATAGGTGTT

190/6881
FIGURE 179

MTNTKGKRRGTRYMF SRPFRKHGVVPLAMYMRIYKKGDIVDIKGMGTVQKGMSHKCYHGKTGRVYNVPQHAVGIV
V NKQVKGKILAKRINVCIEHIKHSKSRDSFLKRVKENDPPP REAQCVRTNGKEPELLETIPYEFMA

191/6881
FIGURE 180A

CGGACGCGTGGGCTGCTGCGGAGCCGGCAGCGCAGGCGGGCGGAGCGGAGCTGCCCCCGTGGTGGCGGGCGATGC
CCCCGTGAGCCTCCCTCGCCGCCCTCCCCGCCCGCGTGCCTATCCACTCGGAGTCCGCGCCAGCCTGGGGCCG
GGCCGCGCCTACTGCCGGGTTGCGGGGGCGGGGTCCCGGGGCAGCACCTGCCCCGCTTGCGGAGCCGCTCGGC
CTGTGGAGGCCCCCTCCCTGTCTGGACCCCGGCCCCACCTCCGGACCCTTTTATCACATCGCCTCCTCTGGGAGC
CTGCCCTGATTGCCTTCACCTCATTTCTTGAAAATTGGTGTGTTTGGCAGAAGTCAATTGAAGCCTTGTGCAAATG
CCCTAGGGGTGTGCTGTTGGGAGGCAGCCCCCTGTGATGCGGAACACCAGGCTCAGATTTCATCAGTTCGAGCTGC
CTGAGGCCCTGCCACCCCGGGGACCATGTTTAACGGGGAGCCAGGTCTGCCTCATCTGGGGCCTCCAGGAATGT
GGTGGCGGAGCTCCAGCATTGGCGGTGAAATCTGCGGATCCCAGCAAGCCGGGGGCGGGGCTGGGACCACCACCGC
CAAGAAGCGGCGGAGCAGCCTGGGTGCCAAGATGGTGGCCATCGTGGGCCTGACTCAGTGGAGCAAGAGCACACT
CCAGCTTCCGCAGCCTGAAGGGGCCACCAAGAAGCTGCGCAGCAACATCCGCCGGAGCACGGAGACAGGCATCGC
GGTGGAGATGCGGAGCCGGGTACACGCCAGGGCAGCCGGGAGTCCACCGATGGGAGCACCAACAGCAACAGCTC
CGACGGCACGTTTCATCTTCCCCACTACCCGGCTAGGGGCTGAAAGCCAGTTCAGCGATTTCTTGATGGGCTGGG
ACCAGCTCAGATTGTGGGGCGACAGACACTGGCAACACCACCCATGGGAGATGTGCACATTGCCATCATGGACCG
GAGTGGCCAGCTGGAGGTGGAAGTGATTGAAGCTCGGGCCTGACCCCAAACCAGGCTCCAAATCCCTCCCAGC
CACCTATATCAAGGTTTACCTGCTGGAGAATGGGGCCTGCTTGGCCAAGAAGAAGACAAAGATGACCAAGAAGAC
CTGTGATCCCTGTACCAGCAGGCTCTGCTCTTTGACGAGGGACCCAGGGCAAGGTGCTGCAGGTGATCGTCTG
GGGAGACTATGGCCGCATGGACCACAAGTGCTTCATGGGCATGGCCCAGATCATGCTGGACGAGCTGGACCTCAG
CGCCGCGGTACCCGGCTGGTACAACTCTTCCCCACCTCCTCAGTGGCAGACTCCACACTCGGATCCCTCACCAG
GCGCCTGTCCCAGTCTTCCCTGGAGAGTGCCACCAGCCCCCTCATGCTCTTAAGGATGTGAGGAAGAGGCCAGGAT
GGTGGTGTGGGGAGGGGTGCCTGCTGGCCCCATGTCTCCCTGTACATAGTCTTCGTGTCTTTCTGGACCCCTT
GTCCTGCTGCATGCCGTGTGGCTACTGGGCTCATCCAGCTGGCAGTGGAGACTGTAGTGTGTGCGTGTGTGCGT
GCGTGTGTGTGTGTGTACGTGACCAGTTCTATCTGTTTCATTGTCTGGGTATAGTCACTCCTGGTGATGATA
TGGGCTGAAATGTCTCCACGTCTCTTTGTGTCTTGTGAAAAGAAACCCAAAGGAGTGTTGTGTGGACATGACTC
ACCCTGAGGAGTCTCCAGGGATGGAGGTGGGGCATGCGGCCACTGGTCGGTGCTGCCTGGTCTCGCCTGGGGCA
GAGCCTGTGTGTTCTTCACCTGTGCCTGCTCCTGGTGGTCTCTGCTTTGTTTTCTGTCTTTGTCTTTTGTTCCT
CTTGACTCTCCCGGCTCTGCCACTGTTTTCTGAGAAATGTAGCATCCGCTGCAGCTGGCCACACTGAGGGCCCTC
TGGGAACCCCAACCCACTGGAGCCGCTCCGGCAGCTCTTCCTGCCACTGAATGCGTTCTGCAGCATGTAGCATGC
CCACCTAGCTCCCTGGCCAGGGCCCTGGGGAGGCAGAGGGTACCCAGGGGACTGAGGGCTTAGAAATGACTTTCT
CTATGAGGCTGGAACCTCCTCCTTCTTCCAGTGAAGCACGAGGTCTTGTTCCAGGGTTCTTGCCAGGTGCCCC
CTTAGCATTTGTTCTTCATCTCCTGTCTCTTCAAGCCTCCCCACTCCACCGTGCCGAAGGAGCTCTGCCAGTGGG
CCTGGGCAGGCAGCCACAGAGGGCATGTTATCTGCTAAAGCAAACAGTCCCTCCTGAGGCCCTGAGGGTGGCCCTG
ACCCCTCAGGGCTCATTCCTGGTGGGCATGACTCGGTAAGGAGGTTCTGTGGGTAGGGCTGTTTGTGGAATAA
GGAGGGCTGAGGCTGAGTTGTTCCCGCCACTGTTGAGGATCCCATCTGACATTTGGGGATTCACTGCATGAAGT
TGTTCAATTTGGGGCTCCAGTTTTTGTGCATTTCCAGACCAGGGTCCCTGTCTGGGAGCTCAGACTTAGCTGGGCT
CCAGCAGCCTGGCTCCGGACTCTCGTCTGCCACCATCACCAGCTCTGTCTAAGCAATACTTACCCCTCCGGGCTT
CCCTGCTTTCTGTGCCCCACTGCTGCCCTCTGCAGAGCCATCTGCTCCAGGCACCCACCTGCCTCTGCTTGCTT
TCTCACCCTATGTCTGGTTGGAGCTTCTCACAGCCACTCAAACCTGACTTGATTGACAACCTGGGCCCTGTTGGT
GGAGACCAGTGCCTGAACTGGACCCCTGTGAAATCTGTCCCGTGGGAATCCTGAAGTCTGACTCAGGAATGCCAG
ACCTGTCCCTGTCCCTCCTCAGCTCTAGGGTGAAAGGCGAGAGGTTGCACAGGACATGGACAGAGCAGCCCTTGG
GTTTGTATCTGGTAGGGGAGAAAGCAGCAGGACAGTGGAGGTGTGTGGAAGGCACTCTTTCCACCTCTCTCCAGG
CATTATCCCCAGGTGCTGAAATGGCTGTGGCCCCAGCACCTGAGGCAGGGGTACGCTACCTGGGGTAGCAGTAGA
AAGGTCTTGGGGTCTGAATGACTTGGGGCCTCCATTTCATAACCAAAGTTGTAGGGGCATGGAGGCAGTGGCGCCT
TATGGATAGGTCTATCTCAGCCCAAAGGGCTCCTTGGCTGGCATGGTTCTGTGTTACGTTGAAGCCAGAGTCTTA
TAACACCTCCCAAGAAAGATAGGGGAAGAAGCCAGAACCCACCTGGCCTGCCACAGGACAAGAAGTGGGTAAAG
GGCAGGAAGGAAATGAACGGAGTTAGCTCCAGGCTCCTATCTCTGCCCTGAGCCTCTATTCTTATATTATCAGAG
AAAGGGACCATTGGGTGCATAGAGATGGGGAGGAGGCCACTGGGCTGAATTTTCTCTTTAGGCGGAAATGCTCTC
CCCAGGCCCATTGCGTTTCGTCAAGTTCTTGAAATGGACAAAGGGCTCTGTCTCCTCGACCCTAGTGGGGGATC
AAGAAGGAACTCCGTTGCAAAAGGGTATTTTAATCTCCTGTTTATGATATATTACCTCTAGAGCAGTCACTGT

192/6881
FIGURE 180B

CAGGGTGTTCGCGAAAATACTCTACACCTTTGGGATGATAGGGTTGTTAGTGACCCACAGGACAGTATAGATGTTT
GTGGATGTAGCACTGAGTGGTGATACCCAGACCAGCAGTCACCCAGGAAGTGGGGGTACCCATACCCTCATT
CTCTGGTGGGGAGCTGCCTGCAGAGAGGCCTGCCACTGGGGGTTCAGGCCGTGGTGACCTTGCTCTGGGGAA
GGGTTAGCACAGGGGAGGTTCTAGCTGGAGGAGGGTCTGATGTGCTGGTAACTTGGGCTGACCTACCTACAGTC
CCTGGCTGCCAAAAGTCTCAGCAGTTGGGCCACTCCACTATTCCACCTCTCTAAAAGAAGGTAATTTCTCCCC
AAATTGACCTTGGGGAATTATTCTTTTAACCCCTTGCACCAAATAAGTTACTCATCCCCACCTGGATTTTACCCC
ATGAGGGTAAAGTTGTGTGAGGCTGACACGTCTGTGTGATGCAGTGTGGCTGCACCTAAGGGTCTGTTTCTCAGC
ATCATGGATGCAGGGGCTTGTCTGAAAAGCCACTCTGGACCTAGCCTGTCCCAGAAGAGGAGAATGCACAAGTGT
AACTCCTGGTTGTTTGTCTGGGGTGGGGGAGCATCTGCTGTTTGGAGACGGGGGTGGGGAAGGAAGGAACATGAT
CCCTCCAGAAGTCTCCACCCCTGGGGCCAACTCACTGCCATGTTTCAAGTGTCCCGGTCCAAATGCCCCCTTGCCC
AGATGAAACCCTGCAGTGGTTACAGGAATGGAGCTCTTTGTCACTCCACCTCCTCTGGTCAGGCGAGGTTCACTG
TGCATATGGCAGAGACAGGAGTGGCCCTGCAGTGATGTTGGGTTGTGGGCAGGGACAGTGATGGATGACTCAGAG
CGTCTGTCTTTGTATTTCTGCTCTGTTTCACTCTGTCCCACTTTCTTCATAGACTCCTTTTTCCCTGCAATGGGTTT
TTGGTATGAAAAAGGCTCCAGTAAATGGAGCCAAGTCTTGGTTTGACAAGGGGAAGTTGATCCTTCAGGGAAGAA
TCATCTCCAAAATGACTCCCCATCTGGTTTCTTCTACCAACCAATTCTACTAGGAAAGGAGCACTTAGGAGGCTC
TTGGGATGCAGCAAGTCCCAGGCAATGCCAGCATTTTATGGGGGTGAGGCAGAACCAGGAGCTCCAAGAAAGG
CCACCCATAGAGCTCATCCTCTGTGGAATCACTGCCGGTTAGAACACTGAGGTCAAGCCAGTCTCCCATGGTCA
TGCCACCCACCAGGGAAGCATGCCTGATCTCTTCTTTACTGCCAGCCTTGAGGAGAGCAGAAGCCTCCATTTTTA
AAGACAATAAAGACCTCCAAGGGTACTTCTTTGGAAATGAAATGTAGCACAATCTTAGCCTACGTTACCAGGAGC
CCTGACATGCAACCAGGGTCCCTCTTCCATGCCCTGCTGCCAGGAGTTGCTGAGCTCCTCTTCCCTTGGGGTTC
CAGCCCTCCTAATACCTCATATTCCCATCTTCCCTCAGCCCAGAAAGCAATGGGGCTTTAGTGATGCTCCTCTTT
TGTGTCTCTCTGGTTGCCTCTAGCACTGTGCAAACTCTGCAAGAAATTGCTGCCTTTGCTTGATGTTGTAGATGA
GTTGCCCTCCACCTGGCTGGAGAGATGGCACATCATTAGGGCCAGAAGGTTGTCCAGCAGTGTCTTCTGCAGTGG
CTGCAGGGAGATGGAAGAAGAGCCCTGCTTCCCTGCCTCCTCTACCTTTCTCTTCCACTCCTCAGAGTTTTT
TTCTCCAGTATCCTGACATGTAAAGAGATTCTTTAAAATGCTGCTTCTTCTACTGGACTGTCTTTCACTGAGTAG
TCAGGGAGGAGATGAAAATGTGGACACATCCCCCGCCTTCTCCCTCAACCTTTTCACTCACGTGAGAAGAGGTT
GGGGCAAAACAAAACAAGCATGATTGAAGAGCAGGGGAAGCCACACAATCAGGTGAGCCCTGATGGGGGCTGGA
CTGGCCTGGTCTGGCTGGGAAAGGATTCTTTTAAAAGCGTGCTGAGCATCTCAGAGCAATGTGAGTGATGCCAA
AGAGAGCAACTTGGCCTCCTTGGGCACCAACTCTGATGGCTGAGTTGCACAAACGTGGCTCAGATGTTGGCATGC
CCGATGGTGGGACCTTGTCTCTGATAAAGGGCTTAATCTTTCCATGTAGCAAAGCAACTTTCCCTCCCTCCCT
CCCCCGAACCCTGAGCTTGGGCTTGTGTGGGCCAGCATGGCTGTGCTGTGAGGGAAGCCACATCAGTGAGAG
AAAGTTGCATTCTCTCAGGGGCCCTAGATTGGCTTGGGGCAGGTGCTTGTGAAAAGCATGAGTGTCTTCTGCTTTG
GGAACCCCTTCCAGGGCTCTGGTTGGAACCTTGCCAGTAAGGACAGGGCCTTGGGCCTCCCAAGGAGTTCACAA
TGATGCCAGGAAGGGTCCCTGAGCCTGGGTCCAGTCAGCTTGGCTAACAGAATGGGGCTTGGGAATTCCAGGGG
CAACTGAGCATCCACCCCATAGCCAGTGATCTGGACAGGGACAGCTGGCTACAGGGAATCAAAGGCTGTTCTGT
ACAGTTTTTACCAGAAACTGTGACCTTGGGTAAGGCTCCTCACTTTTCTGGGCCTCAACTTCCCTCATCTGCAAAAT
CAGAGCATTAGCTGCTCTCCCCATGATTCCCTCCAGTTTTTAATTAAAGTCTCTGATCTGGAGCATGAGGGT
TGCGAGCCTGGTGCACCTGGTTCTGTCTCCGTGGGCTGGTTTCTTCAGCCCTGATGCCAGGCTGGGTGCAG
GCTCTCATCTGGTCCATGCCAGATGCTGCCTCAGACAAGAAGTCTGGGAATCCTAACAGACTCTGCTTTCTCT
CTTCGTGGTTTGTCTCCCTCTTTTATTCTTGTGTAATGATGAGACATAATTAAGGGTCATCTACAATGGACAAT
TTTCAAGGTGCTGATGTGATGTCAACCTCCGCTACATCCTGAGTAAGTCAGTGTCCCAACAGCAGATGAGGC
TGGGTCTTTCTCATTTCTGCTTCTGGGATGACATCAGTGGGAGAGTTGAAGATCTGAGAATTCTAAAGGAAATG
TTCTCTGATGGGAGGAGAGGGAACTTATTTCCCTTCAAAGTAGTTTGTCTTAAAGACCTCCTCCCTCCAG
AATGTCTTTAACCAGACATCATTTCAGAAGGTGGGGCAGCTGCTTCTTAAAGAGTGGGCCTGATAGCTCAAC
CAACTCCTTTAGCATGTAAACTCACAGAAGGCAAGAACCCTTTTTTTAGACTTTCCAAATGCATCCTGCAAGA
GAGAGATAGCTGATAGGGACTGACAAGCACACTGTTTAGATAAGAAGCAATTACCCTTTTATCTGTGCTCTAT
ACATTTTCTATGTGCAGCATCTTCTTAACCTTGTGTGGTTCCTGGGTGGCAGGTGCACAGCTGGGAGGGACTGC
CGGCTGTTTCTGTACAACATTCTTGCCAATTCCTTGAGGAGAAAATTCTTCACATGGCTTCTGCATGTACAGTAT

193/6881
FIGURE 180C

TTGGGCAGCAAAACATGATTAAAGTCAGTTTGAAAATGG

194/6881
FIGURE 181

MFNGEPGPASSGASRNVRSSSIGGEICGSQQAGGGAGTTTAKKRRSSLGAKMVAIVGLTQWSKSTLQLPQPEGA
TKKLRSNIRIRSTETGIAVEMRSRVTRQGSRESTDGSTNSNSSDGTFFPTTRLGAESQFSDFLDGLGPAQIVGRQ
TLATPPMGDVHIAIMDRSGQLEVEVIEARGLTPKPGSKSLPATYIKVYLLENGACLAKKTKMTKKTCDPLYQQA
LLFDEGPQGKVLQVIVWGDYGRMDHKCFMGMAQIMLDELDLSAAVTGWYKLFPTSSVADSTLGSLTRRLSQSSLE
SATSPSCS

195/6881
FIGURE 182

AAGCTGCTGACATCCTGGATCTAGGGTTGTAAAGAAGATTACATGAGCTAATGGATGTGAAAACATCTTAAAAAC
TCTCAAATACTTTTCAACTTTGGAGGATTATTATGATTTTCATTCTGTTTCAGCGGCTATACTCAGACTTTACTCT
AAAAGTCAAATCTTCTGACATTCTTTGAAGTGAAGCATTCTATGAATGTGAGCTGAAGAAATGAATGAAATGAAA
TAATGCAGCATCTAGTGCTTTTTTGCATGGCCCAAAGGGGCTCTGTGCTGCTCCACTACAGAGGAACTTCAAGAA
ATGCTGGTTTGCTACAGTGTTTTAGCTTGTGAGATTCTCTGGGACCTTCCCTGCTCCATCATGGGGTCACCTCTA
GGTCATTTTACCTGGGACAAATACCTAAAAGAAACATGTTTCAGTCCCAGCGCTGTCCATTGCTTCAAGCAGTCC
TACACACCTCCAAGCAACGAGTTCAAGATCAGTATGAAATTGGAAGCACAGGACCCCAGGAACACCACATCCACC
TGTATTGCCACAGTAGTTGGACTGACAGGTGCCCGCCTTCGCCTGCGCCTTGATGGGAGCGACAACAAAATGAC
TTCTGGCGGCTGGTTGACTCAGCTGAAATCCAGCCTATTGGGAAGTGTGAAAAAGATGGGGGTATGCTACAGCCA
CCTCTTGGAATTTTCGGCTGAATGCGTCTTCTTGGCCCATGTTCCTTTTGAAGACGCTAAATGGAGCAGAGATGGCT
CCCATCAGGATTTTCCACAAGGAGCCACCATCGCCTTCCCACTTCTTCAAAATGGGAATGAAGCTAGAAGCT
GTGGACAGGAAGAACCCTCATTTCATTTGCCAGCCACTATTGGGGAGGTTCCGGGGCTCAGAGGTGCTTGTCACT
TTTGATGGGTGGCGAGGGGCCCTTTGACTACTGGTGCCGCTTCGACTCCCAGACATCTTCCCTGTGGGCTGGTGT
TCCTTGACTGGAGACAACCTGCAGCCTCCTGGCACCAAGTTGTGATTCCAAAGAATCCCTATCCTGCCTCCGAT
GTGAATACTGAGAAGCCCAGCATCCACAGCAGCACCAAACTGTCTTGGAACATCAACCAGGGCAGAGGGGGCGT
AAACCAGGAAGAAGCGGGGCCGACACCCAAGACCCTAATTTCCCATCCCATCTCTGCCCCATCCAAGACAGCT
GAACCTTTGAAATTCCCAAAGAAGAGAGGTCCCAAACCTGGCAGCAAGAGGAAACCTCGGACTTTGCTGAACCCA
CCACCTGCCTCACCAACAACCAGCACTCCTGAACCGGATACCAGCACTGTACCCAGGATGCTGCCACCATCCCC
AGCTCAGCCATGCAGGCCCAACAGTTTGTATCTACTTGAACAAGAATGGCAGCACAGGCCCCCACTTAGATAAG
AAGAAGGTCCAGCAACTCCCTGACCATTTTGACCAGCCCGTGCTCTGTGGTGTGTCAGCAGGCTGTCCAGGCC
TGTATCGACTGTGCTTATCACCAGAAAACCGTCTTCAGCTTCTCAAGCAAGGCCATGGTGGTGAGGTTATCTCA
GCCGTGTTTGACCGGGAACAGCATACCCTCAACCTCCAGCAGTCAACAGCATCACCTACGTCTCCGCTTCCCTG
GAGAACTCTGCCACAACCTTCGTAGTGACAATCTGTTTGGCAACCAGCCCTTTACACAGACTCACTTGTCACTC
ACTGCCATAGAGTACAGCCACAGCCACGACAGGTACCTACCAGGTGAAACCTTTGTCTGGGGAATAGTCTGGCC
CGCTCCTTGGAACCACACTCAGACTCAATGGACTCTGCCTCAAATCCCACCAACCTTGTGAGCACTCCCAAAGG
CACCGGCCCTTGCTTTTATCCTGTGGCCTCCACCAAGCACTGCCTCAGCTGTGCGCAGGCTATGCTCCAGGGGA
GTGTTAAAAGGATCAAATGAAAGAAGGGATATGGAATCATTTTGGAACTAAATCGTTCCCCAGGGTTCGGACCGA
TACCTGGAGAGCCGCGATGCCTCTCGACTGAGTGGCCGGGACCCCTCCTCATGGACAGTCGAGGATGTGATGCAG
TTTGTCCGGGAAGCTGATCCTCAGCTTGGACCCACGCTGACCTGTTTCGCAAACACGAGATCGATGGCAAGGCC
CTGCTGCTGCTGCGCAGTGACATGATGATGAAGTACATGGGCCTGAAGCTGGGGCCTGCACTCAAGCTCTCCTAC
CACATTGACCGGCTGAAGCAGGGCAAGTTCTGAACCAGGAGAGGCAGCCTAGACAACCAAGTGGCAGCAGGTGGG
GGCATTCTTCTAGGAATGAGGGGCATCAGCCACCCACAGGCACCTCAGTGGGGTTCCGGGGCCACCTCAGGACTCC
AAGAGGCTGTGTGGAGCCACCCTCCTAGCCACAGCTGCCATGATAAGTCCCTTCCATGAAGGACTGAGGAGGGAG
AGTGGGGGTCCAGGGCTGGTGTGCTCTTCCCTCAGCTCTGCCGGGGCTCTAAGGTCCCTCTATTTATTTCTCAA
CCCTGGCTGGCCTCTCACCAGGAGTTTAGGCTGAATGCCTTCCACGTGATGGAGGAAAAGGCCAACTCTGTCTTG
GTCTTGTGTGGCACCCCATCGCCCCACAGCTCGTACCTTCTCACCAGATTCCCCTGAATCCAAACTCGTGGTGC
AAACCTCTACCTTTTTTACAAAAAGATCTTATTGTTAATTTATTGTTTCTGGCACTTGGGCAAAACCTGTAGTTA
ATACTCCTCCACACTAGACACTGGGTTTCAGGAGGAGGGAGACTGCCCTGCTTTGGTCCCAGAGAGGCCCTCTG
CAGATAGGCGTGGCCCCCTCTTCAGAGGACACTACCCTAGGGCACTTTCTCTTTGAGGTGGAGAGACCCATAAAGC
CTTGACCACATCACTCCATATGGGGAGGAGAAGGATCCCTGTACCTTCTCCTCTCTTCACGGGGCCCTTTTGCA
GCCCTAGGCCTCATCTGTGGGAAGGGAGTCCCTGGCTTATACTGCCCCACCACAGCTCCTTGCCCTGGCCAGAA
CTGCTGTGAAGAAAAATCAGGCCGGAAGGCCAAGAAGGCGTAAGGGGGATGGGAGGGCAGGTTTCCAGGCTGG
AGTCGGTTCCACCCACTCGCCTGTCCACAGGCTTCCCTGTAAAGCAAGTCAGCAGCACAGCTACTCACGCTGCCAT
CTGGACTTATTTTATGTCAATCTGTTTATAAATAAAAAACCAATATAGAT

196/6881
FIGURE 183

GCTGCAGATGGCGGAAATGGATCCGGTAGCCGAGTTCCCCAGCCTCCCGGTGCTGCGCGCTGGGCTGAGGTTAT
GGCTCGCTTCGCGGCCAGGCTGGGCGCGCAGGGCCGGCGGGTGGTGTGGTTACGTCAGGCGGCACCAAGGTCCC
ACTGGAAGCGCGGCCGGTGCGCTTCCTGGACAACCTTCAGCAGCGGGCGGCGCGGTGCAACCTCGGCCGAGGCCTT
CCTAGCCGCCGGCTACGGGGTCTGTTCTTGTATCGCGCTCGCTCTGCCTTCCCCTATGCCCACCGCTTCCCACC
CCAGACTTGCTGTCCGCTCTGCGGCCTTCGGGCCCAGCCCTTTCGGGCTTGCTGAGCCTGGAGGCCGAGGAGAA
TGCACTTCCGGGTTTTGCTGAGGCTCTGAGGAGCTACCAGGAGGCTGCGGCTGCAGGCACCTTCCTGGCAGTAGA
GTTCAACCACTTTGGCGGACTATTTGCATCTGTTGCAGGCTGCGGCCAGGCACTCAATCCGCTAGGCCCTTCTGC
GATGTTTTACCTGGCTGCGGCTGTGTCTGAGATTTCTATGTTCTGTCTCTGAAATGCCTGAACACAAGATCCAGTC
ATCTGGGGGGCCCACTGCAGATAACAATGAAGATGGTGCCAAAACCTGCTTTCTCCTTTGGTTAAAGATTGGGCTCC
CAAAGCATTTATAATTTCTTTAAGTTGGAGACTGACCCCGCCATTGTAATTAATCGAGCTCGGAAGGCTTTGGA
AATTTATCAGCATCAAGTGGTGGTGGCTAATATCCTTGAGTCACGACAGTCCTTTGTGTTTTATTGTAACCAAAGA
CTCGGAAACCAAGTTATTGCTATCAAGGAAGAAATAGAAAAAGGCGTAGAGATAGAAGAGAAAGATAGTGGATAAT
CTTCAGTCTCGACACACAGCTTTTATAGGTGACAGAACTGAAGTAAAAAGCCCTTATAGGATTAAAAATTGTTT
AGGGCTCTTAGAGATGGTGAAAACACAAAAAAACCATGGCTTTCATATGGACAGAGAAAAATGAAAGAAAGGGA
AAAGGCAGTGGTGTGTAGGCAAATATGGTTTGGCATTCTGCTTTTAATGACACCTGATATGATGTCATTTTGATT
TTGAAATTGAACACTAGAACTGTTAATCACCTTTAAAAAGAAGAGCTTATTGGGAATTATATATTCCTTAAAATA
TACATGGGGGCCTGAATGTCAGCCATCTTTATACTATAGAAAAAGGATTATGGATGCATGAATGGTCATGCTTTG
GAGATCAAATATFGGTTGAATGCCTATGTATGTCAGGCCCTGTGCTGAGCCATGAGGATTAAAAAGATGAATAAA
CATATCTTGTTTAGGAAATGGATGTATAAAAAAATCAAGTGCAATAAAGTGTGTGTCCAAAAGCTGACACAATGG
AAAGG

197/6881
FIGURE 184

MAEMDPVAEFPQPPGAARWAEVMARFAARLGAQGRRVVLVTSGGTVPLEARPVRFLDNFSSGRRGATSAEAFLA
AGYGVLFLYRARSAPFYAHRFPQTWLSALRPSGPALSGLLSLEAEENALPGFAEALRSYQAAAAAGTFLAVEFT
TLADYLHLLQAAAQALNPLGPSAMFYLA AAVSDFYVPVSEMPEHKIQSSGGPLQITMKMVPKLLSPLVKDWAPKA
FIISFKLETDP AIVINRARKALEIYQH QVVANILESRSQSFV FIVTKDSETKLLLSRKK

198/6881
FIGURE 185

CGGGAGCGGAGAGCGGACCCAGAGAGCCCTGAGCAGCCCCACCGCCGCCGCCGGCCTAGTTACCATCACACCCC
GGGAGGAGCCGCAGCTGCCGCAGCCGGCCCCAGTCACCATCACCGCAACCATGAGCAGCGAGGCCGAGACCCAGC
AGCCGCCCCGCCGCCCCCCCCCGCCGCCCCCGCCCTCAGCGCCGCCGACACCAAGCCCGGCACTACGGGCAGCGGCG
CAGGGAGCGGTGGCCCCGGGCGGCCTCACATCGGCGGCGCCTGCCGGCGGGGACAAGAAGGTCATCGCAACGAAGG
TTTTGGGAACAGTAAAATGGTTCAATGTAAGGAACGGATATGGTTTCATCAACAGGAATGACACCAAGGAAGATG
TATTTGTACACCAGACTGCCATAAAGAAGAATAACCCCAGGAAGTACCTTCGCAGTGTAGGAGATGGAGAGACTG
TGGAGTTTGATGTTGTTGAAGGAGAAAAGGGTGCGGAGGCAGCAAATGTTACAGGTCCTGGTGGTGTTCAGTTC
AAGGCAGTAAATATGCAGCAGACCGTAACCATTTATAGACGCTATCCACGTCGTAGGGGTCTCCACGCAATTACC
AGCAAAATTACCAGAATAGTGAGAGTGGGGAAAAGAACGAGGGATCGGAGAGTGCTCCCGAAGGCCAGGCCAAC
AACGCCGGCCCTACCGCAGGCGAAGGTTCCACCTTACTACATGCGGAGACCCTATGGGCGTCGACCACAGTATT
CCAACCTCCTGTGCAGGGAGAAGTGATGGAGGGTGCTGACAACCAGGTCAGGAGAACAAAGGTAGACCAGTGA
GGCAGAATATGTATCGGGGATATAGACCACGATTCCGCAGGGGGCCCTCCTCGCCAAAGACAGCCTAGAGAGGACG
GCAATGAAGAAGATAAAGAAAATCAAGGAGATGAGACCCAAGGTCAGCAGCCACCTCAACGTCGGTACCGCCGCA
ACTTCAATTACCGACGCAGACGCCCAGAAAACCTAAACCACAAGATGGCAAAGAGACAAAAGCAGCCGATCCAC
CAGCTGAGAATTTCGTCCGCTCCCGAGGCTGAGCAGGGCGGGGCTGAGTAAATGCCGGCTTACCATCTCTACCATC
ATCCGGTTTAGTCATCCAACAAGAAGAAATATGAAATTCCAGCAATAAGAAATGAACAAAAGATTGGAGCTGAAG
ACCTAAAGTGCTTGCTTTTTTGCCGTTGACCAGATAAATAGAACTATCTGCATTATCTATGCAGCATGGGGTTTT
TATTATTTTTACCTAAAGACGTCTCTTTTTTGTAATAACAAACGTGTTTTTTAAAAAAGCCTGGTTTTTCTCAAT
ACGCCTTTAAAGG

199/6881
FIGURE 186

MSSEAETQQPPAAPPAPALSAADTKPGTTGSGAGSGGPGGLTSAAPAGGDKKVIATKVLGTVKWFNVRNGYGF I
NRNDTKEDVFVHQTAIKKNNPRKYLRVGDGETVEFDVVEGEKGAEAAANVTGPGGVFVQGSKYAADRNHYRRYPR
RRGPPRNYQQNYQNSESGEKNESSESAPEGQAQQRRPYRRRRFPPYYMRRPYGRRPQYSNPPVQGEVMEGADNQG
AGEQGRPVRQNMRYRGYRPRFRRGPPRQRQFPREDGNEEDKENQDETQGGQPPQRRYRRNFNYRRRRPENPKPQDG
KETKAADPPAENSSAPEAEQGGAE

200/6881
FIGURE 187

GGCGGGTGGCTGGCGGTTCCGTTAGGTCTGAGGGAGCGATGGCGGTACGCGGTTGAAGCTGCTGACCACACTGC
TGGCTGTCGTGGCCGCTGCCTCCCAAGCCGAGGTCTGAGTCCGAGGCAGGATGGGGCATGGTGACGCCTGATCTGC
TCTTCGCCGAGGGGACCGCAGCCTACGCGCGCGGGGACTGGCCCCGGGTGGTCCTGAGCATGGAAACGGGCGCTGC
GCTCCCGGGCAGCCCTCCGCGCCCTTCGCCTGCGCTGCCGCACCCAGTGTGCCGCCGACTTCCCGTGGGAGCTGG
ACCCCGACTGGTCCCCCAGCCCGGCCAGGCCTCGGGCGCCGCCGCCCTGCGCGACCTGAGCTTCTTCGGGGGGCC
TTCTGCGCTCGCGCTGCCTGCCTGCGCCGCTGCCTCGGGCGCCGCCGCCCACTCGCTCAGCGAAGAGATGGAGC
TGGAGTTCCGCAAGCGGAGCCCCCTACAACCTACCTGCAGGTCTGCCTACTTCAAGATCAACAAGTTGGAGAAAGCTG
TTGCTGCAGCACACACCTTCTTCGTGGGCAATCCTGAGCACATGGAAATGCAGCAGAACCTAGACTATTACAAA
CCATGTCTGGAGTGAAGGAGGCCGACTTCAAGGATCTTGAGACTCAACCCCATATGCAAGAATTTGACTGGGAG
TGCGACTCTACTCAGAGGAACAGCCACAGGAAGCTGTGCCCCACCTAGAGGCGGCGCTGCAAGAATACTTTGTGG
CCTATGAGGAGTGCCGTGCCCTCTGCGAAGGGCCCTATGACTACGATGGCTACAACCTACCTTGAGTACAACGCTG
ACCTCTTCCAGGCCATCACAGATCATTACATCCAGGTCTCAACTGTAAGCAGAACTGTGTACGGAGCTTGCTT
CCCACCCAAGTCGAGAGAAGCCCTTTGAAGACTTCTTCCCATCGCATTATAATTATCTGCAGTTTGCTACTATA
ACATTGGGAATTATACACAGGCTGTTGAATGTGCCAAGACCTATCTTCTTCTTCCCCAATGACGAGGTGATGA
ACCAAAATTTGGCCTATTATGCAGCTATGCTTGGAAGAAGAACACACCAGATCCATCGGCCCCCGTGAGAGTGCCA
AGGAGTACCGACAGCGAAGCCTACTGGAAGAAAGAACTGCTTTTCTTCGCTTATGATGTTTTTGAATTCCTTTG
TGGATCCGGATTTCATGGACTCCAGAAGAAGTGATTCCCAAGAGATTGCAAGAGAAACAGAAGTCAGAACGGGAAA
CAGCCGTACGCATCTCCAGGAGATTGGGAACCTTATGAAGGAAATCGAGACCCTTGTGGAAGAGAAGACCAAGG
AGTCACTGGATGTGAGCAGACTGACCCGGGAAGGTGGCCCCCTGCTGTATGAAGGCATCAGTCTCACCATGAACT
CCAAACTCCTGAATGGTTCCAGCGGGTGGTGATGGACGGCGTAATCTCTGACCACGAGTGTGAGGAGCTGCAGA
GACTGACCAATGTGGCAGCAACCTCAGGAGATGGCTACCGGGGTCAGACCTCCCCACATACTCCCAATGAAAAGT
TCTATGGTGTCACTGTCTTCAAAGCCCTCAAGCTGGGGCAAGAAGGCAAAGTTCTCTGAGAGTGCCACCTGT
ACTACAACGTGACGGAGAAGGTGCGGCGCATCATGGAGTCTACTTCCGCCTGGATACGCCCTCTACTTTTCTCT
ACTCTCATCTGGTGTGCCGCACTGCCATCGAAGAGGTCCAGGCAGAGAGGAAGGATGATAGTCATCCAGTCCACG
TGGACAACCTGCATCCTGAATGCCGAGACCCCTCGTGTGTGTCAAAGAGCCCCCAGCCTACACCTTCCGCGACTACA
GCGCCATCCTTTACCTAAATGGGGACTTCGATGGCGGAAACTTTTATTTCACTGAACTGGATGCCAAGACCGTGA
CGGCAGAGGTGCAGCCTCAGTGTGGAAGAGCCGTGGGATTCTCTTCAGGCCTGAAAACCCACATGGAGTGAAGG
CTGTACCAGGGGGCAGCGCTGTGCCATCGCCCTGTGGTTACCCCTGGACCCTCGACACAGCGAGCGGGGTGAGAG
CAGCTCGAGCGGGTGAGAGCAGCTGGTGTGTGGTGACCCGTTCCAGAGCGCCCTTGGTTTTGCCTTTCTCTTCC
CCAAATCCCATTTGCCAGTGGCTGAGACACGAAAGGAGCACTTGGGACACCAGCTCCAACGCCCTGTATTATGGT
CACATTGCCTTGTCTCTCCCTGGGCCTGCTGTGAACGGGATCCAGGTGGGGAAAGAGGTCAAGACAGGGAGCGATG
CTGAGTTCTTGGTTCCCTCCTTGGGCCCACTTCAGCTGTCTTTTCCAGAGAGTAGGACCTGCTGGGAAGGAGA
TGAGCCTGGGGCCATTAAGGAACCTTCCTTGTCCCCTGGGAAGTAGCAGCTGAGAGATAGCGAGTGTCTGGAGCG
GAGGCCTCTCTGAATGGGCAGGGGTTTGTCTTGCAGGACAGGGTGCAGGCAGATGACCTGGTGAAGATGCTCTT
CAGCCCAGAAGAGATGGACCTCTCCAGGAGCAGCCCTGGATGCCAGCAGGGTCCCCCGAACCTGCACAAGA
GTCTCTCTCAGGCAGTGAATCGAAGCCCAAGGATGAGCTATGACAGCGTCCAGGTCAGACGGATGGGTGACTAGA
CCCATGGAGAGGAACCTCTTCTGCACTCTGAGCTGGCCAGCCCCCTCGGGGCTGCAGAGCAGTGAGCCTACATCTGC
CACTCAGCCGAGGGGACCCCTGCTCACAGCCTTCTACATGGTGCTACTGCTCTTGGAGTGGACATGACCAGACACC
GCACCCCTTGGATCTGGCTGAGGGCTCAGGACACAGGCCAGCCACCCCGAGGGGCCTCCACAGGCCGCTGCATG
ACAGCGATACAGTACTTAAGTGTCTGTGTAGACAACCAAGAATAAATGATTTCATGGTTTTTTTTT

201/6881
FIGURE 188

TAGTCGCGGGTCCCCGAGTGAGCACGCCAGGGAGCAGGAGACCAAACGACGGGGGTGCGAGTCAGAGTCGCAGTG
GGAGTCCCCGGACCGGAGCACGAGCCTGAGCGGGAGAGCGCCGCTCGCACGCCCCGTGCCACCCGCGTACCCGGC
GCAGCCAGAGCCACCAGCGCAGCGCTGCCATGGAGCCCAGCAGCAAGAAGCTGACGGGTGCGCTCATGCTGGCTG
TGGGAGGAGCAGTGCTTGGCTCCCTGCAGTTTGGCTACAACACTGGAGTCATCAATGCCCCCAGAAGGTGATCG
AGGAGTTCTACAACCAGACATGGGTCCACCGCTATGGGGAGAGCATCCTGCCACCACGCTCACCACGCTCTGGT
CCCTCTCAGTGGCCATCTTTTCTGTTGGGGGCATGATTGGCTCCTTCTCTGTGGGCCTTTTCGTTAACCGCTTG
GCCGGCGGAATTCAATGCTGATGATGAACCTGCTGGCCTTCGTGTCCGCCGTGCTCATGGGCTTCTCGAAACTGG
GCAAGTCCTTTGAGATGCTGATCCTGGGCCGCTTCATCATCGGTGTGTACTGCGGCCTGACCACAGGCTTCGTGC
CCATGTATGTGGGTGAAGTGTCACCACAGCCTTTCGTGGGGCCCTGGGCACCCTGCACCAGCTGGGCATCGTCG
TCGGCATCCTCATCGCCAGGTGTTTCGGCCTGGACTCCATCATGGGCAACAAGGACCTGTGGCCCCCTGCTGCTGA
GCATCATCTTCATCCCGCCCTGCTGCAGTGCATCGTGTGCCCTTCTGCCCCGAGAGTCCCCGCTTCCTGCTCA
TCAACCGCAACGAGGAGAACCAGGGCCAAGAGTGTGCTAAAGAAGCTGCGCGGGACAGCTGACGTGACCCATGACC
TGCAGGAGATGAAGGAAGAGAGTCGGCAGATGATGCGGGAGAAGAAGGTCACCATCCTGGAGCTGTTCCGCTCCC
CCGCCTACCGCCAGCCCATCCTCATCGCTGTGGTGTGCTGCAGCTGTCCAGCAGCTGTCTGGCATCAACGCTGTCT
TCTATTACTCCACGAGCATCTTCGAGAAGGCGGGGGTGCAGCAGCCTGTGTATGCCACCATTGGCTCCGGTATCG
TCAACACGGCCTTCACTGTCTGTCTGTTTGTGGTGGAGCGAGCAGGCCGGCGGACCCTGCACCTCATAGGCC
TCGCTGGCATGGCGGGTGTGCCATACTCATGACCATCGCGCTAGCACTGCTGGAGCAGCTACCCTGGATGTCTCT
ATCTGAGCATCGTGGCCATCTTTGGCTTTGTGGCCTTCTTTGAAGTGGGTCTGGCCCCATCCCATGGTTTCATCG
TGGCTGAACTCTTCAGCCAGGGTCCACGTCCAGCTGCCATTGCCGTTGCAGGCTTCTCCAACCTGGACCTCAAATT
TCATTGTGGGCATGTGCTTCCAGTATGTGGAGCAACTGTGTGGTCCCTACGTCTTCATCATCTTCACTGTGCTCC
TGGTTCTGTTCTTCATCTTCACCTACTTCAAAGTTCCTGAGACTAAAGGCCGGACCTTCGATGAGATCGCTTCCG
GCTTCCGGCAGGGGGGAGCCAGCCAAAGTGATAAGACACCCGAGGAGCTGTTCCATCCCCTGGGGGCTGATTCCC
AAGTGTCAGTCGCCCCAGATCACCAGCCCGGCCTGCTCCAGCAGCCCTAAGGATCTCTCAGGAGCACAGGCAGC
TGGATGAGACTTCCAAACCTGACAGATGTGAGCCGAGCCGGGCCTGGGGCTCCTTTCTCCAGCCAGCAATGATGT
CCAGAAGAATATTACAGGACTTAACGGCTCCAGGATTTTAACAAAAGCAAGACTGTTGCTCAAATCTATTACAGACA
AGCAACAGGTTTTATAATTTTTTTTATTACTGATTTTGTATTATTTTATATCAGCCTGAGTCTCCTGTGCCACATC
CCAGGCTTCACCCTGAATGGTTCCATGCCTGAGGGTGGAGACTAAGCCCTGTGAGACACTTGCCTTCTTCACCC
AGCTAATCTGTAGGGCTGGACCTATGTCCTAAGGACACACTAATCGAACTATGAACTACAAAGCTTCTATCCAG
GAGGTGGCTATGGCCACCCGTTCTGCTGGCCTGGATCTCCCCACTCTAGGGGTCAGGCTCCATTAGGATTTGCC
CTTCCCATCTCTTCTACCCAACCACTCAAATTAATCTTTCTTTACCTGAGACCAGTTGGGAGCACTGGAGTGCA
GGGAGGAGAGGGGAAGGGCCAGTCTGGGCTGCCGGGTCTAGTCTCCTTTGCACTGAGGGCCACACTATTACCAT
GAGAAGAGGGCCTGTGGGAGCCTGCAAACCTCACTGCTCAAGAAGACATGGAGACTCCTGCCCTGTTGTGTATAGA
TGCAAGATATTTATATATATTTTTTGGTTGTCAATATTAAATACAGACACTAAGTTATAGTATATCTGGACAAGCC
AACTTGTAATAACACCACTCACTCCTGTTACTTACCTAAACAGATATAAATGGCTGGTTTTTTAGAAACATGGTT
TTGAAATGCTTGTGGATTGAGGGTAGGAGGTTTGGATGGGAGTGAGACAGAAGTAAGTGGGGTTGCAACCACTGC
AACGGCTTAGACTTCGACTCAGGATCCAGTCCCTTACACGTACCTCTCATCAGTGTCTCTTGCTCAAAAATCTG
TTTGATCCCTGTTACCCAGAGAATATATACATTCTTTATCTTGACATTCAAGGCATTTCTATCACATATTTGATA
GTTGGTGTTCAAAAAACACTAGTTTTGTGCCAGCCGTGATGCTCAGGCTTGAAATCGCATTATTTTGAATGTGA
AGGGAA

202/6881
FIGURE 189

MEPSSKKLTGRLMLAVGGAVLGSLQFGYNTGVINAPQKVIEEFYNQTWVHRYGESILPTTLTTLWSLSVAIFSVG
GMIGSF SVGLFVNRFGRNSMLMMNLLAFVSAVLMGF SKLGKSFEM LILGRFIIGVYCGLTTGFVPMYVGEVSPT
AFRGALGTLHQLGIVVGILIAQVFGLDSIMGNKDLWP LLLSIIFIPALLQCIVLPFCPESPRFLLINRNEENRAK
SVLKKLRGTADVTHDLQEMKEESRQMMREKKVTILELFRSPAYRQPI LIAVVLQLSQQLSGINAVFYSTSI FEK
AGVQQPVYATIGSGIVNTAFTVVSLFVVERAGRRTLHLI GLAGMAGCAILMTIALALLEQLPWMSYLSIVAIFGF
VAF FEVGPGPIPWFI VAE LFSQGPRPAAI AVAGFSNWTSNFIVGMCFQYVEQLCGPYVFIIFTVLLVLFFIFTYF
KVPETKGRTFDEIASGFRQGGASQSDKTPEELFHPLGADSQV

203/6881
FIGURE 190

CACGTCGTTACGGCCTTCTTCGGCCCCTCTAGCACGACATTGAGGCCTGGCTTCAGAAGCCCTCGGGAAAACGC
ATCCTGCAACTCTCTGTCTGTGACAAGGGATTTCATCGGATTCCGACTCCGAATCCGAGAGCGGGGAGTGTCCAT
CTCGCCGCACGCACGTCCCACACAGCTACTGCTCAACTTTTTGATTGGGACTTCCGCTTCCGGCGGCAAACCATAC
TTCCGGTTTGTCTGCTATAGGAACCGCTACGGCGTTTGAAGTGTCCGGGTTGCTTAGGATCCCTACAGGTAG
CGCCTCTGGATACATGCGTGGTCTGCTGACCCAGAGAGAAAACGAAAGCAGAAGTGTGGCGGGAGATCATGTCA
GCCGTGGTAGCTCAGACGCTGCATGTTTTTGGTCTTCGATCCACGTGGCCAACAATATCTTCTACTTTCGATGAA
CAGATCATTATATTTCTTCAGGAAATCACTGTGTGAAGTACAATGTGGATCAGAAATGGCAAAAATTCATTCCA
GGCTCAGAGAAGAGTCAGGGCATGTTGGCCTTGTCCATCAGTCCCAATCGGCGGTACCTCGCTATCTCTGAGACT
GTGCAAGAAAAACCTGCCATCACCATTTATGAATTGTCTCCATCCCTTGCCGGAAGCGCAAAGTTCTTAATAAT
TTTGACTTCCAAGTTCAGAAATTTATTAGCATGGCTTTTTCTCCAGACTCCAAATACCTATTGGCTCAGACGTCA
CCTCCAGAGTCAAATCTTGTCTACTGGCTGTGGGAAAAACAGAAAAGTAATGGCCATTGTTAGAATCGACACTCAG
AACAACCTGTCTACCAGGTGAGCTTCAGTCCACAGGATAACACTCAGGTGTGTGTCACTGGAAATGGGATGTTT
AAGCTTCTCCGTTTTGCTGAGGGAACCTGAAGCAAACAGCTTTCAGAGGGGAGAACCCCAAACTATCTAGCC
CACACCTGGGTGGCTGATGACAAGATTGTCGTTGGCACTGACACAGGCAAACCTCTTCTCTTTGAATCTGGAGAT
CAGCGTTGGGAGACCAGCATAATGGTCAAGGAACCTACCGATGGCTCAAAGAGCCTGGATGTCAATTCAGGAATCA
GAGAGCCTGATTGAATTTCCACCAGTCAGTTCTCCACTCCCTTCCTATGAACAGATGGTGGCGGCCAGTAGCCAT
AGCCAGATGTCCATGCCCCAGGTGTTTGCCATTGCAGCCTATTCAAAGGGATTGCTGCTGTTCTGCTGGGCCAGGG
AGAGTTCTGCTGTTTGAGAAGATGGAAGAAAAGGATTTTTACCGTGAGAGCAGAGAAATCAGGATTCCTGTGGAC
CCGCAGAGCAATGATCCAAGTCAGTCTGACAAACAGGACGTTCTCTGCCTGTGCTTCAGCCCCCTCAGAGGAACT
CTGGTTGCCAGCACCAGTAAGAACCAACTCTACAGCATCACCATGTCCCTGACAGAGATCAGCAAGGGAGCCTGC
TCACTTTGAGTATTTGATGTATCCATTGCACTCAGCACCCATCACCAGGTCTAGCTACCTGCATCCGCAAAACCCCT
TATAGCCACCTGTTCTCTGGATCGATCCATCCGCCTTTGGAATTATGAAACAAACACCCTGGAACCTATTTAAGGA
ATACCAAGAAGAGGCATATTCCATCAGCCTTCATCCATCTGGACACTTCATTGTAGTAGGGTTTGCTGACAACT
ACGCCTCATGAATCTACTCATTGATGATATACGTTCTTTCAAAGAATACTCTGTTAGAGGATGCGGAGAGTGTTC
CTTTAGCAATGGAGGTCACCTGTTTGCTGCAGTCAATGGAATGTGATTACGTTTACACCACCACGAGCCTAGA
GAACATCTCAAGCCTGAAAGGACACACAGGGAAGATTGCTCAATTGTGTGGAATGCAGATTGATAGCAAACTGAT
TTCTGGTGGCACAGATGGTGCTGTGTATGAATGGAATCTGTCCACAGGAAAGAGAGAGACAGATGCGTGCTCAA
GTCTTGAGCTACAACCTGTGTTACTGTCTCCCCGATGCCAAAATTATCTTTGCTGTTGGATCAGACCACACCCCT
CAAGGAGATTGCAGATTCCCTTGCCTTCGAGAGATATCGGCGTTTGATGTCACCTACACCGCCATTGTCATCTCGC
ATTCTGGACGCATGATGTTTGTGGGCACCTCGGTGGGAACCATTCGTGCCATGAAGTACCCTCTGCCTCTGCAGA
AGGAATTCAATGAGTACCAGGCCCATGCCGCTCCTATCACCAAGGTGAGCAGGGCCCTCTCCCCAGGAACCCAGT
CCCACACCTGCCTGCTACGTGCCTTGTTTCATCCCTTCAACCTCCCAATGTCTTTCTCTCTCCTTCTCTCTCTT
ATTTATTCATCCATCATTCAATTGAATCACCATCTATTGACTATGAATATACTCTTTGTTTTAACTACTTCCAGGA
ATTTAGCCTAGGAAATCATCAGAGATACACCTAAAAATGTATGTACAACGTTTTCACCATAATATTATGCATAAT
AAGGGGCCGTTTGGTGGATGCCGTAGCTGCCGTGAGTGTGGGCTGCACTTGACCACAGCTGCCTCCTCCTCCAGA
GAATGCCCCAGACTGAAAGGAGCCATAGCCCTGAAGATTGGCCCCCTACCTCTCCCTGAGGGTACAAAAGGCCACC
CCAGGGGCAATACCATGAGTACACATTTGTAAATTGTCCTTCCATTACCCCTTCTCATAAAGTAGTATCTATGTT
CAACAGTCAAAATGTGGAAGCAACCAAGCATCCATCGACAGACGAATGCATAAGCAAAAGATGGTATATCTATAC
AATGGAACAATACCCTGCCTAAAAAGGAAGGGAATTCTGCAATGTGCTACCACATGGATGAACCTTGAGGATGTT
ATGCTAAATTAAATAAGGCCAACCAAAAAAGATAAGTACAGTGTGATTCCACTTTTAGGAGATACTTGGAGCAG
TCAGAATCACAAAGACAGAGTGGTGGTTGGCAGGGGCTGCAGGAAGGGGGGAATGAGGAATGATTGTTTTCATAGGT
ATAGAGTTTTGGTTTTACAAGACAAAAGGATTATGGGGGTAGTTGGTGGCAATGGCTGCACAACATTACAAATGT
ATTTAATAACATGAAGTGTACACTTGAAAATGGTTAAGATAGCAAATTTTACAGAATATGTATTTTACGACAATT
TTAAAAATGAAATAAAAAAGAATTATCTTGC

204/6881
FIGURE 191

MSAVVAQTLHVFGLRSHVANNIFYFDEQIIIFPSGNHCVKYNVDQKWQKFIPGSEKSQGMLALSISPNRRYLAI
ETVQEKPAITIIYELSSIPCRKRKVLNNFDFQVQKFISMAFSPDSKYLLAQTSPPESENLYVWLWEKQKVMAIVRID
TQNNPVYQVSFSPQDNTQVCVTGNGMFKLLRFAEGTLKQTSFQRGEPQNYLAHTWVADDKIVVGTDGTGKLFLFES
GDQRWETSIMVKEPTNGSKSLDVIQESLIEFPPVSSPLPSYEQMVAASSHSQMSMPQVFIAAAYSKGFAACSAG
PGRVLLFEKMEEKDFYRESREIRIPVDPQSNDPQSQDKQDVLCLCFSPSEETLVASTSKNQLYSITMSLTEISKG
EPAHFEYLMYPLHSAPITGLATCIRKPLIATCSLDRSIRLWNYETNTLELFKEYQEEAYSISLHPSGHFIVVGFA
DKLRLMNLLIDDIRSFKEYSVRGCGECSFSNGGHLFAAVNGNVIHVYTTTSLENISSLKGHTGKSLNCVECR

205/6881
FIGURE 192

GCGATTTCGGTGGCACGTGGAGCCACGGCGTGGGAGTAGGGGGCTGAAGGCAGGCAGCAGCGGCCAGGGCCGCCCT
CTGCTAGCCGCTTGGGTCTCGGGATACCCCGTTTCTTCCTGTAGGTGTGGGACGTGCGTGCGGCGAGATGGACAC
-TCCCCCGCTCTCGGATTTCGGAGTCGGAATCCGATGAATCCCTTGTACAGACAGAGAGTTGCAGGATGCGTTTTTC
CCGAGGGCTTCTGAAGCCAGGCCTCAATGTCGTGCTAGAGGGGGCCGAAGAAGGCCGTGAACGACGTGAATGGCCT
GAAGCAATGTTTGGCAGAATTCAAGCGGGATCTGGAATGGGTGAAAGGCTCGATGTGACACTGGGTCCGGTACC
GGAGATCGGTGGATCTGAGGCGCCAGCACCTCAGAACAAAGACCAGAAAGCTGTTGATCCAGAAGACGACTTCCA
GCGAGAGATGAGTTTCTATCGCCAAGCCCAGGCCGAGTGCTTGCAGTCTTACCCCGCCTCCATCAGCTCAAAGT
CCCTACGAAGCGACCCACTGATTATTTTGCGGAAATGGCCAAATCTGATCTGCAGGTGCAGAAGATTTCGACAGAA
GCTGCAGACTAAACAGGCTGCCATGGAGAGGTCTGAAAAAGCTAAGCAACTGCGAGCACTTAGGAAATACGGGAA
GAAGGTGCAAACGGAGGTTCTTCAGAAGAGGCAGCAGGAGAAAGCCCATATGATGAATGCTATTAAGAAATATCA
GAAAGGCTTCTCTGATAAACTGGATTTCCTTGAGGGAGATCAGAAACCTCTGGCACAGCGCAAGAAGGCAGGAGC
CAAAGGCCAGCAGATGAGGAAGGGGCCAGTGCTAAACGACGGTATAAAAACCAGAAGTTTGGTTTTGGTGGAAA
GAAGAAAGGCTCAAAGTGGAACACTCGGGAGAGCTATGATGATGTATCTAGCTTCCGGGCCAAGACAGCTCATGG
CAGAGGCCTCAAGAGGCCTGGCAAGAAAGGGTCAAATAAGAGACCTGGAAAACGAACAAGAGAGAAGATGAAGAA
CAGAACACACTAAATAGCATCTTTGAATACAAAGAACCAAGAAAAAGGAATGAAGACTCGCAATTTACGACACA
CTTTGATCCCTTCTGTTGGTGTGATGTTGTAAACATTTCTTTCAATAAACTAAAGAAAAATTATTAAAGGAACAC
ATACCTTTGGTTAAATAGTCTAGACTAAAAGATTGAGAAGTTACTTTCCATTGCTATCTATTGATAATTTAGACA
TTGAGTTCAAATTGCCTTCATTTTATGATAAATAATGATTTAACTGAAAA

206/6881
FIGURE 193

MDTPPLSDSESESESLVTDRELQDAFSRGLLKPGLNVLLEGPKKAVNDVNGLKQCLAEFKRDLEWVERLDVTLG
PVPEIGGSEAPAPQNKDQKAVDPEDDFQREMSFYRQAQAAVLAVLPRHLQLKVPTKRPTDYFAEMAKSDLQVQKI
RQKLQTKQAAMERSEKAKQLRALRKYGKKVQTEVLQKRQQEKAHMMNAIKKYQKGFSDKLDFLEGDQKPLAQRKK
AGAKGQQMRKGPSAKRRYKNQKFGFGGKKKGSKWNTRESYDDVSSFRAKTAHGRGLKRP GKKGSNKRPGKRTREK
MKNRTH

207/6881
FIGURE 194

CCACGCGTCCGGGCGTAAGCCAGGCGTGTTAAAGCCGGTCGGAAGTCTCCGGAGGGCACGGGCTCCGTAGGCAC
CAACTGCAAGGACCCCTCCCCCTGCGGGCGCTCCCATGGCACAGTTCGCGTTCGAGAGTGACCTGCACTCGCTGC
TTCAGCTGGATGCACCCATCCCCAATGCACCCCTGCGCGCTGGCAGCGCAAAGCCAAGGAAGCCGCAGGCCCGG
CCCCCTCACCCATGCGGGCCGCCAACCAGATCCACAGCGCCGGCAGGACTCCGGGGCCGAATCCTGGCAAATCCA
GTTCCAAGGTTTCAAGCACTCCTAGCAAACCTGGCGGTGACCGCTATATCCCCCATCGCAGTGCTGCCCAGATGG
AGGTGGCCAGCTTCCTCCTGAGCAAGGAGAACCAGTCTGAAAACAGCCAGACGCCACCAAGAAGGAACATCAGA
AAGCCTGGGCTTTGAACCTGAACGGTTTTGATGTAGAGGAAGCCAAGATCCTTCGGCTCAGTGGAAGAACACAAA
ATGCGCCAGAGGGTTATCAGAACAGACTGAAAGTACTCTACAGCCAAAAGGCCACTCCTGGCTCCAGCCGGAAGA
CCTGCCGTTACATTCTTCCCTGCCAGACCGTATCCTGGATGCGCCTGAAATCCGAAATGACTATTACCTGAACC
TTGTGGATTGGAGTTCTGGGAATGTACTGGCCGTGGCACTGGACAACAGTGTGTACCTGTGGAGTGCAAGCTCTG
GTGACATCCTGCAGCTTTTGCAAATGGAGCAGCCTGGGGAATATATATCCTCTGTGGCCTGGATCAAAGAGGGCA
ACTACTTGGCTGTGGGCACCAGCAGTGCTGAGGTGCAGCTATGGGATGTGCAGCAGCAGAAACGGCTTCGAAATA
TGACCAGTCACTCTGCCCCGAGTGGGCTCCCTAAGCTGGAACAGCTATATCCTGTCCAGTGGTTTACGTTCTGGCC
ACATCCACCACCATGATGTTGGGTAGCAGAACACCATGTGGCCACACTGAGTGGCCACAGCCAGGAAGTGTGTG
GGCTGCGCTGGGCCCCAGATGGACGACATTTGGCCAGTGGTGGTAATGATAACTTGGTCAATGTGTGGCCTAGTG
CTCCTGGAGAGGGTGGCTGGGTTCTCTGCAGACATTCACCCAGCATCAAGGGGCTGTCAAGGCCGTAGCATGGT
GTCCCTGGCAGTCCAATGTCTGGCAACAGGAGGGGGCACCAGTGATCGACACATTCGCATCTGGAATGTGTGCT
CTGGGGCCTGTCTGAGTGCCGTGGATGCCATTCCAGGTGTGCTCCATCCTCTGGTCTCCCCATTACAAGGAGC
TCATCTCAGGCCATGGCTTTGCACAGAACCAGCTAGTTATTTGGAAGTACCAACCATGGCCAAGGTGGCTGAAC
TCAAAGGTCACACATCCCGGCTCCTGAGTCTGACCATGAGCCCAGATGGGGCCACAGTGGCATCCGCAGCAGCAG
ATGAGACCCTGAGGCTATGGCGCTGTTTTGAGTTGGACCCTGCGCGGCGCGGGAGCGGGAGAAGGCCAGTGCAG
CCAAAAGCAGCCTCATCCACCAAGGCATCCGCTTGAAGACCAACCCATCACCTCAGTTGTTTTTTATTTTTCTAAT
AAAGTCATGTCTCCCTTCATGTTTTTTTTTTTTAAAA

208/6881
FIGURE 195

MAQFAFESDLHSLQLDAPIPNAPPARWQRKAKEAAGPAPSPMRAANRSHSAGRTPGRTPGKSSSKVQTTPSKPG
GDRYIPHRSAQMEVASFLLSKENQSENSQTPTKKEHQKAWALNLNGFDVEEAKILRLSGKPQNAPEGYQNRLKV
LYSQKATPGSSRKTCRYIPSLPDRILDAPFIRNDYYLNLVDWSSGNVLAVALDNSVYLWSASSGDILQLLQMEQP
GEYISSVAWIKEGNYLAVGTSSAEVQLWDVQQQKRLRNMTSHSARVGSLSWNSYILSSGSRSGHIHHHDVRVAEH
HVATLSGHSQEVCGLRWAPDGRHLASGGNDNLVNVWPSAPGEGGWVPLQTFHQHQAQVAVAWCPWQSNVLTATGG
GTSDRHIRIWNVCSGACLSAVDAHSQVCSILWSPHYKELISGHGFAQNQLVIWKYPTMAKVAVELKGHTSRVLSLT
MSPDGATVASAAADETLRLWRCFELDPARRREREKASAAKSSLIHQGIR

209/6881
FIGURE 196

GGCACGAGGGGAACCGTCCGCAGCCGCCGGAGCCGGGAGCCCTGCCCAAGTCGGAGCGGCGTCCCCTGCTGAGCCC
CGAGCGCCGGGGCCAGCAGCCGGATGCCCCGGGCCACTGGGCGGGCCAGTGGCCGCCTGCGGGGATGAGCAGACTGC
TGGGGGGGACGCTGGAGCGCGTCTGCAAGGCTGTGCTCCTTCTCTGCCTGCTGCACTTCCTCGTGGCCGTCATCC
TCTACTTTGACGTCTACGCCCAGCACCTGGCCTTCTTCAGCCGCTTCAGTGGCCGAGGCCCTGCCCATGCCCTCC
ACCCAGCTGCTAGCAGCAGCAGCAGCAGCAGCAACTGCTCCCGGCCAACGCCACCGCCTCTAGCTCCGGGCTCC
CTGAGGTCCCCAGTGCCCTGCCCCGGTCCACGGCTCCACGCTGCCACCCTGTCTGACTCGCCACCTGGTCTTG
CGGGTGACAGGGAGAACCCAGGCGTGCTCATGGGCGGGCGATACACACCGCCCGACTGCACCCCAGCCCAGACG
GTGGCGGTCTATCATCCCTTTAGACACCGGGGAACACCACCTGCGCTACTGGCTCCACTATCTACACCCATCTTG
AGGCGGCAGCGGCTGCGCTACGGCGTCTATGTCTATCAACCAGCATGGTGAGGACACCTTCAACCGGGCCAAGCTG
CTTAACGTGGGCTTCTTAGAGGCGCTGAAGGAGGATGCCGCCTATGACTGCTTTCATCTTCAGCGATGTGGACCTG
GTCCCCATGGATGACCGCAACCTATACCGCTGCGGCGACCAACCCCGCCACTTTGCCATTGCCATGGACAAGTTT
GGCTTCCGGCTTCCCTATGCTGGCTACTTTGGAGGTGTGTGTCAGGCCTGAGTAAGGCTCAGTTTCTGAGAATCAAT
GGCTTCCCCAATGAGTACTGGGGCTGGGGTGGCGAGGATGATGACATCTTCAACCGGATCTCCCTGACTGGGATG
AAGATCTCACGCCCAGACATCCGAATTGGCCGCTACCGCATGATCAAGCACGACCGCGACAAGCATAACGAACCT
AACCCTCAGAGGTTTACCAAGATTCAAAACACGAAGCTGACCATGAAGCGGGACGGCATTGGGTGAGTGCGGTAC
CAGGTCTTGGAGGTGTCTCGGCAACCACTCTTCACCAATATCACAGTGGACATTGGGCGGCCTCCGTCTGGCCC
CCTCGGGGCTGACACTAATGGACAGAGGCTCTCGGTGCCGAAGATTGCCTGCCAGAGGACTGACCACAGCCTGGC
TGGCAGCTGCTCTGTGGAGGACCTCCAGGACTGAGACTGGGCTCTGTTTTCCAAGGGTCTTCACTAGGCCCCCTA
GCTACACCTGGAAGTTTCAAGAACCACTTTGGGGGGCCTCCTGCCTGGGCAGGCTCTTCAAGTGTGGCCCTCTTT
GGAGTCAACCCCTCCTTCCCGACCCCTCCCCCTAGCCAGCCCCAGTCACTGTGAGGGTCGGGCCAGCCCCTGCA
CTGCCTCGCAGAGTGGCCTGGGCTAGGTCACTCCACCTCTCTGTGCCTCAGTTTCCCCCCTTGAGTCCCCTAGG
GCCTGGAAGGGTGGGAGGTATGTCTAGGGGGCAGTGTCTCTTCAGGGGGAATTCTCAGCTCTTGGGAACCCCT
TGCTCCCAGGGGAGGGGAAACCTTTTTTCATTCAACATTGTAGGGGGCAAGCTTTGGTGCGCCCCCTGCTGAGGAG
CAGCCCCAGGAGGGGACCAGAGGGGATGCTGTGTGCTGCCTGGGATCTTGGGGTTGGCCTTTGCATGGGAGGCA
GGTGGGGCTTGGATCAGTAAGTCTGGTTCCCGCCTCCCTGTCTGAGAGAGGAGGCAGGAGCCCCAGGGCCGGCTT
GTGTTTGTACATTGCACAGAACTTGTGTGGGTGCTTTAGTAAAAACGTGAATGGAAAAAAAAAAAAAAAAAAAA

210/6881
FIGURE 197

MSRLLGGLTERVCKAVLLLCLLHFLVAVILYFDVYAQHLAFFSRFSARGPAHALHPAASSSSSSSSNCSRPNATAS
SSGLPEVPSALPGPTAPTLPDPCDPPGLAGAQGEPRRAHGRPIHTARLHPSPDGGGHHPL

211/6881
FIGURE 198

CCCAGTGCCCTGCCCGGTCCCACGGCTCCCACGCTGCCACCCTGTCCTGACTCGCCACCTGGTCTTGTGGGCAGA
CTGCTGATCGAGTTCACCTCACCCATGCCCCTGGAGCGGGTGCAGAGGGCCTGGAAGGGTGGGAGGTATGTCTAG
GGGGCAGTGTCTCTTCCAGGGGGAATTCTCAGCTCTTGGGAACCCCTTGCTCCCAGGGGAGGGGAAACCTTTTT
CATTCAACATTGTAGGGGGCAAGCTTTGGTGCGCCCCCTGCTGAGGAGCAGCCCCAGGAGGGGACCAGAGGGGAT
GCTGTGTCGCTGCCTGGGATCTTGGGGTTGGCCTTTGCATGGGAGGCAGGTGGGGCTTGGATCAGTAAGTCTGGT
TCCCGCCTCCCTGTCTGAGAGAGGAGGCAGGAGCCCCAGGGCCGGCTTGTGTTTGTACATTGCACAGAACTTGT
GTGGGTGCTTTAGTAAAAAACGTGAATGG

212/6881
FIGURE 199

GCCAGCAGCCGGATGCCCCGGGCCCACTGGGCGGGCCAGTGGCCGCCTGCGGG**ATG**AGCAGACTGCTGGGGGGGAC
GCTGGAGCGCGTCTGCAAGGCTGTGCTCCTTCTCTGCCTGCTGCACTTCCTCGTGGCCGTCATCCTCTACTTTGA
CGTCTACGCCCAGCACCTGGCCTTCTTCAGCCGCTTCAGTGCCCGAGGCCCTGCCCATGCCCTCCACCCAGCTGC
TAGCAGCAGCAGCAGCAGCAGCAACTGCTCCCGGCCCAACGCCACCGCCTCTAGCTCCGGGCTCCCTGAGGTCCC
CAGTGCCCTGCCCCGGTCCCACGGCTCCCAAGCTGCCACCCTGTCTGACTCGCCACCTGGTCTTGTGGGCAGACT
GCTGATCGAGTTACCTCACCCATGCCCCCTGGAGCGGGTGCAGAGGGAGAACCAGGCGTGCTCATGGGCGGCCG
ATACACACCGCCCCGACTGCACCCAGCCCAGACGGTGGCGGTCATCATCCCCTTTAGACACCGGGAACACCACCT
GCGCTACTGGCTCCACTATCTACACCCATCTTGAGGCGGCAGCGGCTGCGCTACGGCGTCTATGTCATCAACCA
GCATGGTGAGGACACCTTCAACCGGGCCAAGCTGCTTAACGTGGGCTTCCTAGAGGCGCTGAAGGAGGATGCCGC
CTATGACTGCTTCATCTTCAGCGATGTGGACCTGGTCCCCATGGATGACCGCAACCTATAACCGCTGCGGCGACCA
ACCCCGCCACTTTGCCATTGCCATGGACAAGTTTGGCTTCCGGCTTCCCTATGCTGGCTACTTTGGAGGTGTGTC
AGGCCTGAGTAAGGCTCAGTTTCTGAGAATCAATGGCTTCCCCAATGAGTACTGGGGCTGGGGTGGCGAGGATGA
TGACATCTTCAACCGGATCTCCCTGACTGGGATGAAGATCTCACGCCCAGACATCCGAATCGGCCGCTACCGCAT
GATCAAGCACGACCGCGACAAGCATAACGAACCTAACCCCTCAGAGGTTTACCAAGATTCAAAACACGAAGCTGAC
CATGAAGCGGGACGGCATTGGGTGAGTGCAGTACCAGGTCTTGGAGGTGTCTCGGCAACCACTCTTCACCAATAT
CACAGTGGACATTGGGCGGCCTCCGTCGTGGCCCCCTCGGGGCT**TGAC**ACTAATGGACAGAGGCTCTCGGTGCCGA
AGATTGCCTGCCAGAGGACTGACCACAGCCTGGCTGGCAGCTGCTCTGTGGAGGACCTCCAGGACTGAGACTGGG
CTCTGTTTTTCCAAGGGTCTTCACTAGGCCCCCTAGCTACACCTGGAAGTTTCAAGACCCACTTTGGGGGGCCTCC
TGCCTGGGCAGGCTCTTCAAGTGTGGCCCTCTTTGGAGTCAACCTCCTTCCCGACCCCTCCCCCTAGCCCAGC
CCCAGTCACTGTGAGGGTCGGGCGCAGCCCCTGCACTGCCTCGCAGAGTGGCCTGGGCTAGGTCACTCCACCTCTC
TGTGCCTCAGTTTCCCCCCTTGAGTCCCCTAGGGCCTGGAAGGGTGGGAGGTATGTCTAGGGGGCAGTGTCTCT
TCCAGGGGGAATTCTCAGCTCTTGGGAACCCCTTGCTCCCAGGGGAGGGGAAACCTTTTTTATTCAACATTGTA
GGGGGCAAGCTTTGGTGCGCCCTTGCTGAGGAGCAGCCCCAGGAGGGGACCAGAGGGGATGCTGTGTCGCTGCC
TGGGATCTTGGGGTTGGCCTTTGCATGGGAGGCAGGTGGGGCTTGGATCAGTAAGTCTGGTTCCCGCCTCCCTGT
CTGAGAGAGGAGGCAGGAGCCCCAGGGCCGGCTTGTGTTGTACATTGCACAGAACTTGTGTGGGTGCTTTAGT
AAAAACGTGAATGG

213/6881
FIGURE 200

MSRLGGTLERVCKAVLLLCLLHFLVAVILYFDVYAQHLAFFSRFSARGPAHALHPAASSSSSSSSNCSRPNATAS
SSGLPEVPSALPGPTAPTLPDPPGLVGRLLIEFTSPMPLEERVQRENPGVLMGGRYTPPDCTPAQTVAVIIP
FRHREHHLRYWLHYLHPILRRQRLRYGVYVINQHGEDTFNRAKLLNVGFLEALKEDAAYDCFIFSDVDLVPMDR
NLYRCGDQPRHFAIAMDKFGFRLPYAGYFGGVSGLSKAQFLRINGFPNEYWGWGGEDDDIFNRISLTGMKISRPD
IRIGRYRMIKHDRDKHNEPNPQRF TKIQNTKLTMKRDGIGSVRYQVLEVSQRPLFTNITVDIGRPPSWPPRG

214/6881
FIGURE 201

GCGGAGAAACAGTAGTTAGGATGGCTGAAGGGGATACTCACCGGCTGAAGGCCGACTGTGATTCCCCCTACCCCC
ACAAGGCGATTTTGACCCCCCTGAGGGCTGCTCTAGAGGACTCAGGCCCCGAAGCTGTCCCAGGGAGGTCCCCGCT
GCATCCCAACCAAGCTGTGCCTCATGGAGTCGATGTTTAGCAGCCCTGCCGAGGCGGCGCTGCAGCGAGAGA
CCGGGGTGCCAGGACTGCTTACTCCTCTTCCGGACCTGGACGGAGTGACGAGCTGGAGCGAGTCGCTGGATTG
TCCGCGACCTGGGGTGTGAACGAGTTGCCTTGCACTTCCCTGACCAGCTATTGGGAGATGCTGTGGCTGTGGCTG
CACGACTGGAGGAGACGACAGGGTCAAAGATGTTTATTCTGGGTGACACAGCCTACGGCAGCTGCTGCGTGGATG
TGCTGGGTGCTGAGCAAGCTGGAGCTCAGGCTCTCATACATTTTGGCCCTGCCTGCTTAAGCCCTCCAGCCCCGC
CACTGCCCGTTGCCTTCGTGCTTCGTCAACGTTCTGTGGCCTTGAGCTCTGTGTCAAGGCCTTTGAGGCCCCAGA
ACCCAGACCCCAAAGCGCCTGTGGTGTCTGCTGAGTGAGCCGGCCTGTGCCCATGCCCTGGAGGCTTTGGCTACTC
TCCTGCGCCACGGTACCTGGACCTGCTAGTCTCCAGCCCAGCTTTTCCCCAACCAGTGGGTTCCCTGAGTCCAG
AGCCTATGCCCTAGAGCGTTTGGGCGCCGCTTCCCCCTTGCCCCAGGGAGGCGTCTAGAAGAGTATGGTGCCT
TCTATGTAGGGGGCTCTAAGGCCAGCCCTGACCCAGACCTTGACCCAGACCTGAGTCGGCTGCTCTTGGGGTGGG
CACCAGGTCAACCCTTCTCCTCCTGCTGTCCAGATACAGGGAAGACTCAGGATGAGGGTGCCCGGGCTGGACGGC
TAAGGGCACGAAGACGATATCTGGTAGAGAGGGCCAGAGATGCCCCGCTGGTAGGGCTGCTGGCAGGCACACTGG
GTGTAGCCCAACACCGTGAGGCACTGGCCCACTTGCGGAACCTGACTCAGGCTGCTGGCAAGCGTAGCTATGTGT
TGGCCCTGGGGCGGGCCACCCCTGCCAAGCTTGCCAACCTTCCCTGAGGTGGATGTCTTTGTGCTATTAGCCTGTC
CTCTGGGTGCTCTAGCCCCCAGCTTTCTGGTAGCTTCTTCCAGCCTATACTGGCACCATGTGAGCTGGAAGCTG
CCTGCAACCCTGCCTGGCCACCTCCAGGCCTGGCTCCCCACCTCACACATTATGCGGACTTATTGCCTGGCTCTC
CCTTCCACGTGGCTCTCCCAACACCTGAGTCAGAGCTGTGGGAAACCCAGACGTGTCACTCATTACTGGAGATC
TCCGACCCCACTGCCTGGAAGTCATCAAATGATCATGGAAGCTTGGCTCTGACCCACGGCCCCAGCTGGAGC
TGGCTGAGAGCAGTCTGCAGCCTCATTCCTTAGTTCCCGGAGCTGGCAAGGGCTGGAGCCCCGCCTGGGTGAGA
CGCCAGTGACAGAAGCTGTGAGTGGAAGACGAGGGATTGCCATCGCCTATGAGGATGAGGGAAGCGGCTGATACC
ATGTGGGGCTGGAGACATAGATGGACTTATGAATGGCTGCTAGGACCTTTAGTGCTCCCTGCACCAACCTCCCAT
CCCCCTGCCAAGATCCTTGAAGGACCCTGGAAGGAGGGAGAGCAGGCAGCCCTTACAGGATAGGATCCGTCTCT
GTCCTGTCCTGGCACTGGCACAAGCTCAGCCCATGCCAGTAATGCGTGTTGTTTGGCTGATGGAATAAAGGGCT
TAGGGACTTCCCTGAGGCCTCTGGACCCATCTGTCTTCTGAGGGCAGCCAGGACCTTTGGCCAATCCCAGTTC
CCAGGCTGCAGTTGAGGGTCTGTCTTGTCAAAAGGCAGGTGCTAGACAGTCTAGACCAGGGTTTCTCAAACCTCG
TACTTGACATTTGGGGCCAGATAATTCTTTGTTGTGGGGCTGTCTGGTGTATGGTAGGGTGCTCAGCAGCATCCC
TGGCCTCTGCCCACTAGACATCAGAAGCACTCCCCAGTTGTGACAACCAAAAAATATCTCCAGACCTTGGCAAAT
GTTATCTGTGGGGGAAAATTGCCCTCAATTGAGAACCCTGGTCTAGCTAGACCTGCACTGTCCAGTACAGTAGC
CACTAAATACATGTGGCTAAACTTAAATTTAAGTTAATTAAGATTAAGCTCAGTTTCTCAGTCACATTAGTCA
TTCAAGTGTTTCAAGACAGCCACATGAGGGGACAGTGCAGCTACAGGATATGCCATCATGGCAGAAAGTTCTGTTGG
TTGGACAGCGTTGGTCTATACTGACTCTTATTTCTCAGGGAGATCACAGCAACCTAAATAAACCAGATACCTTTT
C

215/6881
FIGURE 202A

GCCTTCGCCTGCTGGAAAAGCAGTAGGATCGGCCAGTGGCGACAGCAGGAGCTGAGCCTAAGCCCTGGCGGGGCT
TTGGGCTGTAGATTCTGTCTGACTAAAGGGACCTCAAAAAGGAGGGGAAAATGGCTTCTGAGTCTGAAACTCTGA
ATCCCAGTGCTAGGATAATGACCTTTTATCCAACCTATGGAAGAGTTCCGAAACTTCAGTAGATACATTGCCTACA
TTGAATCCCAAGGAGCTCATCGGGCAGGGCTAGCCAAGGTTGTTCTCCAAAAGAGTGGAAGCCACGAGCATCCT
ATGATGACATTGATGATTGGTCATTCTGCCCCATTCAACAGCTGGTGACGGGGCAGTCTGGCCTCTTTACTC
AGTACAACATACAGAAGAAAGCCATGACTGTTTCGAGAGTTCCGCAAGATAGCCAATAGCGATAAGTACTGTACCC
CACGCTATAGTGAGTTTGAAGAGCTCGAGCGGAAATACTGGAAAAATCTTACATTCAATCCTCCAATCTATGGTG
CAGATGTGAATGGTACCCCTCTATGAAAAGCATGTTGATGAGTGGAATATTGGCCGGCTGAGAAACAATCCTGGACT
TGGTGGAAAAGGAGAGTGGGATCACCATTGAGGGTGTGAACACCCCATACCTGTACTTTGGCATGTGGAAGACAT
CCTTTGCTTGGCACACTGAAGACATGGACCTCTACAGCATCAACTACCTGCACTTTGGAGAACCAGTCTGGT
ACTCTGTTCCACCTGAGCATGGAAAGCGGTTGGAACGCCTCGCCAAAGGCTTTTTCCAGGAAGTGCTCAAAGCT
GTGAGGCATTTCTCCGCCACAAGATGACCCTGATTTCCCGTTAATGCTGAAGAAATATGGAATTCCCTTTGACA
AGGTGACTCAAGAGGCTGGAGAGTTTATGATCACTTTCCCTTATGGTTACCATGCCGGCTTTAACCATGGTTTTA
ACTGTGCGGAGTCTACCAATTTTGCTACCCGTCGGTGGATTGAGTACGGCAAGCAAGCTGTGCTGTGCTCCTGTA
GAAAGGACATGGTGAAGATCTCCATGGATGTGTTTGTGAGAAAGTTCCAGCCAGAAAGGTACAAACTTTGAAAAG
CTGGGAAGGACAACACAGTTATTGACCATACTCTGCCACGCCAGAAGCAGCTGAGTTTCTTAAGGAGAGTGAAC
TGCCTCCAAGAGCTGGCAACGAGGAGGAGTGGCCAGAGGAGGACATGGAAGGGGTGGAGGATGGAGAGGAAGGAG
ACCTGAAGACAAGCCTGGCCAAGCACCGAATAGGGACAAAGAGGCACCGAGTTTGTCTTGAATACCAAGGAGG
TGAGTCAGAGTGAGCTCTTCCCAAGGAGGATCTGAGTTCTGAGCAGTATGAGATGACGGAGTGCCCGGCAGCCC
TCGCCCCCTGTGAGGGCCACCCATAGCTCTGTGCGGCAAGTTGAGGATGGTCTTACCTTCCAGATTATTCTGACT
CCACTGAAGTCAAATTTGAAGAGCTTAAAAATGTCAAACCTAGAAGAGGAGGATGAGGAGGAAGAACAAGAAGCAG
CTGCCTTGGATCTTTCTGTGAATCCTGCGTCTGTAGGGGGACGCTTGTCTTCTCAGGCTCCAAAAGAAATCAT
CTTCTAGCCTGGGCTCTGGCTCTTACGGGATTCTATCTCTTCTGATTGAGAACTAGTGAGCCTCTCTCCTGCC
GAGCCCAAGGGCAAACGGGAGTTCTCACTGTGCACAGTTATGCCAAAGGGGATGGCAGGGTCACTGTGGGAGAGC
CATGCACGAGGAAGAAAGGAAGCGCCGCTAGAAGTTTCAGTGAGCGGGAGCTGGCAGAGGTTGCAGATGAATACA
TGTTTTCCCTAGAAGAGAATAAGAAGTCCAAGGGACGCGCTCAGCCTTTAAGCAAGCTCCCCGCCATCACCCAC
TTGTGCTGCAGGAGTGTGTGATGATGAGACATCTGAACAGCTGACCCCTGAGGAAGAGGCTGAGGAGACAG
AGGCCTGGGCCAAGCCTCTGAGCCAACTGTGGCAGAACCAGCCTCCAAACTTTGAGGCTGAGAAGGAATTCAATG
AGACCATGGCCCAACAGGCCCCCTCACTGCGCTGTCTGTATGATCTTCCAGACTTATCATCAGGTTGAATTTGGAG
GCTTTAATCAGAACTGTGGAAAATGCTTCAGATTTAGCCCCCAGAAGCAGAGGACCAAGCCATTGATTCCAGAAA
TGTGCTTCACTTCGACTGGCTGCAGCACGGACATCAACCTTTCTACTCCTTATCTTGAGGAGGATGGCACCAGCA
TACTCGTTTTCTGCAAGAAAGTGACAGCTCCGGGTCCATGCCAGTTGCTATGGGGTCCCCCTGCAAAGGCTTCTG
AAGACTGGATGTGTTCTCGGTGTTTCAAGCAATGCCCTAGAGGAGGAGTCTGTTTATGCTCATTACGAGGAGGGG
CCCTGCAGAGAGCAAATGATGACAGGTGGGTCCACGTTTCTATGTGCTGTGGCAATTCTGGAAGCAAGGTTTGTCA
ACATTGCAGAAAGAAGTCCGGTGGATGTGAGCAAAATCCCCCTGCCCCGCTTCAAAGTGAATGTATCTTCTGTA
AGAAGCGGAGGAAAAGAAGTCTGGCTGCTGTGTGCAGTGTCTCACGGCCGCTGCCCAACTGCCTTCCATGTGA
GCTGCGCCCAGGCTGCCGGTGTGATGATGCAGCCTGACGACTGGCCTTTTGTGGTCTTCACTTACCTGCTTTCCGC
ACAAGATTCTTAATTTGGAGCGTGCCAAGGGGGCCTTGCAAAGCATCACTGCAGGCCAGAAAGTCATTAGCAAGC
ATAAGAACGGGCGCTTCTACCAAGTGTGAAGTGGTCAGGCTCACCACCGAGACCTTCTATGAAGTCAACTTTGATG
ATGGCTCCTTACGCGACAATCTTTATCTGAGGACATAGTGAGCCAGGACTGTCTCCAGTTTGGTCTCCTGTCTG
AAGGGGAAGTGGTCCAAGTGAGATGGACAGACGGCCAAGTCTATGGAGCCAAGTTTGTGGCTTCCACCCTATCC
AAATGTACCAGGTGGAGTTTGGAGATGGCTCACAACCTGTGGTTAAGAGAGATGATGTATACACTGGATGAAG
AGCTTCCCAAGAGAGTCAAATCTAGACTGTGATGAGCTCAGACATGCGCTTCAATGAGATTTTACAGAGAAAG
AGGTTAAGCAAGAAAAGAAACGGCAACGAGTTATCAACTCAAGATACCGGGAAGATTATATTGAGCCTGCACTAT
ACCGGGCCATCATGGAGTAGGTGCTTCCAGGGTCCAAGGGATTCTCAGCCATCCAGGCAAGAGCACTCTGGGTTC
CACAGCACAGCAGACATGGAACGCTGAACTCTCTGAAAGTGAAGTTGTAAAAAGAAAAGGAATGAAATAACCGAC
CCATCATCTTCTCACCCACCCTCATTGCATTCCGCTGTAGTGAAAGGACGAGCCATTTCTGGGCACGTGGCAGCA
GTCGCTGATCTCCAGCTGAGGGGGCTGAGCACTGGAATGCTGTGGCTGCACTGGCCCCAGTCCATAGAGGGGTCA

216/6881
FIGURE 202B

ACTATGCTGGCTGGACTGGCTGCCTTGTTCTGGCCTAGGACTTAGCTTCATAACTATCACCTGCACCGACTAGG
CTGAGGTGCTGGTACTTGCCCCAACCCTACTTTTGTATTTATATGTGTGTGTGTGTGTGCGTGCGTGCGTGCGT
GCGTGATGTTTGGTCTGGACCAGCTTCTGCCAGCCCCTGGCCTTTACTTTCTTCCTTGCCTATGCAGGGCAAAC
AAAATGTGAAATTCTGCCCTCAGCTGAGCTGAGTAAGGGCTCCTGGGGGTTGGCTGGAGATGGGTGTGGCATCTG
TCCAGGCCTGGAACCGTCTCAAGACAGTGCTGGCAAAGCTGCAGTATTGAGATGCTAAGGAGCTGATGCCACCTC
TTTGTCTTCCCCCTAAAGGAGAACATGGGGATAACATGGGTGTGTGCCACAACACTCTAGGTGCAGAGCCCCTGT
GGCAAAGTATTACAGGGTGTGGGTGGGGATTACCCTGAATCGGGGATTTTAATGATGGAAGCAGGCAGAGCCTGG
TGGGTGATTCTGTCAACAGAAAATTGCAATCATGCAGGGGCTGGGAGGGTTAGGATGAAAAAACTGGGGCCATTG
GAGGCCCACTGTAGGTGGGAGGGAGCTGATTTTGGGGTGGGGGGTGGGACTAGAGGGCAATACTGAAGGGGTTAA
ACAGGTTTTTGTCTCCTCAAGAATTTGTTTGCCTGGGCCCAGGATTGGAGGGCTTCACACCAATACCCTGTGTATA
CAAGAATCAGATTTATAATACTTCCCCTTTTTTGTACGTATGAACACTATAAACCAAATTATTTTG

217/6881
FIGURE 203

MASESETLNPSARIMTFYPTMEEFRNFSRYIAYIESQGAHRAGLAKVVPPKEWKPRASYDDIDDLVIPAPIQQLV
TGQSGLEFTQYNIQKKAMTVREFRKIANS DKYCTPRYSEFEELERKYWKNLTFNPP IYGADVNGTLYEKHVDEWNI
GRLRTILDLVEKESGITIEGVNTPYLYFGMWKTSFAWHTEDMDLYSINYLFHFGEPKSWYSVPPEHGKRLERLAKG
FFPGSAQSCEAFLRHKMTLISPLMLKKYGIPFDKVTQEAGEFMITFPYGYHAGFNHGFNCAESTNFATRRWIEYG
KQAVLCSCRKDMVKISMDVVFVRKFQPERYKLWKAGKDNTVIDHTLPTPEAAEFLKESELPPRAGNEEECPPEEDME
GVEDGEEGDLKTS LAKHRIGTKRHRVCLEIPQEVSQSELPKEDLSSEQYEMTECPAALAPVRPTHSSVRQVEDG
LTFPDYSDSTEVKFEELKNVKLEEEDEEEEQEAAALDLSVNPASVGGRLVFSGSKKKSSSLGSGSSRDSISSDS
ETSEPLSCRAQQGTGVLTVHSYAKGDGRVTVGEPCTRKKGSAARSF SERELAEVADEYMF SLEENKKSKGRRQPL
SKLPRHHPVLVQECVSDDDETSEQLTPEEEAEETEAWAKPLSQLWQNRPPNF EAEKEFNETMAQQAPHCAVCMIFQ
TYHQVEFGGFNQNCGNASDLAPQKQRTKPLIPEMCFTSTGCSTDINLSTPYLEEDGTSILVSCKKCSVRVHASCY
GVPPAKASEDWMCSRCSANALEEDCCLCSLRGGALQRANDDRWVHVSCAVAILEARFVNIAERSPVDVSKIPLPR
FKLKCIFCKKRRKRTAGCCVQCSHGRCP TAFHVSCAQAAGVMMQPDDWPFVVFITCFRHKIPNLERAKGALQSIT
AGQKVISKHKNGRFYQCEVVRLTTETFYEVNFDDGSFSDNLYPEDIVSQDCLQFGPPAEGEVVQVRWTDGQVYGA
KFVASHPIQMYQVEFEDGSQLVVKRDDVYTLDEELPKRVKSRLSVASDMRFNEIFTEKEVKQEKKRQRVINSRYR
EDYIEPALYRAIME

218/6881
FIGURE 204

AGTTACAGACAGCTGACCATGGGAAGCGAATGGGTGGGACCTCAGGGTTTTCCGGAGCTGAAGAATGACACATTCTGCGAGCAGCCTGGGGAGAGGAAACAGACTACACTCCCGTTTGGTGCATGCGCCAGGCAGGCCGTTACTTACCA GAGTTTAGGGAAACCCGGGCTGCCCAGGACTTTTTCAGCACGTGTCGCTCTCCTGAGGCCTGCTGTGAAGTACTGACT CTGCAGCCACTGCGTCGCTTCCCTCTGGATGCTGCCATCATTCTCCGACATCCTTGTTGTACCCAGGCACTG GGCATGGAGGTGACCATGGTACCTGGCAAAGGACCCAGCTTCCCAGAGCCATTAAGAGAAGAGCAGGACCTAGAA CGCCTACGGGATCCAGAAGTGGTAGCCTCTGAGCTAGGCTATGTGTTCCAAGCCATCACCCCTACCCGACAACGA CTGGCTGGACGTGTGCCGCTGATTGGCTTTGCTGGTGCCCCATGGACCCTGATGACATACATGGTTGAGGGTGGT GGCTCAAGCACCATGGCTCAGGCCAAGCGCTGGCTCTATCAGAGACCTCAGGCTAGTCACCAGCTGCTTCGCATC CTCACTGATGCTCTGGTCCCATATCTGGTAGGACAAGTGGTGGCTGGTGCCAGGCATTGCAGCTGTTTGAGTCC CATGCAGGGCATCTTGCCCCACAGCTCTTCAACAAGTTTGACTGCCTTACATCCGTGATGTGGCCAAGCAAGTG AAGGCCAGGTTGCGGGAGGCAGGCCTGGCACCAAGTGCCCATGATCATCTTTGCTAAGGATGGGCATTTTGCCCTG GAGGAGCTGGCCCAAGCTGGCTATGAGGTGGTTGGGCTTGACTGGACAGTGGCCCCAAAGAAAGCCCGGAGTGT GTGGGGAAGACGGTGACATTGCAGGGCAACCTGGACCCCTGTGCCTTGATGATCTGAGGAGGAGATCGGGCAG TTGGTGAAGCAGATGCTGGATGACTTTGGACCACATCGCTACATTGCCAACCTGGGCCATGGGCTTTATCCTGAC ATGGACCCAGAACATGTGGGCGCCTTTGTGGATGCTGTGCATAAACACTCACGTCTGCTTCGACAGAACTGAGTG TATACCTTTACCCTCAAGTACCACTAACACAGATGATTGATCGTTTCCAGGACAATAAAAGTTTCGGAGTTGAAC TATTGTGTAGTTTTGTTTGTGAAAGATTGTGCCCATATCCTCAGTTCTTCTTAGCCTCTGCTCCTTCCCTGGGAA CCCTCTCTATATCCTCTT

219/6881
FIGURE 205

MEANGLGPQGFPPELKNDTFLRAAWGEETDYTPVWCMRQAGRYLPEFRETRAQAQDFFSTCRSPEACCELTLOPLRR
FPLDAAIIFSDILVVPQALGMEVTMVPGKGPSFPEPLREEQDLERLRDPEVVASELGYVFQAITLTRQRLAGRVP
LIGFAGAPWTLMTYMVEGGGSSTMAQAKRWLYQRPQASHQLLRILTALVPYLVGQVVAGAQAALQLFESHAGHLG
PQLFNKFALPYIRDVAKQVKARLREAGLAPVPMIIFAKDGHFALEELAQAQAGYEVVGLDWTVPKKARECVGKTVT
LQGNLDPICALYASEEEIGQLVKQMLDDFGPHRYIANLGHGLYPDMDPEHVGAFVDAVHKHSRLLRQN

220/6881
FIGURE 206

AGCTTTGCGCAGTGGCAGTATCGTAGCCAATGAGGTTTATCCGAGGCGCGATTATTGCTAATTGAAAACTTTTCC
CAATACCCCGCCATGACGACTTGAAATATAGTCGGCATTGGCAATTTTTGACAGTCTCTACGGAGACTGCATGTG
CTGGTGAAGCTCCTGGAAGTGATGGGAAGGAATGGACAAGGAGACGTTTGAGTTCAAGTTTGGGAAGGAAC TAACA
TTCACCACTGTACTGAGTGACCAACAGGTGGTGGAGCTGATCCCTGGGGGTGCAGGCATCGTCGTGGGATATGGG
GACCGTTCTCGTTTCATCCAAC TGGTCCAGAAGGCACGGCTAGAGGAGAGCAAGGAGCAGGTGGCAGCTATGCAG
GCAGGTCTGCTGAAGGTGGTACCACAGGCTGTGCTGGACTTGCTGACCTGGCAAGAGTTGGAGAAGAAAAGTGTGT
GGGGATCCAGAGGTCACTGTGGATGCTCTGCGCAAGCTCACCCGGTTTGAGGACTTCGAGCCATCTGACTCGCGG
GTGCAGTATTTCTGGGAGGCACTGAACAAC TACCAACGAGGACCGGAGCCGCTTCCCTGCGCTTTTGTCACGGGC
CGCAGTCGCCTGCCAGCACGGATCTACATCTACCCAGACAAGCTGGGCTACGAGACCACAGACGCGCTGCCCCGAG
TCTTCCACTTGCTCCAGCACCCCTCTTCCCTGCCACACTATGCCAGTGCCAAGGTATGCGAGGAGAAGCTCCGCTAT
GCGGCCTACAAC TCGTGCCATCGACACTGACATGAGCCCTTGCGAGGAGTGAGAGGCGTGCCGCCGGCTGTGGGA
CCAGCAAGACTGCACGTGTCCCTCTTGCCCTTGCCAGGGCGAAGACACCTTCCCTGCCCTGGTTTGGCTGACGT
GCTCAGCAAAACCCCATGTGCCCTGCTCCTGTGTGCAGTTGGGGTAGGGGCAGCTGGCATGGTCAGGTAACACTA
GTGGCCCAGCCCCGAGACCCACAAGCCCTACCCGTGCTGGGGCTTGCTTCCCGAGGTATTTACCTCTTAAGAG
GGAATCTTCCACAAGCCCAGCACAAAGCTGCCAGGCCTGAGCTACTTGAAGGGGGCCATCTAGGTCCCCAACCCAT
GGACTTTGCCTCCATTTTCAGCTCCGCCTTTTTTCTCCTATTTTCTCTCTGGCTTTCTTCAGCCATGACTCACAA
CTAAAAACATAAAACACTGGAGGTTAGTGGAGGCCCTCCCCAAGCAGGGAGCCTGGGATGGGCAGGGAGTGATA
GCCAAACTCCTTGGTCACCTGCTCCAAGAAGGAAGCAGTAGCTGAGCACCTGCCCTCACATACTGCTCTTTTCCC
CTCTCCCTCCACACCAGAGATGTGGTGAGCTCTGTTCTTCTACCAACCCAGTCTCAACACACAAAGTGCCACCAC
CTTCCCTGACTCAGAACCCACATCCACTCAATGTGAACTCTACTACCACGACCTCCCCATATTCTCACTTCTCC
ATCACCTCCAGCCTGACTCCCTGTCTGCCCTTTACCCCCAAGATTTTGACACAGGTTAAGGCCAGTTATGGCCTT
TTTGAAATCTGTAATAGCTCCCCTTTCCCCAACTCTAAAGCCTAGACCTTAAACCTGTTTCTAGAGCTATGCACA
CCCCTGCCCCAGTTTACCGTTCCCTCCCTCAGGGCCTCCGTGACACTCCATGAAAAGAAGTTCTTGCATACCGGAA
AGTTGAATAAATGGATGAATTCAAAAAAAAAAAAAAAAAAAA

221/6881
FIGURE 207

MEGMDKETFEFKFGKELTFTTVLSDQQVVELIPGGAGIVVGYGDRSRFIQLVQKARLEESKEQVAAMQAGLLKVV
PQAVLDLLTWQELEKKVCGDPEVTVDALRKLTRFEDFEPDSRVQYFWEALNNFTNEDRSRFLRFVTGRSRLPAR
IYIYPDKLGYETTDALPESSTCSSTLFLPHYASAKVCEEKLRYYAAYNCVAIDTDMSPWEE

222/6881
FIGURE 208

CACAATGGTGCGCATGAATGCCCTGGCAGATGCTCTCAAGAGCATCAACAATGCCGAAAAGAGAGGCCAAACGCCA
GGTGCTTCTTAGGCCATGCTCCAAAGTCATCGTCCAGTTTCTCACTGTGATGATGAAGCATGGTTACATTGGCGA
ATTTGAAATCACTGATGATCACAGAGCTGGGAAAATTGTTGTGAACCTCACAGGCAGGCTAAACAAGTGTGGAGC
GATCAGCCCCAGATTTGATGTGCAACTCAAAGATCTGGAAAAATGGCAGAATAATCTGCTTCCATCCCGCCAGTT
TGATTTCAATTGTACTGACAACCTCAGCTGGCATCATGGACCATGAAGCAAGACGAAAACACACAGGAGGGAAAAAT
CCAGGGATTCTTTTTCTAGGGATGTAATACATATATTTACAAATAAAATGCCTCAAGGAC

223/6881
FIGURE 209

MVRMNALADALKSINNAEKRGRQVLLRPCSKVIVQFLTVMMKHGYIGEFEITDDHRAGKIVVNLTGRLNKCGAI
SPRFDVQLKDLEKWQNNLLPSRQFDFIVLTTSAGIMDHEARRKHTGGKIQGFFF

224/6881
FIGURE 210

CTCTTTCCAGCCAGCGCCGAGCGATGGGGCATCTCTCGGGACAACTGGCACAAAGCGCCGCAAAACCGGGGGCAAGA
GAAAGCCCTACCACAAGAAGCGGAAGTATGAGTTGGGGCGCCCAGCTGCCAACACCAAGATTGGCCCCCGCCGCA
TCCACACAGTCCGTGTGCGGGGAGGTAACAAGAAATACCGTGCCCTGAGGTTGGACGTGGGGAATTTCTCCTGGG
GCTCAGAGTGTTGTACTCGTAAAACAAGGATCATCGATGTTGTCTACAATGCATCTAATAACGAGCTGGTTTCGTA
CCAAGACCCTGGTGAAGAATTGCATCGTGCTCATCGACAGCACACCGTACCGACAGTGGTACGAGTCCCACTATG
CGCTGCCCCTGGGCCGCAAGAAGGGAGCCAAGCTGACTCCTGAGGAAGAAGAGATTTTAAACAAAAACGATCTA
AAAAAATTCAGAAGAAATATGATGAAAGGAAAAAGAATGCCAAATCAGCAGTCTCCTGGAGGAGCAGTTCCAGC
AGGGCAAGCTTCTTGCGTGCATCGCTTCAAGGCCGGGACAGTGTGGCCGAGCAGATGGCTATGTGCTAGAGGGCA
AAGAGTTGGAGTTCTATCTTAGGAAAATCAAGGCCCGCAAAGGCAAATTAAATCCTTGTTTTGTCTTCACCCATGT
AATAAAGGTGTTTATTGTTTTGTTCACCA

225/6881
FIGURE 211

MGISRDNWHKRRKTGGKRKPYHKKRKYELGRPAANTKIGPRRIHTVRVRGGNKKYRALRLDVGNFSWGSECCTRK
TRIIDVVYNASNNELVRTKTLVKNCIVLIDSTPYRQWYESHYALPLGRKKGAKLTPEEEEEILNKKRSKKIQKKYD
ERKKNAKISSLEEQFQQGKLLACIASRPGQCGRADGYVLEGKELEFYLRKIKARKGK

226/6881
FIGURE 212

ACGCTTGCGCGCGGGATTAACTGCGGCGGTTTACGCGGCGTTAAGACTTCGTAGGGTTAGCGAAATTGAGGTT
TCTTGGTATTGCGCGTTTCTCTTCCTTGCTGACTCTCCGAATGGCCATGGACTCGTCGCTTCAGGCCCGCCTGTT
TCCCGGTCTCGCTATCAAGATCCAACGCAGTAATGGTTTAATTCACAGTGCCAATGTAAGGACTGTGAACTTGGA
GAAATCCTGTGTTTCAGTGGAATGGGCAGAAGGAGGTGCCACAAAGGGCAAAGAGATTGATTTTGATGATGTGGC
TGCAATAAACCCAGAACTCTTACAGCTTCTTCCCTTACATCCGAAGGACAATCTGCCCTTGCAAGAAAATGTAAC
AATCCAGAAACAAAAACGGAGATCCGTCAACTCCAAAATTCTGCTCCAAAAGAAAGTCTTCGAAGCCGCTCCAC
TCGCATGTCCACTGTCTCAGAGCTTCGCATCACGGCTCAGGAGAATGACATGGAGGTGGAGCTGCCTGCAGCTGC
AACTCCCGCAAGCAGTTTTTCAGTTCTCTGCCCCACTAGGCCTTCTGCCCTGCAGTGGCTGAAATACCATT
GAGGATGGTCAGCGAGGAGATGGAAGAGCAAGTCCATTCCATCCGAGGCAGCTCTTCTGCAAACCTGTGAACTC
AGTTCGGAGGAAATCATGTCTTGTGAAGGAAGTGGAAAAATGAAGAACAAGCGAGAAGAGAAGAAGGCCAGAA
CTCTGAAATGAGAATGAAGAGAGCTCAGGAGTATGACAGTAGTTTTCCAACTGGGAATTTGCCGAATGATTAA
AGAATTTGGGGTACTTTGGAAATGTCATCCACTTACTATGACTGATCCTATCGAAGAGCACAGAATATGTGTCTG
TGTTAGGAAACGCCCACTGAATAAGCAAGAATTGGCCAAGAAAGAAATTGATGTGATTTCCATTCTAGCAAGTG
TCTCCTCTTGGTACATGAACCCAGTTGAAAGTGGACTTAACAAAGTATCTGGAGAACCAAGCATTCTGCTTTGA
CTTTGCATTTGATGAAACAGCTTCGAATGAAGTTGTCTACAGGTTACACGAAGGCCACTGGTACAGACAATCTT
TGAAGGTGGAAGCAACTTGTTTTGCATATGGCCAGACAGGAAGTGGCAAGACACATACTATGGGCGGAGACCT
CTCTGGGAAAGCCCAGAATGCATCCAAAGGGATCTATGCCATGGCCTCCCGGGACGTCTTCTCTGAAGAATCA
ACCCTGCTACCGGAAGTTGGGCCTGGAAGTCTATGTGACATTCTTCGAGATCTACAATGGGAAGCTGTTTGACCT
GCTCAACAAGAAGGCCAAGCTGCGCGTGCTGGAGGACGGCAAGCAACAGGTGCAAGTGGTGGGGCTGCAGGAGCA
TCTGGTTAACTCTGCTGATGATGTCATCAAGATGATCGACATGGGCAGCGCCTGCAGAACCTCTGGGCAGACATT
TGCCAACTCCAATTCTCCCGCTCCCACGCGTGCTTCCAAATTATTCTTCGAGCTAAAGGGAGAATGCATGGCAA
GTCTCTTTGGTAGATCTGGCAGGGAATGAGCGAGGCGCGGACACTTCCAGTGCTGACCGGCAGACCCGCATGGA
GGGCGCAGAAATCAACAAGAGTCTCTTAGCCCTGAAGGAGTGCATCAGGGCCCTGGGACAGAACAAAGGCTCACAC
CCCGTTCCGTGAGAGCAAGCTGACACAGGTGCTGAGGGACTCCTTCATTGGGGAGAACTCTAGGACTTGCAAGATT
GCCACGATCTCACCAGGCATAAGCTCCTGTGAATATACTTTAAACACCCTGAGATATGCAGACAGGGTCAAGGAG
CTGAGCCCCCACAGTGGGCCCAGTGGAGAGCAGTTGATTCAAATGGAAACAGAAGAGATGGAAGCCTGCTCTAAC
GGGCGCTGATTCCAGGCAATTTATCCAAGGAAGAGGAGGAAGTGTCTTCCAGATGTCCAGCTTTAACGAAGCC
ATGACTCAGATCAGGGAGCTGGAGGAGAAGGCTATGGAAGAGCTCAAGGAGATCATACAGCAAGGACCAGACTGG
CTTGAGCTCTCTGAGATGACCGAGCAGCCAGACTATGACCTGGAGACCTTTGTGAACAAAGCGGAATCTGCTCTG
GCCCAGCAAGCCAAGCATTCTCAGCCCTGCGAGATGTATCAAGGCCTTGCGCCTGGCCATGCAGCTGGAAGAG
CAGGCTAGCAGACAAATAAGCAGCAAGAAACGGCCCCAGTGACGACTGCAAATAAAAAATCTGTTTGGTTTGACAC
CCAGCCTCTTCCCTGGCCCTCCCCAGAGAACTTTGGGTACCTGGTGGGTCTAGGCAGGGTCTGAGCTGGGACAGG
TTCTGGTAAATGCCAAGTATGGGGGCATCTGGGCCAGGGCAGCTGGGGAGGGGGTCAGAGTGACATGGGACACT
CCTTTTCTGTTTCTCAGTTGTGCCCCCTCACGAGAGGAAGGAGCTCTTAGTTACCCCTTTGTGTTGCCCTTCTTTC
CATCAAGGGGAATGTTCTCAGCATAGAGCTTTCTCCGCAGCATCCTGCCTGCGTGGACTGGCTGCTAATGGAGAG
CTCCCTGGGGTTGTCTGGCTCTGGGGAGAGAGACGGAGCCTTTAGTACAGCTATCTGCTGGCTCTAACCTTCT
ACGCCCTTTGGGCCGAGCACTGAATGTCTGTACTTTAAAAAATGTTTCTGAGACCTCTTCTACTTTACTGTCT
CCCTAGAGATCCTAGAGGATCCCTACTGTTTTCTGTTTTATGTGTTTATACATTGTATGTAACAATAAAGAGAAA
AAATAAA

227/6881.
FIGURE 213A

TAGGCAGGCGGCTGAGCCGGCGGCGGGTGGCCTGCCAACGTGTGCTGGGTGGGAGAAGGCGAGGCGTCAGCGAT
GCTGTCTCTTCCGTGAGGAGCGCAGAGGAGGTGCGGGCGCCGGAGGCCCCAGAAGGCTCGAAGGCGCCGCGGGCT
GGGGTCGGTGGCTTAGGGAGCCCGTCCGGCCATGGTGGCCGCGGGTGGTGGTTGGCGCGGCTGCGCTGCGGCCCCG
GGGCAGTGCGGAGCCGGGACAGTCGCGGCGCTGACGCCCCGCGGGCCCCAGCTGCAGATATGAAGCGGAGCCGCTG
CCGCGACCGACCGCAGCCGCGCGCCGCCCCGACCGCCGGGAGGATGGAGTTCAGCGGGCAGCGGAGCTGTCTCAGTC
TTTGCCGCGCGCCGGCGAGCGCCGCCCCGGGAGGCAGCGGCTGGAGGAGCGGACGGGCCCCGCGGGGCCCCGAGGG
CAAGGAGCAGGATGTAGTAACCTGGAGTTAGTCCCCTGCTCTTCAGGAACTCAGTAATCCTGACATATTTTCATC
CACTGGAAAAGTTAAACTTCAGCGACAACCTGAGTCAGGATGATTGTAAGTTATGGAGAGGAAACCTGGCCAGCTC
TCTATCGGGTAAGCAGCTGCTCCCTTTGTCCAGCAGTGTACATAGCAGTGTGGGACAGGTGACTTGGCAGTCGTC
AGGAGAAGCATCAAACCTGGTTTCAATGAGAAACAGTCCCTTGGACAGTCTGCACCTTCTCTTACTGCTGGCCT
GAAGGAGTTGAGCCTTCCAAGAAGAGGCAGCTTTTGTGCGACAAGTAACCGCAAGAGCTTGATTGTGACCTCTAG
CACATCACCTACACTACCACGGCCACACTCACCCTCCATGGCCACACAGGTAACAGTCCCTTGGACAGCCCCCG
GAATTTCTCTCCAAATGCACCTGCTCACTTTTCTTTTGTCTGCCCCGTAGGACTGATGGGCGGCGCTGGTCTTT
GGCCTCTTTGCCCTCTTCAGGATATGGAATAACACTCCTAGCTCCACTGTCTCATCATGCTCCTCACAGGA
AAAGCTGCATCAGTTGCCCTTCCAGCCTACAGCTGATGAGCTGCACTTTTTGACGAAGCATTTACAGCACAGAGAG
CGTACCAGATGAGGAAGGACGGCAGTCCCCAGCCATGCGGCTCGCTCCCGGAGCCTCAGTCCCGGACGATCCCC
AGTATCCTTTGACAGTGAAATAATAATGATGAATCATGTTTACAAAGAAAGATTCCCAAAGGCCACCGCACAAAT
GGAAGAGCGACTAGCAGAGTTTATTTCTCCAACTCCAGACAGCGTGTGCCCTTGGCAGATGGAGCCCTGAG
CTTTATTATCATCATCAGGTGATTGAGATGGCCGAGACTGCCTGGATAAATCTCGGAGTGGCCTCATTACATCACA
ATACTTCTACGAACCTCAAGATAATTTGGAGAACTTTTACAAGATGCTCATGAGCGCTCAGAGAGCTCAGAAAT
GGCTTTTGTGATGCAGCTGGTGAAAAAGCTGATGATTATCATTGCCCCGCCAGCACGTCTCCTGGAATGCCTGGA
GTTTGACCCTGAAGAGTTCTACCACCTTTTAGAAGCAGCTGAGGGCCACGCCAAAGAGGGACAAGGGATTAAATG
TGACATTCCCCGCTACATCGTTAGCCAGCTGGGCCTCACCCGGGATCCCCCTAGAAGAAATGGCCAGTTGAGCAG
CTGTGACAGTCTGACACTCCAGAGACAGATGATTCTATTGAGGGCCATGGGGCATCTCTGCCATCTAAAAAGAC
ACCCTCTGAAGAGGACTTCGAGACCATTAAGCTCATCAGCAATGGCGCCTATGGGGCTGTATTTCTGGTGCGGCA
CAAGTCCACCCGGCAGCGCTTTGCCATGAAGAAGATCAACAAGCAGAACCTGATCCTACGGAACCAGATCCAGCA
GGCCTTCGTGGAGCGTGACATACTGACTTTTCGTGAGAACCCCTTTGTGGTCAGCATGTTCTGCTCCTTTGATAC
CAAGCGCCACTTGTGCATGGTGATGGAGTACGTTGAAGGGGGAGACTGTGCCACTCTGCTGAAGAATATTGGGGC
CCTGCCTGTGGACATGGTGCGTCTATACCTTTGCGGAACTGTGCTGGCCCTGGAGTACTTACACAACCTATGGCAT
CGTGACCCGTGACCTCAAGCCTGACAACCTCCTAATTACATCCATGGGGCACATCAAGCTCACGGACTTTGGACT
GTCCAAAATTGGCCTCATGAGTCTGACAACGAACCTTGATGAGGGTCATATTGAAAAGGATGCCCGGGAATTCCT
GGACAAGCAGGTATGCGGGACCCCGAATAACATTGCGCCTGAGGTGATCCTGCGCCAGGGCTATGGGAAGCCAGT
GGACTGGTGGGCCATGGGCATTATCCTGTATGAGTTCTGGTGGGCTGCGTCCCTTTTTTTGGAGATACTCCGGA
GGAGCTCTTTGGGCAGGTGATCAGTGATGAGATTGTGTGGCCTGAGGGTGATGAGGCACTGCCCCCAGACGCCCA
GGACCTCACCTCCAACTGCTCCACCAGAACCCTCTGGAGAGACTTGGCACAGGCAGTGCCCTATGAGGTGAAGCA
GCACCCATTCTTTACTGGTCTGGACTGGACAGGACTTCTCCGCCAGAAGGCTGAATTTATTCCTCAGTTGGAGTC
AGAGGATGATACTAGCTATTTTGACACCCGCTCAGAGCGATACCACCACATGGACTCGGAGGATGAGGAAGAAGT
GAGTGAGGATGGCTGCCTTGAGATCCGCCAGTTCTCTTCTGCTCTCCAAGGTTCAACAAGGTGTACAGCAGCAT
GGAGCGGCTCTCACTGCTCGAGGAGCGCCGGACACCACCCCGACCAAGCGCAGCCTGAGTGAGGAGAAGGAGGA
CCATTGAGATGGCCTGGCAGGGCTCAAAGGCCGAGACCGGAGCTGGGTGATTGGCTCCCCCTGAGATATTACGGAA
GCGGCTGTGCGGTGTCTGAGTCATCCACACAGAGAGTGACTCAAGCCCTCCAATGACAGTGCGACGCCGCTGCTC
AGGCCTCCTGGATGCGCCTCGGTTCCCGGAGGGGCCCTGAGGAGGCCAGCAGCACCCCTCAGGAGGCAACCACAGGA
GGGTATATGGGTCTTGACACCCCATCTGGAGAGGGGGTATCTGGGCCTGTCACTGAACACTCAGGGGAGCAGCG
GCCAAAGCTGGATGAGGAAGCTGTTGGCCGGAGCAGTGGTTCCAGTCCAGCTATGGAGACCCGAGGCCGTGGGAC
CTCACAGCTGGCTGAGGGAGCCACAGCCAAGGCCATCAGTGACCTGGCTGTGCGTAGGGCCCCGCCACCGGCTGCT
CTCTGGGGACTCAACAGAGAAGCGCACTGCTCGCCCTGTCAACAAAGTGATCAAGTCCGCCTCAGCCACAGCCCT
CTCACTCCTCATTCTTTCGGAACACCACACCTGCTCCCCGTTGGCCAGCCCCATGTCCCCACATTCTCAGTCGTC
CAACCCATCATCCCGGGACTCTTCTCCAAGCAGGACTTCTTGCCAGCCCTTGGCAGCATGAGGCCTCCCATCAT

228/6881
FIGURE 213B

CATCCACCGAGCTGGCAAGAAGTATGGCTTCACCCTGCGGGCCATTGCGGTCTACATGGGTGACTCCGATGTCTA
CACCGTGCACCATATGGTGTGGCACGTGGAGGATGGAGGTCCGGCCAGTGAGGCAGGGCTTCGTCAAGGTGACCT
CATCACCCATGTCAATGGGGAACCTGTGCATGGCCTGGTGACACGAGGTGGTAGAGCTGATCCTGAAGAGTGG
AAACAAGGTGGCCATTTCAACAACCTCCCCTGGAGAACACATCCATTAAAGTGGGGCCAGCTCGGAAGGGCAGCTA
CAAGGCCAAGATGGCCCGAAGGAGCAAGAGGAGCCGCGGCAAGGATGGGCAAGAAAGCAGAAAAAGGAGCTCCCT
GTTCCGCAAGATCACCAAGCAAGCATCCCTGCTCCACACCAGCCGAGCCTTTCTTCCCTTAACCGCTCCTTGTC
ATCAGGGGAGAGTGGGCCAGGCTCTCCACACACAGCCACAGCCTTTCCCCCGATCTCCCACTCAAGGCTACCG
GGTGACCCCCGATGCTGTGCATTTCAGTGGGAGGGAATTCATCACAGAGCAGCTCCCCAGCTCCAGCGTGCCAG
TTCCCCAGCCGGCTCTGGGCACACACGGCCCAGCTCCCTCCACGGTCTGGCACCCAAGCTCCAACGCCAGTACCG
CTCTCCACGGCGCAAGTCAGCAGGCAGCATCCCCTGTACCACTGGCCCACACCCCTTCTCCCCACCCCCAAC
AGCTTACCTCAGCGGTCCCCATCGCCCCTGTCTGGCCATGTAGCCCAGGCCTTTCCCACAAAGCTTCACTTGTC
ACCTCCCCTGGGCAGGCAACTCTCACGGCCCAAGAGTGGCGGAGCCACCCGTTTCACTACTCAAGAGGGGTGCA
GTCGGCTGAGAACTGGCAGCAGCACTTGCCGCCTCTGAGAAGAAGCTAGCCACTTCTCGCAAGCACAGCCTTGA
CCTGCCCCACTCTGAACTAAAGAAGGAAGTGCAGCCAGGGAAGTGGAGCCTCTGGAGGTAGTTGGAGCCAGGAG
TGTGCTGTCTGGCAAGGGGGCCCTGCCAGGGAAGGGGGTGTCTGAGCCTGCTCCCTCACGGGGCCCTAGGCACCCCT
CCGGCAGGACCGAGCCGAACGACGGGAGTCGCTGCAGAAGCAAGAAGCCATTTCGTGAGGTGGACTCCTCAGAGGA
CGACACCGAGGAAGGGCCTGAGAACAGCCAGGGTGCACAGGAGCTGAGCTTGGCACCTCACCCAGAAGTGAGCCA
GAGTGTGGCCCCATAAAGGAGCAGGAGAGAGTGGGGAAGAGGATCCTTTCCCGTCCAGAGACCCCTAGGAGCCTGGG
CCCAATGGTCCCAAGCCTATTGACAGGGATCACACTGGGGCCTCCCAGAATGGAAAGTCCAGTGGTCCCCACAG
GAGGCTCGGGAGCCCAAGCCATTGAGGAGGCTGCCAGCTCCTCCTCAGCAGGCCCAACCTAGGTGAGTCTGG
AGCCACAGACCCCATCCCTCCTGAAGGTTGCTGGAAGGCCCAGCACCTCCACACCCAGGCACTAACAGCACTTTC
TCCCAGCACTTCGGGACTCACCCCCACCAGCAGTTGCTCTCCTCCCAGCTCCACCTCTGGGAAGCTGAGCATGTG
GTCCTGGAAATCCCTTATTGAGGGCCCAGACAGGGCATCCCCAAGCAGAAAGGCAACCATGGCAGGTGGGCTAGC
CAACCTCCAGGATTTGGAAAACACAACCTCCAGCCCAGCCTAAGAACCTGTCTCCAGGGAGCAGGGGAAGACACA
GCCACCTAGTGCCCCCAGACTGGCCCATCCATCTTATGAGGATCCCAGCCAGGGCTGGCTATGGGAGTCTGAGTG
TGCACAAGCAGTGAAAGAGGATCCAGCCCTGAGCATACCCAAGTGCTGATGCCTCAGGTGACAGAAGGCAGGA
CGTTCCATGCCGAGGCTGCCCCCTCACCCAGAAGTCTGAGCCCAGCCTCAGGAGGGGCCAAGAACCAGGGGGCCA
TCAAAGCATCGGGATTTGGCATTGGTTCCAGATGAGCTTTTAAAGCAAACATAGCAGTTGTTTGCCATTTCTTG
CACTCAGACCTGTGTAATATATGCTCCTGGAAACC

229/6881
FIGURE 214

GCAAGATGGTGGGTGAAAAAGTTGAGAAGCCAGATGCTAAAGAGAAGAAACCCAAAGCCAAGAAGGCTGATGTTG
GTGGCAAGGTGAAAAAGGGTAACCTCAAGGCTAAAAAGCCCAAGAAGGGGAAAGCCCCATTGCAGCCGCAACCCTG
TCCTTGTGAGAGGAATTGGCAGGTATTGCCGATCTGCCATGTATTCCAGAAAGGCCATGTACAAGAGGAAGTACT
CAGCCGCTAAATCTAAGGTTGAAAAGAAAAAGAAGGAGAAGGTTCTTGCAACTGTTACAAAACCAGTTGGTTGTG
ACAAGAATGGCGGTGCCCCGGGTGGTTAAACTTCGCAAAATGCCTAGATATTATCCTACTGAAGATGTGCCTCGAA
AGCTGTTGAGCCATGGCAAAAAATCCTTCAGTCAGCACGTGAGGCCATAGGGGCAAGAAGGTGGTTTTCTGAAG
CAGCTGGCTAGTGGTTTGTTACTTGTGACTGGACCTCTGGTCCTCAATCGAATTCCTCTACGAAGAACATACCAG
AAATTTGTCATTGCCAC

230/6881
FIGURE 215

MVGEKVEKPDAKEKKPKAKKADVGGKVKKGNLKAKKPKKGKPHCSRNPVLVRGIGRYCRSAMYSRKAMYKRKYSA
AKSKVEKKKKKEKVLATVTKPVGCDKNGGARVVKLRLKMPRYPTEDVPRKLLSHGKKSFSQHVRP

231/6881
FIGURE 216

AAATCTGCCATTTTCTGTCCCTGAGTGAGTCTCTGGCGTCCCAAATGCTGTGTTTTCTCGCAGGCTCTATTCCGT
TCGCTGGTTTCGCCACCTCAGGGGAACGATGGCCATGGAGTCCACAGCCACTGCCGCCGTCGCCGCGGAGCTGGTT
TCTGCCGACAAAATTGAAGATGTTCCCTGCTCCTTCTACATCTGCAGATAAAGTGGAGAGTCTGGATGTGGATAGT
GAAGCTAAGAACTATTGGGTTTAGGACAGAAACATCTGGTGATGGGGGATATTCCAGCAGCTGTCAATGCATTC
CAGGAAGCAGCTAGTCTTTTAGGTAAGAAGTATGGAGAGACAGCTAATGAGTGTGGAGAAGCCTTCTTTTCTAT
GGGAAATCACTTCTGGAGTTGGCAAGAATGGAGAATGGTGTGTTGGGAAACGCCTTGGAAGGTGTGCATGTGGAA
GAGGAAGAAGGAGAAAAACAGAAGATGAATCTCTGGTAGAAAATAATGATAACATAGATGAGGAAGCAAGGGAA
GAGTTGAGAGAACAGGTTTATGACGCCATGGGAGAAAAAGAAGAAGCCAAAAAACAGAAGACAAGTCTTTGGCA
AAGCCTGAAACTGATAAAGAACAGGACAGTGAATGGAGAAGGGTGGAGAGAAGATATGGATATAAGTAAATCT
GCAGAGGAGCCACAGGAAAAAGTTGACTTGACTCTAGATTGGTTAACTGAAACCTCTGAAGAGGCAAAAGGAGGA
GCAGCACCAGAAGGACCGAATGAAGCTGAGGTCACTTCTGGGAAGCCAGAACAGGAAGTACCAGATGCTGAGGAA
GAAAAATCAGTTTCTGGAAGTATGTCCAAGAAGAGTGCAGAGAAAAAGGAGGTGAGGAGAAGCAGGGAGAGGTA
ATTGTGAGCATAGAGGAGAAGCCAAAAGAAGTTTTCAGAAGAGCAGCCTGTGGTGACTCTAGAAAAGCAGGGCACT
GCAGTGGAGGTAGAAGCAGAGTCTTTAGACCCGACAGTCAAGCCAGTGGATGTGGGTGGGGACGAGCCAGAGGAG
AAGGTAGTTACCTCTGAAAACGAGGCAGGAAAGGCGGTTCTTGAACAACTGGTAGGTCAAGAAGTACCACCTGCT
GAAGAGTCACCAGAGGTGACAACAGAGGCTGCAGAGGCCTCAGCTGTAGAGGCTGGATCAGAAGTCTCTGAAAAG
CCTGGGCAGGAGGCTCCAGTTCTCCCTAAGGATGGTGAGTCAATGGACCGTCAGTTGTAGGAGATCAGACTCCT
ATTGAACCACAGACTTCTATAGAAAGACTGACAGAAACAAAAGATGGCTCAGGACTAGAGGAGAAGGTGAGGGCA
AAGCTGGTTTCTAGTCAAGGAGGAGACTAAGCTGTCTGTAGAAGAGTCTGAGGCAGCTGGAGATGGGGTTGATACC
AAGGTAGCCCAGGGAGCTACTGAGAAATCACCTGAAGACAAAGTTCAGATAGCTGCTAATGAAGAGACACAAGAG
AGAGAAGAACAGATGAAAAGAGGGTGAAGAACTGAAGGCTCAGAAGAGGATGATAAAGAAAATGATAAGACCGAA
GAAATGCCAAATGATTCACTCCTTGAACAAGTCTCTTCAAGAAAATGAGGAGGAGGAGATTGGGAACCTAGAG
CTTGCCCTGGGATATGCTGGATTTAGCAAAGATCATTTTTTAAAGGCAAGAAACAAAAGAAGCACAGCTTTATGCT
GCCCAGGCACATCTTAACTCGGAGAAGTTAGTGTTGAATCTGAAAACATATGTGCAAGCTGTGGAGGAGTTCCAG
TCCTGCCTTAACCTGCAGGAACAGTACCTGGAAGCCCACGACCGTCTCCTTGCAGAGACCCACTACCAGCTGGGC
TTGGCTTATGGGTACAACCTCTCAGTATGATGAGGCAGTGGCACAGTTCAGCAAATCTATTGAAGTCATTGAGAAC
AGAATGGCTGTACTAAACGAGCAGGTGAAGGAGGCTGAAGGATCGTCTGCTGAATACAAGAAAGAAATTGAGGAA
CTAAAGGAAGTCTACCCGAAATTAGAGAGAAGATAGAAGATGCAAAGGAGTCTCAGCGTAGTGGGAATGTAGCT
GAACTGGCTCTGAAAGCTACTCTGGTGGAGAGTTCTACTTCAGGTTTCACTCCTGGTGGAGGAGGCTCTTCAGTC
TCCATGATTGCCAGTAGAAAAGCCAACAGACGGTGCTTCCCTCATCAAATTGTGTGACTGATATTTCCACCTTGTC
AGAAAGAAGAGGAAACCAGAGGAAGAGAGTCCCCGAAAGATGATGCAAAGAAAGCCAAACAAGAGCCGGAGGTG
AACGGAGGCAGTGGGGATGCTGTCCCCAGTGGAAATGAAGTTTCGGAAAACATGGAGGAGGAGGCTGAGAATCAG
GCTGAAAGCCGGGCAGCAGTGGAGGGGACAGTGGAGGCTGGAGCTACAGTTGAAAGCACTGCATGTTAAGAGGGG
GCACAGCCCTCCTCCCAAGGGAAGTGTGTTTTGTATATAATGTATTTTTTCACTTTTGGAGGATTCTTTTGTAT
AACTTCAATAAAGATTGTAAGCAAAGGTTGAGGCTTTGATGGTTTTTTTCTTAATTATTGGCTGAATCTGCCTTG
GAGCACTGCTGGTTTTATATATTAGCCAAAGGTTTTGTTCTGGCCTTCTGTACTGATCTGTGTTCCCTGATCCTAA
TTCCCTATCTGTCTAACGTGGAGGTGATCAAGTGTGGCTGTAGGCCTTTGTTTTCCAATGGTGCTATATTCTGTTT
TCAAACACTTCACTGAACCCAGCTGTCTTGCAAACCTTTCAGTGGTGCTGTCCCTGGATGGGGGCTACAAAAACAA
GAATTGGTGAAGATCTTGCTCTTCAGTGCTGAAAATGGATGATGGACTTTGGCTGTGAGCCAGGCCTAGGATGGT
TCTTGTCTATATCCACCTAGTCTTCACCTGGGGCTATAATTCTGTCTGGAAGAAAGTCTGAAAACCTGGGT
CAGGGGAATGATTCTAAGGAAAAAGGCTCTGCATTTGAGCTCTGGTTTGAAAGTAGCCAAGGGGACTGATGGTGG
ACACTCCAGATGTGGTTGGAAGCATATGTGGGGAGGCTGGCTGGTTGAGTTTTGTATTTTTCTGTATAGAAAGGT
TGAGATATATCAACACTTGAATTGTTACCCATCTGCAGAATTGACTTCTCAAATAAAGATGCTAAAAATCT

232/6881
FIGURE 217

MAMESTATAAVALVSAADKIEDVPAPSTSDKVESLDVDSEAKKLLGLGQKHLVMGDIPAAVNAFQEAASLLGK
KYGETANECGEAFFFYGKSLLELARMENGLGNALGVHVEEEEGEKTEDESLENNDNIDEEAREELREQVYDA
MGEKEEAKKTEDKSLAKPETDKEQDSEMEKGGREDMDISKSAEPPQEKVDLTLDWLTETSEEAKGGAAPEGPNEA
EVTSGKPEQEVPADEEEKSVSGTDVQEECREKGGQEKQGEVIVSIEEKPKEVSEEQPVVTLKQGTAVEVEAESL
DPTVKPVDVGGDEPEEKVVTSENEAGKAVLEQLVGQEVPPAEESPEVTTEAAEASAVEAGSEVSEKPGQEAPVLP
KDGAVNGPSVVGDTPIEPQTSIERLTETKDGSGLEEKVRAKLVPSQEETKLSVEESEAAAGDGVDTKVAQGATEK
SPEDKVQIAANEETQEREEQMKEGEETEGSEEDDKENDKTEEMPNDVLENKSLQENEEEEIGNLELAWDMLDLA
KIIFFKRQETKEAQLYAAQHLKLGEVSVESENVVQAVEEFQSCLNLQEQYLEAHDRLAETHYQLGLAYGYNSQY
DEAVAQFSKSI EVIENRMAVLNEQVKEAEGSSAEYKKEIEELKELLPEIREKIEDAKESQRSGNVAELALKATLV
ESSTSGFTPGGGSSVSMIASRKPTDGASSSNCVTDISHLVRKKRKPEEESPRKDDAKKAKQEPEVNGGSGDAVP
SGNEVSENMEEEAENQAESRAAVEGTVEAGATVESTAC

233/6881
FIGURE 218

AGCCAGAAATGTGAAGTGCTAGCTGAAGGATGAGCAGCAGCTAGCCAGGCAAAGGGGGCAATGGCGGCTTCCTGT
GTTCTACTGCACACTGGGCAGAAGATGCCTCTGATTGGTCTGGGTACCTGGAAGAGTGAGCCTGGTCAGGTAAAA
GCAGCTGTTAAGTATGCCCTTAGCGTAGGCTACCGCCACATTGATTGTGCTGCTATCTACGGCAATGAGCCTGAG
ATTGGGGAGGCCCTGAAGGAGGACGTGGGACCAGGCAAGGCGGTGCCTCGGGAGGAGCTGTTTGTGACATCCAAG
CTGTGGAACACCAAGCACCAACCCCGAGGATGTGGAGCCTGCCCTCCGGAAGACTCTGGCTGACCTCCAGCTGGAG
TATCTGGACCTGTACCTGATGCACTGGCCTTATGCCTTTGAGCGGGGAGACAACCCCTTCCCAAGAATGCTGAT
GGGACTATATGCTACGACTCCACCCACTACAAGGAGACTTGGAAGGCTCTGGAGGCACTGGTGGCTAAGGGGCTG
GTGCAGGCGCTGGGCCTGTCCAACCTCAACAGTCGGCAGATTGATGACATACTCAGTGTGGCCTCCGTGCGTCCA
GCTGTCTTGCAGGTGGAATGCCACCCATACTTGGCTCAAAATGAGCTAATTGCCCACTGCCAAGCACGTGGCTTG
GAGGTAAGTGCCTTATAGCCCTTTGGGCTCCTCTGATCGTGCATGGCGTGATCCTGATGAGCCTGTCCTGCTGGAG
GAACCAGTAGTCCTGGCATTGGCTGAAAAGTATGGCCGATCTCCAGCTCAGATCTTGCTCAGGTGGCAGGTCCAG
CGGAAAGTGATCTGCATCCCCAAAAGTATCACTCCTTCTCGAATCCTTCAGAACATCAAGGTGTTTGACTTCACC
TTTAGCCCAGAAGAGATGAAGCAGCTAAATGCCCTGAACAAAAATTGGAGATATATTGTGCCTATGCTTACGGTG
GATGGGAAGAGAGTCCCAAGGGATGCAGGGCATCCTCTGTACCCCTTTAATGACCCGTACTGAGACCACAGCTTC
TTGGCCTCCCTTCCAGCTCTGCAGCTAATGAGGTCCTGCCACAACGGAAAGAGGGAGTTAATAAAGCCATTGGAG
CATCCAT

234/6881
FIGURE 219

MAASCVLLHTGQKMPLIGLGTWKSEPGQVKA AVKYALSVGYRHIDCAA IYGNEPEIGEALKEDVGPGKAVPREEL
FVTSKLWNTKHHPEDVEPALRKTLADLQLEYLDLYLMHWPYA FERGDNPFPKNADGTICYDSTHYKETWKALEAL
VAKGLVQALGLSNFNSRQIDDILSVASVRPAVLQVECHPYLAQNELIAHCQARGLEVTAYSPLGSSDRAWRPDE
PVLLEEPVVLALAEKYGRSPAQILLRWQVQRKVICIPKSITPSRILQNIKVFDFTF SPEEMKQLNALNKNWRYIV
PMLTVDGKRVP RDAGHPLYPFNDPY

235/6881
FIGURE 220

GTTCCTGCCTGGTGTGCGGTGGTTAGTTTCTGCGACTTGTGTTGGGACTGCTGATAGGAAGATGTCTTCAGGAAAT
GCTAAAATTGGGCACCCTGCCCCAACTTCAAAGCCACAGCTGTTATGCCAGATGGTCAGTTTAAAGATATCAGC
CTGTCTGACTACAAAGGAAAAATATGTTGTGTTCTTCTTTTACCCTCTTGACTTCACCTTTGTGTGCCCCACGGAG
ATCATTGCTTTCAGTGATAGGGCAGAAGAATTTAAGAACTCAACTGCCAAGTGATTGGTGCTTCTGTGGATTCT
CACTTCTGTCACTCTAGCATGGGTCAATACACCTAAGAAACAAGGAGGACTGGGACCCATGAACATTCCCTTTGGTA
TCAGACCCGAAGCGCACCATTGCTCAGGATTATGGGGTCTTAAAGGCTGATGAAGGCATCTCGTTTCAGGGGCCTT
TTTATCATTGATGATAAGGGTATTCTTCGGCAGATCACTGTAAATGACCTCCCTGTTGGCCGCTCTGTGGATGAG
ACTTTGAGACTAGTTCAGGCCTTCCAGTTCACTGACAAACATGGGGAAAGTGTGCCCAGCTGGCTGGAAACCTGGC
AGTGATACCATCAAGCCTGATGTCCAAAAGAGCAAAGAATATTTCTCCAAGCAGAAGTGAGCGCTGGGCTGTTTT
AGTGCCAGGCTGCGGTGGGCAGCCATGAGAACAAAACCTCTTCTGTATTTTTTTTTTCCATTAGTAAAACACAAG
ACTTCAGATTCAGCCGAATTGTGGTGTCTTACAAGGCAGGCCTTTCCTACAGGGGGTGGAGAGACCAGCCTTTCT
TCCTTTGGTAGGAATGGCCTGAGTTGGCGTTGTGGGCAGGCTACTGGTTTGTATGATGTATTAGTAGAGCAACCC
ATTAATCTTTTGTAGTTTGTATTAAACTTGAAGTGAAG

236/6881
FIGURE 221

MSSGNAKIGH PAPNFKATAVMPDGQFKDISLSDYKGKYVVFYPLDFTFVCPTEIIAFSDRAEEFKKLNQVIG
ASVDSHFCHLAWVNTPKKQGGLGPMNIPLVSDPKRTIAQDYGVKKADEGISFRGLFIIDDKGILRQITVNDLPVG
RSVDETLRLVQAFQFTDKHGEVCPAGWKPGSDTIKPDVQKSKEYFSKQK

237/6881
FIGURE 222

GCTCGGCTCACTGAGACCCGGTGGTCCAGACGCTGCTCCTGGCTGGGGTGGCGCTGCAGGGAGAACCGCGAGCTC
TCAGGGGTTCGGCGGGTGACTTCTTTCCGGAAGAAAGCGAGGAACGCGCTCTGCGGGGTGAGCCGGACTCCCCAAC
TCCGGACGATCAGCCCAGGACTGAGAGCCCCGAAGTCCCCAACCAAGTAAGCGGCCCCAGAAAGGACAAGTCTA
GGTCGCCGTCCAGAGCGCCATGGCCGCGCCCGCCCTTCGTTTGTGCCACATCGCCTTCCACGTGCCCCGCCGGCA
GCCCCTAGCCCGGAACCTGCAGCGCCTCTTCGGCTTCCAGCCCCTGGCTTCGCGGGAGGTGGACGGCTGGCGGCA
GCTAGCCCTGCGCAGCGGGCAGCGGCTCTTTTGGTGAACGAGGGCGCAGGGTCTGGAGAGCCGCTGTACGGCCT
GGATCCGCGTCACGCCGTGCCAGCGCCACAAACCTGTGCTTCGACGTGGCGGACGCCGGCGCTGCAACCCGGGA
GCTGGCAGCGCTGGGCTGCAGCGTGCCTGTCCCTCCGTTTCGCGTGCGGGACGCGCAGGGTGCCGCCACTTACGC
CGTGGTCAGCTCGCCTGCCGGCATCCTCAGCCTGACCTTGCTGGAGCGCGCTGGCTACCGCGGACCCTTCCTACC
CGGCTTCAGGCCCCTGTCTCTGCGCCTGGCCCCGGGTGGGTTCAGCCGCGTGGACCACCTGACCTTGGCCTGCAC
CCCCGGCAGCTCCCCACACTTTTTCGCTGGTTCCACGACTGCCTGGGCTTTTGCCACTTGCCGCTGAGCCCAGG
TGAGGATCCCAGCTGGGCCTCGAAATGACAGCAGGGTTTGGGCTTGGGGGACTGAGGCTTACAGCCCTGCAGGC
CCAGCCGGGCAGCATTGTCCCCACTCTTGTCTGGCTGAGTCCCTTCGGGGGCGACGACACGACAGGACCAGGT
GGAGCAGTTCCTGGCCCCGACAAAGGGGCCAGGCCTGCAGCACGTGGGGCTGTATACGCCTAACATTGTGGAGGC
CACTGAGGGGGTGGCAACTGCTGGAGGCCAGTTCCTGGCTCCCCCTGGGGCATACTACCAGCAGCCAGGAAAGGA
GAGGCAGATCCGAGCTGCAGGGCACGAGCCTCATCTGCTTGCTCGACAGGGGATCCTGCTAGATGGTGATAAAGG
CAAGTTTCTGCTTCAGGTCTTCACCAAGTCCCTTTTTTACTGAGGACACTTTCTTCCTGGAGCTGATTAGAGGCA
GGGGGCCACTGGCTTTGGTCAGGGCAACATCAGAGCTCTGTGGCAGTCCGTACAGGAGCAATCTGCCAGGAGCCA
GGAAGCCTAAGGATGCCAGGGCTGGGTGCAGCCAGCTGTCTGCAGCTCTGGGGAGACCAGCACAGAAGTGGG
AACATCTGCAGGAGGCCCAACTAGTGAAAGGCTTTGCCTCCGGGGGCGAGGTGTGACTTCCATTTTCATCAGTGCC
TGCCAGAAGCTGTGTCTCTCATTGGGCTCCAAAGAGGTGGGATTTTTTAAAGTAAACATTTCTTATATACAGT
CTATAATAAATATGTAAGATACAAAGAACAATAAAAGAATTACACACTAGGAAAAAAAAAAAAAAAAAAAAA

238/6881
FIGURE 223

MAAPALRLCHIAFHVPAGQPLARNLQRLFGEQPLASREVDGWRQLALRSGDAVFLVNEGAGSGEPLYGLDPRHAV
PSATNLCFDVADAGAATRELAALGCSVPVPPVVRVRDAQGAATYAVVSSPAGILSLTLERAGYRGPFLPGFRPVS
SAPGPGWVSRVDHLTLACTPGSSPTLLRWFDCLGFCFLPLSPGEDPELGLEMTAGFGLGGLRLTALQAQPGSIV
PTLVLAESLPGATTRQDQVEQFLARHKGPGLQHVGLYTPNIVEATEGVATAGGQFLAPPGAYYQQPGKERQIRAA
GHEPHLLARQGILLDGDGKGKFLQVFTKSLFTEDTFFLELIQRQGATGFGQGNIRALWQSVQEQSARSQEA

239/6881

FIGURE 224

GACCACGATGAGTGTGCCGCACTTCCGGCCAGATCGCCGGATTTCGCTGAGTGACCCTTACAAGTCCTTCTTGA
TCCTGAACTGGGTTAGGTGCCGCTGTTGCTGCTCGTGTTGAATCTAGAACCGTAGCCAGACATGGGACTGGAGGA
CGAGCAAAAGATGCTTACCGAATCCGGAGATCCTGAGGAGGAGGAAGAGGAAGAGGAGGAATTAGTGGATCCCCT
AACAAACAGTGAGAGAGCAATGCGAGCAGTTGGAGAAATGTGTAAAGGCCCGGGAGCGGCTAGAGCTCTGTGATGA
GCGTGTATCCTCTCGATCACATACAGAAGAGGATTGCACGGAGGAGCTCTTTGACTTCTTGCAIGCGAGGGACCA
TTGCGTGGCCACAACTCTTTAACAACTTGAATTAAATGTGTGGACTTAATTCACCCCAGTCTTCATCATCTGG
GCATCAGAATATTTCTTATGGTTTTGGATGTACCATTTGTTTCTTATTTGTGTAAGTTACATGAACC
TCATGGGTTTGGCTTAGGCTGGTAGCTTCTATGTAATTCGCAATGATTCCATCTAAATAAAAGTTCTATGATCTG
C

240/6881
FIGURE 225

MGLEDEQKMLTESGDPEEEEEEEELVDPLTTVREQCEQLEKCVKARERLELCDERVSSRSHTTEEDCTEELFDFL
HARDHCVAHKLFNNLK

241/6881
FIGURE 226

CGCGCCTGAGGAGGAGGAGGAGGCGGGGGCGGCCATGGCTGCTGTGGTGGTGGCGGCTGCGGGTGGCGCGGGACC
GGCGGTCTCTGCAGGTGGCCGGTCTCTACCGGGGCCTGTGCGCGGTGCGCAGCCGCGCCCTGGGCCTGGGGCTCGT
GTCACCCGCGCAGCTGCGCGTCTTCCAGTGCGCCCCGGCTCGGGCCGGCCCGAGGGGGGCGCCGACAGCAGCGG
GGTCGGGGCCGAGGCCGAGCTCCAGGCCAACCCCTTTCTACGACCGCTACCGCGACAAGATCCAGCTGCTGCGCAG
GTCAGACCCAGCTGCTTTTGTAGTCCCGCCTGGAGAAACGCAGTGAATTTGGAAGCAGCCAGTGGGGCATTCCAG
GCAAGGTGATTTTATCAAATGTGTGGAACAGAAGACAGATGCCTTGGGGAAACAGTCTGTGAACAGAGGATTAC
TAAGGACAAGACTCTCAGTTCAATCTTTAACATTGAGATGGTAAAAGAAAAAAGTGCAGAAGAAATAAACAGAT
TTGGCAGCAATATTTTGCAGCAAAAGATACAGTCTACGCAGTTATTCTGCAGAAAAGTTTGATTTGATCTGGAA
CCGGGCTCAGTCTGTCCAACATTTCTATGTGCTCTGCCAAGAAGGGAAGGTTATGAGTTTTTGTAGGACAATG
GACAGGTACTGAACTCCACTTCACTGCACTTATAAATATTTCAGACCCGAGGGGAAGCTGCAGCCAGCCAGCTGAT
TTTATATCACTATCCTGAACTTAAGGAAGAAAAGGGCATACTGCTGATGACTGCAGAAATGGATTCCACATTTCT
GAATGTTGCTGAGGCACAGTGCATCGCCAACCAAGTTTCTACGCTACTGATCGGAAAAGAGACCTACGG
GTTAGTGGAGACCTTTAACCTCAGACCAAATGAGTTCAAATATATGTCTGTCATCGCTGAATTGGAGCAAAGCGG
ACTTGGAGCAGAACTGAAATGTGCCCAGAACCAAAATAAGACTTAGAACTGTACAGGTTGGCCCTTCACCTAGTT
GACTCAGCCCTCGATAGTCTAGAGCCACCCCTCCTCAGGAAGTCAAGAGCTCAGCATTATATAATGAGCAGTTG
GTAATGAGTTGCCCTATGTGCTTGTGCAAGCAGTCACAGAGATGAGCCCTATTACTTGATATTCAGGAACAAAG
GTACCTGAACATTCTGATAATTATCTCAGCATACTTGAGGTTTCCTTTTTTAAGTGTTTCGAGGTTATAACAAGAG
ACAGCCAAGGACCTACAAGACAGTTGACTTGATTTTGCACAGTGTAAACAGCGCAGTTGCATTCTGGCCACTTTGA
CCTTATAGTCCCAAATGATGAGTTTGTCTCTTTATGAACTCATGACAGGATAATAAGCTTGAAGACCTGCTGT
AGTTAGATATGGGCTTTAATCCTTCCAGGCACCAGTCAGCTGAACAAAAGCATAAGCCAAACATCCTGTTTAAA
CTGTAGAATAACCAGATATTCCCATCAGGTTAAAGACTTCATCTAGATGATGCCCCCAGAGATGCCTTTAGTGT
AAGTAGCTGGCTTGGGGTATCAGCAAATTTAGGTATAGTTAGATAAACAGGTACAGGGCCTGCATACTATTAAA
CCATAGTTTGTGGCACCCGCTTTTCTAACTCCACCTGTTAGAAGCTATGTGTTTGAAGGAATGAATCAGTGCAGT
ATAAAATAAAATTCTTTTGTAAAGGAG

242/6881
FIGURE 227

MAAVVVAAAGGAGPAVLQVAGLYRGLCAVRSRALGLGLVSPAQLRVFPVRPGSGRPEGGADSSGVGAEEAELQANP
FYDRYRDKIQLLRRSDPAAFESRLEKRSEFRKQPVGHSRQGDFIKCVEQKTDALGKQSVNRGFTKDKTLSSIFNI
EMVKEKTAAEIKQIWQQYFAAKDTVYAVIPAEEKFDLIWNRAQSCPTFLCALPRREGYEFFVGQWTGTELHFTALI
NIQTRGEAAASQLILYHYPELKEEKGIVLMTAEMDSTFLNVAEAQCIANQVQLFYATDRKETYGLVETFNLRPNE
FKYMSVIAELEQSGLGAELEKCAQNQNKT

243/6881
FIGURE 228

ACCTGCCCTCATCTGGCCCGCGACTGTAAGACCGGACCCACATCCAGACCAATCTTCCTGTCCGGCTGCTGCGA
CGCGGTCCGCAGGTTGCAGGCGGGCGGCCGGGGCGCCTGAAGGTTACCGAGTGCATGACGGCCTCAGTTCCCGCG
CTGCCCCGCCCCGCTGGCCCGCCGACCTCCCCGCCGCTCGCCCGCCAGCCCCTCGGGCCCCGGCGGCGGCGGCG
GTGGCGGCGACGGTCGCAGGAGGTGCCGTCTGCCTCCCAGGTGCGCGCTTCGCTCCCGGAGCCGCGGAACCTCGGT
CGCGCCATGGCGTCCAACATGGACCGGGAGATGATCCTGGCGGATTTTCAGGCATGTACTGGCATTGAAAACATT
GACGAAGCTATTACATTGCTTGAACAAAATAATTGGGACTTAGTGGCAGCTATCAATGGTGTAAATACCACAGGAA
AATGGCATTCTACAAAGTGAATATGGAGGTGAGACCATAACCAGGACCTGCATTTAATCCAGCAAGTCATCCAGCT
TCAGCTCCTACTTCCTCTTCTTCTTCAGCGTTTCGACCTGTAATGCCATCCAGGCAGATTGTAGAAAGGCAACCT
CGGATGCTGGACTTCAGGGTTGAATACAGAGACAGAAATGTTGATGTGGTACTTGAAGACACCTGTACTGTTGGA
GAGATTAAACAGATTCTAGAAAATGAACTTCAGATACCTGTGTCCAAAATGCTGTTAAAAGGCTGGAAGACGGGA
GATGTGGAAGACAGTACGGTCCTAAAATCTCTACACTTGCCAAAAACAACAGTCTTTATGTCCTTACACCAGAT
TTGCCACCACCTTCATCATCTAGTCATGCTGGTGCCCTGCAGGAGTCATTAAATCAAAACTTCATGCTGATCATC
ACCCACCGAGAAGTCCAGCGGGAGTACAACCTGAACTTCTCAGGAAGCAGTACTATTCAAGAGGTAAAGAGAAAT
GTGTATGACCTTACAAGTATCCCCGTTCCGCCACCAATTATGGGAGGGCTGGCCAACTTCTGCTACAGACGACTCA
ATGTGTCTTGCTGAATCAGGGCTCTCTTATCCCTGCCATCGACTTACAGTGGGAAGAAGATCTTCACCTGCACAG
ACCCGGGAACAGTCGGAAGAACAATCACCAGTGTTTCATATGGTTAGTGATAGCGATGGAGATGACTTTGAAGAT
GCTACAGAATTTGGGGTGGATGATGGAGAAGTATTTGGCATGGCGTCATCTGCCTTGAGAAAATCTCCAATGATG
CCAGAAAACGCAGAAAATGAAGGAGATGCCTTATTACAATTTACAGCAGAGTTTTCTTCAAGATATGGTGATTGC
CATCCTGTATTTTTTATTGGCTCATTAGAAGCTGCTTTTCAAGAGGCCTTCTATGTGAAAGCCCCGAGATAGAAAG
CTTCTTGCTATCTACCTCCACCATGATGAAAGTGTGTTAACCAACGTGTTCTGCTCACAAATGCTTTGTGCTGAA
TCCATTGTTTCTTATCTGAGTCAAAAATTTTATAACCTGGGCTTGGGATCTGACAAAGGACTCCAACAGAGCAAGA
TTTCTCACTATGTGCAATAGACACTTTGGCAGTGTTGTGGCACAACCATTCGGACTCAAAAAACGGATCAGTTT
CCGCTTTTCTGATTATTATGGGAAAAGCGATCATCTAATGAAGTGTTGAATGTGATACAAGGGAACACAACAGTA
GATGAGTTAATGATGAGACTCATGGCTGCAATGGAGATCTTCACAGCCCCAACAAACAGGAAGATATAAAGGACGAG
GATGAACGTGAAGCCAGAGAAAAATGTGAAGAGAGAGCAAGATGAGGCCTATCGCCTTTCACCTGAGGCTGACAGA
GCAAAGAGGGAAGCTCACGAGAGAGAGATGGCAGAACAGTTTCGTTTGGAGCAGATTCGCAAAGAACAAGAAGAG
GAACGTGAGGCCATCCGGCTGTCTTAGAGCAAGCCCTGCCTCCTGAGCCAAAGGAAGAAAATGCTGAGCCTGTG
AGCAAACCTGCGGATCCGGACCCCCAGTGGCGAGTTCTTGAGCGGCGTTTCCTGGCCAGCAACAAGCTCCAGATT
GTCTTTGATTTTGTAGCTTCCAAAGGATTTCCATGGGATGAGTACAAGTTACTGAGCACCTTTCTAGGAGAGAC
GTAACCTCAACTGGACCCAAATAAATCATTATTGGAGGTAAAGTTGTTCCCTCAAGAAACCCTTTTCTTGAAGCA
AAAGAGTAAACACGGCCCAGCGGTGGAACCGCCATTCTTGACAAGCCAGCAGCCTGCGTCAGGAGAAGGGCTC
CTGCCAACCCACCCACACGCTCGTCTCACTCAATTCAATGTACACTTCTGCCTCTTGCAAATGCTGGAAAA
AGTAATAATAAATATAGCTACTTAAAAA

244/6881
FIGURE 229

CTCTGCCGAGCCTCCTTAAAACTCTGCCGTTAAATGGGGGCGGGTTTTCACACTCAAAAAGCGCTCAATTTTTT
TCTTTTTCAAAAAAGCTGATGAGTTCGGA AAAAAGGGAGAAGAAACCGGCACCCTCTCTGAGAGGCAACAGAAGC
AGCAATTGTTTTCAGCGAAAAAGCAGCAAGGGAGGGAGTGAAGGAAAAAAGCAAAAAAGGGGGCGACACGCAAGT
GCCTGTAGGGGTGAAAGGAGCAGGGACCGGCATCTAGGGGGGGATCAGCTACAAAAGAACTGTCACTGGGAGC
GGTGCGGCCAAGGAGGAAGCAGTGTCTGCCAGGCTCTGCTCCAGGGCACAGCTGGCTGGCGGCTGCCCTGTCCGCA
GCAAAGGGGCACAGGCCGGGGACCGCGAGAGGTGGCAAAGTGGCACC GGCGCCGAGGCTGCTGAGCGCTCGCCG
AGACGGCGACCGGACTGGCTGCCCCGGA ACTGCGGCGACTCTCCCTACTCAGAACTTGCCCTACGTTTTCCAGGA
CTCTCCCCATCTCCAGAGGCCCCCAAAAACCGGGAAAGGAAGGAAAGGACAGCGGCGGCAGCAGCTCAATGAGT
GCCTACAGCAGAAAGCCTGAACGAGCTCGGTTCGTAGGCGGGAA GTTCCCGGGGGGGCTGCCCAGTGCAGCCGCAA
TGCTGCCGCGAGCTGCCCCAGCAGTCCGGGCTCCGTAGACGCTTTCCGCATCACTCTCCTTCCCTCGGGCTGCCGG
GAGTCCC GGGACCTGGCGGGGCGCGCATGACGGGCTTCTCGGGGGCCCGCCGCACGCCCGGCAGCCTCCGGAGAC
GCGCGCCGAGCCCCGGCTCCACGGCCTCTGAGGCTCGGCGGGGCTGCGGCTGCCCTGGCGGGCGGGCTCCGGAGCT
TTCCTGAGCGGCATTAGCCACGGCTTGGCCCGGACGCGACCAAAGGCTCTTCTGGAGAAGCCCAGAGCACTGGG
CAATCGTTACGACCTGTAACTTGAGGGCCACCGAACTGCTACTCCGTTTCGCCTTTGGCGATCATCTTTTAACCC
TCCGGAGCACGT CAGCATCCAGCCACCGCGGCGCTCTCCAGCAGCGGAGGACCCAGGACTATCCCTTCGGCGAG
ACGGATGGAACCGAGCCCCCTGGAGGACCTGCCCCCTGCAGTTCCTGCCTCACACGGCTCAAGTACCACCGTGAA
CAAGGGACCCCTAAAGAATGCGCCGAGCCTTGCGGGGAACGAGTTGGCGTCCGCAGCTGCCAGGGGGGACCTAGAGCA
ACTTACTAGTTTGTGCAAAATAATGTAAACGTCAATGCACAAAATGGATTGGAAGGACTGCGCTGCAGGTTAT
GAAACTTGGAATCCCGAGATTGCCAGGAGACTGCTACTTAGAGGTGCTAATCCCGATTTGAAAGACCGAACTGG
TTTCGCTGTCAATTCATGATGCGGCCAGAGCAGGTTTCTTGACACTTTACAGACTTTGCTGGAGTTTCAAGCTGA
TGTTAACATCGAGGATAATGAAGGGAACCTGCCCTTGCACTTGCGTGCCAAAGAAGGCCACCTCCGGGTGGTGGA
GTTCTTGGTGAAGCACACGGCCAGCAATGTGGGGCATCGGAACCATAAGGGGGACACCGCCTGTGATTTGGCCAG
GCTCTATGGGAGGAATGAGGTTGTTAGCCTGATGCAGGCAAACGGGGCTGGGGGAGCCACAAATCTTCAATTAAC
GTGGGGAGGGCTCCCCACGTTGCCTCTACTTTATCAATTA ACTGAGTAGCTCTCCTGACTTTTAATGTCAATTG
TTAAAATACAGTTCTGTCAATATGTTAAGCAGCTAAATTTTCTGAACTGCATAAGTGAAAATCTTACAACAGGCT
TATGAATATATTTAAGCAACATCTTTTTTAACCTGCAAATCTGTTCTAACATGTAATTGCAGATAACTTTGACTT
TCTTCTGAATATTTTATCTTTCTTGCTTTTCCCTTGCTTCCCCTTTTGCCAATCTCAACACCCAAGTTGAAGA
CTTTGTTTTTAAAATGGTTTGCTCTGATGCTTTTGTCTAATTA AAACACTTTCAAAACAGGAAAAAAAAAAAAA
AAAA

245/6881
FIGURE 230

MAEPWGNELASAAARGDLEQLTSLLQNNVNVNAQNGFGRTALQVMKLGNPEIARRLLLRGANPDLKDRTGFAVIH
DAARAGFLDTLQTLLEFQADVNIEDNEGNLPLHLAAKEGHLRVVEFLVKHTASNVGHRNHKGDTACDLARLYGRN
EVSLSMQANGAGGATNLQ

246/6881
FIGURE 231

AAAACACCAAATGGTGGATGACACCAGTGCAGCGGGGGGGGGCCCCGGAGGCCCTGGGATGGGGAAGTGCGGTGGC
TTCCGCGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGTCGCAGCCGTAGACGGGGCCGGGGCCGAGGCCGCGGA
GCTCGCGGAGGCAAGGCCGAGGATAAGGAGTGGATGCCCCGTACCAAGCTGGGCTGCTTGGTGAAGGACATGAAG
ATCAAGTCCCTGGAGGAGATCTATCTCTTCTCCCTGCCCATTAAAGGAATCAGAGATCATTGACTTTTTCTGGGG
GCCTCTCTCAAGGATGAGGTTTTGAAGATTATGCCAGTGCAGACGCAGACCCGTGCTGGCCAGCGCACCAGGTTC
AAGGCGTTTGTGTGCTATCGGGGACTACAATGGCCACGTGCGTCTGGGTGTTAAGTGCTCCAAGGAGGTGGCCACC
GCCATCCATGGGGCCATCATCCTGGCCAAGCTCTCCATTGTCCCCGTGCGCAGAGGCTACTGGGGGAACAAGATT
GGCAAGCCCCACACCGTCCCTTGCAAGGTGACAGGCCGCTGCGGCTCTGCACTGGTGCACCTCATCCCTGTACCC
AGGGGCACTGGCATTGTCTCCGCACCTGTGCCAAGAAGCTGCTCATGATGGCTGGTATCGATGACTGCTGCACC
TCAGCCTGGGGCTGCACTGCCACCCTGGGCAACTTCGCCAAGGCCACCTTTGATGCCATTTCTAAGACCTACAGC
TACCTGACCCCCGACCTCTGGAAGGAGACTGTATTTACCAAGTCTCCCGATCAGGAATTCAGTACCACCTCATC
AAGGCCACGCCAGAGTCTCCGTGCAGCGGACCCAGGCTCCAGCTGTGGCTACAACATTAGGGTTTTTAGACAAGG
AAAATAAAGCGAATTAAGCGT

247/6881
FIGURE 232

MCNCGGFRGGFGSGIRGRGRSRRRGRGRGRGARGGKAEDKEWMPVTKLGCLVKDMKIKSLEEIYLFSLPIKESEI
IDFFLGASLKDEVLKIMPVQTQTRAGQRTREKAFVAIGDYNGHVGLGVKCSKEVATAIHGAILAKLSIVPVRRG
YWGNIKIGKPHTVPCKVTGRCGSALVHLIPVPRGTGIVSAPVPKKLLMMAGIDDCCTSAWGCTATLGNFAKATFDA
ISKTYSYLTPDLWKETVFTKSPDQEFTDHLIKAHARVSVQRTQAPAVATT

248/6881
FIGURE 233

ATGTCTAAGTCAGAATCTCTTAAAGAGCCCGAACAGCTGCAGAAACTCCTCACTGGAGGGTTGAGCATTGAAGCA
ACCAATGAGAGCCTGAGGAGCCATTTTGAGCAATGGGGAACGCTCACGGACTGTGTGGTCCTGAGAGATCCAAAC
ACTAAGTGCTCCAGGGGCTTTGGGTTTGTACATATGCCACTGTGGAGGAGGTGGATGCAGCCACAAATGCAAGG
CCACACAAGGTGGATGGAAGAGTTGTGAAACAAAGAGAGCTGTCTCAAGAGAAGATTCCCAAAGACCAGGTGCT
CACTTAACTGTGAAAAAGTTTGGAAAAATGGAAGTGATTGAAATCATGACTGACCATGGCAGTGGCAAGAAAAGG
GACTTTGCCTTTGTAACCTTTGATGACCATGACTCCGTGGATAAGACTGTCATTGAGAAATACCATATTGTGAAT
GGCCACAACCTGTGAAGTTAGGAAAGCCCTGTCAAAGCAAGAGATGGCTAGTGCTTCATCCAGCCAAAGAGGTCGA
ACAGGCTCCTTGATGCCTAAAGCCCAATGTCTGGCATTGAGCCCTCCATGACAGGTTCCAGCTTTCTCTGCAAG
GCCATGCTCCTCACGGCCTATGACTGCCTCCTGTTCTGCGCCTGTCAGGTCTTCCACCTCACCCCTCTTCTCAGC
CTATCCAAGCCCATTGAGTCTTCAGGCGAGCTCTAG

249/6881
FIGURE 234

MSKSESLKEPEQLQKLLTGGLSIEATNESLRSHFEQWGTLTDCVVLDPNTKCSRGFGFVITYATVEEVDAATNAR
PHKVDGRVVETKRAVSREDSQRPGAHLTVKKFGKMEVIEIMTDHGSGKKRDFAFVTFDDHDSVDKTVIQKYHIVN
GHNCEVRKALSKQEMASASSSQRGRTGSLMPKAQCLAFEPSMTGSQLSCKAMLLTAYDCLLFCACQVFHLTFLLS
LSKPIQSSGEL

250/6881
FIGURE 235

CGGTCCCGCACTGGTGCAGCCATGTCCTCTTCCCCGTGGGAGCCTGCGACCCTGCGCCGGGTGTTTCGTGGTGGGG
GTTGGCATGACCAAGTTTGTGAAGCCTGGAGCTGAGAATTCAAGAGACTACCCTGACTTGGCAGAAGAAGCAGGC
AAGAAGGCTTTAGCTGATGCACAGATCCCTTATTCAGCAGTGGACCAGGCATGTGTTGGCTATGTTTTTGGTGAC
TCTACCTGTGGGCAGAGGGCTATCTATCACAGTTTGGGAATGACTGGAATTCCTATAATCAATGTCAACAATAAC
TGTGCTACTGGTTCCTACTGCTTTGTTTATGGCCCCGCCAGCTGATTCAGGGTGGTGTGGCAGAATGTGTCTTGGCT
CTTGGGTTTGAGAAGATGAGTAAGGGAAGCCTTGGAATAAAATTTTCAGATAGAACCATTCCCCTGATAAGCAT
GTTGACCTCCTGATCAATAAGTATGGATTGTCTGCTCACCCAGTTGCTCCTCAGATGTTTGGGTATGCTGGAAAA
GAACATATGGAAAAATATGGAACAAAAATTGAACACTTTGCAAAAATTGGATGGAAAAATCATAAACATTTCAGTT
AATAACCCGTATTCCCAGTTCCAAGATGAATACAGTTTAGATGAAGTGATGGCATCTAAAGAAGTTTTTGATTTT
TTGACTATCTTACAATGTTGTCCCCTTCAGATGGTGTGTCAGCAGCAATTTTGGCCAGTGAAGCATTGTGTACAG
AAGTATGGCCTGCAATCCAAAGCTGTGGAAATTTTGGCACAAGAAATGATGACTGATTTGCCAAGCTCGTTTGAA
GAAAAAAGCATTATTAAATGTTTGGCTTTTGATATGAGTAAAGAAGCTGCAAGAAAATGCTATGAGAAATCTGGC
CTGACACCAAATGATATTGACGTAATAGAACTTCACGATTGCTTTTCTACCAACGAACCTCTGACTTATGAAGCA
CTCGGACTCTGTCCAGAAGGACAAGGTGCAACGCTGGTTGATAGAGGAGATAATACATATGGAGGAAAAGTGGGTC
ATAAATCCTAGTGGTGGACTGATTTCAAAGGGACACCCACTAGGCGCTACAGGTCTTGCTCAGTGTGCAGAACTC
TGCTGGCAGCTGAGAGGGGAAGCCGGAAGAGGCAAGTTCCCTGGTGCAAAGGTGGCTCTGCAGCATAATTTAGGC
ATTGGAGGAGCTGTGGTTGTAACACTCTACAAGATGGGTTTTCCGGAAGCCGCCAGTTCTTTTAGAACTCATCAA
ATTGAAGCTGTTCCAACCAGCTCTGCAAGTGATGGATTTAAGGCAAATCTTGTTTTTAAGGAGATTGAGAAGAAA
CTTGAAGAGGAAGGGGAACAGTTTGTGAAGAAAATCGGTGGTATTTTTGCCTTCAAGGTGAAAGATGGCCCTGGG
GGTAAAGAGGCCACCTGGGTGGTGGATGTGAAGAATGGCAAAGGATCAGTGCTTCCTAACTCAGATAAGAAGGCT
GACTGCACAATCACAATGGCTGACTCAGACTTCCTGGCTTTAATGACTGGTAAAATGAATCCTCAGTCGGCCTTC
TTTCAAGGCAAATTGAAAATCACTGGCAACATGGGTCTCGCTATGAAGTTACAAAATCTTCAGCTTCAGCCAGGC
AACGCTAAGCTCTGAAGAAGCTCCCTTTGGCTACTTTTGAAAATCAAGATGAGATATATAGATATATATCCATACA
TTTTATTGTCAGAATTTAGACTGAACTACACATTGGCAAATAGCGTGGATAGGATTTGTTTCTTAATGGGTGTG
ACCAATCCTGTTTTTCTATGCTCTGGGTGAATAGAGCCTGATGGTATACTACTGCTTTGCGGAATTGCATACAA
CTGTGCATTACAAAGTTAATATGGTAATTATGGTCTGGGGTAAAATTGAGTTTCAGAATAAAATTAGGAACAGTA
AAATCCAAAAGAACTATGTAAACAAAAAGCTTTTGTGTTGCTTACAAAGTATATTTAAGGATTATTCTGCTGAAG
ATTCAGTTTAAAGAGTTTTCTTGGGAGAACTAAGTAAGAAACACAATGCCAACAGCTGGCCAGTAATTAGTGTG
TGCACCTTCATGTCATTAATCAATTTCTCAATAGTTCTTAAAATTAGTGAGATTAAAAATCTAAAAATTTTGCATT
TCATGCTATCAGAAACAGTATTTTTCTTCCCAAATCAAAATAAAAGAAATATGATCAGAGCTTGAACACAGGCTTA
TTTTTAAAAATAAAATATTTTTAACATGGGTTTCTTATTGAAAAATCAGTGTATTAGTCATAAAACACCATCAT
TAAGAATAATTGAACAATAAAGTTTGGCTTTTCAGATGCAGTTTTTCAAATTATAATCTCATTTCAATTTATAACGTT
CTCAGTCCTTTGTTATAATTTTCTTTTTTCATGTAAGTTTAATTATCTGCATTTATCTTTTTTCTAGTTTTTCT
AATACTAATGTTATTTCTTAAAATTCAGTGAGATATAGGATAAAATAATGCTTTGAGAAGAATGTTTAATAGAAA
ATTAAAAATACTTTTTTCTGGCA

251/6881
FIGURE 236

MSSSPWEPATLRRVFVVGVMGTFVKPGAENSRDYPDLAEEAGKKALADAQIPYSAVDQACVGYVFGDSTCGQRA
IYHSLGMTGIPIINVNNNCATGSTALFMARQLIQGGVAECVLALGF EKMSKSLGIKFSDR TIPTDKHVDLLINK
YGLSAHPVAPQMFGYAGKEHMEKYGTKIEHFAKIGWKNNHKSNNPYSQFQDEYSLDEV MASKEVFDFLTILQCC
PTSDGAAAAILASEAFVQKYGLQSKAVEILAQEMMTDLPSSFEEKSIIKMVGFDMSKEAARKCYEKSGLTPNDID
VIELHDCFSTNELLYEALGLCPEGQGATLVDRGDNTYGGKWVINPSGGLISKGHPLGATGLAQCAELCWQLRGE
AGKRQVP GAKVALQHNLGIGGAVVVTLYKMGFPEAASSFRTHQIEAVPTSSASDGFKANLVFKEIEKKLEEEGEQ
FVKKIGGIFAFKVKGDPGGKEATWVVDVKNGKGSVLPSDKKADCTITMADSDFLALMTGKMNPQSAFFQGLKI
TGNMGLAMKLQNLQLQPGNAKL

252/6881
FIGURE 237

GGCCCTGCGCGCGGCAACATGGCGGGGTCCAGGTGGAGGTCTTGAGGCTATCAGATCGGTATGGCATTGGCGTCC
GGGCCCCGCAAGGCGGGCGCTAGCTGGCTCCGGGCAGCTCGGCCTTGGGGGCTTCGGGGCCCCGAGACGCGGGGCG
TATGAGTGGGGCGTGCGCTCCACGCGGAAGTCGGAGCCTCCTCCCCCTGGATAGGGTGTACGAGATCCCTGGACTG
GAGCCCATCACCTTTGCGGGGAAGATGCACTTCGTGCCCTGGCTGGCGCGGCCGATCTTTCCGCCCTGGGACCGC
GGCTACAAGGACCCAAGGTTCTACCGCTCGCCCCCTCTTCACGAGCATCCGCTGTACAAAGACCAGGCCTGCTAT
ATCTTTCACCACCGTTGCCGCCTTCTCGAGGGTGTAAAGCAGGCCCTCTGGCTCACCAAGACCAAGTTAATAGAA
GGCCTTCCCGAGAAAGTGCTTAGCCTTGTTGATGATCCAAGGAACCACATAGAGAACCAAGACGAGTGCGTTCTG
AATGTGATCTCTCACGCCCCTCTCTGGCAGACCACTGAGGAAATCCCCAAGAGAGAGACCTACTGCCCGGTCATC
GTGGACAACCTAATACAGCTGTGTAAATCTCAGATTCTCAAGCATCCTTCTCTGGCCAGGAGGATCTGTGTCCAA
AACTCCACGTTTTCTGCTACCTGGAACCGAGAGTCTCTTCTCCTTCAAGTCCGTGGTTCTGGTGGAGCCCGACTG
AGCACTAAGGATCCTCTGCCCACCATCGCCTCCAGAGAGGAGATTGAAGCTACTAAGAATCATGTTCTAGAGACC
TTCTACCCCATATCACCCATCATCGATCTTCATGAATGCAATATTTATGATGTGAAAAATGACACAGGATTCCAG
GAAGGCTATCCTTACCCCTATCCCCATACCCTGTACTTACTGGACAAAGCCAATTTACGACCACACCGCCTTCAA
CCAGATCAGCTGCGGGCCAAGATGATCCTGTTTGCTTTTGGCAGTGCCCTGGCTCAGGCCCCGGCTCCTCTATGGG
AATGATGCCAAGGTCTTGGAGCAGCCCGTGGTGGTGCAGAGCGTGGGCACGGATGGACGTGTCTTCCATTTCTTA
GTGTTTCAACTGAATACCACAGACCTGGACTGTAACGAGGGTGTCAAGAATTTGGCCTGGGTGGACTCAGACCAG
CTCCTCTATCAGCATTTTTGGTGTCTCCAGTGATCAAAAAGAGAGTGTTGTGGAACCTGTTGGGCCAGTTGGT
TTCAAGCCAGAGACATTAGAAAAGTTTTAGCTCTATATTTGCATGGTGCTGCGTAGCGGAGGACCCCTCTGAA
TCCTGAAACCCCTCTTGCTCTCTTCCACGGAAGAGGGCCTGGGCCCCGTGGAGCCTCAGTGCCCGTTTGGCCTG
CTGCTCTCGCTGACAATAAAGAGCCCTTGCGTTGC

253/6881
FIGURE 238

MALASGPARRALAGSGQLGLGGFGAPRRGAYEWGVRSTRKSEPPPLDRVYEIPGLEPITFAGKMHFVPWLARPIF
PPWDRGYKDFRFYRSPPLHEHPLYKDQACYIFHHRCRLLEGVKQALWLTKTKLIEGLPEKVLSLVDDPRNHIENQ
DECVLNVISHARLWQTTEEIPKRETYCPVIVDNLIQLCKSQILKHPSLARRICVQNSTFSATWNRESLLLQVRGS
GGARLSTKDPLPTIASREEIEATKNHVLETFYPISPIIDLHECNIYDVKNDTGFGQEGYPYPYPHTLYLLDKANLR
PHRLQPDQLRAKMILFAFGSALAQARLLYGNDKVLQPVVVQSVGTDGRVFHFLVFQLNTDLDLCNEGVKNLAW
VDSDQLLYQHFWCLPVIKKRVVVEPVGPVGFKPETFRKFLALYLHGAA

254/6881
FIGURE 239

CCGCGGCCGGGGCTGACGCTTTGACAGCTGGAAAGAGCGCGGAGCCAGCGCCTGGGGGGGAGGGAGGGGAGCGCG
GCGAGGAGAGCGCCAGCGAGCGAGAGAGCGAGCGAGCGCGGGGAGGGGGCCGGGAGCGAGGGGCAGCTCGGGAG
AGCCGGAGCGGTAGCGGCGGCGGCGGCGGCGGCGGAGGCTCGGCGCCCTCTTCCCTGCAAACCATGTTTGCCA
AAGGCAAAGGCTCGGCGGTGCCCTCGGATGGGCAGGCTCGGGAAAAAGTTAGCTTTATACGTCTACGAATATTTAC
TGCACGTAGGAGCACAGAAATCTGCACAGACCTTCTTATCGGAGATTCGATGGGAAAAAACATCACGTTGGGAG
AACCGCCTGGGTTTTTGCACCTCGTGGTGGTGTGTATTTTGGGACCTTTACTGTGCAGCTCCTGAAAGGAGAGACA
CTTGTGAACATTCAAGTGAAGCAAAAGCCTTTCATGATTATAGTGCAGCAGCTGCCCGAGCCCCGTGCTTGGCA
ACATTCCCCCAACGATGGGATGCCGGGAGGCCCATCCCGCCAGGTTTCTTTCAGGGTCCTCCGGGGTCACAGC
CCTCGCCGCACGCACAGCCTCCACCTCACAATCCTAGCAGCATGATGGGACCCACAGTCAGCCTCCGGGAGGAG
TTCCTGGGACACAGCCATTGCTGCCCAATTCTATGGATCCCACACGACAACAAGGCCACCCCAACATGGGAGGAT
CAATGCAGAGAATGAACCTTCCCCGAGGCATGGGGCCCATGGGTCCCAGGCCACAGAATTACGGCAGCGGCATGA
GACCACCACCAACTCCCTCGGCCCCGCCATGCCCGGGATTAAACATGGGCCCCGGGAGCTGGCAGACCCTGGCCCA
ATCCTAACAGTGCTAACTCAATTCCATACTCCTCCTCATCACCTGGTACCTATGTGGGACCCCTGGTGGTGGCG
GTCCTCCAGGAACACCCATTATGCCAGTCCCGCAGATTCAACAAATTCAGTGACAACATCTACACAATGATTA
ATCCAGTGCCGCCTGGAGGCAGCCGGTCCAACCTCCCGATGGGTCCCAGGCTCGGACGGTCCGATGGGCGGCATGG
GTGGCATGGAGCCACACCACATGAATGGATCATTAGGGTCAGGCGACATAGACGGACTTCCAAAAAATTCTCCTA
ACAACATAAGTGGCATTAGCAATCCTCCAGGCACCCCTCGAGATGACGGCGAGCTAGGAGGGAACCTCCTCCACT
CCTTTCAGAACGACAATTATTCTCCAAGCATGACGATGAGTGTGTGATCCCCCCTTCTCCGAGACGCTGAGAGAG
CAGGCATTGCAGGCGGGAAGATGCCAGAAATTATGCAAGAAGTGAGGTGTCATTATCCAGGAGCTGGTGGGGAGG
GCATCTCCCTGCTCCCCCTCAACCCCTCCACCCCATCCACGCCCCCTACCTTTCCCAATTTTAGTTTCATGCAA
TAAAAAGGCCAACTTTTTATTCCATAAAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA ,

255/6881
FIGURE 240

MFAKGKGS AVPSDGQAREKLALYVY EYLLHVGAQKSAQTFLSEIRWEKNITLGEPPGFLHSWWCVFWDLYCAAPE
RRDTCEHSSEAKAFHDYSAAAAPSPVLGNIPPNDGMPGGPIPPGFFQGPPGSQPSPHAQPPPHNPSSMMGPHSQP
PGGVPGTQPLLPNSMDPTRQQGHPNMGGSMQRMNPPRGMGPMGPGPQNYGSGMRPPPNLGPAMPGINMGPGAGR
PWPNPNSANSIPYSSSSPGTYVGPPGGGGPPGTPIMPSPADSTNSSDNIYTMINPVPPGGSRSNFPMPGPGSDGPM
GGMGGMEPHHMNGSLGSGDIDGLPKNSPNNISGISNPPGTPRDDGELGGNFLHSFQNDNYSPSMTMSV

256/6881
FIGURE 241

ATGTACGCCTTTGTGCGGTTTCCTGGAGGACAACGTCTGCTACGCGCTGCCCCTGTGCTGCGTGCGCGACTTCAGC
CCCCGCTCGCGGCTGGATTTTGACAACCAGAAGGTGTACGCCGTGTACCGGGCCCGGAGGAATTGGGCGCCGGG
CCCGAGAGCCCCCGCGCGCCCCCGCGACTGGGGCGCGCTGTTGCTCCACAAGGCCAGATCCTGGCGCTGGCA
GAAGACAAATCTGACCTTGAAAACAGTGTGATGCAGAAGAAAATAAAAATCCCCAAGCTTTCTCTTAATCATGTA
GAAGAAGATGGAGAGGTTAAAGATTATGGGGAAGAAGATTTACAGCTTAGACACATCAAGGATTGTCTGGGGAAA
TATTGATCTGCAGTCCAAGAAAATCCCAGCTGCCCTTGCCCTGAACTGATTCTCGTTGTCTTACACAGAGACCTGA
GGGGCGGAAGCCGAGCGAAGTGGCGCACAAGAGCATCGAGGCAGTGGTGGCTCGGCTAGAGAAGCAGAACGGCCT
GAGCCTGGGCCATAGCACGTGTCCGGAAGAGGTCTTCGTGGAGGCCTCGCCAGGCACAGAGGACATGGACAGTCT
AGAAGATGCTGTGGTGCCCCGGGCTCTGTATGAGGAGCTGCTGCGCAACTACCAGCAGCAACAGGAAGAGATGCG
CCACCTCCAGCAGGAGCTGGAGCGGACTCGGAGGCAGCTGGTACAACAGGCCAAGAAGCTCAAGGAGTACGGGGC
ACTTGTGTCTGAAATGAAGGAGCTCCGTGACCTTAACCGGAGGCTCCAGGACGTGCTGCTCCTGAGGCTTGCGCAG
CGGTCCCGCCATTGATCTGGAAAAAGTAAAGTCAGAATGTCTCGAGCCCGAGCCGGAGTTACGGAGCACTTTCAG
TGAGGAAGCAAATACGTCGTCCTATTACCCCGCTCCTGCGCCTGTCATGGACAAGTATATCCTAGACAATGGCAA
GGTCCATCTGGGAAGCGGGATTGCGGTTGATGAGGAGAAATGGCACCAGCTACAAGTAACCCAAGGAGATTCCAA
GTACACGAAGAACTTGGCAGTTATGATTTGGGGAACAGATGTTCTGAAAAACAGAAGCGTTCACAGGCGTCGCCAC
AAAAAAAAAAGAAAGATGCAGTCCCTAAACCACCCCTCTCGCCTCGCAAATAAGCATCGTCAGAGAGTGTTTGTA
TGACAGAATAGCACAGAAGAACTGTGGATGAACTGAAATTGCACAGAGACTCTCCAAAGTCAACAAGTACATCTG
TGAAAAAATCATGGATATCAATAAATCCTGTAAAAATGAAGAACGAAGGGAAGCAAAATACAATTTGCAATTAAAC
TTTGATTTTTTCAT

257/6881
FIGURE 242

MDSLEDVAVPRALYEELLRNYQQQQEEMRHLQQELERTRRQLVQQAKKLKEYGALVSEMKELRDLNRRLQDVLLL
RLGSGPAIDLEKVKSECLEPEPELRSTFSEEANTSSYYPAPAPVMDKYILDNGKVHLGSGIWVDEEKWHQLQVTQ
GDSKYTKNLAVMIWGTDLKNRSVTGVATKKKKDAVPKPPLSPRKLSIVRECLYDRIAQETVDETEIAQRLSKVN
KYICEKIMDINKSCKNEERREAKYNLQ

258/6881
FIGURE 243

CCITTCGTTGCCTGATCGCCGCCATCATGGGTCGTATGCGTGCTCCTGAGAAGGGCCTGTCCCAGTCGGCTTTAC
CCTATCGACGCAGCTTCCCCACTTG GTTGAAGTTGACATCTGACGACGTGAAGGAGCAGATTTACAAACTGGCCA
AGAAGGGCCTTACTCCTTCACAGATCGGTGTAATCGTGAGAGAATCACATGGTGTTGCACAAGTACGTTTTGTGA
CAGGCAATCTCTACCATTTAATTAAGAAAGCAGTTGCTGTTCAAAGCATCTTGAGAGGAACAGAAAGGATAAGGA
TGCTAAATTCCATCTGATTCTGATAGAGAGCCAGATTCACCGTTTG

259/6881
FIGURE 244

CGCCGCCATCATGGGTCGTATGCGTGCTCCTGAGAAGGGCCTGTCCCAGTCGGCTTTACCCTATCGACGCAGCTT
CCCCACTTGGTTGAAGTTGACATCTGACGACGTGAAGGAGCAGATTTACAACTGGCCAAGAAGGGCCTTACTCC
TTCACAGATCGGTGTAATCGTGAGAGAATCACATGGTGTTGCACAAGTACGTTTTGTGACAGGCAATAAAATTTT
AAGAATTCTTAAGTCTAAGGGACTTGCTCCTGATCTTCCTGAAGATCTCTACCATTTAATTAAGAAAGCAGTTGC
TGTTCAAAGCATCTTGAGAGGAACAGAAAGGATAAGGATGCTAAATTCCATCTGATTCTGATAGAGAGCCAGATT
CACCGTTTGGCTCAATATTATAAGACCAAGCGAGTCCTCCCTCCCAGTTGGAAATATGAATCATCTACAGCCTCT
GCCCTGGTCGCATAAAATTTGTCTGTGTACTCAAGCAATAAAATGATTGTTTAACTAAAATAAAACAAAAACAAAA
ACAAAAAA

260/6881
FIGURE 245

AGAAGATGCCTTCAAATTCAACCCGAGAAGGATATCATTGTAGAGTTTATCAAAAATGGAGATTTCAAGTATGTCC
GCATGCTGGGGGCACTTTACATGAGGCTGACAGGCACTGCAATTGATTGCTACAAGTACTTGGAACCTTTGTACA
ATGACTATCGAAAAATCAAGAGCCAGAACCGAAATGGGGAGTTTGAATTGATGCATGTTGATGAGTTTATTGATG
AACTATTGCACAGTGAGAGAGTCTGTGATATCATTCTGCCCCGACTACAGAAACGCTATGTATTAGAGGAAGCTG
AGCAACTGGAGCCTCGAGTTAGTGCTCTGGAAGAGGACATGGATGATGTGGAGTCCAGTGAAGAGGAAGAAGAGG
AGGATGAGAAGTTGGAAAGAGTGCCATCACCTGATCACCGCCGGAGAAGCTACCGAGACTTGGACAAGCCCCGTC
GCTCTCCCACTGCGCTACAGGAGGAGTAGGAGCCGGTCTCCCAAGGCGGAGTCGATCTCCAAAAGGAGAA
GCCCCCTCCCCTCGCCGAGAAAGGCATCGGAGCAAGAGTCCAAGACGTCACCGCAGCAGGTCCCGAGATCGGCGGC
ACAGATCCCGTTCCAAGTCCCCAGGTATCACCGTAGTCACAGACACAGGAGCCACTCAAAGTCTCCCGAAAGGT
CTAAGAAGAGCCACAAGAAGAGCCGGAGAGGGAATGAGTAAATGGACTCAGTTTGGTTTTAGTCCACATGGCCTCC
TGTGGATATAAGGATATCTGTATGTGGAAGGATTAAGATCTCCCCAGGCAGCTATAAGAATATTTTAGTTTTTT
TCTTATCAAGTTTCTCAACCTTTATTTTTTAATGAAGGAGGTGCTGAGTTTTGTATCTTTTTAATCATAATCAACA
TCAGTTTTTTGACCCAACTAACCTTGACTGTATTCAAATTTATGAGAGTATAAAGGATCTGGAGGTTGGGGATATG
ACTGACAAGGAAAGGCTGTGGCCACCTGATGACCCTTTCCCTTTTTATTAAACCGGACACACCTGTTTTCCATTT
CGCTGTAGTTTTAGTTTTTGGTTTTGTTGTGGTTGGAAGTCTTTGAGAAATCCTGGGATTTGTGCTGCTGCTGTTAT
TCAAAGATCAAAGGAGTAAAAACATAGTTGCTCCTAACTTTTTTCCAGCAGCAGCAAGTGGTAATAAACATGAAAA
CTGGTTTGTAGCAGTTTTTGAAAAGATAGAATGCATTCAAATGTAAGGCTGCTTCTGGATCATTAAGCCAGTTTC
ATCAAACAGTTCAACAGAGAGCAGCACTTAATACCCTTTATACAGCCCATTTTTTTCATAGTTTCATTTGTTCTTG
CCCACAAGCTTGAAATCCAGGTTAAGGTATCCAGCCTTTATCATATAAGCATTGACATTATCCAGGCCTAGTCAG
TAGCAGTAGGGTAACGGGATTGAAAAAGATTTGATGGAGAGGAAAGTATCTAATATTAGTCATGGTTTTGACCTA
AATTGCTAGACAGTCGTGCCATTACAAAGTCAGAAAATACAGCAGGAAGAGACAGCTTTTAGAGGGGCAGAGAA
TTAGAGGATGGTGGTAGTAATGAAAAAGATGCATTGAGTTTAACAAGTTTAATTTGAGACAGCTATGGTATAGCT
AAAAACAAAAGCCCATAAAGTTGGAGATAGGGACCAGAGTTTAACATAGCGATCTAGGCCAGAATTGACAATGTT
TAAGTAATGGTGAATCTGTCAATAAGACTTCCAGAGTGTTAATATATATCAGAAATGCACACAACAGAACCAT
AGGCAACACCAACACAGGAAGAAATAGAAGTCACCTATTGAAAACCTGGAATGGCCCATTCAGAAAGACAGGAGAA
TTAGGAGAGAGTGAGTGAAAGAAGCCAAGGGTCAAGAATGCAGAAGCAAAGGAAGGACTAAAAAGCCTCCACGGA
CATCGATAATCAAGAGATTATTAAGATCTTTGCTAGAAGAGTTCCCTTACCTGTACTTAACTCCCTTAAAAAGAG
AAAAGTGATGGAATGACTTCTGCAACTGTAGTCCCAGCAGGAAGTGTGAAGACCAGCTGCCCTGCAGGATCCAGT
TTTTCTTGGGAGGTTGTATCTGGTCATAAGGTAAACATTCTATATATTCTATGCCTGCTCTAGAATTGAAAGACT
TCAGCAGTATTAAAGCATTTTTTTAATCTT

261/6881
FIGURE 246

MLQIQPEKDIIVEFIKNGDFKYVRMLGALYMRLTGTAIDCYKYLEPLYNDYRKIKSQNRNGEFELMHVDEFIDEL
LHSEVCDIILPRLQKRYVLEEAEQLEPRVSALEEDMDDVESSEEEEEDEKLERVSPDHRRRSYRDLDPKPRS
PTLRYRRSRSRSEPRRRSRSPKRRSPSPRRERHRSKSPRRHRSRSDRRHRSRSKSPGHHRSHRHRSHSKSPERSK
KSHKKSRRGNE

262/6881
FIGURE 247

GTTTCGGGCCAGATGCGCTCCATCATGGAAGGGCCGCTGAGCAAATGGACTAACGTGATGAAGGGCTGGCAGTACC
GTTGGTTCGTGCTGGACTACAATGCAGGACTGCTCTCCTACTACACGTCCAAGGACAAAATGATGAGAGGCTCTC
GCAGAGGATGTGTTAGACTCAGAGGAGCTGTGATTGGTATAGACGATGAGGACGACAGCACCTTCACAATAACTG
TTGATCAGAAAACCTTCCATTTCCAGGCCCGTGATGCTGATGAGCGAGAGAAGTGGATCCATGCCTTAGAAGAAA
CAATTCCTTCGACATACTCTCCAGCTTCAAGGTTTGGATTTCAGGATTTGTTCCCTAGTGTCCAAGATTTTGATAAGA
AACTTACAGAAGCTGATGCTTACCTACAAATCTTGATTGAACAATTAAAGCTTTTTGATGACAAGCTTCAAAAC
GCAAAGAAGATGAACAGAGAAAGAAAATTGAAACTCTCAAAGAGACAACAAATAGCATGGTAGAATCAATTAAAC
ACTGCATTGTGTTGCTGCAGATTGCCAAAGACCAGAGTAATGCGGAGAAGCACGCAGATGGAATGATAAGTACTA
TTAATCCCGTAGATGCAATATATCAACCTAGTCCTTTGGAACCTGTGATCAGCACAAATGCCTTCCCAGACTGTGT
TACCTCCAGAACCTGTTTCAGTTGTGTAAGTCAGAGCAGCGTCCATCTTCCCTACCAGTTGGACCTGTGTTGGCTA
CCTTGGGACATCATCAGACTCCTACACCAAATAGTACAGGCAGTGGCCATTACCACCGAGTAGCAGTCTCACTT
CTCCAAGCCACGTGAACCTTGTCTCCAATACAGTCCCAGAGTTCTCTTACTCCAGCAGTGAAGATGAATTTTATG
ATGCTGATGAATTCATCAAAGTGGCTCATCCCCAAAGCGCTTAATAGATTCTTCTGGATCTGCCTCAGTCCCTGA
CACACAGCAGCTCGGGAAATAGTCTAAAACGCCAGATACCACAGAATCACTTAATTCTTCCCTGTCCAATGGAA
CAAGTGATGCTGACCTGTTTGATTACATGATGACAGAGATGATGATGCGGAGGCAGGGTCTGTGGAGGAGCACA
AGAGCGTTATCATGCATCTCTTGTGCGAGGTTAGACTTGAATGGATCTTACTAAGGTAGTTCTTCCAACGTTTA
TTCTTGAAAGAAGATCTCTTTTAGAAATGTATGCAGACTTTTTTGCACATCCGGACCTGTTTGTGAGCATTAGTG
ACCAGAAGGATCCCAAGGATCGAATGGTTTCAGGTTGTGAAATGGTACCTCTCAGCCTTTCATGCGGGAAGGAAAG
GATCAGTTGCCAAAAGCCATACAATCCCATTTTGGGCGAGATTTTTCAGTGTGATTGGACATTACCAATGATA
CTGAAGAGAACACAGAAGTAGTTTCAGAAGGACCAGTTCCCTGGGTTTCCAAAACAGTGTAACATTTGTGGCTG
AGCAGGTTTCCCATCATCCACCCATTTTCAGCCTTTTATGCTGAGTGTTTTAACAAGAAGATACAATTCAATGCTC
ATATCTGGACCAAATCAAATTCCTTGGGATGTCAATTGGGGTGCACAACATAGGGCAGGGCTGTGTCTCATGTC
TAGACTATGATGAACATTACATTCTCACATTCCCCAATGGCTATGGAAGGTCTATCCTCACAGTGCCCTGGGTGG
AATTAGGAGGAGAATGCAATATTAATTGTTCCAAAACAGGCTATAGTGCAAATATCATCTTCCACACTAAACCCT
TCTATGGGGGCAAGAAGCACAGAATTACTGCCGAGATTTTTTCTCCAAATGACAAGAAGTCTTTTTGCTCAATTG
AAGGGGAATGGAATGGTGTGATGTATGCAAAATATGCAACAGGGGAAAATACAGTCTTTGTAGATACCAAGAAGT
TGCTTATAATCAAGAAGAAAGTGAGGAAGTTGGAAGATCAGAACGAGTATGAATCCCGCAGCCTTTGGAAGGATG
TCACTTTCAACTTAAAAATCAGAGACATTGATGCAGCAACTGAAGCAAAGCACAGGCTTGAAGAAAGACAAAGAG
CAGAAGCCCCGAGAAAGGAAGGAGAAGGAAATTCAGTGGGAGACAAGGTTATTTTCATGAAGATGGAGAATGCTGGG
TTTATGATGAACCATTACTGAAACGTCTTGGTGCTGCCAAGCATTAGGTTGGAAGATGCAAAGTTTATACCTGAT
GATCAGGGCAGTAGGCATAATTCAGCAACAAACAATCTTCCCTTTGGGAGAAACCTGTTTCATTCCAATCTTCTAAT
TACAGTGGTTCCCTATCTCAGGGATACTGGACTTTCTGACGCAGATGAACAATTAAGGGGAAAAGCTTCCCTTTTC
CCTCTGTGGCAGTTACGATTTTGACTTCAGTCCTGAGAAAACTTCAGGTTTTGAAAATCAGATGATGTCTTCTC
CTTTTCCAAACACCACACGTTGAAAGCATTATATAATCCAAGTCTGAAACTCTGCGCTCTAGTACTGCTGTTAAG
ATACACAACCTTGTTTCTTAGTTCATATAATCTCGGGATACACACACACACATATATATACACACACATACG
TATACACACACATACATATATATAAATATACCTGATGCCAGATTTTTTTTCATAAATATCTGCCTACTGTAAATA
TGGGTTCCCTCTGAGTTGTTTTAGAAAATTAGCGCAATGTATTAATCAAGTGTTAGGAAATTTTCATGGTCTTAC
CTACAATAACTTTTTATTTTGGAATTGAACTATTATTAATTTGTATCTAATCCTGGATTACAGTTTAATTAATTAT
TCTTAGTGCTTAAGGCTTCATAAAGTAATTTTTCCAACCTTTTTTTTTAAAAAAAAAAAAA

263/6881
FIGURE 248

MASIMEGPLSKWTNVMKGWQYRWFVLDYNAGLLSYTTSKDKMMRGSRRGCVRLRGAVIGIDDEDDSTFTITVDQK
TFHFQARDADEREKWIHALEETILRHTLQLQGLDSGFVPSVQDFDKKLTEADAYLQILIEQLKLFDDKLQNKED
EQRKKIETLKETTNSMVESIKHCIVLLQIAKDQSNAEKHADGMISTINPVDALYQPSPLEPVIISTMPSQTVLPPE
PVQLCKSEQRPSLPVGPVLATLGHHQTPTPNSTGSGHSPSSSLTSPSHVNLSPNTVPEFSYSSSEDEFYDADE
FHQSGSSPKRLIDSSGSASVLTHSSSGNSLKRPDTTESLNSSLNGTSDADLFDSDHDDRDDDAEAGSVEEHKSVI
MHLLSQVRLGMDLTKVVLPTFILERRSLLEMYADFFAHPDLFVSISDQKDPKDRMVQVVKWYLSAFHAGRKGSVA
KKPYNPILGEIFQCHWTLPNDTEENTELVSEGPVPWVSKNSVTFVAEQVSHHPPISAFYAECFNKKIQFNAHIWT
KSKFLGMSIGVHNIGQGCVSCLDYDEHYILTFPNGYGRSILTPWVELGGECNINCSKTGYSANIIFHTKPFYGG
KKHRITAEIFSPNDKKSFCSIEGEWNGVMYAKYATGENTVFVDTKKLPIIKKKVRKLEDQNEYESRSLWKDVTFN
LKIRDIDAATEAKHRLEERQRAEARERKEKEIQWETRLFHEDGECWVYDEPLLKRLGAAKH

264/6881
FIGURE 249A

CCCCGGCTGTGGGCTACAGGCGCAGAGCGGGCCAGGCGCGGAGCTGGCGGCAGTGACAGGAGGCGCGAACCCGCA
GCGCTTACCGCGCGGCGCCGCACCATGGAGCCCGCCGTGTCGCTGGCCGTGTGCGCGCTGCTCTTCCTGCTGTGG
GTGCGCCTGAAGGGGCTGGAGTTCTGTGCTCATCCACCAGCGCTGGGTGTTCTGTGTGCCTCTTCCTCCTGCCGCTC
TCGCTTATCTTCGATATCTACTACTACGTGCGCGCCTGGGTGGTGTTCAGCTCAGCAGCGCTCCGCGCCTGCAC
GAGCAGCGCGTGCGGGACATCCAGAAGCAGGTGCGGGAATGGAAGGAGCAGGGTAGCAAGACCTTCATGTGCACG
GGGCGCCCTGGCTGGCTCACTGTCTCACTACGTGTCGGGAAGTACAAGAAGACACACAAAAACATCATGATCAAC
CTGATGGACATTCTGGAAGTGGACACCAAGAAACAGATTGTCCGTGTGGAGCCCTTGGTGACCATGGGCCAGGTG
ACTGCCCTGCTGACCTCCATTGGCTGGACTCTCCCCGTGTTGCCTGAGCTTGATGACCTCACAGTGGGGGGCTTG
ATCATGGGCACAGGCATCGAGTCATCATCCACAAGTACGGCCTGTTCCAACACATCTGCACTGCTTACGAGCTG
GTCTTGCTGATGGCAGCTTTGTGCGATGCACTCCGTCCGAAAACCTCAGACCTGTTCTATGCCGTACCTGGTCC
TGTGGGACGCTGGGTTTCTGGTGGCCGCTGAGATCCGCATCATCCCTGCCAAGAAGTACGTCAAGCTGCGTTTC
GAGCCAGTGCGGGGCCTGGAGGCTATCTGTGCCAAGTTCACCCACGAGTCCCAGCGGCAGGAGAACCACCTTCGTG
GAAGGGCTGCTCTACTCCCTGGATGAGGCTGTCAATTATGACAGGGGTGATGACAGATGAGGCAGAGCCCAGCAAG
CTGAATAGCATTGGCAATTACTACAAGCCGTGGTTCCTTTAAGCATGTGGAGAATACTGAAGACAAACCGAGAG
GGCCTGGAGTACATTCCCTTGAGACACTACTACCACCGCCACACGCGCAGCATCTCTGGGAGCTCCAGGACATT
ATCCCTTTGGCAACAACCCCATCTTCCGCTACCTCTTTGGCTGGATGGTGCCTCCCAAGATCTCCCTCCTGAAG
CTGACCCAGGGTGAGACCCTGCGCAAGCTGTACGAGCAGCACACGTGGTGCAGGACATGCTGGTGGCCATGAAG
TGCCTGCAGCAGGCCCTGCACACCTTCCAAAACGACATCCACGTCTACCCCATCTGGCTGTGTCCGTTTCATCCTG
CCCAGCCAGCCAGGCCTAGTGCACCCCAAAGGAAATGAGGCAGAGCTCTACATCGACATTGGAGCATATGGGGAG
CCGCGTGTGAAACACTTTGAAGCCAGGTCCCTGCATGAGGCAGCTGGAGAAGTTTGTCCGCAGCGTGCATGGCTTC
CAGATGCTGTATGCCGACTGCTACATGAACCGGGAGGAGTTCTGGGAGATGTTTGATGGCTCCTTGTAACACAAG
CTGCGAGAGAAGCTGGGTTGCCAGGACGCCCTTCCCGAGGTGTACGACAAGATCTGCAAGGCCGCCAGGCACTGA
GCTGGAGCCCGCCTGGAGAGACAGACACGTGTGAGTGGTCAGGCATCTTCCCTTCACTCAAGCTTGGCTGCTTTC
CTAGATCCACACTTTCAAAGAGAAAACCCCTCCAGAATCCACCCCTGACAGCCCAACACCACCTTCTCCTGGCT
TCCAGGGGGCAGCCAGTGAATGGAAAGAATGTGGGATTTGGAGTCAGACAAGCCTGAGTCCAGTTCCCGTTT
AGAACTCATTAGCTGTGTGACTCTGGGTGAGTCCCTTAACCCCTCTGAGCCCGGTCTCTTCATTAGTTGAAAGG
GATAGTAATACCTACTTGCAGGTTGTTGTCTGAGTTGAGCACTGGTCACATTGAAGGTGCTGGGTAAGTGGT
AGCTCTTGTGCTTCCCGTTCAGCGTCACATCTGCAGTGGAGCCTGAAAAGGCTCCACATTAGGTACCTGTGCA
CAGCCATGGCTGGAATGATGAAGGGGATACGCTGGAGTTGCCCTGCCATCGCCTCCATCAGCCAGACGAGGTCTT
CACAGGAGAAGGACAGCTCTTCCCCACCCCTGGGATCTCAGGAGGGCAGCCACGGAGTGGGGAGGCCCCAGATGCG
CTGTGCCAAAGCCAGGTCCGAGGCCAAAGTTCTCCCTGCCATCCTTGGTGCCGTCTGCCCCCTTCTCCTTCATG
CCTGGGCCCTGCAGGCCCCACCCAGCCACCCTGAGTCCACTCGGAGTGCCCTGTGTTCTGGAGAAGGCATTCCA
GGGTTGAATCTTGTCCAGCCTCAGCCTGGGACACCTAGGTGGAGAGAGTGGTCTCCGCTCTGAATTGGATCCAG
GGGACCTGGGCTCATTCTTCTGGCTCACCAACCCTGCAGGCCTCATCTTCCCAAACCCACTTTGTCTTGGTG
GGAGTGGGTCCGCGCTGCTCTGCAGCAGGGGCTGGGGAGTGGACAGCATCAGGTGGGAAAGTGGAGTCCACCCTC
ATGTTTCTGTAGGATTCTCACCGTGGGGCTGGAAGAAAAGAGCATCGACTTGATTTCTCCAACCACTCATCCCTC
TTTTTCTTTCTTCCACCACTCCCCACCCAGCTGTAGTTAATTTAGTGCTTACAAATCCTAAGCTCAGAGAAA
GTTCCATTTCCGTTCCAGAGGGAAGGGAACCTCCCTAGGTCTTCCCTGGCTTGTTATAACGCAAAGCTTGGTTG
TTTATGCAACTCTATCTTAAGAACTGCCAGCCTCAGCTGAAAACCCGAATCTGAGAAGGAATTGCGTCATGTAA
GGGAAGCTGGAATTAAGGGAGCTGAGCCAGTCATGGTTGTGGCGTGTGAGTCAGGAGACCTAGGTTTCAGCCCT
CTCTACTGTGAGCGAGCTGTGCAACGTGGGCAAGTCATTGTCTCTGAGCTGCAGTTTCTCATCTGTACATCG
CTACAGACAAGACCTCCCTGGAAACCCTTCTGATTGTCTTAGACACTGTGGTTGCAAAACCCACGGAAAGCCTCAT
TTGTGTGGAAGTCAAGAGGAAAAATGATCCAGTGGACACTTGGGGATTATCTGTCAATTCAAGATCCTTCTTCAA
CCCCAAGGTCAAGTCCCATCTCATTTCCAGAAAGGCTCATACCTGGCTTGCCAGGGAAGCATCTGTCTTGTCAATC
CAGGTGCCAGAATCCTCTCAGAGTCATTGAAGGGTGTTCACCCATCCCAACCAAGGCTTGGCACACTGCCAGTGT
CTTAGCAGGGTCTTGTGAGGGCTGGGGGCATCCAGGCACTCAGAAGGCAAAGGAACCAACCTACCCATTTGGCT
CTGGAGGGGGCAGAAGAAAGAAATAAACCTCATCTATATTTTACAAAGCATGTGAATTCTGGCATTAGCTCTCA
TAGGAGACCCATGTGCTTCTTGCTCAGTGCAAAACTGATGATTCTACTTGCTGTAGATGAATGGTTAACACGAG

265/6881
FIGURE 249B

CTAGTTAAACAGTGCCATTGTTTTGCCAGTGAAGCCTCCAACCCTAAGCCACTGGGACGGTGGCCAGAGATGCCA
GCAGCCTCTGTGCGCCCTTAGTCATATAACCAAAATCCAGACCTTATCCACAACCCGGGGCTTGGAAGGAAGGTA
TTTTGGAATCACACCCTCCGGTTATGTTGCTCCAGTAAATCTTGCCCTGGAAAGAGGCAGTCTTCTTAGCATGGT
GAGCTGAGTTCATGGCTTTTTTTTGTAGCCAGTCCTGTCCCTGGCCATCCATGTGATGGTTTTGGATGGAGTTAA
ACTTGATGCCAGTGGGCAGTGCATGTGGAAGTATCAGAGTAAGGCTCTCCCCTCCAGAGCCCTGAGTTTCTTGG
CTGCATGAAGGTTTTCTTTAGAATCAGAATTGTAGCCAGTTTCTTTGGCCAGAAGGATGAATACTTGGATATTAC
TGAAAGGGAGGGGTGGAGATGGGTGTGGCAGTGTATGGTGTGTGATTTTTATTTTCTTCTTTGGTCATGGGGGCC
AAGGAGAAAGGCATGAATCTTCCCTGTCAGGCTCTTACAGCCACAGGCACTGTGTCTACTGTCTGGAAGACATGT
CCCCATGGCTGTGGGGCCGCTGCTTCTGTTTAAATAAAAAGTGGCCTGG

266/6881
FIGURE 250

GACATCATGGGCTATTTTTAGGGGTTGACTGGTAGCAGATAAGTGTTGAGCTCGGGCTGGATAAGGGCTCAGAGT
TGCACTGAGTGTGGCTGAAGCAGCGAGGCGGGAGTGGAGGTGCGCGGAGTCAGGCAGACAGACACAGCCAG
CCAGCCAGGTTCGGCAGTATAGTCCGAAC TGCAAATCTTATTTTTCTTTTACCTTCTCTAACTGCCCAGAGCTA
GCGCTGTGGCTCCCGGGCTGGTGTTCGGGAGTGTCCAGAGAGCCTGGTCTCCAGCCGCCCCGGGAGGAGAGC
CCTGCTGCCCAGGCGCTGTTGACAGCGGCGGAAAGCAGCGGTACCCACGCGCCCGCCGGGGGAAGTCGGCGAGCG
GCTGCAGCAGCAAAGAACTTTCCCGGCTGGGAGGACCGGAGACAAGTGGCAGAGTCCCGGAGCCAAC TTTTGCAA
GCCTTTCCTGCGTCTTAGGCTTCTCCACGGCGGTAAAGACCAGAAGGCGGCGGAGAGCCACGCAAGAGAAGAAGG
ACGTGCGCTCAGCTTCGCTCGCACCGGTTGTTGAACTTGGGCGAGCGCGAGCCGCGGCTGCCGGGCGCCCCCTCC
CCCTAGCAGCGGAGGAGGGGACAAGTCGTGCGAGTCCGGGCGGCCAAGACCCGCGCCGCGGCCGCGCCACTGCAGGG
TCCGCACTGATCCGCTCCGCGGGGAGAGCCGCTGCTCTGGGAAGTGAGTTGCGCTGCGGACTCCGAGGAACCGCT
GCGCACGAAGAGCGCTCAGTGAGTGACCGCGACTTTTCAAAGCCGGGTAGCGCGCGCGAGTCGACAAGTAAGAGT
GCGGGAGGCATCTTAATTAACCTTGCCTCCCTGGAGCGAGCTGGTGAGGAGGGCGCAGCGGGGACGACAGCCAG
CGGGTGCGTGCGCTCTTAGAGAAACTTTCCCTGTCAAAGGCTCCGGGGGGCGCGGGTGTCCCCGCTTGCCACAG
CCCTGTTGCGGCCCCGAAACTTGTGCGCGCAGCCCAAACCTACAGTGAAGTGACGGACTGTTCTATGACTG
CAAAGATGGAAACGACCTTCTATGACGATGCCCTCAACGCCTCGTTTCTCCCGTCCGAGAGCGGACCTTATGGCT
ACAGTAACCCCAAGATCCTGAAACAGAGCATGACCTTGAACCTGGCCGACCCAGTGGGGAGCCTGAAGCCGCACC
TCCGCGCCAAGAACTCGGACCTCCTCACCTCGCCCGACGTGGGGCTGCTCAAGCTGGCGTCGCCCAGCTGGAGC
GCCTGATAATCCAGTCCAGCAACGGGCACATCACCACCACGCCGACCCCCACCCAGTTCTGTGCCCCAAGAACG
TGACAGATGAGCAGGAGGGCTTCGCGGAGGGCTTCGTGCGCGCCCTGGCCGAAGTGCACAGCCAGAACACGCTGC
CCAGCGTCACGTGCGGCGCGCAGCCGGTCAACGGGGCAGGCATGGTGGCTCCCGCGGTAGCCTCGGTGGCAGGGG
GCAGCGGCAGCGGCGGCTTCAGCGCCAGCCTGCACAGCGAGCCGCGGCTTACGCAAACCTCAGCAACTTCAACC
CAGGCGCGCTGAGCAGCGGCGGCGGGGCGCCCTCCTACGGCGCGGCGGCGCTGGCCTTTCCCGCGCAACCCACG
AGCAGCAGCAGCCGCGCACCACTGCCCCAGCAGATGCCCGTGCAGCACCCGCGGCTGCAGGCCCTGAAGGAGG
AGCCTCAGACAGTGCCCGAGATGCCCGGCGAGACACCGCCCTGTCCCCATCGACATGGAGTCCCAGGAGCGGA
TCAAGGCGGAGAGGAAGCGCATGAGGAACCGCATCGCTGCCTCCAAGTGCCGAAAAAGGAAGCTGGAGAGAATCG
CCCGGCTGGAGGAAAAAGTGAAAACCTTGAAAGCTCAGAACTCGGAGCTGGCGTCCACGGCCAACATGCTCAGGG
AACAGGTGGCACAGCTTAAACAGAAAGTCATGAACCACGTTAACAGTGGGTGCCAACTCATGCTAACGCAGCAGT
TGCAAACATTTTGAAGAGAGACCGTCCGGGGCTGAGGGGCAACGAAGAAAAAATAACACAGAGAGACAGACTT
GAGAACTTGACAAGTTGCGACGAGAGAAAAAAGAGTGTCCGAGAACTAAAGCCAAGGGTATCCAAGTTGGACT
GGGTTGCGTCTTGACGGCGCCCCCAGTGTGCACGAGTGGGAAGGACTTGGCGCGCCCTCCCTTGGCGTGGAGCCA
GGGAGCGGCCCTGCGGGCTGCCCGCTTTGCGGACGGGCTGTCCCCGCGCGAACGGAACGTTGGACTTTTCGT
TAACATTGACCAAGAAGTGCATGGACCTAACATTCGATCTCATTAGTATTAAAGGGGGAGGGGGAGGGGGTTA
CAAAGTGCAATAGAGACTGTAGATTGCTTCTGTAGTACTCCTTAAGAACACAAAGCGGGGGGAGGGTTGGGGAGG
GGCGGCAGGAGGGAGGTTTGTGAGAGCGAGGCTGAGCCTACAGATGAACTCTTCTGGCCTGCCTTCGTAACTG
TGTATGTACATATATATATTTTTTAATTTGATGAAAAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTGTAG
TTATTTCTTGTGTTTGTGTTTGGGTATCCTGCCCAGTGTGTTTGTAAATAAGAGATTGGAGCACTCTGAGTTT
ACCATTTGTAATAAAGTATATAATTTTTTTATGTTTTGTTTCTGAAAATTCCAGAAAGGATATTTAAGAAAATAC
AATAAACTATTGGAAAGTACTCCCCTAACCTCTTTTCTGCATCATCTGTAGATACTAGCTATCTAGGTGGAGTTG
AAAGAGTTAAGAAATGTCGATTAAAATCACTCTCAGTGCTTCTTACTATTAAGCAGTAAAACTGTTCTCTATTAG
ACTTTAGAAATAAATGTACCTGATGTACCTGATGCTATGGTCAGGTTATACTCCTCCTCCCCAGCTATCTATAT
GGAATTGCTTACCAAAGGATAGTGCATGTTTCAGGAGGCTGGAGGAAGGGGGTTCAGTGGAGAGGGACAGCC
CACTGAGAAGTCAAACATTTCAAAGTTTGGATTGTATCAAGTGGCATGTGCTGTGACCATTTATAATGTTAGTAG
AAATTTTACAATAGGTGCTTATTCTCAAAGCAGGAATTGGTGGCAGATTTTACAAAAGATGTATCCTTCCAATTT
GGAATCTTCTCTTGACAATTCCTAGATAAAAAGATGGCCTTTGCTTATGAATATTTATAACAGCATTCTTGTC
CAATAAATGTATTCAAATACC

FIGURE 251A

[illegible]

268/6881
FIGURE 251B

CCATTGTTAACTCACAGGCCTCATAAAACATAGGCTGTTGGCTATTATTCTCCAACCCCTTGATCTAGAGAATTTT
AAACATTAGAATTTTGTGTTTACATTTGTTAAGCTTTACGTCATCTTCAAATGACACCAAACTCAGAATTATGAT
CTGCATTTAAGCCAATTTTAAAATAAAATAAGCAGTCAATGCTGCCTCATTTATTGAAATTCAGTAGATTTTAGT
TTATTTCTTAGTAGTCAGAGAATTGATTTATAGCTATTCACCAAACATTCTTACTAACGTTTCCTTATATCTAAA
TCAGATTGATTCTATATTTTGTCTTTGTTTGTAAATCAATAGCCAATGAAGAATAAGGAGTATTGGAAGAAGCAGTG
AGTCAGCTTTAGGTGACCTGGTTCTTGTCTCAACTTTGTGATTGTTGGGGAGATACAGTTTACTTTCCTGAGCCTT
AATTCTTGTGTAAGTCTAACTTAACTTCTTAATGTCCTTCCAGAACTAAAATTTTATTGTTTCATTCTAAT
CGTTGGACTACTCTTGTGAAGTTTATATTTTGTAGTTAATACAGTTTCCAAATTAACATACATTTAAAAAAAAG
GGTAGTATTTTCCATTTCTCTGTGTGCACTTAGGATAAACAGTGAAGTATAGCTTATAAAACAATTAGTTTGAG
GGCTGAGAGTGTAAGAGGAACTATACAAAAGTCAGGAAACCTGAGCTCTTACCCTAACTCTGTTACCAACTTTG
CTGTGTGACCTTAATCAAAACACATAACCTGGACCCCATGCTCCTCACCAGTAAATCAAGGGCCTGAATTTTATG
GCTTAGTATTTCCCTTCCAAGCTCCGAAGTTGCGTGATTCTGTGAAAGGCAGTGATTGATTCCCTTGTACTCATCT
TCCTTTTGTACCTGTTTCCCTCATGATATATTGGGGAACAAATACTAAAAAGTGTTTTATACTAGCTTTCTTGATTG
ACATTTCCCTATAATACTGATGAATTTGGGTGATGGAAAGTAATGGAAATTGTTAAAAGTTCTGCTCTCAAATCT
GAGTCTCCTTGCCCTGTGTGCCAATGTTTAACCATATTTGCTAATCTAAGCCATATTGCGAGGATCTCAAGGATG
ATACTTGTCAAGAGTTTGGGGCCTTGAGAGCACAGTTTTCAAATAATACTTAGTATTTTCTGACTATAGAGTAC
ATTTGTCTTGTAAGTATATTTTAAAATACAGAGAAGTGTGAAGTACAAATATCTCAGTGCTACTATTTAAAAAA
ACACAATTAGTATATAAATCCTTCCCCATTTTTTTGACAGTATAATTTTAGTATGTTAACTTGGTTACTTCTTT
CTCTCTTCCCTCCATCATTTTTCCCTGCTTCTTTTTCTTTTGTGTCATATTCTTAAACAATTTTGCAACCACAGGTA
CCCACATTGCTGGCACTACCAGCCTTGGGCTACTACCGAGGATAATGGAGCCAGGGCCTTGTAAGAAGCACAGAGG
AAGTCTAGAAGTGAAGGGGCTATGATACAGGAAGTTCAGGAGGCAGAGTCTCAAAGGAACACCTGCCTTTAATA
ATGTTTACAGAAGTGGAGAAAGGACTAAAGGACTTAAAGACATGCAGGTGTCTTCATCCTGATTCTGTCTTTGTT
ATTGCACAATGACTATAAATAATGACCTAATTTTTTTTTTTTTCTGGCTTGGCTAATGGAAATCGACACTAGCG
CTTCCCCAGTATTAGACTTAATCTAATTCCAAAGTAACATTCAAGAAAAGAAAAACCAGTGGAACAGGATCAGTA
AGCTCAGACTCTCCATCTCCATTATTTTAGCCTTGACCATTCTTCTCTAATCCTTTTAAATTATCTTCAGTTTCC
AGTTCAAGTTACATTGCTTCAGTTACAGTTTGTGTTGACCCGTGATTTCAGAGCTGCATTATGATTCTTGTGGGCCC
TAGATAGTTTTGCCATCTTAGACCCCTTCTTCCATACAAAATTAAAAGTGATATTTTACAATTGTATCTGTATGA
AATGAATGTATTAATATTTTAGATTAAAACATTTGTTTGAAGTTTCAGTTTTTTCTTATGAGGCTAAAAAAAT
TAAAACATTTTTGTGGGCTTCTAAAAAACTGTGGGCCTTAGGTACTGTGCCTAATGGATAAGTTGGCATTGCCTG
TATTCTGAAGGGCATCATTGGAAAAATAGCAGTCATTATTCTGTCCCCTTCTCCCACCACCACAGTCCTTGGAGA
AGCCTTTGCCACTCCATCCAGGAGCACTGCAGTTTCCACGGTTATAGATCTATAGACTTGAACCTACTTCTCTCC
CAACCTAACGAAAACCTACAAGGATTACTTGGGACCATTTCATCCTCAAAAAAGATAGGAGGCAGTGTTTGTGTTT
AGTCTTCAGATATTTTGTGTTTGGTCAGTCCCTAATCTGTAGTTTTGAAACTCGTGCCACACTTGAAAGGGAAAC
ATCCTACTACCTTTCTTCTCTCCATTTCCCACAAACCCTTCTCTCATCATCACTCCCTGCATTCTTACTTCT
CAGCATATAAATACAAGACCCTTCTTCTATTATTTGTTGAAAGCTAGGCCTGTAAAATAGAGATGGACAGACCA
TGCATGTTTCCATGAAGCTATTTAATGCTGCTCCAGTCTTCTGTCCATACCATTCCCTTCCCTGCCCCTAGGAGT
GGGGTTGAGGTCTGTGACATGCAGACTGTAAGCACAGTCAGAACCTCTGCAGCTCTCAACCCAACAGAGGAGACT
GTGGCTTCAACATGCCAACCTGAGCAGGTCTCCTCTGCATTACCTTCCCTCCATTTCTCTTCCCTGGGTCTGATG
AGGTGAGCTGGAGGAACCAATAGTCAGGATGCCCTGGAATTGATGTTGCTCTGTTTTGTGCTCACAAAACAGCCA
TGTAACACATGAGCACCTGAGTTGAAGCCATCCAGTCGCAAGTCAGCAGACAGCAGTTGATGGAATTCTCAGTAG
AAATTCAGTAAGGGTGCCCAAATTTTATTTTTTTTTTACCTATACTCTACCAATATATGGTATTTAGGAAAAC
TCTTTTATCCAAGCACAAAGAAAAGCACACACATTTTATAATCATCTGCTTCATCAGGGTAAATAAATAATTTA
ACAAATTTGATCAGCATCTCTAGTTTACCAGTACTTTAATATTAGTTTTCTTACAAATTAATGTATTTTGAATA
TTTCCAGAAAATCACTGTGGGAGAATAATGTAATATACTTTAGGATATATTTCCCTGACCTTTTCTTAAATGGCTT
CATGTGCTATTCCCCCAAATCTGCTTTCTCTATTTTCTTTTTTATTTAACCTATAATTATACTTTCTAGTATAT
TCTGAGTCTATCTTCTAAGCCACCTTACATTTTCTTGGAACAAGGGAGGGAATAAATAGTTGCCCTCCACTAAAT
CAGGAAAAAATAAATAATATCCCAGGGGAGCTGTGATTATGCCAAGAGCTCTAAACAGAAGTTTGAGAAGGTAAAA
ATTAAGTTGTAGTATCTGAGTTGTTTTTATTTTCTTCCCTTGGTGTGTTATGAAGGTATTCATAAGAACTTTAAT

269/6881
FIGURE 251C

TCAGGGGAAAAAATGCCTGATTTGCTATTTTTGACATTTCCCTCGTCTCTTAAGAAGTCAGTTAAATATGTTTTTC
ATAGTTTATATTCCTGTTTCATAGATTACTGTGAAACATGTATTTAAACCTATGAATTATAAAATAGTATTTAGA
TTCTAGCGTGAGTTAAATAGATTAGTCATATATCTTTTAGATTTGTGGATTTGACATGTAAATTATGTGTTGTGT
ATAAGTAAGTTAGTTACTAAACATATGGCATGGTTATTGATAAACTTGTTGCTATTTTTTTCCAAATGCTATCAG
TGTTTGTGGACTTTTAAAAATTAGTTTGAATTTTGGAATGTTCTGTGATAAAATGTAATTTCAACTATTTTGTAC
ATTTAAATATGCCATGTTGTATATGTCTGTATTTAAAAATGTTGTAAATACCTGCATTTTAAGAATTATGAAAGA
TTTTCTCAAAAATGACAGAACTCTCCATACTTAATTGTGACACATTATAAGATATCTGATTTTAAGCTTTTGGA
TTTTGTTCTAAAAATTAAGTTTAAACATGCTGAAAATTCATAAAAATAAAATTTGAAAATAAA

270/6881
FIGURE 252

MHETNQGEFITSDSQEALFSKSSRGCLQNEKQDETLSSEITLWTEKQSNQDKKSIELNDQKFNELIKNCNKHDG
RGIIVDARQLPSPEPCETIQKNLNDNEMLFHSCQMVESHEEEELKPPEQEIEIDRNIIQEEEEKQAIPEFFEGRQA
KTPERYLKIRNYILDQWEICKPKYLNKTSVRPGLKNCQDVNCIGRIHTYLELIGAINFGCEQAVYNRPQTVDKVR
IRDRKDAVEAYQLAQRLQSMRTRRRRVDRDPWGNWCDAKDLEGQTFEHLSAEELAKRREEEEKGRPVKSLKVPRTK
SSFDPFQLIPCNEFFSEEKQEPFQVKVASEALLIMDLHAHVSMAEVIGLLGGRYSEVDKVVEVCAAEP CNSLSTGL
QCEMDPVSQTQASETLAVRGFSVIGWYHSHPAFDPNPSLRDIDTQAKYQSYFSRGGAKFIGMIVSPYNNRNNPLPY
SQITCLVISEEISPDGSYRLPYKFEVQQMLEEPQWGLVFEKTRWIEKYRLSHSSVPMDKIFRRDSDLTCLQKLL
ECMRKTLKVTNCFMAEEFLTEIENLFLSNYKSNQENGVTENCTKELLM

271/6881
FIGURE 253

CTCTCTCTGGTCCGTGCCTCCAAGATGACAAAGAAAAGAAGGAACAATGGTCGTGCCAAAAAGGGCCGCGGCCAC
GTGCAGCCTATTTCGCTGCACTAACTGTGCCCCGATGCGTGCCCAAGGACAAGGCCATTAAGACATTCGTCATTCTGA
AACATAGTGAAGGCCGCAGCAGTCAGGGACATTTCTGAAGCGAGCGTCTTCGATGCCTATGTGCTTCCCAAGCTG
TATGTGAAGCTACATTACTGTGTGAGTTGTGCAATTCACAGCAAAGTAGTCAGGAATCGATCTCGTGAAGCCCGC
AAGGACCGAACACCCCCATCCCGATTTAGACCTGCGGGTGCTGCCCCACGTCCCCCACCAAAGCCCATGTAAGGA
GCTGAGTTCTTAAAGACTGAAGACAGGCTATTCTCTGGAGAAAAATAAAATGGAAATTGTACTT

272/6881
FIGURE 254A

ATGGCACAAACCGGGCAAATGCTCTGAAAAACGGATAAAATAAAATGCTGGTCACAGATGAGAACATCAGTCTAGCA
GAGCTTGCGAAGGCAGCAGGGAGGAGAAAAACCTCTGAGCTGTGTTTTGCCAGTGTCCACAGAGGGTTAGGAGGA
CCCAATGAAGGAATGACCCCTGAAATGTGAACAGGGCGAAGAACTAGGCCCCAGCTCCCTGCAGAGAAGATACATC
AAAGCCCCACATGAGGATTTTTATAGCTCCACATTGGACAAGCTTCCTCTTCCTGAGATAGAGCCTACAGGGAAG
GGACAGATTTGGGGCAAGGAGAGGAGTCTGAAAGAGATGGGGTACGCCGTAGTGAAAGCTGGAGTGAGAGCCTTC
GTATTCGAAGGCGGGGACTCGGGCGCTGTTGGCAGCTGGCGACGCGGGGCGAAGCCGCGGCTGGCGGCGCCTGGC
CAGTCCCCGATCCGCCGCGTGCACCCGGAGGTTGCGTGCGCTCCGAAGCCGGGGTGTGCGCCTAGCTGCCCCGGC
CCCGTGACCCGCGGGCCGCTCGCGCAGGACTTCGCGAGCTCGCCAAGCCTGGGGTCTGCGACAGAAAAAGGAGCG
GGGCTGCTCGGGCTGCCCAAAGGGTCAATGGTTATTAAGGAAGAAAAACAGAAATGGGGCCCTTGTATGGACTCTAT
TACCAAGTGCCATTGGACACGCAGGCAGTGTACTGGGAGACAGTCTGTTGTGCTCAGAGGTATTGCCACGGCCT
GAAGTTCTCTCTTTGGCCGAGCTGCCCCCACTCTGCTGCAATCTTCTGGGGAGGGCTTCACCTGCCACTGCCTC
CTGCAATGCCAGCATCGCTGCTGCAGACTGCAGAGCTGGGGTGCCAAAGACCAGTCTCTCAGGGGGATGAAGAG
AAAGACCCTCCGAAGAGCCACCTTATTCTGTGGAGACCCATATGGCTTTCATTTAGACCTGGACTTCCTCAAG
TATGTGGATGACATCGAGAAGGGAAACACTATCAAAAGAATTCCTATCCACAGAAGGGCCAAGCAGGCCAAATTT
AGCACTCTGCCCCGAACTTCAGCCTTCCTGACAGTGGGGCTCGCCCCCTGCAGCCCCGCCCCCTCCAAACTGG
TCTCCCGTGGTGCCAAGGGAGGCATCACTTGGGACACAGGAGCAAAACCAGTCACCACCGCTTGGTAA1'GCCCC
CAGGCCTCAACAAGCAGGAGTGAGGTGAGCTACCACAGGAAGGCTCTGTTGGCAGAGGCCACCAGACAGTTGGAA
GCTGCTGAGCCAGAGGATGCCGAGCTCACTTTTGGGAGTGACGCGCCCCAGCTCTTGAGAGCATCCAGCATGCCT
GCCACGCTGCTGCACAGCAGGGCTTCTGAGGAGCCAGGCCTGAGCCTGGGGCCCCCTGCCCTCTGCCCCCTCCT
CCCCTTCAGGGTGAAGGCAGTGTCTGTGATGGCACCTTTGAACCTGCAGAAGGATTGGCAGGTTTCCACAGCTCC
AGCCCACGAGCATCAACTCGGATTCCAGAGCTGGTCCAGGAGGGAGCTGAGCCTCCAGAGGGTGTGGTGAAGGTT
CCAAATCACCTCCCTCTCCAGGCCCTCCTTTCTCATTCCAGAATGTGCTTGTAGTTCTAGAGGACAAGGAAGAT
GAACACAATGCCAGAGAAGCAGAGGTGTTGTTACCCCTGGCTCCCCTACGCCAAGCCCGCCACCTCTGCCATCA
CCCATCCCTGAGAATGAGCTCCTCCTGGAAGAAATCGAGCTCAACATCAGCGAGATTCCACCCCGCCACCTGTGA
GAGGTGGACATGAGAAGCATTGGCATCAGGGTAACTGAGGAAAGCCTGGGCCTTGCCAGGGTGGATCCAGGCAGC
ATCTCCAGCCTGAAACAGCAGGTCTCGGCCCTGGAGGGAGAGTTGTCTGGAAGAACCAGGAACTGGCACAGGTC
AGAAGTGTCTCTCCAGCAGCAGGAAGAGGAAATCAAAGCTAGGGAGCAAAAGAAATTCAGAGCTGGAGTTCACTGTA
GCCCAACTGGAAGGACAGTTTACCAAGAGAACGCCAAAGACACTCAGGGCCAGACGGACGTGATGGTGAACACT
GACCCTGTCCATGGACTCTTGACCAGGGAGTCTGTGTGATAAGGGCATTGAAGTCAACCTTCTAGGCAGCATGGAG
TCTGAAAGCTGGGGGCACCGAGGAGAGGAGAATGGCCTCCTATGGGGGCCAGATGGTGCATAAACAAGGGAATCAG
AGCCCAGCAGAACGTGTGCTTCTGCCCCAGCTGTCACTGCCACAGGGACCCGAGCAGGTCTTACCTCCTCTGTGA
CATAGCTTCTCTCCACTGAACTCAGGATTGAAGAAGCAGGCACTGAACAGGAAGGAGGGCCCTCAGGGAGGAACC
AGGGGAGCAGGAGGCTTTCTGTGGGGCAGCGACAGAAAGACTCCCCAGCAGGGAGGGAGGAGACCAGTTCCAAT
CTCCCAGGGAAGGAGCACCCGGGAAGGCCACCAAGCTCGCCAACGGATGCCACTATTGGGCAGTATGTGAAGAAG
ATCCAGGAGCTCCTGCAGGAGCAGTGGAAGTGCCTGGAGCATGGGTACCCGAGCTGGCCAGCGCCATCAAGCAG
CCAGCCTCCAAGCTCAGCAGCATCCAGAGCCAGCTGCTGAGCTCCCTCAACCTGCTGCTGTCTGGCCTACTCGGCC
CAGGCTCACCCACCCAAGGAGCCACCGGCCTCCTCCTCCTCCCCGCCAGTGAGATCTCCCCATCGACCAGCCTT
AAATCCATAATGAAAAAGAAAGACTATGGCTTCCGTGCAGGAGGTAATGGGACCAAAAAGAACCTTCAGTTTGT
GGGGTTAACGGTGGGTATGAGACCACCTCAAGTGAGGAGACCAGCGGTGAGGACAGCACCCAGAGGACTTGTCT
GACAGCGAGGCAGAGAAGAAGTGTGACGGCCCAGATCACAAGCATGTCAAAGATGCCCATCTCACCTGCGAGGCT
GGGCAGGGCATCCCTGAGGGCACCTGCCATGCTGCCCAGGAAAGTGGGCCTGGGGAAGAAGTCCCCCACTCCAAG
GCCGAGAGCCGGAAGTCTGTAGCCCCCGCGTGGTGGCCTCCTACCTCCACGAGGTCCAGCCTCACTCCCCACAC
TTCTTGAAACTGCTTGTCAACTTGGCCGATCACAACGGGAACACGGCCCTTCACTACAGCGTGTCCCACTCCAAC
TTCTCCATCGTGAAGCTGCTGCTGGAGACAGGCGTCTGCAATGTGGACCATCAGAACAAGCTGGCTACACTGCC
GTAATGATCACTCCCTTGGCTTCCGCGAGAGACCAATGAAGACATGGCTGTTGTCTGGAAGCTCTTAAGAGAAGGA
AATGTGAACATTCAAGCTACTCAGGGAGGGCCAGACTGCGCTGATGCTGGGAGTCAGCCACGACAGGGAGGACATG
GTTCAAGCGCTGCTTAGCTGCCAGGCAGATGTCAATCTGCAGGACCACGATGGATCCTCGGCCCTCATGGTGGCC
TGTCACCATGGCAACGTGGACCTGGTGC GGCTGCTCCTGGCACACCCAGCCTGCGACAGCAGCCTGACTGACAAG

273/6881
FIGURE 254B

GCTGGCCGCACAGCTTTGTCCATCGCTCTGAAGTCACCCACCCATATGGAAATTGCTGGGCTTCTGAGAGCCCAC
GCGGAGCAGGGCAGGTCCCTGGGGCTGTAG

274/6881
FIGURE 255

MASVQEVMGPKRTFSLGLTVGMRPPQVRRPAVRTAPQRTCLTARQRRSVTAQITSMKMPI SPARLGRASLRAP
AMLPRKVGLGKKSPTRPRDINPQKNFLMHAGH

275/6881
FIGURE 256A

GCGGCGGCCGCGGAGTATCCTGGAGCTGCAGACAGTGCGGGCCTGCGCCCAGTCCCGGCTGTCTCGCCGCGACC
CCTCCTCAGCCCTGGGCGCGCGCACGCTGGGGCCCCGCGGGGCTGGCCGCCTAGCGAGCCTGCCGGTCGACCCCA
GCCAGCGCAGCGACGGGGCGCTGCCTGGCCCAGGCGCACACGGAAGTGCCTTCTCTGAAGTAGCTTTGGAAAGT
AGAGAAGAAAAATCCAGTTTGCTTCTTGGAGAACACTGGACAGCTGAATAAATGCAGTATCTAAATATAAAAGAGG
ACTGCAATGCCATGGCTTTCTGTGCTAAAATGAGGAGCTCCAAGAAGACTGAGGTGAACCTGGAGGCCCTTGAGC
CAGGGGTGGAAGTGATCTTCTATCTGTGCGACAGGGAGCCCCCTCCGGCTGGGCAGTGGAGAGTACACAGCAGAGG
AACTGTGCATCAGGGCTGCACAGGCATGCCGTATCTCTCTCTTTGTGTCACAACCTCTTTGCCCTGTATGACGAGA
ACACCAAGCTCTGGTATGCTCCAAATCGCACCATCACCGTTGATGACAAGATGTCCCTCCGGCTCCACTACCGGA
TGAGGTTCTATTTACCAATTGGCATGGAACCAACGACAATGAGCAGTCAGTGTGGCGTCAATTCTCCAAAGAAGC
AGAAAAATGGCTACGAGAAAAAAAAGATTCCAGATGCAACCCCTCTCCTTGATGCCAGCTCACTGGAGTATCTGT
TTGCTCAGGGACAGTATGATTTGGTGAAATGCCTGGCTCCTATTGAGACCCCAAGACCGAGCAGGATGGACATG
ATATTGAGAACGAGTGTCTAGGGATGGCTGTCTGGCCATCTCACACTATGCCATGATGAAGAAGATGCAGTTGC
CAGAACTGCCCCAAGGACATCAGCTACAAGCGATATATTCCAGAAACATTGAATAAGTCCATCAGACAGAGGAACC
TTCTCACCAGGATGCGGATAAATAATGTTTTCAAGGATTTCTTAAAGGAATTTAACAACAAGACCATTGTGACA
GCAGCGTGTCCACGCATGACCTGAAGGTGAAATACTTGGCTACCTTGGAACCTTTGACAAAACATTACGGTGCTG
AAATATTTGAGACTTCCATGTTACTGATTTTCATCAGAAAATGAGATGAATTGGTTTCATTGCAATGACGGTGAA
ACGTTCTCTACTACGAAGTGATGGTGACTGGGAATCTTGGAATCCAGTGGAGGCATAAACCAAATGTTGTTTCTG
TTGAAAAGGAAAAAATAAACTGAAGCGGAAAAAACTGGAAAATAAACACAAGAAGGATGAGGAGAAAAACAAGA
TCCGGGAAGAGTGGAACAATTTTTCTTACTTCCCTGAAATCACTCACATTGTAATAAAGGAGTCTGTGGTCAGCA
TTAACAAGCAGGACAACAAGAAAATGGAAGTGAAGCTCTCTTCCCACGAGGAGGCCTTGTCTTTGTGTCCCTGG
TAGATGGCTACTTCCGGCTCACAGCAGATGCCCATCATTACCTCTGCACCGACGTGGCCCCCCCCGTTGATCGTCC
ACAACATACAGAATGGCTGTCTATGGTCCAATCTGTACAGAATACGCCATCAATAAATTGCGGCAAGAAGGAAGCG
AGGAGGGGATGTACGTGCTGAGGTGGAGCTGCACCGACTTTGACAACATCCTCATGACCGTCACCTGCTTTGAGA
AGTCTGAGCAGGTGCAGGGTGCCGAGAAGCAGTTCAAGAACTTTCAGATCGAGGTGCAGAAGGGCCGCTACAGTC
TGCACGGTTCCGACCGCAGCTTCCCCAGCTTGGGAGACCTCATGAGCCACCTCAAGAAGCAGATCCTGCGCACGG
ATAACATCAGCTTCATGCTAAAACGCTGCTGCCAGCCCCAAGCCCCGAGAAATCTCCAACCTGCTGGTGGCTACTA
AGAAAGCCCAGGAGTGGCAGCCCGTCTACCCCATGAGCCAGCTGAGTTTCGATCGGATCCTCAAGAAGGATCTGG
TGCAGGGCGAGCACCTTGGGAGAGGCACGAGAACACACATCTATTCTGGGACCCTGATGGATTACAAGGATGACG
AAGGAACCTTCTGAAGAGAAGAAGATAAAAGTGATCCTCAAAGTCTTAGACCCCAGCCACAGGGATATTTCCCTGG
CCTTCTTCGAGGCAGCCAGCATGATGAGACAGGTCTCCACAAAACACATCGTGACCTCTATGGCGTCTGTGTCC
GCGACGTGGAGAATATCATGGTGGAAGAGTTTGTGGAAGGGGGTCTCTGGATCTCTTCATGCACCGGAAAAAGCG
ATGTCTTTACCACACCATGGAATTTCAAAGTTGCCAAACAGCTGGCCAGTGGCCCTGAGCTACTTGGAGGATAAAG
ACCTGGTCCATGGAATGTGTGTACTAAAAACCTCCTCCTGGCCCGTGAGGGCATCGACAGTGAGTGTGGCCCAT
TCATCAAGCTCAGTGACCCCGGCATCCCCATTACGGTGCTGTCTAGGCAAGAATGCATTGAACGAATCCCATGGA
TTGCTCCTGAGTGTGTTGAGGACTCCAAGAACCTGAGTGTGGCTGCTGACAAGTGGAGCTTTGGAACACGCTCT
GGGAAATCTGCTACAATGGCGAGATCCCCTTGAAAGACAAGACGCTGATTGAGAAAGAGAGATTCTATGAAAGCC
GGTGCAGGCCAGTGACACCATCATGTAAGGAGCTGGCTGACCTCATGACCCGCTGCATGAACATATGACCCCAATC
AGAGGCCCTTTCTTCCGAGCCATCATGAGAGACATTAATAAGCTTGAAGAGCAGAATCCAGATATTGTTTCAGAAA
AAAAACCAGCAACTGAAGTGACCCACACATTTTGAAGAGCGCTTCTTAAAGAGGATCCGTGACTTTGGGAGAGG
GCCACTTTGGGAAGGTTGAGCTCTGCAGGTATGACCCCGAAGGGGACAATACAGGGGAGCAGGTGGCTGTTAAAT
CTCTGAAGCCTGAGAGTGGAGGTAACCACATAGCTGATCTGAAAAAGGAAATCGAGATCTTAAGGAACCTCTATC
ATGAGAACATTGTGAAGTACAAAGGAATCTGCACAGAAGACGGAGGAAATGGTATTAAGCTCATCATGGAATTTT
TGCTTCCGGGAAGCCTTAAGGAATATCTTCCAAAGAATAAGAACAAAATAAACCTCAAACAGCAGCTAAAATATG
CCGTTTCAGATTTGTAAGGGGATGGACTATTTGGGTTCTCGGCAATACGTTTCAACGGGACTTGGCAGCAAGAAATG
TCCTTGTGAGAGTGAACACCAAGTGAAAATTGGAGACTTCGGTTTAAACCAAAGCAATTGAAACCGATAAGGAGT
ATTACACCGTCAAGGATGACCGGGACAGCCCTGTGTTTTGGTATGCTCCAGAATGTTTAAATGCAATCTAAATTTT
ATATTGCCTCTGACGTCTGGTCTTTTGGAGTCACTCTGCATGAGCTGCTGACTTACTGTGATTGAGATTCTAGTC
CCATGGCTTTGTTCTCTGAAAATGATAGGCCCAACCCATGGCCAGATGACAGTCAACAAGACTTGTGAATACGTTAA

276/6881
FIGURE 256B

AAGAAGGAAAACGCCTGCCGTGCCACCTAACTGTCCAGATGAGGTTTATCAACTTATGAGGAAATGCTGGGAAT
TCCAACCATCCAATCGGACAAGCTTTCAGAACCTTATTGAAGGATTTGAAGCACTTTTAAAAATAAGAAGCATGAA
TAACATTTAAATTCCACAGATTATCAAGTCCTTCTCCTGCAACAAATGCCCAAGTCATTTTTTAAAAATTTCTAA
TGAAAGAAGTTTGTGTTCTGTCCAAAAAGTCACTGAACTCATACTTCAGTACATATACATGTATAAGGCACACTG
TAGTGCTTAATATGTGTAAGGACTTCCTCTTTAAATTTGGTACCAGTAACTTAGTGACACATAATGACAACCAAA
ATATTTGAAAGCACTTAAGCACTCCTCCTTGTGGAAAGAATATACCACCATTTCATCTGGCTAGTTCACCATCAC
AACTGCATTACCAAAAGGGGATTTTTGAAAACGAGGAGTTGACCAAAATAATATCTGAAGATGATTGCTTTTCCC
TGCTGCCAGCTGATCTGAAATGTTTTGCTGGCACATTAATCATAGATAAAGAAAGATTGATGGACTTAGCCCTCA
AATTTCAGTATCTATACAGTACTAGACCATGCATTCTTAAATATTAGATACCAGGTAGTATATATTGTTTCTGT
ACAAAAATGACTGTATTCTCTCACCAGTAGGACTTAACTTTGTTTCTCCAGTGGCTTAGCTCCTGTTCCCTTTGG
GTGATCACTAGCACCCATTTTTGAGAAAGCTGGTTCATCATGGGGGATAGCTGTGGAATAGATAATTTGCTGCA
TGTTAATTCTCAAGAACTAAGCCTGTGCCAGTGCTTTCCTAAGCAGTATACCTTTAATCAGAACTCATTCCCAGA
ACCTGGATGCTATTACACATGCTTTTAAGAAACGTCAATGTATATCCTTTTATAACTCTACCCTTTGGGGCAAG
CTATTCCAGCACTGGTTTTGAATGCTGTATGCAACCAGTCTGAATACCACATACGCTGCACTGTTCTTAGAGGGT
TTCCATACTTACCACCGATCTACAAGGGTTGATCCCTGTTTTTACCATCAATCATCACCCCTGTGGTGCAACACTT
GAAAGACCCGGCTAGAGGCACCTATGGACTTCAGGATCCACTAGACAGTTTTTCAGTTTGCTTGAGGTTAGCTGGGT
AATCAAAAATGTTTAGTCATTGATTCAATGTGAACGATTACGGTCTTTATGACCAAGAGTCTGAAAATCTTTTTG
TTATGCTGTTTAGTATTGTTTTGATATTGTTACTTTTCACCTGTTGAGCCCAAATTCAGGATTGGTTCAGTGGCA
GCAATGAAGTTGCCATTTAAATTTGTTTCATAGCCTACATACCAAGGTCTCTGTGTCAAACCTGTGGCCACTCTA
TATGCACCTTGTTTACTCTTTATACAAATAAATATACTAAAGACTTT

277/6881
FIGURE 257

CTCTTCATAAGCCGGCGCTCGGCGAGTTCTCCCAGGAGAAGGCCATGTTTCAGTTTCGAGCGCCAAGATCGTGAAAC
CCAACGGCGAGAAGCCGGAGGAGTTTCGAGTCCGGCATCTCCCAGGCTCTTCTGGAGCTGGAGATGAACTCAGAAC
TCAAGGCTCAGCTCAGAGAGCTGAATATTACGGCAGCCAAGGAAATTGAAGTTGGTGGTGGTTCGGAAAGCTATCA
TAATACTTGTTCCCGTTACTCAACTGAAATCTTTCCAGAAAATCCAAATCCGGCTAGTAAGTGAATTGGAGAAAA
AGTTTCAGTGGGAAGCATGTCGTCTTTATCGCTCAGAGGAGAATTCTGCCTAAGCCAACTCGAAAAAGCTGTACAA
AAAATAAGCAAAAGCGTCCCAGGAGCAGCACTGTGACAGCTGTGCACGATGCCATCCTTGAGGACTTGGTCTTCC
CAAGTGAAATTGTGGGCAAGAAAATCCGCGTCAAAC TAGATGGCAGCCGGCTCATAAAGGTTCAATTTGGACAAAG
CACAACAGAACAATGTGGAACACAAGGTTGAAACTTTTTCTGGTGTCTATAAGAAGCTCATGGGCAAGGATGTTA
ATTGTGAATTCACAGAGTTTCAATAGTAAACAAAAATGACTAAATAAAAAATATATATATATTCATAGT

278/6881
FIGURE 258

MFSSSAKIVKPNGEKPEEFESGISQALLELEMNSELKAQLRELNITAAKEIEVGGGRKAIILVPVTQLKSFQKI
QIRLVSELEKKFSGKHVVFIAQRRILPKPTRKCTKNKQKRPRSSTVTAVHDAILEDLVFPSEIVGKKIRVKLDG
SRLIKVHLDKAQQNNVEHKVETFSGVYKKLMGKDVNCEFPEFQS

279/6881
FIGURE 259

GGAGAAGGCCATGTTTCAGTTCGAGCGCCAAGATCGTGAAACCCAACGGCGAGAAGCCGGAGGAGTTCGAGTCCGG
CATCTCCCAGGAAATTGAAGTTGGTGGTGGTTCGGAAAGCTATCATAATACTTGTTCCCGTTACTCAACTGAAATC
TTTCCAGAAAAATCCAAATCCGGCTAGTAAGTGAATTGGAGAAAAAGTTCAGTGGGAAGCATGTCGTCTTTATCGC
TCAGAGGAGAATTCTGCCTAAGCCAACCTCGAAAAAGCTGTACAAAAAATAAGCAAAGCGTCCCAGGAGCAGCAC
TGTGACAGCTGTGCACGATGCCATCCTTGAGGACTTGGTCTTCCCAAGTGAAATTGTGGGCAAGAAAAATCCGCGT
CAAAC TAGATGGCAGCCGGCTCATAAAGGTTCAATTTGGACAAAGCACACAGAACAATGTGGAACACAAGGTTGA
AACTTTTTCTGGTGTCTATAAGAAGCTCATGGGCAAGGATGTTAATTGTGAATTCCCAGAGTTTCAATAGTAAAC
AAAAATGACTAAATAAAAAATATATATATTCATAGTAAAAAAAAAAAAAAAAAATCTC

280/6881
FIGURE 260

GGGGGTGGGAAGAGCTGAAGCAGGCGCTCTTGGCTCGGCGCGGGCCCGCTGCAATCCGTGGAGGAACGCGCCGCCG
AGCCACCATCATGCCTGGGCACTTACAGGAAGGCTTCGGCTGCGTGGTCACCAACCGATTTCGACCAGTTATTTGA
CGACGAATCGGACCCCTTCGAGGTGCTGAAGGCAGCAGAGAACAAGAAAAAGAAGCCGGCGGGGGCGGCGTTGG
GGGCCCTGGGGCCAAGAGCGCAGCTCAGGCCGCGGCCAGACCAACTCCAACGCGGCAGGCAAAACAGCTGCGCAA
GGAGTCCCAAGAACCGCAAGAACCCGCTGCCCCCAGCGTTGGCGTGGTTGACAAGAAAAGAGGAGACGCAGCC
GCCCCGTGGCGCTTAAGAAAGAAGGAATAAGACGAGTTGGAAGAAGACCTGATCAACAACCTTCAGGGTGAAGGGAA
AATAATTGATAGAAGACCAGAAAGGCGACCACCTCGTGAACGAAGATTTCGAAAAGCCACTTGAAGAAAAGGGTGA
AGGAGGCGAATTTTCAGTTGATAGACCGATTATTGACCGACCTATTTCGAGGTCTGTTGGTGGTCTTGGAAGAGGTCTG
AGGGGGCCGTGGACGTGGAATGGGCCGAGGAGATGGATTTGATTCTCGTGGCAAACGTGAATTTGATAGGCATAG
TGGAAGTGATAGATCTGGCCTGAAGCACGAGGACAAACGTGGAGGTAGCGGATCTCACAACCTGGGGAACGTGTCAA
AGACGAATTAAGTACTTGGATCAATCAATGTGACTGAGGAAACACCTGAAGGTGAAGAACATCATCCAGTGGC
AGACACTGAAAATAAGGAGAATGAAGTTGAAGAGCTAAAAGAGGAGGGTCCAAAAGAGATGACTTTGGATGAGTG
GAAGGCTATTCAAATAAGGACCGGGCAAAGTAGAATTTAATATCCGAAAACCAAATGAAGGTGCTGATGGGCA
GTGGAAGAAGGGATTTGTTCTTCATAAATCAAAGAGTGAAGAGGCTCATGCTGAAGATTCGGTTATGGACCATCA
TTTCCGGAAGCCAGCAAATGATATAACGTCTCAGCTGGAGATCAATTTTGGAGACCTTGGCCGCCAGGACGTGG
CGGCAGGGGAGGACGAGGTGGACGTGGGCGTGGTGGGCGCCCAAACCGTGGCAGCAGGACCGACAAGTCAAGTGC
TTCTGCTCCTGATGTGGATGACCCAGAGGCATTCCCAGCTCTGGCTTAACTGGATGCCATAAGACAACCCTGGTT
CCTTTGTGAACCCTTCTGTTCAAAGCTTTTGCATGCTTAAGGATTCCAAACGACTAAGAAATTAAAAAAAAG
ACTGTCATTCATACCATTACACCTAAAGACTGAATTTTATCTGTTTTAAAAATGAACTTCTCCCGCTACACAGA
AGTAACAAATATGGTAGTCAGTTTTGTATTTAGAAATGTATTGGTAGCAGGGATGTTTTTATAATTTTCAGAGAT
TATGCATTCTTCATGAATACTTTTGTATTGCTGCTTGCAAATATGCATTTCCAAACTTGAAATATAGGTGTGAAC
AGTGTGTACCAGTTTAAAGCTTTCACTTCATTTGTGTTTTTTAATTAAGGACTTAGAAGTCCCCCAATTACAAA
CTGGTTTTTAAATATTGGACATACTGGTTTTTAATACCTGCTTTGCATATTACACATGGTCAACTGGGACATGTTA
AACTTTGATTTGTCAAATTTTATGCTGTGTGGAATACTAATAATATGATTTTTAACTTAGTTTTAATATTTTCAT
ITTGGGGGAAAAATCTTTTTTCACTTCTCATGATAGCTGTTATATATATATGCTAAATCTTTATATACAGAAATA
TCAGTACTTGAACAAATTCAAAGCACATTTGGTTTATTAACCCTTGCTCCTTGCTATGGCTCATTAGGTTCAAATT
ATAACTAATTTACATTTTCAGCTATATTTACTTTTTAAATGCTTGAGTTTCCATTTTAAAAATCTAACTAGACA
TCTTAATTGGTGAAAGTTGTTTAACTACTTATTGTTGGTAGGCACATCGTGTCAAGTGAAGTAGTTTTATAGGT
ATGGGTTTTTTCTCCCCCTTACCAGGGTGGGTGGAATAAGTTGATTTGGCCAATGTGTAATATTTAACTGTTC
TGTAATAAAAAAAAAAAAAAAAAA

281/6881
FIGURE 261

MPGHLQEGFGCVVTNRFDQLFDDESDPFEVLKAAENKKKEAGGGVGGPGAKSAAQAAAQTNNAAGKQLRKESQ
KDRKNPLPPSVGVVDKKEETQPPVALKKEGIRRVGRRPDQQLQGEKIIDRRPERRPPRERRFEKPLEEKGE
FSVDRPIIDRPIRGRGGLGRGRGGRGRGMGRGDGFDSRGKREFDRHSGSDRSGLKHEDKRGGSGSHNWGT
TKDEL
TDLDQSNVTEETPEGEEHHPVADTENKENEVEEVKEEGPKEMTLDEWKAIQNKDRAKVEFNIRKPN
EGADGQWKK
GFVLHKSSEEAHAEDSVMDHHRKFPANDITSQLEINFGDLGRPGRGGRGGRGGRGGRGGRPNRGS
RTDKSSASAP
DVDDPEAFPALA

282/6881
FIGURE 262

ACCTTTAAGCGTCACGGGTGGGGCTGCAGCTTCTGGACCTAGGACTTTGAACATGTCGCGCCTGAAGCGGATAGC
GGGGCAGGATCTCCGCGCTGGTTTCAAAGCAGGTGGAAGAGACTGCGGTACCTCGGTACCCCAAGGGCTGTTGAA
GGCAGCGAGGAAGAGCGGCCAGTTAAACCTGTCGGGTAGAAACCTCAGTGAAGTGCCGCAGTGTGTCTGGAGAAT
AAATGTGGATATCCCTGAGGAAGCTAATCAGAATCTTTCGTTTGGTGCTACTGAAAGATGGTGGGAGCAGACAGA
TTTGACCAAATAATAATATCAAACAATAAACTTCAGTCACTTACAGATGACCTGCGACTCTTGCCCTGCACTGAC
TGTTCTTGATATACATGATAATCAGTTGACATCCCTTCTTCTGCTATAAGAGAGCTAGAAAATCTTCAGAACT
TAATGTCAGCCATAATAAACTGAAAATACTCCCTGAAGAAATTACAAACCTAAGAAACCTGAAGTGCCGTGATCT
CCAGCATAATGAATTAACCTGCATATCAGAGGGATTTGAACAACTTTCCAATTTAGAAGATTTAGATCTTTCAA
CAATCATCTTACAACCTGTTCCCTGCTAGTTTTTCTTCTCTGTCCAGTCTGGTGCGACTCAATCTTTCTAGTAATGA
ACTGAAGAGTTTGCCAGCAGAAATAAATAGAATGAAAAGGTTGAAGCATTGTTGATTGTAATTCAAATCTCTTGGA
AACTATACCTCCTGAATTGGCTGGCATGGAATCACTAGAATTGCTTTATTTGCGGAGGAATAAATTACGTTTTCT
ACCAGAATTTCTTCTGTAGTCTATTGAAGGAATTGCACGTAGGTGAAAACCAGATTGAAATGTTAGAGGCAGA
ACATCTTAAACATCTGAATTCAATTCTTGTGCTAGACCTGAGGGATAACAAGTTAAATCTGTTCCAGATGAAAT
TATACTACTACGGTCCCTTGGAAGGCTTGACCTAAGCAACAATGATATTAGTAGTCTTCCCTATTTCATTGGGGAA
CCTTCATTTGAAATTTTGGCATTAGAAGGAAATCCTTTGAGAACAATTGGAAGAGAAATTATAAGTAAAGGAAC
ACAAGAAGTCCTAAATATCTACGAAGCAAGATCAAAGATGATGGACCTAGCCAAAGTGAGTCTGCTACTGAGAC
TGCCATGACACTACCAAGTGAATCCAGAGTCAATATACATGCCATCATTACATTAAAAATATTAGACTATAGTGA
TAAACAAGCAACTTTGATTCCCTGATGAGGTGTTTGATGCAGTAAAAAGCAACATCGTCACTTCTATTAACCTCAG
TAAGAATCAACTATGTGAAATTCCAAAAGGATGGTAGAACTGAAGGAAATGGTTTCTGATGTCGATCTCAGTTT
TAATAAACTTTTCTTTATATCCTTGAGATTATGTGTGCTTCAGAAATTGACTTTTTTTAGATCTCAGGAACAATTT
TTTAAATTCCTTTGCCAGAAGAAATGGAATCACTGGTAAGACTGCAACGATCAATCTTTCTTTAATAGGTTTAA
AATGCTACCTGAAGTTCTATATCGTATCTTCACACTTGAAACAATTCTGATTAGTAATAATCAGGTTGGATCTGT
GGACCCTCAGAAAATGAAGATGATGGAAAATCTGACCACGTTGGACCTTCAAATAATGACCTCTTACAAATTC
ACCAGAGCTCGGTAAATTGTGTAACTTAAGAACATTACTATTGGATGGAAATCCATTCCGAGTTCTCGAGCAGC
CATATTAATGAAAGGAACAGCTGCTATACTTGAATATTTGAGAGACCGAATTCCTACTTAACATGGAGTTGCTTT
ATAACCCTTGTCATGTATTATTAACCCTGGTTAATTCTAAGGAGGATGTAACATTTGTTTTAGTATCATCTTAAA
AGGTGATTATTGTAATTGATCTTGTAGTTTCCCAGTATCACCTACCCGTTGGTATAATTAGCCTGGGCCATATTC
ACTGCCAGTAAATATTTTTACATTTTTATTTAAGATTTTTGTAAGGTGTTGTGTACATTTGTAATGGTGATAACC
ACAATGTGTTTCATACATTTGTTCTAAATGTTTTGCTTATGATTTATCCTGCTAACTTTCAATTTTCTTATAGCAAG
CAGTTTTTTCAAATAATGAATTTTTATTTAATGTGGTTCAGTATTATAATAACAAAGCATTTTTGTAGAACTGGTT
TTTTTTCTCATTTATTTTTGTATTCCATACAATGTGACCAATTGACTTGAATATGACTAGCCAGTTTCTATGTTT
TTGTTAGATATAAAATTAATTCGAATTTTGTGTAATACTGTTCTTTGGCATTAAAAAATAAGACCTTCTTATCT
TGGGCCACATGTCAAAAGAAAAAGGAAACAAAAATATATTAATAAATAAGACTTTTCATTACCCATGATAGGACTT
TTGTGATATGGCTAATCTCAGTACACATTTCAACTTAAAACCTTTTTATTTACAGCACCATAATTTTAAAAATTA
CTTGCAATCTTGGAAGACTAACTTGCAAGTGTTTTTCTAAAAGGGAATTTGATAGGTAACTTGATTTAATAAA
AATTAAATATCATTTTTGTTTACACCAAAATTATCAGAAGTAGGTTGATTAGTCATTATAACACTTACCATATGA
TTCTATTAAGAAGTCAATTCAGTAGCATGTATATCAATTTATATAGATAGGTAGATAGCTTTTGATGATTGAGG
CATGCTTATATTATGAAAAAATTGCTAATAAAGATAAATACTACATGTTTCAGAATAAAAGTTACATTTTTTC

283/6881
FIGURE 263

MSRLKRIAGQDLRAGFKAGGRDCGTSVPQGLLKAARKSGQLNLSGRNLSEVPQCVWRINVDIPEEANQNLSFGAT
ERWWEQTDLTCLIISNNKLQSLTDDLRLLPALTVLDIHDNQLTSLPSAIRELENLQKLNVSHNKLKILPEEITNL
RNLKCLYLQHNELTICISEGFEQLSNLEDLDLSNNHLTTVPASFSSSLVRLNLSNELKSLPAEINRMKRLKHL
DCNSNLETIPPELAGMESLELLYLRRNKLRLPEFPSCSLLKELHVGENQIEMLEAEHLKHLNSILVLDLRDNK
LKSVPEIILLRSLERLDLSNNDISSLPYSLGNLHLKFLALEGNPLRTIRREIISKGTQEVLYLRSKIKDDGPS
QSESATETAMTLPSESRVNIHAIITLKILDYSDKQATLIPDEVF DAVKSNIVTSINFSKNQLCEIPKRMVELKEM
VSDVDLSFNKLSFISLELCVLQKLTFLDLRNNFLNSLPEEMESLVRLQTINLSFNRFKMLPEVLYRIFTLETILI
SNNQVGSVDPQKMKMMENLTTLDLQNNDLQIPPELGNCVNLRTLLLDGNPFRVPRAAILMKGTAAILEYLRDRI
PT

284/6881
FIGURE 264

GCTCTTTCCCTAAGCAGCCTGAGGTAATCTGTGAAAATGGTTCGCTACTCACTTGACCCGGAGAACCCACGAAA
TCACTCGTGAAACTGCTCAGGCCATCAAGGGTATGCATATACAAAAGCCACGAAGTATCTGAAAGATGTCACTT
TACAGAAACAGTGTGTACCATTCCGACGTTACAATGGTGGAGTTGGCAGGTGTGCGCAGGCCAAGCAGTGGGGCT
GGACACAAGGTCGGTGGCCCCAAAAGAGTGCTGAATTTTTGCTGCACATGCTTAAAAACACAGAGAGTAATGCTG
AACTTAAGGGTTTAGATGTAGATTCTCTGGTCATTGAGCATATCCAAGTGAACAAAGCACCTAAGATGCGCCGCC
GGACCTACAGAGCTCATGGTCGGATTAAACCCATACATGAGCTCTCCCTGCCACATTGAGATGATCCTTACGGAAA
AGGAACAGATTGTTCCCTAAACCAGAAGAGGAGGTTGCCCAGAAGAAAAAGATATCCCAGAAGAACTGAAGAAAC
AAAAACTTATGGCACGGGAGTAAATTCAGCATTAAAAATAAATGTAATTAAAAGGAAAAATAAAAAATAAAATAA
ATAAATAAATAAATAAAAAAAAAAAAAAAAAAAAAAG

285/6881
FIGURE 265

GCTCTTTCCCTAAGCAGCCTGAGGTAATCTGTGAAAATGGTTCGCTACTCACTTGACCCGGAGAACCCACGAAA
TCATGCAAATCAAGAGGTTCCAATCTTCGTGTTCACTTTAAGAACACTCGTGAAACTGCTCAGGCCATCAAGGGT
ATGCATATACAAAAAGCCACGAAGTATCTGAAAGATGTCACCTTACAGAAACAGTGTGTACCATTCCGACGTTAC
AATGGTGGAGTTGGCAGGTGTGCGCAGGCCAAGCAGTGGGGCTGGACACAAGGTCGGTGGCCCCAAAAAGAGTGCT
GAATTTTTGCTGCACATGCTTAAAAACACAGAGAGTAATGCTGAACTTAAGGGTTTAGATGTAGATTCTCTGGTC
ATTGAGCATATCCAAGTGAACAAAGCACCTAAGATGCGCCGCGGACCTACAGAGCTCATGGTCGGATTAAACCA
TACATGAGCTCTCCCTGCCACATTGAGATGATCCTTACGGAAAAGGAACAGATTGTTCTAAACCAGAAGAGGAG
GTTGCCCAGAAGAAAAAGATATCCCAGAAGAACTGAAGAAACAAAACTTATGGCACGGGAGTAAATTCAGCAT
TAAATAAATGTAATTAAAAGG

286/6881
FIGURE 266

MVRYSLDPENPTKSCKSRGSNLRVHFKNTRETAQAIGMYIQGTYLKDVTLQKQCIPFRHYNGGVGRCAQAKQ
WGTIQGRWPKKSAEFLHVLKNTESNAELKGRFSGH

287/6881
FIGURE 267

CGGGAAGGATTGAATACGAGACGCTGTCTGCTTGCTGCCTTAAGACAGCTAGCTGAATTGCTGATTAACTTTTAA
AATACCCAGCTTGTTTTATTTTTCTTAGAATCTGTTGCTAAGACTGGGGACGCTGTTTTCTTTACAAAGGGAAA
TCTAAGTTAATTTCAAGGCATTTCGAAATGCGGGAAAGACTATTATTGCATTTTGGGAATTGAGAAAGGAGCTTCAG
ATGAAGATATTAAAAAGGCTTACCGAAAACAAGCCCTCAAATTTTCATCCGGACAAGAACAAATCTCCTCAGGCAG
AGGAAAAATTTAAAGAGGTCGCAGAAGCTTATGAAGTATTGAGTGATCCTAAAAAGAGAGAAATATATGATCAGT
TTGGGGAGGAAGGTTGAAAGGAGGAGCAGGAGGTACTGATGGACAAGGAGGTACCTTCCGGTACACCTTTCATG
GCGATCCTCATGCTACATTTGCTGCATTTTTCGGAGGGTCCAACCCCTTTGAAATTTTCTTTGGAAGACGAATGG
GTGGTGGTAGAGATTCTGAAGAAATGGAATAGATGGTGATCCTTTTAGTGCCTTTGGTTTTCAGCATGAATGGAT
ATCCAAGAGACAGGAATTCTGTGGGGCCATCCCGCCTCAAACAAGATCCTCCAGTTATTCATGAACCTTAGAGTAT
CACTTGAAGAGATATATAGTGGTTGTACCAAACGGATGAAGATTTCTCGAAAAAGGCTAAACGCTGATGGAAGGA
GTTACAGATCTGAGGACAAAATTCTTACCATTGAGATTAAAAAAGGGTGGAAAGAAGGCACCAAAATTACTTTTC
CAAGAGAAGGAGATGAAACACCAAATAGTATTCCAGCAGACATTGTTTTTATCATTAAAGACAAAGATCATCCAA
AATTTAAAAGGGATGGATCAAATATAATTTATACTGCTAAAATTAGTTTACGAGAGGCATTGTGTGGCTGCTCAA
TTAATGTACCAACACTGGATGGAAGAAACATACCTATGTCAGTAAATGATATTGTGAAACCCGGAATGAGGAGAA
GAATTATTGGATATGGGCTGCCATTTCCAAAAAATCCTGACCAACGTGGTGACCTTCTAATAGAATTTGAGGTGT
CCTTCCCAGATACTATATCTTCTTCATCCAAAGAAGTACTTAGGAAACATCTTCCTGCCTCATAGAAATGAAGAAC
TTTGTTACACATATTTTGATAAGGCACTGAAAATATAAAAGGACTGGTAGTTTACTGATGTAGATGTGAATTCTG
TATAAAGATGTGTAAATTGTTTTGAGGGTTCATTAAATTGCAT

288/6881
FIGURE 268

MGKDYYCILGIEKGASDEDIKKAYRKQALKFHPDKNKSPQAEKFKAEAEVLSDPKKREIYDQFGEEGLKGG
AGGTDGQGGTFRYTFHGDPHATFAAFFGGSNPFIEIFFGRMGGRDSEEMEIDGDPFSAFGFSMNGYPRDRNSVG
PSRLKQDPFVIHELVSLEEIYSGCTKRMKISRKRLNADGRSYRSEDKILTIEIKKGWKEGTKITFPREGDETPN
SIPADIVFIIKDKDHPKFKRDGSNIIYTAKISLREALCGCSINVPTLDGRNIPMSVNDIVKPGMRRRIIGYGLPF
PKNPDQRGDLLEFEVSFPDTISSSSKEVLRKHLPAS

289/6881
FIGURE 269

GCGCACGGCCTGTCCGCTGCACACCAGCTTGTTGGCGTCTTCGTGCGCCGCGCTCGCCCCGGGCTACTCCTGCGCG
CCACAATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCAACCCTTCTCCACTTGACCAGGCTGGCGCTCT
CCACCTGCCCCGCTGCCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCGCCGGGAGTGGGGCTGGTCCGGGACG
GCTGCGGGCTGCTGTAAGGTCTGCGCCAAGCAGCTCAACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCA
AGGGGCTGGAATGCAACTTCGGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGAC
CCTGTGAATATAACTCCAGAATCTACCAAAACGGGGAAAAGTTTCCAGCCCAACTGTAAACATCAGTGCACATGTA
TTGATGGCGCCGTGGGCTGCATTCTCTGTGTCCCCAAGAACTATCTCTCCCAACTTGGGCTGTCCCAACCCTC
GGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGG
ACCAGGACGGCCTCCTTGGAAGGAGCTGGGATTTCGATGCCTCCGAGGTGGAGTTGACGAGAAAACAATGAATTGA
TTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGATCCCTGTTTTTGGGAATGGAGCCTCGCATCCGATAACAACCTT
TACAAGGCCAGAAATGTATTGTTCAAACAACCTTCATGGTCCAGTGCTCAAAGACCTGTGGAACCTGGTATCTCCA
CACGAGTTACCAATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGAC
AGCCAGTGACAGCAGCCTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCGAACCAGTCAGGTTTA
CTTACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCTGCGTGGACGGCCGATGCTGCA
CGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGGGAGACATTTTCCAAGAACGTCATGA
TGATCCAGTCCCTGCAAATGCAACTACAACCTGCCCCGATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCA
ATGACATTACAAATTTAGGGACTTAAATGCTACCTGGGTTTCCAGGGCACACCTAGACAAACAAGGGAGAAGAGT
GTCAGAATCAGAATCATGGAGAAAATGGGCGGGGGTGGTGTGGGTGATGGGACTCATTGTAGAAAGGAAGCCTTG
CTCATTCTTGAGGAGCATTAAAGGTATTTGAAACTGCCAAGGGTGCTGGTGCGGATGGACACTAATGCAGCCACG
ATTGGAGAATACTTTGCTTCATAGTATTGGAGCACATGTTACTGCTTCATTTTGGAGCTTGTGGAGTTGATGACT
TTCTGTTTTTCIGTTTGTAATTATTTGCTAAGCATATTTTCTCTAGGCTTTTTTCTTTTGGGGTTCTACAGTCG
TAAAAGAGATAATAAGATTAGTTGGACAGTTTAAAGCTTTTATTCGTCCTTTGACAAAAGTAAATGGGAGGGCAT
TCCATCCCTTCTGAAGGGGGACACTCCATGAGTGCTGTGAGAGGCAGCTATCTGCACTCTAAACTGCAAACAG
AAATCAGGTGTTTTAAGACTGAATGTTTTATTTATCAAAATGTAGCTTTTGGGGAGGGAGGGGAAATGTAATACT
GGAATAATTTGTAAATGATTTTAATTTTATATTTCAGTGAAAAGATTTTATTTATGGAATTAACCATTTAATAAAG
AAATATTACCT

290/6881
FIGURE 270

MSSRIARALALVVTLLHLTRLALSTCPAACHCPLAEPKCAPGVGLVRDGCCKVCAKQLNEDCSKTQPCDHTKG
LECNFGASSTALKGICRAQSEGRPC EYNSRIYQNGESFQPNCKHQCTCIDGAVGCIPLCPQELSLPNLGCPNPRL
VKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKELGFDASEVELTRNNELIAVGKGSSLKRIPVFGMEPRIRYNPLQ
GQKCI VQTTSWSQSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFY
AGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCPHANEAAFPFYRLFND
IHKFRD

[illegible]

292/6881
FIGURE 272

MVNP GSSSQPPPV TAGSLSWKRCAGCGGKIADRFLLYAMDSYWHSRCLKSCCQAQLGDIGTSCYTKSGMILCRN
DYIRLFGNSGACSACGQSIPASELVMRAQG NVYHLKCFTCSTCRNRLVPGDRFHYINGSLFCEHDRPTALINGHL
NSLQSNP LLLPDQKVC

293/6881
FIGURE 273

AGCGATGGCGGCTGGGCCGAGTGGGTGCTCTGGTGCCGGCGTTTGGGCTACGGTTGTTGTTGGCGACTGTGCTTCA
AGCGGTGTCTGCTTTTGGGGCAGAGTTTTTCATCGGAGGCATGCAGAGAGTTAGGCTTTTCTAGCAACTTGCTTTG
CAGCTCTTGATCTTCTCGGACAGTTCAACCTGCTTCAGCTGGATCCTGATTGCAGAGGATGCTGTCAGGAGGA
AGCACAAATTTGAAACCAAAAAGCTGTATGCAGGAGCTATTCTTGAAGTTTGTGGATGAAAATTGGGAAGGTTCCC
TCAAGTCCAAGCTTTTGTAGGAGTGATAAACCCAACTGTTTCAGAGGACTGCAAATCAAGTATGTCCGTGGTTC
AGACCCTGTATTAAAGCTTTTGGACGACAATGGGAACATTGCTGAAGAACTGAGCATTCTCAAATGGAACACAGA
CAGTGTAGAAGAAATTCCTGAGTGAAAAGTTGGAACGCATATTAAATCTTGCTTAAATTTTGTCTATCCTTTTGT
ACCTTATCAAATGAAATATTACAGCACCTAGAAAATAATTTAGTTTGTCTTGCTTCCATTGATCAGTCTTTTACT
TGAGGCATTAAATATCTAATTAAATCGTGAAATGGCAGTATAGTCCATGATATCTAAGGAGTTGGCAAGCTTAAC
AAAACCCATTTTTTATAAATGTCCATCCTCCTGCATTTGTTGATACCACTAACAAAATGCTTTGTAAACAGACTTG
CGGTAAATTATGCAAATGATAGTTTGTGATAATTGGTCCAGTTTTACGAACAACAGATTTCTAAATTAGAGAGGT
TAACAAGACAGATGATTACTATGCCTCATGTGCTGTGTGCTCTTTGAAAGGAATGACAGCAGACTACAAAGCAAA
TAAGATATACTGAGCCTCAACAGATTGCCTGCTCCTCAGAGTCTCTCCTATTTTTGTATTACCCAGCTTTCTTTT
TAATACAAATGTTATTTATAGTTTACAATGAATGCACTGCATAAAAACCTTTGTAGCTTCATTATTGTAAAACATA
TTCAAGATCCTACAGTAAGAGTGAAACATTACAAAGATTTGCGTTAATGAAGACTACACAGAAAACCTTTCTAG
GGATTTGTGTGGATCAGATACATACTTGGCAAATTTTGTAGTTTACATTCTTACAGAAAAGTCCATTTAAAAGT
GATCATTTGTAAGACCAAAATATAAATAAAAAGTTTCAAAAATCTATCTGAATTTGGAATTCTTCTGTTTTGTTT
TTTCATGTTTAAAAATGATGTTTTTCAATGCATTTTTTTCATGTAAGCCCTTTTTTTAGCCAAAATGTAAAAATG
GCTGTAATATTTAAACCTTATAACATCTTATTGTTGGTAATAGTGCTTTATATTTGTCTGATTTTATTTTTTCAA
GTTTTTTCATTTATGAACACATTTTCATTGGTATATTATTTAAGGAATATCTCTTGATATAGAATTTTTATATTA
AAAATGATTTTTCTTTGGC

294/6881
FIGURE 274

MAAGPSGCLVPAFGLRLLLATVLQAVSAFGAEFSSEACRELGFSSNLLCSCDLLGQFNLLQLDPDCRGCCQEEA
QFETKKLYAGAILEVCGENWEGSLKSKLLLGVINPNCSEDCKSSMSVVQTLYLKLLDDNGNIAEELSILKWNTDS
VEEFLSEKLERI

295/6881
FIGURE 275

GCTCTTTCCCTAAGCAGCCTGAAGTAATCTGTGAAAATGGTTCGCTATTCACTTGACCCGGAGAACCCCATGAAA
TCACACTCGTGAAACTGCTCAGGCCATCAAGGGTATGCATATACGAAAAGCCACGAAGTATCTTAAAGATGTCAC
TTTACAGAAACAGTGCATACCATTCCGACGTTACAATGGTGGAGTTGGCAAGTGTGCGCAGGCCAAGCAGTGGGG
CTGGACACAAGGTCGGTGGCCCCAAAAGAGTGCTGAATTTTGTCTGCACATGTTTAAAAACGCAGAGGGTAATAC
TGAACCTTAAGGGTTTAGATGTAGATTCTCTGGTCATTGAGTATATCCAAGTGAACAAAGCACCTAAGATGCTCCG
CCGGACCTACAGAGCTCATGGTCGGATTAACATACATGAGCTCTCCCTGGCACATTGAGATGATCCTTACTGA
AAAGGAACAGATTGTTCC'TAAACCAGAAAAGGAGGTTGCCCAGAAGAAAAAGATATCCCAGAAGAAACTGAAGAA
ACAAAAACTTATGGCCCGGAAGTAAATTCAGCATTAAAAATAAATGTAATTAAAAGGAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAG

296/6881
FIGURE 276

GCTCTTTCCCTAAGCAGCCTGAAGTAATCTGTGAAAATGGTTCGCTATTCACCTTGACCCGGAGAACCCCATGAAA
TCATGCAAATCAAGAGGTTCCAATCTTCGTGTTCACTTTAAGGACACTCGTGAAACTGCTCAGGCCATCAAGGGT
ATGCATATACGAAAAGCCACGAAGTATCTTAAAGATGTCACCTTACAGAAACAGTGCATACCATTCGGACGTTAC
AATGGTGGAGTTGGCAAGTGTGCGCAGGCCAAGCAGTGGGGCTGGACACAAGGTCGGTGGCCCCAAAAAGAGTGCT
GAATTTTTGCTGCACATGTTTAAAAACGCAGAGGGTAATACTGAACTTAAGGGTTTAGATGTAGATTCTCTGGTC
ATTGAGTATATCCAAGTGAACAAAGCACCTAAGATGCTCCGCCGGACCTACAGAGCTCATGGTCCGATTAACTCA
TACATGAGCTCTCCCTGGCACATTGAGATGATCCTTACTGAAAAGGAACAGATTGTTCTAAACCAGAAAAGGAG
GTTGCCCAGAAGAAAAAGATATCCAGAGAACTGAAGAAACAAAACTTATGGCCCGGAAGTAAATTCAGCAT
TAAATAAATGTAATTAAAGG

297/6881
FIGURE 277

CTTTTTTACAACGGGTTTGCTGCCAGAACACAGGTGTCGTGAAAACCTACCCCTAAAAGCCAAAATGGGAAAAGAA
AAGACTCATATCAACATTGTCGTCATTGGACACGTAGATTTCGGGCAAGTCCACCACTTCTGGCCATCTGATCTAC
AAATGCGGTGGCATCGACAAAAGAACAATTGAAAAATTGCAGAAAAGAGGCTGCTGAGATGGGAAAGGGCTCCTTC
AAGTATGCCTGAGTCTTGGATAAACTGAAAGCTGAGCGTGAACTGGTATCACCATTGATATCTCCTTGTGGAAA
TTTGAGACCAGCAAGTACTATGTGACTATCATTGATGCCCCAGGACACAGAGACTTCATCAAAAACATGATTACA
GGGACATCTCAGGCTGGTTGTGCTGTCCTAATTGTTGCTGCTGGTGGTGAATTTGAAGCTGGTATCTCCAAG
AATGGGCAGACCCGAGAGCATGCCCTTCTGGCATATACACTGGGTGTGAAACAATAATTGTTGATGTTAACAAA
ATGGATTCCACTGAGCCACCCTACAGCCAGAAGAGATATGAGGAAATTGTTAAGGAAATCAGCACTTACATTAAG
AAAATTGGCTACAACCCCAACACAGTAGCATTGTGCAATTTCTGGTTAGAATGGTGACAACATGCTGGAGCCA
AGTGCTAACATGCCTTGGTTCAAGGGATGGAAGTCACCCATAAGGATGGCAATGCCAGTGGAACCATGCTGCTT
GAGGCTCTGGACTGCATCCTACCACCAACTCGTCCAAGTGAAGCCCTTGCGCCTGCCTCTCCAGGATGTCTAC
AAAATTGGTGGTATTGGTACTGTTCTTGTGGCCGAGTGGAGACTGGTATTCTCAAACCTGGTATGGTGGTCACC
TTTGCTCCAGTCAGCGTTACAACAGAAGTAAAATCTGTGAAATGCACCATGAAGCTTTGAATGAAGCTCTTCCT
GGGGACAATATGGGCTTCAATGTCAAGAATGTGTCTGTCAAGGATGTTTCATCGTGGCAACGTTGCTGGTGACAGC
AAAAATGACCCACCAATGGAAGCAGCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGT
CGCTTTACTGTTTCATGATATGAGACAGACACTTGCGGTGGGTGTCATCAAAGCAGTGGACAAGAAGGCTGCTGGA
GCTGGCAAGGTCACCAAGTCTGCCCAGAAAGCTCAGAAGGCTAAATTGAATATTATCCCTAATACCTGCCACCCCA
CTCTTAATCAGTGGTGGGAAGACGGTCTCAGAACTGTTTGTTTCAATTGGCCATTTAAGTTTAGTAGTAAAAGAC
TGGTTAATGATAATAATGCAACATAAAACCTTCAGAAGGAAAGGAGAATGTTTTGTGGACCACCTTTGGTTTTCTT
TTTCGCATGCAGCAGTTTTTAAGTTATTAGTTTTTAAATCAGTACTTTTTAAATGGAACAACCTTGACCAAAAAT
TTGTCA.CAGAATTTTGAGACCCATTAAAAAAGTTTAATGAG

298/6881
FIGURE 278

MLEPSANMPWFKGWKVTHKDGNASGTMLLEALDCILPPTRPDKPLRLPLQDVYKIGGIGTVLVGRVETGILKPG
MVVTFAPVSVTTEVKSVEMHHEALNEALPGDNMGFNVKNVSKDVHRGNVAGDSKNDPPMEAAGKPMCYESFSY
PPLGRFTVHDMRQTLAVGVKAVDKKAAGAGKVTKSAQKAQKAK

299/6881
FIGURE 279

CACAGGTGTCGTGAAAAC TACCCCTAAAAGCCAAAATGGGAAAAGAAAAGACTCATATCAACATTGTCGTCATTG
GACACGTAGATTCTGGGCAAGTCCACCACTTCTGGCCATCTGATCTACAAATGCCGTGGCATCGACAAAAGAACAA
TTGAAAAATTGCAGAAAGAGGCTGCTGAGATGGGAAAGGGCTCCTTCAAGTATGCCTGAGTCTTGGATAAACTGA
AAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTGTGGAAATTTGAGACCAGCAAGTACTATGTGACTA
TCATTGATGCCCTTCTGGCATATACACTGGGTGTGAAACAACATAATTGTTGATGTTAACAAAATGGATTCCACTG
AGCCACCCTACAGCCAGAAGAGATATGAGGAAATTGTTAAGGAAATCAGCACTTACATTAAGGGTGACAACATGC
TGGAGCCAAGTGCTAACATGCCTTGGTTCAAGGGATGGAAAGTCACCCATAAGGATGGCAATGCCAGTGGAACCA
TGCTGCTTGAGGCTCTGGACTGCATCCTACCACCAACTCGTCCAAC TGACAAGCCGGCCAAATAAGCTCTGGCTA
TGCACCTGTATTGGATTGCCACACAGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCG
TTCTGGTAAAAAGCTGGAAGATGGCCCTAAATTCTTGAAGTCTGGTGATGCTGCCATTGCTGATATGGTTCCTGG
CAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTGCGCTTTACTGTTTCATGATATGAGACAGAC
ACTTGCGGTGGGTGTCATCAAAGCAGTGGACAAGAAGGCTGCTGGAGCTGGCAAGGTCACCAAGTCTGCCCAGAA
AGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGG

300/6881
FIGURE 280

GCCAAAATGGGAAAAGAAAAGACTCATATCAACATTGTCGTCATTGGACACGTAGATTGCGGCAAGTCCACCACT
TCTGGCCATCTGATCTACAAATGCGGTGGCATCGACAAAAGAACAATTGAAAAATTGCAGAAAGAGGCTGCTGAG
ATGGGAAAGGGCTCCTTCAAGTATGCCTGAGTCTTGGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATT
GATATCTCCTTGTGGAAATTTGAGACCAGCAAGTACTATGTGACTATCATTGATGCCCCAGGACACAGAGACTTC
ATCAAAAACATGATTACAGGGACATCTCAGGCTGGTTGTGCTGTCCTAATTGTTGCTGCTGGTGTGGTGAATTT
GAAGCTGGTATCTCCAAGAATGGGCAGACCCGAGAGCATGCCCTTCTGGCATATACACTGGGTGTGAAACAATA
ATTGTTGATGTTAACAAAATGGATTCCACTGAGCCACCCTACAGCCAGAAGAGATATGAGGAAATTGTTAAGGAA
ATCAGCACTTACATTAAGAAAATTGGCTACAACCCCAACACAGTAGCATTGTGCCAAATTCTTGAAGTCTGGTG
ATGCTGCCATTGCTGATATGGTTCCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTC
GCTTTACTGTTTCATGATATGAGACAGACACTTGCGGTGGGTG

301/6881
FIGURE 281

GTGGAGACTGGTATTCTCAAACCTGGTATGGTGGTCACCTTTGCTCCAGTCAGCGTTACAACAGAAGTAAATCT
GTCGAAATGCACCATGAAGCTTTGAATGAAGCTCTTCCTGGGGACAATATGGGCTTCAATGTCAAGAATGTGTCT
GTCAAGGATGTTTCATCGTGGCAACGTTGCTGGTGACAGCAAAAATGACCCACCAATGGAAGCAGCTGGCTTCACT
GCTCAGGTGATTATCCTGAACCATCCGGGCCAAAATAAGCTCTGGCTATGCACCTGTATTGGATTGCCACACAGCT
CACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCGTTCTGGTAAAAAGCTGGAAGATGGCCCT
AAATTCTTGAAGTCTGGTGATGCTGCCATTGCTGATATGGTTCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCA
GACTATCCACCTTTGGGTCGCTTTACTGTTTCATGATATGAGACAGACACTTGCGGTGGGTGTCATCAAAGCAGTG
GACAAGAAGGCTGCTGGAGCTGGCAAGGTCACCAAGTCTGCCCAGAAAGCTCAGAAGGCTAAATGAATATTATCC
CTAATACCTGCCACCCCACTCTTAATCAGTGGTGGAAGAACGGTCTCAGAACTGTTTGTTTCAATTGGCCATTTA
AGTTTAGTAGTAAATTTTGTGGACCACTTTGGTT

302/6881
FIGURE 282

GTTACTCAAAGACTACCTACTGCGTGGTGCTCCAAGTGAAATTCGTGAAGAATTAGAAAAGCAGCTTTATTCTTG
TATTGCTCTCAAAGTCACAGCAAATCAAATGGAAATGGAACATTCTTTGATACTAAATAACCTAAAAACATTATT
GTGGAAGAAAAATTTCTTACACTAATGACTCTTAGTTTCATTTGGACATAATTACCATTTTAAGAAACCTGCCACTT
TTAAAGAACAATTTTGAGCATTAAAAAAAATGGCTTCAAATTCGGGCCAGTTACACAAAACCTCTTCCCCCAG
GCCTGAGAAGCCATCAGTATGTGATCACTGAAGTAATGGCAGGTGTAGGATCAACAGGTCCCCAAGATGTCATTCT
CTGCCCTTTTAGAAGCCCTGTTACATCTCCGAAGTACATTTCATTGTGTAACATTTTGGACTGACTTTAAAAACCA
ATGCTGTGAAAAGCTTCATTCCATAAACATCAACAGTGAGTGATTTGTAGATTTACCTTAGCCAAAAATACCAATG
CTGGAAGCATTGTGTTTGCATTGAAGCTGCTGTTCAACAAGAAAATTTATAAATTTACTAATGTCTTAGCATGGT
AAAGTTTGCACATTAACAGAAATTAAGACTGCAAAGCAGGTTAAACTTGCTTCTTTATAAAACAGATGTTGGGTT
AATAGCATGGTTTACTGTATTAAAGACTTATACACCCATTTTAACTTCATTTCAGACATCAAGTTATGTGTAGCT
TCACAATGGTTCAAGTGGCTTACTTCAAGAAATCTTATACTTGACAGTACACCAATTTTATTGACTAAAAATGGA
TGAATTTTCTAAAGATTCAAAGGGCCCATCTTAGTATCACGCAGCTGACTGAGCCCTTCAAACCTGACATCTTA
AGGCCCAATCAAGATCCACATATCCTGATTTTGAAGTATGTGAAAGTGGGACTGTAAGTGCAAGACTAAAAATAA
TTATAGCAGACTTTTGTAGTAATAACTTTCCATTTTCAAACAGTATATCCTGTGGGCCAAAGGGCTATTTCTTAA
GAGGCATGTAAATGTATTTATTTATCTAATGTTTTTTTCCCATGTAAACTTGATATACAAGGTTTAGTATTTGC
TCCTCTTTCATATTATTTTACACGTATACTCAGATTTGGCATGTACCTTTCACATCTCCATAAAATTAACAC
CTTTTGGAGAAAAGAACCCTATTTTCTGCTCAAAGGTTTCGCCTACCTAAAGTGAACATGTTAAAAATCTATG
TGACCATCACTGGACAGCTTTCTCTCAAACCTTCTCTCAACGCCATGGATTAGCACCAGTTTTGTTTACTTTAA
GGTACTTTTCCCATTCATCATCTGGTTATAATAAATGGATGGAAGAAATATTTCCCACTGATGGTTGGTCTGTTG
CTTGCCAAATTTTATAGGGAGAGCTGTTTCATCATACAACATAAGGGATAATGACTCCTGTGAGGTAAACAGAAAGC
CCAAGAAATAACAACCTTTTTTTCTTAAAAAGTTAGTTACACTTGTTTTCTTGAGAAAAAAACCTGTCAACTCCT
TTGCTTTTCCAAAATATTTTCAAGGTATTTCTTATAAGGTTTATAAGAATAAGAGCTTAACACAGAAATAGTTGCT
GTTTATAAGTTTATTATCTATATCTGAAAAATCATAGAAAATTGCTGGGTTTAGCTCTCAGCAGCCCGCTCCTG
AGCTCTGAGGAAGCTTGCCTTCTTTTGTAGCTACCCGATCCTTCTTCTGAGCAAGGGACATTTTGGGACGGTTCCA
CCTACAAAAGATAGGAATATATATTTTTTAACTATAACTGAAGAGAATAGAATATTTAATTTAAAAATTTAATA
AAATTTAATTTTGATAGAGAATATTTAAGACTTTGCAATCAGAAGGTTAAATAATCCAAGTTCAAATACATTTAC
TTATGTATGATCTTAAGCTAACTTTCCCAAACCCCAACTTCTGTGATGTCCTACTACCATAGGGCCAAAAAGTCAA
ATAGAAGACATGTTAGATTTCAGTAATACCCTTCTAGGTATTTGCCCAAATGTTTTGAAATCAGTTTGTCCAAGA
GAGTGGCACTCCCATGTTTCATTGCAGCACTATATATTAATAGCAACAGATAAATGGATAAAGGAAATGTGGTATA
CATATACATAATGGATTATTACCCAGTCTTTAAAAATGATGGAAATTCCTGTCAATTTGCAACATGAATGAAGTGGA
GAATATTGTGCTCAGTGAAATAAGCCAGGCACAAAAAGACAAATACTTCATATTTCATATAGAATCTAAAAACAATG
GAACTCAGAGAAGCAGAGAGCAGAATGGTGGTTACAGAGGCTGGTGGGTGCAAGAATGGGCAGATGATAGTCAA
GTATAAAATCTCCAACAGGAGGAGTATGATTTTGTGTTTGTAGTTCTATTGCACAGCATGATGAATATAGAATATCG
TACATTTACAAATTAAGAGAATAAATTTCAAATGTTGTTGCCACAAAGTGTTAAGTATTTGAGGTGAATATGTTA
AATACATTGATTTAATTACTATACATTGTATTTGTGGGCCATCACATCACTTTATGCTTACATGTTTCATTAAGTA
TTACTTTCTATTCCATTTAAAGATCAAACATGAAAGATCAACAAAAAGCAACTTGTCAGCCAATAAAAAAATGC
AGTAACCAGTACTTAGACTGTACTAGGATAGAAAGAACCACCTCAGTAGTGTCTGAGGCTAACACATTTCCATCA
CCACAGTTACTTTTGCAAACCTGGTTCCCTTCGCTTCTGCCACATCACGCAGAGCTAGTGATCGAGTTTGACAA
TTACACCAACAGTCTGCCCCACGTGGGAACCATTTCCCAACCTGTTTTCTTGAAAAGACAAAAAAGACGACAT
ACCTCTTCTTTTAACTTCTTTCTTGGGCTTCTTTTCATAGACTGGATTCTCTCGTATAGCAGCATGAGCTTTCT
TATACATCTCCTCCATCTGAAACAAAGGAAAGCAAACAGTACTTGTTTCATTTTCATGTGCCCTACTATATTAAT
GCAACCATAACTTATCTTGTCTTCTAAGCCAGATTCTCAAAGGAACATAAATAAATCAATGTTGGTAAACACT
TTAACTTCTAAATGTAACCTCACCTTTTCTAACAATTTCCCAATTTTACCTTATGCAATGTGAATTATCACTAC
AGAACTCCATCTTACTCAAGAAAAAATCAGGCCAGGTGTGGTGGTTCATGCCTGTAATCTCAAGCACTTTGGGA
GTCTGAAGTGGGAGGATCACTTCAGCCCAGGAGTTTGAGACCAGCTAAGGCAACACAGTGAGACCTGTCTCCATA
AAAAAATAATTAGCCAGGTGGCAATTATTAATGGTGGCATGCACCTGTAGTCCCAGCTACAGGACTACACGTGA
GTCCAGGAGGTCAAGGCTGCAGTGGCACAATCACAGCTCACTGGACCCAGCCTAGATGACAGAATGAGACCTCA
TCTCTACCAAAATTAATAAAAAAAAAAAAAAAAAAATTAGCAGGG

303/6881
FIGURE 283

MFFSPCKLDIQGLVFAPLSYYFHTYTTQIWHVPFNISIKLNTFWRKEPLFSAQRFRLPKVEHVKNLCDHHWTAFSQ
NFPSTPWISTSFVYFKVLEFPFIWL

304/6881
FIGURE 284

CCTAGCGCCGCTGGGCCTGCAGGTCTCTGTGAGCAGCGGACGCCGGTCTCTGTTCCGCAGGATCGGGTTTGTTA
AAGTTGTTAAGAATAAGGCCTACTTTAAGAGATACCAAGTGAAATTTAGAAGACGACGAGAGGGTAAAACTGATT
ATTATGCTCGGAAACGCTTGGTGATACAAGATAAAAAATAAATACAACACACCCAAATACAGGATGATAGTTCGTG
TGACAAACAGAGATATCATTGTGTCAGATTGCTTATGCCCGTATAGAGGGGGATATGATAGTCTGCGCAGCGTATG
CACACGAAC TGCCAAAATATGGTGTGAAGGTTGGCCTGACAAATTATGCTGCAGCATATTGTACTGGCCTGCTGC
TGGCCCGCAGGCTTCTCAATAGGTTTGGCATGGACAAGATCTATGAAGGCCAAGTGGAGGTGACTGGTGATGAAT
ACAATGTGGAAAGCATTGATGGTCAGCCAGGTGCCTTCACCTGCTATTTGGATGCAGGCCTTGCCAGAACTACCA
CTGGCAATAAAAGTTTTTGGTGCCCTGAAGGGAGCTGTGGATGGAGGCTTGTCTATCCCTCACAGTACCAAACGAT
TCCCTGGTTATGATTCTGAAAGCAAGGAATTTAATGCAGAAGTACATCGGAAGCACATCATGGGCCAGAAATGTTG
CAGATTACATGCGCTACTTAATGGAAGAAGATGAAGATGCTTACAAGAAACAGTTCTCTCAATACATAAAGAACA
GCGTAACTCCAGACATGATGGAGGAGATGTATAAGAAAGCTCATGCTGCTATACGAGAGAATCCAGTCTATGAAA
AGAAGCCCAAGAAAGAAGTTAAAAAGAAGAGGTGGAACCGTCCCAAAATGTCCCTTGCTCAGAAGAAGGATCGGG
TAGCTCAAAAGAAGGCAAGCTTCCTCAGAGCTCAGGAGCGGGCTGCTGAGAGCTTAAACCCAGCAATTTTCTATGA
TTTTTTCAGATATAGATAATAAACTTATGAACAGCAACTAAAAAAAAAAAAAAAAAAAAA

305/6881
FIGURE 285

MGFVKVVKNKAYFKRYQVKFRRRREGKTDYYARKRLVIQDKNKYNTPKYRMIVRVNTRDIICQIAYARIEGDMIV
CAAYAHHELPKYGVKVGLTNYAAAYCTGLLLARRLNRFGMDKIYEGQVEVTGDEYNVESIDGQPGAFTCYLDAGL
ARTTTGNKVFGALKGAVDGGLSIPHSTKRFPGYDSESKEFNAEVHRKHIMGQNVADYMRYLMEEDEDAYKKQFSQ
YIKNSVTPDMMEEMYKKAHAAIRENFPVYEKKPKKEVKKKRWNRPKMSLAQKKDRVAQKKASFLRAQERAAES

306/6881
FIGURE 286

ATGGTAAATGTTAAGACAAATCTTGGGAGAAACATTTATCAATTCCAATACCTCTCTCCACCCCAATACTGTATG
CTCTTGGAAGAAGATGAAGATGCTTACAAGAAACAGTTCTCTCAATACATAAAGAACAGTGTA ACTCCAGACATG
ATGGAGGAGATGTATAAGAAAGCTCATGCTGCTGTACCAGAGAATCCGGTCTATGAAAAGAAGCCCAAGAAAGAA
GTTAAAAAGAAGAGGTGGAACCGTTCCAAAATGTCCCTTGCTCAGAAGAAGGATTGGGTAGCTCAAAAGAAGGCA
AGCTTCCTCAGAGCTTAG

307/6881
FIGURE 287

MVNVKTNLGRNIYQFQYLSPQYCMLLEDEEDAYKKQFSQYIKNSVTPDMMEEMYKKAHAAPENPVYEKKPKKE
VKKKRWNRSKMSLAQKKDWVAQKKASFLRA

308/6881
FIGURE 288

GCTGACTCCAGTGTCCCGAGAGGCGCCGCTTCTTCCGCTTTCTCGTCAGGCTCCTGCAACCCCAGGCATGAACCA
AGGTTTCTGAACTACTGGGCGGGAGCCAACGTCTCTTCTTTCTCCCGCTCTGGCGGAGGCTTTGTGCTGCGGGC
TGGGCCCCAGGGTGTCCCCCATGGCGGGGCGCGGGTGGAGGTGCGATGGCAGCATCATGGAAGGGGGCGGCCAGA
TCCTGAGAGTCTCTACGGCCTTGAGCTGTCTCCTAGGCCTCCCCCTGCGGGTGCAGAAGATCCGAGCCGGCCGGA
GCACGCCAGGCCTGAGGCCTCAACATTTATCTGGACTGGAAATGATTTCGAGATTTGTGTGATGGGCAACTGGAGG
GGGCAGAAATTGGCTCAACAGAAATAACCTTTACACCAGAGAAGATCAAAGGTGGAATCCACACAGCAGATACCA
AGACAGCAGGGAGTGTGTGCCCTTTGATGCAGGTCTCAATGCCGTGTGTTCTCTTTGCTGCTTCTCCATCAGAAC
TTCATTTGAAAGGTGGAATAATGCTGAAATGGCACACAGATCGATTATACAGTGATGGTCTTCAAGCCAATTG
TTGAAAAATTTGGTTTCATATTTAATTGTGACATTAAAAACAAGGGGATATTACCCAAAAGGGGGTGGTGAAAGTGA
TTGTTTCGAATGTCACCAGTTAAACAATTGAACCCTATAAATTTAACTGAGCGTGGCTGTGTGACTAAGATATATG
GAAGAGCTTTTCGTTGCTGGTGTTTTGCCATTTAAAGTAGCAAAAAGATATGGCAGCGGCAGCAGTTAGATGCATCA
GAAAGGAGATCCGGGATTTGTATGTTAACATCCAGCCTGTTCAAGAACCTAAAGACCAAGCATTGCGCAATGGAA
ATGGAATAATAATTATTGCTGAGACCTCCACTGGCTGTTTGTGTTGCTGGATCATCGCTTGGTAAACGAGGTGTAA
ATGCAGACAAAGTTGGAATTGAAGCTGCCGAAATGCTATTAGCAAATCTTAGACATGGTGGTACTGTGGATGAGT
ATCTGCAAGACCAGCTGATTGTTTTTCATGGCATTAGCCAATGGAGTTTCCAGAATAAAAACAGGACCAGTTACAC
TCCATACGCAAACCGCGATACATTTTGTGTAACAAATAGCAAAGGCTAAATTTATTGTGAAGAAATCAGAAGATG
AAGAAGACGCCGCTAAAGATACTTATATTATTGAATGCCAAGGAATTGGGATGACAAATCCAAATCTATAGAGTA
TTTGCCTCTTAAATGATACCTCATTGATATATTGCACTATTTATAAATACTATAAAATAATGACTAGGAAGTAA
CTTATTAAAGGCTATGACTTAAATTTGAAGATGAAGTACAGTGTCTAGGTTTGCTGAGAAGGCTTCATTAAATT
AATCTCACTTTGAATATCTCCTGAGAGATGGACAATGAAATATCAGTTGGTGGATATGTGTGATAGCTGATTTC
ATATTGAAGTATTGAAATAAAATATTCTTTACACCTGAG

309/6881
FIGURE 289

MAGPRVEVDGSIMEGGGQILRVSTALSCLLGLPLRVQKIRAGRSTPGLRPQHLSGLEMIRDLC DGQLEGAEIGST
EITFTPEKIKGGIHTADTKTAGSVCLLMQVSMPCVLF AASPSELHLKGGTNAEMAPQIDYTVMVFKPIVEKFGFI
FNCDIKTRGYYPKGGGEVIVRMSPVKQLNFINLTERGCVTKIYGRAFVAGVLPFKVAKDMAAAAVRCIRKEIRDL
YVNIQPVQEPKDQAFGNGNGIIIIAETSTGCLFAGSSLGKRGVNADKVGIEAAEMLLANLRHGGTVDEY LQDQLI
VFMALANGVSRIKTGPVTLHTQTAIHF AEQIAKAKFIVKKSEDEEDA AKDTYII ECQGIGMTNPNL

310/6881
FIGURE 290

GCTTTTCCTTGCTACCTGCAGAGGGGTCCATACGGCGTTGTTCTGGATTCCCGTCGTAACCTAAAGGGAAACTTT
CACAATGTCCGGAGCCCTTGATGTCCTGCAAATGAAGGAGGATGTCCTTAAGTTCCTTGCAGCAGGAACCCACTT
AGGTGGCACCAATCTTGACTTCCAGATGGAACAGTACATCTATAAAAGGAAAAGTGATGGCATCTATATCATAAA
TCTGAAGAGGACCTGGGAGAAGCTTCTGCTGGCAGGTCGTGCTATTGTTGCCATTGAAAACCCTGCTGATGTCAG
TGTTATATCCTCCAGGAATACTGGCCAGAGGGCTGTGCTGAAATTTGCTGCTGCCACTGGAGCCACTCCAATTGC
TGGCCGCTTCACTCCTGGAACCTTCACTAACC GGATCCAGGCAGCCTTCCGGGAGCCACGGCTTGTTGTGGTTAC
TGACCCAGGGCTGACCACCAGCCTCTCACAGAGGCATCTTATGTTAACCTACCTACCATTGCGCTGTGTAAACAC
AGATTCTCCTCTGTGCTATGTGGACATTGCCATCCCATGCAACAACAAGGGAACCTCACTCAGTGGGTTTGATGTG
GTGGATGCTGGCTCGGGAAGTTCTGCGCATGTGTGGCACCATTTCCCGTGAACACCCATGGGAGGTCATGCCTGA
TCTGTACTTCGACAGAGATCCTGAAGAGATTGAAAAAGAAGAGCAGGCTGCTGCTGAGAAGGCAGTGACCAAGGA
GGAATTTAGGGTGAATGGACTGCTCCAGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAGACTGGTCTGA
AGGTGTACAGGTGCCCTCTGTGCCTATTAGCAATTCCCTACTGAAGACTGGAGCGCTCAGCCTGCCACGGAAGA
CTGGTCTGCAGCTCCCCTGCTCAGGCCACTGAATGGGTAGGAGCAACCACTGACTGGTCTTTAAGCTGTTCTTGC
ATAGGCTCTTAAGCAGCATGGAAAAATGGTTGATGGAAAATAAACATCAGTTTCT

311/6881
FIGURE 291

MSGALDVLQMKEDVLKFLAAGTHLGGTNLDFQMEQYIYKRKSDGIYIINLKRTWEKLLLAGRAIVAIENPADVSV
ISSRNTGQRAVLKFAAATGATPIAGRFTPGTFTNRIQAAFREPRLVVVTDPRAHQPLTEASYVNLPTIALCNTD
SPLCYVDIAIPCNNKGTHSVGLMWWMLAREVLRMCGTISREHPWEVMPDLYFDRDP EEIEKEEQAAAEKAVTKEE
FQGEWTAPAPEFTATQPEVADWSEGVQVPSVPIQQFPTEDWSAQPATEDWSAAPT AQATEWVGATTDWS

312/6881
FIGURE 292

GGCACGAGGAAGAATCAGGAGCTTAGGATGTATTAACACCAACTCATTAATATACTAACCGGACAATGTTCTACA
AACAATTCTACATTGTAAAGGACTGGATTGGCACAAAATAAAATAATTTTATTTTATTTACAGCTTATAATATGACT
CGATGGAGGAAAATTTGATAAGCATGAGAGAAGACCATTCTTTTCATGTTTCGTTACAGAATGGAAGCTTCTTGCC
TAGAGCTGGCCTTGGAAGGGGAACGTCTATGTAAATCAGGAGACTGCCGCGCTGGCGTGTCAATTCTTTGAAGCTG
CAGTTCAAGTTGGAAGTGAAGACCTAAAAACACTTAGCGCTATTTACAGCCAGTTGGGCAATGCTTATTTCTATT
TGCATGATTATGCCAAAGCATTAGAATATCACCATCATGATTTAACCCTTGCAAGGACTATTGGAGACCAGCTGG
GGGAAGCGAAAAGCTAGTGGTAATCTGGGAAACACCTTAAAAGTTCTTGGAATTTTGACGAAGCCATAGTTTGTT
GTCAGCGACACCTAGATATTTCCAGAGAGCTTAATGACAAGGTGGGAGAAGCAAGAGCACTTTACAATCTTGGA
ATGTGTATCATGCCAAAGGGAAAAGTTTTGGTTGCCCTGGTCCCCAGGATGTAGGAGAATTTCCAGAAGAAGTGA
GAGATGCTCTGCAGGCAGCCGTGGATTTTTATGAGGAAAACCTATCATTAGTGACTGCTTTGGGTGACCGAGCGG
CACAAGGACGTGCCCTTTGGAAATCTTGGAACACACATTACCTCCTTGGAACCTTCAGGGATGCAGTTATAGCTC
ATGAGCAGCGTCTCCTTATTGCAAAAGAATTTGGAGATAAAGCAGCTGAAAGAAGAGCATATAGCAACCTTGGA
ATGCATATATATTTCTTGGTGAATTTGAAACTGCCTCGGAATACTACAAGAAGACACTACTGTTGGCCCGACAGC
TTAAAGACCGAGCTGTAGAAGCACAGTCTTGTTACAGTCTTGGAATAACATATACTTTACTTCAAGACTATGAAA
AGGCCATTGATTATCATCTGAAGCACTTAGCAATTGCTCAAGAGCTGAATGATAGAATTGGTGAAGGAAGAGCAT
GTTGGAGCTTAGGAAATGCATACACAGCACTAGGAAATCATGATCAAGCAATGCATTTTGCTGAAAAGCACTTGG
AAATTTCAAGAGAGGTTGGGGATAAAAGTGGTGAACCTAACAGCACGACTTAATCTCTCAGACCTTCAATGGTTC
TTGGTCTGAGCTACAGCACAAATAACTCCATAATGTCTGAAAATACTGAAATTGATAGCAGTTTGAATGGTGTAC
TCCCCAAGTTGGGACGCCGGCATAGTATGGAATAATGGAACCTTATGAAGTTAACACCAGAAAAGGTACAGAACT
GGAACAGTGAAATCTTGCTAAGCAAAAACCTCTTATTGCCAAACCTTCTGCAAAGCTACTCTTTGTCAACAGAC
TGAAGGGGAAAAAATACAAAACGAATTCCTCCACTAAAGTTCTCCAAGATGCCAGTAATTTCTATTGACCACCGAA
TTCCAAATTTCTCAGAGGAAAATCAGTGCAGATACTATTGGAGATGAAGGGTTCTTTGACTTATTAAGCCGATTC
AAAGCAATAGGATGGATGATCAGAGATGTTGCTTACAAGAAAAGAACTGCCATACAGCTTCAACAACAACCTTCTT
CCACTCCCCCTAAAATGATGCTAAAAACATCATCTGTTCTGTGGTATCCCCAACACGGATGAGTTTTTAGATC
TTCTTGCCAGCTCACAGAGTCGCCGTCTGGATGACCAGAGGGCTAGTTTCAGTAATTTGCCAGGGCTTCGTCTAA
CACAAAACAGCCAGTCGGTACTTAGCCACCTGATGACTAATGACAACAAAGAGGCTGATGAAGATTTCTTTGACA
TCCTTGTAATAATGTCAAGGATCCAGATTAGATGATCAAAGATGTGCTCCACCACCTGCTACCACAAAGGGTCCGA
CAGTACCAGATGAAGACTTTTTTCAGCCTTATTTTACGGTCCCAGGGAAAGAGAATGGATGAACAGAGAGTTCTTT
TACAAAGAGATCAAAACAGAGACACTGACTTTGGGCTAAAGGACTTTTTTGCAAAATAATGCTTTGTTGGAGTTTA
AAAATTCAGGGAAAAAATCGGCAGACCATTAGTTACTATGGATTTATTTTTTTTCTTTTCAAAACACGGTAAGGAA
ACAATCTATTACTTTTTTCTTAAAGGAGAATTTATAGCACTGTAATACAGCTTAAAAATATTTTTTAGAATGATG
TAAATAGTTAA

313/6881
FIGURE 293

MREDHSFHVRYRMEASCLELALALEGERLCKSGDCRAGVSFFEAAVQVGTEDLKTLSSAIYSQLG NAYFYLHDYAKAL
EYHHHDLTLARTIGDQLGEAKASGNLGNLTKVLGNFDEAIVCCQRHLDISRELNDKVGEARALYNLGNVYHAKGK
SFGCPGPGQDVGEFPPEVRDALQAAVDIFYEENLSLVTALGDRAAQGRAFGNLGNTHYLLGNFRDAVIAHEQRLLIA
KEFGDKAAERRAYSNLGNAYIFLGEFETASEYYKKTLLLLARQLKDRAVEAQSCYSLGNTYTLLQDYEKADYHLK
HLAIAQELNDRIGEGRACWSLGNAYTALGNHDQAMHFAEKHLEISREVGDKSGELTARLNLSDLQMV LGLSYSTN
NSIMSENTEIDSSSLNGVLPKLGRRHSMENMELMKLTPEKVQNWNSEILAKQKPLIAKPSAKLLFVNRLKGKKYKT
NSSTKVLQDASNSIDHRIPNSQRKISADTIGDEGFFDLLSRFQSNRMDDQRCCLQEKNCHTASTTTSSTPPKMML
KTSSVPVVPNTDEFD LLLASSQSRRLDDQRASF SNLPGLRLTQNSQSVLSHLM TNDNKEADEDFFDILVKCQGS
RLDDQRCAPPPATTKGPTVPDEDDFFSLILRSQGKRMDEQRVLLQRDQNRDTDFGLKDFLQNNALLEFKNSGKKSA
DH

314/6881
FIGURE 294

AAGCAGCCTGAGGTAATCTGTGAAAATGGTTCGCTATTTCACTTGACCCGGAGAACCCACGAAATCATGCAAATC
AAGAGGTTCCAATCTTCGTGTTCACTTTAAGAACAACCTCGTGAAACTGCTCAGGCCATCAAGGGTATGCATATACG
AAAAGCCACGAAGTATCTGAAAGATGTCACTTTACAGAAACAGTGTGTACCATTCCGACGTTACAATGGTGGAGT
TGGCAGGTGTGCGCAGGCCCTGCACATGCTTAAAAACACAGAGAGTAATGCTGAACTTAAGGGTTTAGATGTAGA
TTCTCTGGTCATTGAGCATATCCAAGTGAACAAAGCACCTAAGATGCGCCGCCGGACCTACAGAGCTCATGGTCG
GATTAACCCATACATGAGCTCTCCCTGCCACATTGAGATGATCCTTACGGAAAAGGAACAGATTGTTTCCTAAACC
AGAAGAGGAGGTTGCCCAGAAGAAAAGGATATCCCAGAAGAACTGAAGAAACAAAACTTATGGCACGGGAGTA
AATTCAGCAT

315/6881
FIGURE 295

GCAGGCTCTGCCTGTGGCCACTAGCAGAGAAGCTGCTGTCCTTCCACCACCAGCACCGGACCACCTGCTCCAAGA
CCAGCCTCCTGGGGGGACCAGGCACCCGGCCTTCACTGGCACCCAGGGAGCCGTCCTCAGCAGCGTCAACATGTC
AAGGCCCAGCAGCAGAGCCATTTACTTGACCCGGAAGGAGTACTCCAGAACCTCACCTCAGAGCCCCACCTCCT
GCAGCACAGGGTGGAGCACTTGATGACATGCAAGCAGGGGAGTCAGAGAGTCCAGGGGCCCCGAGGATGCCTTGCA
GAAGCTGTTTCGAGATGGATGCACAGGGCCGGGTGTGGAGCCAAGACTTGATCCTGCAGGTTCAGGGACGGCTGGCT
GCAGCTGCTGGACATTGAGACCAAGGAGGAGCTGGACTCTTACCGCCTAGACAGCATCCAGGCCATGAATGTGGC
GCTCAACACATGTTCCCTACAACCTCCATCCTGTCCATCACCGTGCAGGAGCCGGGCCTGCCAGGCACTAGCACTCT
GCTCTTCCAGTGCCAGGAAGTGGGGGCAGAGCGACTGAAGACCAGCCTGCAGAAAGGCTCTGGAGGAAGAGCTGGA
GCAAAGACCTCGACTTGGAGGCCTTCAGCCAGGCCAGGACAGATGGAGGGGGCCTGCTATGGAAAGGCCGCTCCC
TATGGAGCAGGCACGCTATCTGGAGCCGGGGATCCCTCCAGAAACAGCCCCACCAGAGGACCCTAGAGCACAGCCT
CCCACCATCCCCAAGGCCCCGTGCCACGCCACACCAAGTGCCCGAGAACCAAGTGCCTTTACTCTGCCTCCTCCAAG
GCGGTCTCTTCCCCCGAGGACCCAGAGAGGGACGAGGAAGTGCTGAACCATGTCTTAAGGGACATTGAGCTGTT
CATGGGAAAGCTGGAGAAGGCCCAGGCAAAGACCAGCAGGAAGAAGAAATTTGGGAAAAAAACAAGGACCAGGG
AGGTCTCACCCAGGCACAGTACATTGACTGCTTCCAGAAGATCAAGCACAGCTTCAACCTCCTGGGAAGGCTGGC
CACCTGGCTGAAGGAGACAAGTGCCCTGAGCTCGTACACATCCTCTTCAAGTCCCTGAACCTTCATCCTGGCCAG
GTGCCCTGAGGCTGGCCTAGCAGCCCAAGTGATCTCACCCCTCCTCACCCCTAAAGCTATCAACCTGCTACAGTC
CTGTCTAAGCCCACCTGAGAGTAACCTTTGGATGGGGTTGGGGCCAGCCTGGACCACTAGCCGGGCCGACTGGAC
AGGCGATGAGCCCCTGCCCTACCAACCCACATTCTCAGATGACTGGCAACTTCCAGAGCCCTCCAGCCAAGCACC
CTTAGGATACCAGGACCCTGTTTCCCTTCGGCGGGGAAGTCATAGGTTAGGGAGCACCTCACACTTTCTCAGGA
GAAGACACACAACCATGACCTCAGCCTGGGGACCCCAACTCCAGGCCCTCCAGCCCCAAACCTGCCCAGCCAGC
CCTGAAAATGCAAGTCTTGTACGAGTTTGAAGCTAGGAACCCACGGGAAGTACTGTGGTCCAGGGAGAGAAGCT
GGAGGTTCTGGACCACAGCAAGCGGTGGTGGCTGGTGAAGAATGAGGCGGGACGGAGCGGCTACATTCCAAGCAA
CATCCTGGAGCCCCTACAGCCGGGGACCCCTGGGACCCAGGGCCAGTCACCCCTCTCGGGTTCCAATGCTTCGACT
TAGCTCGAGGCCTGAAGAGGTCACAGACTGGCTGCAGGCAGAGAAGTCTCCACTGCCACGGTGAGGACACTTGG
GTCCCTGACGGGGAGCCAGCTACTTCGCATAAGACCTGGGGAGCTACAGATGCTATGTCCACAGGAGGCCCCACG
AATCCTGTCCCGGCTGGAGGCTGTCAGAAGGATGCTGGGGATAAGCCCTTAGGCACCAGCTTAGACACCTCCAAG
AACCAGGCCCCGCTGATGCAAGATGGCAGATCTGATACCCATTAGAGCCCCGAGAATTCCTCTTCTGGATCCCAG
TTTGCAGCAAACCCACACCCAGCTCACACAGCAAAAACAATGGACAGGCCCCAGAGGCTGAAGCAAACAGTGTC
CCTTCTGGCTGTGTTGGAGCCTCCCCAGTAACCACCTATTTATTTTACCTCTTTCCCAAACCTGGAGCATTTATG
CCTAGGCTTGTCAGAATCTGTTCACTCCCTCTCCTTCTCAATAAAAGCATCTTCAAGCTTGT

316/6881
FIGURE 296

GGGAGAAAGCCTGTTGCGTGGAAGATAAGGCGGCGCGGGAAGTGGACACAGGGTGGGCTGGAGCTCAGATCTAAC
TGGACTCTCGCTCCTGCTGGCTGGACATGGAGGATTTGGAGGAAGATGTAAGGTTTATTGTGGATGAGACCTTGG
ACTTTGGGGGGCTGTCACCATCTGACAGCCGTGAGGAGGAAGACATAACAGTGTGGTGAAGTCCAGAGAAACCAC
TTGACAGGGGGCCTCTCCCACCGAAGTGACCCAAATGCAGTGGCACCTGCCCCCAGGGTGTGAGGCTCAGCCTAG
GCCCCCTCAGTCCAGAGAAGCTGGAGGAGATCCTCGATGAGGCCAACC GGCTGGCCGCTCAGCTGGAGCAGTGTG
CCCTGCAGGATCGGGAGAGCGCAGGCGAGGGCCTGGGGCCTCGCCGAGTGAAGCCCAGTCTCGGCGGGAGACCT
TTGTGCTGAAGGATAGTCCTGTCCGAGACCTGCTGCCCCACTGTGAACCTCTTTGACGCGGAGCACCCCCCTCCCCAA
GCAGCCTGACGCCCTCGACTCCGGAGTAATGATAGGAAGGGGTGAGTCAGGGCTCTCCGGGCTACATCTGGAAAGA
GGCCCTCCAACATGAAGAGGGAGTCACCCACTTGCAATCTGTTCCCTGCATCCAAAAGCCCAGCATCTTCTCCTC
TTACCCGATCGACTCCCCCAGTCCGGGGGAGAGCCGGGGCCAGTGGGAGAGCAGCAGCCAGCCCACCCACCCCCA
TCAGATCCGTCCTGGCCCCACAGCCTTCTACCAGCAACTCTCAACGCCTGCCCCGGCCGCAGGGAGCAGCTGCTA
AATCTTCCAGTCAACTGCCCATTCCTCGGCCATCCCCAGGCCTGCCAGCCGAATGCCACTCACCAGCCGGAGTG
TGCCACCTGGCAGAGGTGCCCTACCTCCGGATTCTCTGTCAACTCGAAAAGGGCTTCCAAGACCAAGCACTGCAG
GACACAGAGTGCGGGAAAGTGGACACAAGGTTCTGTTTCCCAGCGACTAAATCTTCTGTGTCATGGGTGCCACTC
GCAGCAATCTGCAGCCCCCAGGAAAGTGGCAGTCCCAGGACCTACCAGGTAAAGAGATCAGGACAGCAAGCAAG
ACTTCAGTAGCAAACCACTACAGTCAGTACCTGGACTCGCCTCTACCCAGCAGACCCTGACTCCAGCAGATTCTG
GCCAGGGACAGGAGGAAGAGATGCCACCAGGGCTGGTCTCCCAGGAGTAGAGACCATGGGAAATGGGGTGGATT
AGGATTGAGCTGGAGAAGACTTAAACTCTCTGGGTTGAAAGAAGATTAGGGGAAAAGAGGTCACCTTCCAGCAGT
GAAATGAACAAATAGAAGATGAGAAGTACAGGCAAGTGGTTTGTCTTTATCCACCCCCACTGTTGTGGTCAGCCC
CAGAGAATTTTATCTTCTTCTTGGCATTGGTTCACTGGACATTTCCACGTGAGCGGCCTCCGTAGCTAACCTCC
CTGCCCTCTGAGGAGCCATCTTCTGAATCGCATTCTCTACTGGACTCTGGCCTGCTTGGAGAGGTGGCAGCAGG
CACCTGGTCTTCAGAAATTGTTTCTGTGAATTCTGTGACTCCTAATAGGCCAGTTTGTGATAAGCTTACTCTAT
GAGTCTTCATTTTCTAAAATAAAGTGAATGTATTTTAAAAAAAAAAAAAAAAAAAAA

317/6881
FIGURE 297

MEDLEEDVRFIVDETLDFFGGLSPSDSREEEDITVLVTPEKPLRRGLSHRSDPNAVAPAPQGVRLSLGPLSPEKLE
EILDEANRLAAQLEQCALQDRESAGEGLGPRRVKPSPRRETFLVKDSPVRDLLPTVNSLTRSTPSPSSLTPRLRS
NDRKGSVRALRATSGKRPSNMKRESPTCNLFFASKSPASSPLTRSTPPVRGRAGPSGRAAASPPTPIRSVLAPQP
STSNSQRLPRPQGAAAKSSSQLPIPSAIPRPASRMPLTSRSVPPGRGALPPDSLSTRKGLPRPSTAGHRVRESGH
KVPVSQRLNLPVMGATRNLQPPRKVAVPGPTR

318/6881
FIGURE 298

GCAGTGCGGCGGTACAGGCTGAGTGCTGCGGCGCGATCCTTGCTTCCCTGAGCGTTGGCCCGGGAGGAAAGAAG
ATGGTGCTGGATCTGGATTTGTTTCGGGTGGATAAAGGAGGGGACCCAGCCCTCATCCGAGAGACGCAGGAGAAG
CGCTTCAAGGACCCGGGACTAGTGGACCAGCTGGTGAAGGCAGACAGCGAGTGGCGACGATGTAGATTTCCGGCA
GACAACTTGAACAAGCTGAAGAACCTATGCAGCAAGACAATCGGAGAGAAAATGAAGAAAAAGAGCCAGTGGGA
GATGATGAGTCTGTCCAGAGAATGTGCTGAGTTTCGATGACCTTACTGCAGACGCTTTAGCTAACCTGAAAGTC
TCACAAATCAAAAAGTCCGACTCCTCATTGATGAAGCCATCCTGAAGTGTGACGCGGAGCGGATAAAGTTGGAA
GCAGAGCGGTTTGAGAACTCCGAGAGATTGGGAACCTTCTGCACCCTTCTGTACCCATCAGTAACGATGAGGAT
GTGGACAACAAAGTAGAGAGGATTTGGGGTGATTGTACAGTCAGGAAGAAGTACTCTCATGTGGACCTGGTGGTG
ATGGTAGATGGCTTTGAAGGCGAAAAGGGGGCCGTGGTGGCTGGGAGTCGAGGGTACTTCTTGAAGGGGGTCTCTG
GTGTTCTTGAACAGGCTCTCATCCAGTATGCCCTTCGCACCTTGGGAAGTCGGGGCTACATTCCCATTTATAACC
CCCTTTTTTCATGAGGAAGGAGGTTCATGCAGGAGGTGGCACAGCTCAGCCAGTTTGATGAAGAACTTTATAAGGTG
ATTGGCAAAGGCAGTGAAGAGTCTGATGACAACCTCCTATGATGAGAAGTACCTGATTGCCACCTCAGAGCAGCCC
ATTGCTGCCCTGCACCGGGATGAGTGGCTCCGGCCGGAGGACCTGCCCATCAAGTATGCTGGCCTGTCTACCTGC
TTCCGTCAGGAGGTGGGCTCCCATGGCCGTGACACCCGTGGCATCTTCCGAGTCCATCAGTTTGAGAAGATTGAA
CAGTTTGTGTACTCATCACCCATGACAACAAGTCATGGGAGATGTTTGAAGAGATGATTACCACCGCAGAGGAG
TTCTACCAGTCCCTGGGGATTCTTACCACATTGTGAATATTGTCTCAGGTTCTTTGAATCATGCTGCCAGTAAG
AAGCTTGACCTGGAGGCCTGGTTTCCGGGCTCAGGAGCCTTCCGTGAGTTGGTCTCCTGTTCTAATTGCACGGAT
TACCAGGCTCGCCGGCTTCGAATCCGATATGGGCAAACCAAGAAGATGATGGACAAGGTGGAGTTTGTCCATATG
CTCAATGCTACCATGTGCGCCACTACCCGTACCATCTGCGCCATCCTGGAGAACTACCAGACAGAGAAGGGCATC
ACTGTGCCTGAGAAATTGAAGGAGTTCATGCCGCCAGGACTGCAAGAACTGATCCCTTTGTGAAGCCTGCGCCC
ATTGAGCAGGAGCCATCAAAGAAGCAGAAGAAGCAACATGAGGGCAGCAAAAAGAAAGCAGCAGCAAGAGACGTC
ACCCTAGAAAACAGGCTGCAGAACATGGAGGTCACCGATGCT**TGA**ACATTCTGCCTCCCTATTTGCCAGGCTTT
CATTTCTGTCTGCTGAGATCTCAGAGCCTGCCCAACAGCAGGGAAGCCAAGCACCCATTCTCCCCCTGCCCCA
TCTGACTGCGTAGCTGAGAGGGGAACAGTGCCATGTACCACACAGATGTTCTGTCTCCTCGCATGGGCATAGGG
ACCCATCATTGATGACTGATGAAACCATGTAATAAAGCATCTCTGGGGAGGGCTTAGGACTCTTCCTCAGTCTTC
TTCCCCGGGCTTGAACCCCGAAA

319/6881
FIGURE 299

MVLDDLDFRVDKGGDPALIRETQEKRFKDPGLVDQLVKADSEWRRRCRFRADNLNKLKNLCSKTIGKMKKKKEPVG
DDESVPENVLVSFDDLTADALANLKVSQIKKVRLIDEAILKCDARIKLEAERFENLREIGNLLHPSVPISNDED
VDNKVERIWGDCTVRKKYSHVDLVVMVDGFEKEKGAVVAGSRGYFLKGVLVFLEQALIQYALRTLGSRGYIPIYT
PFFMRKEVMQEVAQLSQFDEELYKVIGKGSEKSDDNSYDEKYLIATSEQPIAALHRDEWLRPEDLP IKYAGLSTC
FRQEVGSHGRDTRGIFRVHQFEKIEQFVYSSPHDNKSWEMFEEMITTAEEFYQSLGIPYHIVNIVSGSLNHAASK
KLDLEAWFPGSGAFRELVSCSNCTDYQARRLRIRYGQTKKMDKVEFVHMLNATMCATTRTICAILENYQTEKGI
TVPEKLKEFMPPGLQELIPFVKPAPIEQEPSKKQKKQHEGSKKKAAARDVTLENRLQNMEVTD

320/6881
FIGURE 300

CAGAGTGCCCTTTCTCCCCGCTCTTCCCCCTCCCGGGAGCTGCCAGTACTTGACGTGGCGTCACCGCCCTCTAC
CCTCGCTTTGCGTGCGTGTTTGCCTACAGCGGAGGTGGCGGCGCGGGCAGGTCGGAGCTCGGAGCTGCTGCTTCT
GGTTCTCTTGTTGGCCACCGTCGCTGTCCGGCTGCCTTGGGCTGCCGAACAGACAAGGCGTGGGCCACAGCACCTC
AGAAGCCGACGCAGCTCGACGCAGGGGCCGGCAGGAGGGTGGGCGATCGCGTGTCCGAGGGCGCCGCGCGGGCAG
GCGGGCGGGCGCCAGAGGGGGAAAGAGGCGGGGGCGGCGGGTTCAGCCGCTGGCCGGGGCCGGCGGGGGAATGTCGA
TGCCTGACGCGATGCCGCTGCCCGGGGTCCGGGGAGGAGCTGAAGCAGGCCAAGGAGATCGAGGACGCCGAGAAGT
ACTCCTTCATGGCCACCGTCACCAAGGCGCCCAAGAAGCAAATCCAGTTTGCTGATGACATGCAGGAGTTACCA
AATTCCCCACCAAACTGGCCGAAGATCTTTGTCTCGCTCGATCTCACAGTCTCCTGACAGCTACAGTTTCAG
CTGCATCCTACACAGATAGCTCTGATGATGAGGTTTCTCCCCGAGAGAAGCAGCAAACCAACTCCAAGGGCAGCA
GCAATTTCTGTGTGAAGAATCAAGCAGGCAGAAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGT
CTGCTCTGATTTCACTCAGGAAACGTGCTCAGGGGGAGAAAGCCCTTGGCTGGTGCTAAAATAGTGGGCTGTACAC
ACATCACAGCCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCTGGGGGGCTCAGTGCCGCTGGTCTGCTTGTA
ACATCTACTCAACTCAGAAATGAAGTAGCTGCAGCACTGGCTGAGGCTGGAGTTGCAGTGTTTCGCTTGGAAGGGCG
AGTCAGAAGATGACTTCTGGTGGTGATTGACCGCTGTGTGAACATGGATGGGTGGCAGGCCAACATGATCCTGG
ATGATGGGGGAGACTTAACCCACTGGGTTTATAAGAAGTATCCAAACGTGTTTAAGAAGATCCGAGGCATTGTGG
AAGAGAGCGTGACTGGTGTTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTGTGTTCCGGCCATGAACG
TCAATGATTCTGTTACCAACAGAAGTTTGATACTTGTAAGTGTGCTGCTGCCGAGAATCCATTTTGGATGGCCTGAAGA
GGACCACAGATGTGATGTTTGGTGGGAAACAAGTGGTGGTGTGTGGCTATGGTGAGGTAGGCAAGGGCTGCTGTG
CTGCTCTCAAAGCTCTTGGAGCAATTGTCTACATTACCGAAATCGACCCCATCTGTGCTCTGCAGGCCTGCATGG
ATGGGTTTCAGGGTGGTAAAGCTAAATGAAGTCATCCGGCAAGTCGATGTGTAATAACTTGCACAGGAAATAAGA
ATGTAGTGACACGGGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAATATGGGCCACTCCAACACAG
AAATCGATGTGACCAGCCTCCGCACTCCGGAGCTGACGTGGGAGCGAGTACGTTCTCAGGTGGACCATGTCATCT
GGCCAGATGGCAAACGAGTTGTCTCCTGCGCAGAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCACCT
TTGTTCTGTCCATCACAGCCACAACACAGGCTTTGGCACTGATAGAACTCTATAATGCACCCGAGGGGCGATACA
AGCAGGATGTGTACTTGTCTCCTAAGAAAATGGATGAATACGTTGCCAGCTTGCATCTGCCATCATTGATGCCC
ACCTTACAGAGCTGACAGATGACCAAGCAAAATATCTGGGACTCAACAAAATGGGCCATTCAAACCTAATTATT
ACAGATACTAATGGACCATACTACCAAGGACCAGTCCACCTGAACCACACACTCTAAAGAAATATTTTTTAAGAT
AACTTTTATTTTCTTCTTACTCCTTTCTCTTGATTTTTTTCCTATAATTTTATTCTTGTTTTTTTCATCTCATT
TCCAAGTTCTGCAGACCACACAGGAACCTTGCTTCATGGCTCTTTAGATGAAATAGAAGTTCAGGGTCCCTCACTC
TAGTCACTAAAGAAGGATTTTACTCCCCAGCCCAGAAAGGTGATTCTTCTCTTTACCATTCTTGGGGACTTTAG
TCTTAATTAGGTACCTTATTAACAGGAAATGCTAAGGTACCTTCTCTGTGGAACAATCTGCAATGTCTAAATCGC
CTTAAAGAGCCCCATTTCTTAGCTGCTGAAATCAGTGTCTTTCACTTCTTCAGAGAAGCAGGGATGGTACCTAC
CCGGCAGGTAGGTTAGATGTGGGTGGTGCATGTTAATTTCCCTTAGAAGTTCCAAGCCCTGTTTCTGCGTAAAG
GTGGTATGTCCAGTTTCAGAGATGTGTATAATGAGCATGGCTTGTTAAGATCAGGAGGCCCACTTGGATTTATAGT
ATAGCCCTTCTCCACTCCCACCAGACTTGCTCATTTTTTCGAGTTTTTAACTAGACTACACTCTATTTGAGTTTA
ATTTTGTCTCTAGGATTTATTTCTGTTGTCCAAAAAAAAAAAAAAAAAAAAA

321/6881
FIGURE 301

MSMPDAMPLPGVGEELKQAKEIEDAEKYSFMATVTKAPKKQIQFADDMQEF TKFPTKTGRRSLSRISISQSSTDSY
SSAASYTDSDDDEVSPREKQQTNSKGSSNFCVKNIKQAEFGRRREIEIAEQDMSALISLRKRAQGEKPLAGAKIVG
CTHITAQTAVLIETLCALGAQCRWSACNIYSTQNEVAAALAEAGVAVFAWKGESEDDFWWCIDRCVNMDGWQANM
ILDDGGDLTHWVYKKYPNVFKKIRGIVEESVTGVHRLYQLSKAGKLCVPAMNVNDSVTKQKFDNLYCCRESILDG
LKRTTDMFEGGKQVVVCGYGEVGKCCAALKALGAIVYITEIDPICALQACMDGFRVVKLNEVIRQVDVVITCTG
NKNVVTREHLDRMKNSCIVCNMGHSNTEIDVTSLRTPELTWERVRSQVDHVIWPDGKRVLLEAGRLLNLSCSTV
PTFVLSITATTQALALIELYNAPEGRYKQDVYLLPKKMDEYVASLHLP SFDAHLTELTDQAKYLGLNKNGPFKP
NYYRY

322/6881
FIGURE 302A

GCTTATGGCGGCGCTGGAGAGGGGGCGCTGAGCTGTTGGGTATGAAGTGTAAACAGAACAGACTTTACCACCTGAA
ACTGCTGCTTCAAGTTTCAGATCAGGCAAGGAACAAACCTCGTAACAACCTAACAGACCAAGAAGAGTACACTTA
AGTTGAAGACACAACACTTGATCTGAAACAAGAAGTTTGTGCCTACTCAACAGCTTTGAAAGAGCACTTCCCAAC
GCTGCTAGTAGTCTTTGTTTTCTTCAGTGCTGTACTGTGAGATTGCCCGGTACAGCAGCAGTTGTATTCTTTATT
AGCTTGGTAGATCATTTTCTCTCGCTCTTTTTTTAATACTAGCAACTTTCATCCTTTGAAACGTGTGCTGAAAA
AGAAGAATCAGCAAATACTACTGAAAGTGCAATATTTGAGTATCACTGCGAGATGAGCTTTGATCCAAACCTTCT
CCACAACAATGGACATAATGGGTACCCTAATGGTACTTCAGCAGCACTGCGTGAAACTGGGGTTATTGAAAACT
GTTAACCTCTTACGGATTTATTTCAGTGTTTCAGAACGTCAAGCTAGACTTTTCTTCCACTGTTTCACAGTATAATGG
CAACCTGCAAGACTTAAAAGTAGGAGATGATGTTGAATTTGAAGTATCATCGGACCGACGGACTGGGAAACCCAT
TGCTGTTAAACTGGTGAAGATAAAACAAGAAATCCTCCCTGAAGAACGAATGAATGGACAAGTTGTGTGCGCTGT
TCCTCACAACTTAGAGAGTAAATCTCCAGCTGCCCCGGGTGAGAGTCCAACAGGGAGTGTATGCTACGAACGTAA
TGGGGAAGTGTTTTATCTGACTTACACCCCTGAAGATGTGGAAGGGAACGTTTCAGCTGGAAACTGGAGATAAAAT
AAACTTTGTAATTGATAACAATAAACATACTGGTGCTGTAAGTGCTCGCAACATTATGCTGTTGAAAAAGAAACA
AGCCCGCTGTCAGGGAGTAGTTTGTGCCATGAAGGAGGCATTTGGCTTTATTGAAAGAGGTGATGTTGTAAAAGA
GATATTCTTTCACTATAGTGAATTTAAGGGTGACTTAGAAACCTTACAGCCTGGCGATGATGTGGAATTCACAAT
CAAGGACAGAAATGGTAAAGAAGTTGCAACAGATGTCAGACTATTGCCTCAAGGAACAGTCATTTTGAAGATAT
CAGCATTGAACATTTTGAAGGAAGTGAACCAAGTTATCCCAAAGTACCCAGTAAAAACCAGAATGACCCATT
GCCAGGACGCATCAAAGTTGACTTTGTGATCCCTAAAGAACTTCCCTTTGGAGACAAAGATACGAAATCCAAGGT
GACCCTGCTGGAAGGTGACCATGTTAGGTTTAATATTTCAACAGACCGACGTGACAAATTAGAGCGAGCAACCA
TATAGAAGTTCTGTCAAATACATTTTCAGTTCATAATGAAGCCCGAGAAATGGGTGTGATTGCTGCCATGAGAGA
TGGTTTTGGTTTCATCAAGTGTGTGGATCGTGATGTTTCGTATGTTCTTCCACTTCAGTGAAATTCTGGATGGGAA
CCAGCTCCATATTGCAGATGAAGTAGAGTTTACTGTGGTTCCTGATATGCTCTCTGCTCAAAGAAATCATGCTAT
TAGGATTAAAAACTTCCCAAGGGCACGGTTTCATTTTATTCCCATTCAGATCACCGTTTTCTGGGCACGGTAGA
AAAAGAAGCCACTTTTTCCAATCCTAAAACCACTAGCCCAAATAAAGGCAAAGAGAAGGAGGCTGAGGATGGCAT
TATTGCTTATGATGACTGTGGGGTGAACCTGACTATTGCTTTTCAAGCCAAGGATGTGGAAGGATCTACTTCTCC
TCAAATAGGAGATAAGGTTGAATTTAGTATTAGTGACAAACAGAGGCCTGGACAGCAGGTTGCAACTTGTGTGCG
ACTTTTAGGTGCTAATTCTAACTCCAAGAGGCTCTTGGGTTATGTGGCAACTCTGAAGGATAATTTTGGATTTAT
TGAAACAGCCAATCATGATAAGGAAATCTTTTTCCATTACAGTGAGTTCTCTGGTGATGTTGATAGCCTGGAAC
GGGGGACATGGTCGAGTATAGCTTGTCCAAAGGCAAAGGCAACAAAGTCAGTGCAAAAAAGTGAAACAAAACACA
CTCAGTGAATGGCATTACTGAGGAAGCTGATCCCACCATTACTCTGGCAAAGTAATTCGCCCCCTGAGGAGTGT
TGATCCAACACAGACTGAGTACCAAGGAATGATTGAGATTGTGGAGGAGGGCGATATGAAAGGTGAGGTCTATCC
ATTTGGCATCGTTGGGATGGCCAACAAAGGGGATTGCCTGCAGAAAGGGGAGAGCGTCAAGTTCCAATTGTGTGT
CCTGGGCCAAAATGCACAACTATGGCTTACAACATCACACCCCTGCGCAGGGCCACAGTGGAATGTGTGAAAGA
TCAGTTTGGCTTCATTAACATATGAAGTAGGAGATAGCAAGAAGCTCTTTTTCCATGTGAAAGAAGTTCAGGATGG
CATTGAGCTACAGGCAGGAGATGAGGTGGAGTTCTCAGTGATTCTTAATCAGCGCACTGGCAAGTGCAGCGCCTG
TAATGTTTGGCGAGTCTGTGAGGGCCCCAAGGCTGTTGCAGTCCTCGACCTGATCGGTTGGTCAATCGCTTGAA
GAATATCACTCTGGATGATGCCAGTGCTCCTCGCCTAATGGTTCTTCGTCAGCCAAGGGGACCAGATAACTCAAT
GGGGTTTGGTGCAGAAAGAAAGATCCGTCAAGCTGGTGTCAATTGACTAACCACATCCACAAAGCACACCATTAAT
CCACTATGATCAAGTTGGGGGAATCTGGTGAAGGGTTCTGAATATCTCCCTCTTCATCCCTCCCGAAATCTGGA
ATACTTATTCTATTGAGCTATTACACCAGTTTTAACACCTTCCTCGTGTTATGTTTAAAAAATAAATAAATTTA
AGAAAACCATTTTAAATAATGCACAGTTGCAGCCTGGAAAACTTAAGGTGGCGCCTTATAGTATCAATTTTAGG
AGCTTTATTTGGTGCATTTAACGCAACTGGTAATTGCAGAATCCACTTTGCCTGTGTAAGTGAAAAATATAGACT
GTTATCTTGTGGCCCTATGAAATTCTGCACTTTTTATTATATACTCTACCTTCATTAATTACTTCTGGCAAGAT
GTTCTGCCTTAGCACTCAGTTGCATTCTTTTCTTTTCTTCTTCTGTTTATTGCTTTAATTCTGAGGACCATAT
GAGGGTAGAATATATATCTTTTAAAAATTACAAAAATTTGTATAGGCAAACCATTTCTTAAAGTTGATGGCCAA
ATTTTAAATGTTATTTTTCATATCATTTATAATCTTGTACAAATCCACTTAAAGAAGTTTGGTTATATTTTCAGT
GAAATTTTCTTCCAGAGTAGGTTTTTTTTCTGTTGGGTTGGGGGGTAACTTTACTACAATTAGTAAGTATGGTGCA
GAATTTTCATGCAAATGAGGAGTGCCAGCAGTGATGATAATTTAAACATATTTAAACAAAAACAAAAAATGAATG

323/6881

FIGURE 302B

CACAAACTTGCTGCTGCTTAGATCACTGCAGCTTCTAGGACCCGGTTTCTTTTACTGATTTAAAAACAAAACAAA
AAAAAATAAAAAAGTTGTGCCTGAAATGAATCTTGTTTTTTTTTATAAGTAGCCGCCTGGTTACTGTGTCCTGTA
AAATACAGACACTTGACCCTTGGTGTAGCTTCTGTTCAACTTTATATCACGGGAATGGATGGGTCTGATTTCTTG
GCCCTCTTCTTGAATTGGCCATATACAGGGTCCCTGGCCAGTGGACTGAAGGCTTTGTCTAAGATGACAAGGGTC
AGCTCAGGGGATGTGGGGGAGGGCGGTTTTATCTTCCCCCTTGTCGTTTGAGGTTTTGATCTCTGGGTAAAGAGG
CCGTTTATCTTTGTAAACACGAAACATTTTGTCTTCTCCAGTTTTCTGTTAATGGCGAAAGAATGGAAGCGAAT
AAAGTTTTACTGATTTTTTGAGACACT

324/6881
FIGURE 303

MSFDPNLLHNNGHNGYPNGTSAALRETGVIEKLLTSYGFIQCSEARLFFHCSQYNGNLQDLKVGDDVEFEVSS
DRRTGKPIAVKLVKIKQEILPEERMNGQVVCAPHNLESKSPAAPGQSPTGVCYERNGEVLYLTYTPEDVEGNV
QLETGDKINFVIDNNKHTGAVSARNIMLLKKKQARCQGVVCAMKEAFGFIERGDVVKEIFFHYSEFKGDLETLP
GDDVEFTIKDRNGKEVATDVRLLPQGTIVFEDISIEHFEGTVTKVIPKVP SKNQNDPLPGRIKVDVIPKELPFG
DKDTKSKVTLLLEGDHVRFNISTDRRKLERATNIEVLSNTFQFTNEAREMGVIAAMRDGFGFIKCVDRDVRMFFH
FSEILDGNQLHIADEVEFTVVPDMLSAQRNHAIKIKLPKGTVSFHSRSHRFLGTVEKEATFSNPKTTSNKGK
EKEAEDGIIAYDDCGVKLTIAFQAKDVEGSTSPQIGDKVEFSISDKQRPQQVATCVRLGRNSNSKRLLGYVAT
LKDNFGFIETANHDKEIFFHYSEFSGDVDSLELGDMVEYSLSKGKGNKVSÆKVNKTHSVNGITEADPTIYSGK
VIRPLRSVDPTQTEYQGMIEIVEEGDMKGEVYPPFGIVGMANKGDCLOKGESVKFQLCVLGQNAQTMAYNITPLRR
ATVECVKDQFGFINYEVGDSKKLFFHVKEVQDGIELQAGDEVEFSVILNQRTGKCSACNVWRVCEGPKAVAAPRP
DRLVNRLKNITLDDASAPRLMVLROPRGPDNSMGFGÆERKIRQAGVID

325/6881
FIGURE 304

GCTGAAGATGGGAGCCACTCTCAAAATCATGCTGGATAACACCTACATGAAAAAGTGTGACGAGAACATCCTGTG
GCTGGACTACAAGAACATCTGCAAGGTGATGGAAGTGGGCAGCAAGATCTACGTGGATGATGGGCTTATTTCTCT
CCAGGTAAAGCAGAAAGGTGCTGACTTCCTGGTGACGGAGGTGGAAACTGGTGGTTCCTCGGGCAGCAAGAAGGG
TGTGAACCTTCCTGGGGCTGCTGTGGACTTGCTGCTGTGTCAGAGGACATCCAGGACCTGAATTTGGGGTCGA
GCAGGATGTCGATATGGTGTTTTCGTCGTTTCATCCGCAAGGCATCTGATGTCCATGAAGTTAGGGAGGCCCTGGG
AGAGAAGGGAAAGAAAACACTCCACCCTCCACCTTCCATTTTCCCCCACTACTGCAGCACCTCCGGGCCTGTTGC
TATAGAGCCTACCTGTATATCAATAAACAACAGCTTGAAG

326/6881
FIGURE 305

MGATLKIMLDNTYMKKCDENILWLDYKNICKVMEVGSKIYVDDGLISLQVKQKGADFLVTEVETGGSSGSKKGVN
LPGAAVDLPVASEDIQDLNFGVEQDVMVFASFIRKASDVHEVREALGEKGKCTLHPPPSIFPHYCSTSGPVAIE
PTCISINNS

327/6881
FIGURE 306

AGAAGAAGCTGGCCAAGGATATGGGAGCAACCACCATGGACCAGAAAGTCTCTCTGGGCAGGTGTAGTGGTCTTGCTGCTTCTCCAGGGAGGATCTGCCTACAACTGGTTTGCTACTTTACCAACTGGTCCCAGGACCGGCAGGAACCAGGAAAATTCACCCCTGAGAATATTGACCCCTTCCTATGCTCTCATCTCATCTATTTCATTGCCCAGCATCGAAAACAACAAGGTTATCATCAAGGACAAGAGTGAAGTGATGCTCTACCAGACCATCAACAGTCTCAAAACCAAGAATCCCAAACTGAAAATTCCTTGTCCATTGGAGGGTACCTGTTTGGTTCCAAAGGGTTCCACCCTATGGTGGATTCTTCTACATCACGCTTGGAATTCATTAACCTCCATAATCCTGTTTCTGAGGAACCATAACTTTGATGGACTGGATGTAAGCTGGATCTACCCAGATCAGAAAGAAAACACTCATTTCACTGTGCTGATTCATGAGTTAGCAGAAGCCTTTCAGAAGGACTTCACAAAATCCACCAAGGAAAGGCTTCTCTTGACTGCGGGCGTATCTGCAGGGAGGCAAATGATTGATAACAGCTATCAAGTTGAGAACTGGCAAAAGATCTGGATTTTCATCAACCTCCTGTCCTTTGACTTCCATGGGTCTTGGGAAAAGCCCCCTTATCACTGGCCACAACAGCCCTCTGAGCAAGGGGTGGCAGGACAGAGGGCCAAGCTCCTACTACAATGTGGAATATGCTGTGGGGTACTGGATACATAAGGGGAATGCCATCAGAGAAGGTGGTCATGGGCATCCCCACATATGGGCACTCCTTCACACTGGCCTCTGCAGAAACCACCGTGGGGGCCCTGCCTCTGGCCCTGGAGCTGCTGGACCCATCACAGAGTCTTCAGGCTTCCTGGCCTATTATGAGATCTGCCAGTTCCTGAAAGGAGCCAAGATCACGCGCCTCCAGGATCAGCAGGTTCCCTACGCAGTCAAGGGGAACCAAGTGGGTGGGCTATGATGATGTGAAGAGTATGGAGACCAAGGTTCAAGTCTTAAAGAATTTAAACCTGGGAGGAGCCATGATCTGGTCTATTGACATGGATGACTTCACTGGCAATCCTGCAACCAGGGCCCTTACCCTCTTGCTCCAAGCAGTCAAGAGAAGCCTTGGCTCCTTGTGAAGGATTAATTACAGAGAAGCAGGCAAGATGACCTTGCTGCCTGGGGCCTGCTCTCTCCAGGAATTCTCATGTGGGATTCCCTTGCCAGGCTGGCCTTTGGATCTCTCTTCCAAGCCTTTCCTGACTTCCTCTTAGATCATAGATTGGACCTGGTTTTGTCTTCTGCAGCTGTTGACTTGTTGCCCTGAAGTACAATAAAAAAATTCATTTTGCTCCAGTA

328/6881
FIGURE 307

MDQKSLWAGVVVLLLLQGGSAYKLVCFYFTNWSQDRQEPGKFTPENIDPFLCSHLIYSFASIENNKVVIKDKSEVM
LYQTINSLKTKNPKLKILLSIGGYLFGSKGFHPMVDSSSTRLEFINSIILFLRNHNFDGLDVSWIYPDQKENTHF
TVLIHELAEAFQKDFTKSTKERLLLTAGVSAGRQ MIDNSYQVEKLAKDLDFINLLSFDFHGSWEKPLITGHNSPL
SKGWQDRGPSSYYNVEYAVGYWIIHKGMPSEKVVMGIPTYGHSFTLASAETTVGAPASGPGAAGPITESSGFLAYY
EICQFLKGAKITRLQDQQVPYAVKGNQWVGYYDDVKSMETKVQFLKLNLLGGAMIWSIDMDDFTGKSCNQGPYPLV
QAVKRSLGSL

329/6881
FIGURE 308

GGGGAGACTTGTGAGCGGCCATCTTGGTCCTGCCCTGACAGATTCTCCTATCGGGGTCACAGGGACGCTAAGATT
GCTACCTGGACTTTCGTTGACCATGCTGTCCC GGTTGGTACTTTCGCGCCGCCACAGCGGCCCCCTCTCTGAA
GAATGCAGCCTTCCTAGGTCCAGGGGTATTGCAGGCAACAAGGACCTTTCATACAGGGCAGCCACACCTTGTCCC
TGTACCACCTCTTCCTGAATACGGAGGAAAAGTTCGTTATGGACTGATCCCTGAGGAATTCTTCCAGTTTCTTTA
TCCTAAAACCTGGTGTAAACAGGACCCTATGTACTCGGAACTGGGCTTATCTTGTACGCTTTATCCAAAGAAATATA
TGTGATTAGCGCAGAGACCTTCACTGCCCTATCAGTACTAGGTGTAATGGTCTATGGAATTAAAAAATATGGTCC
CTTTGTTGCAGACTTTGCTGATAAACTCAATGAGCAAAAACCTTGCCCACTAGAAGAGGCGAAGCAGGCTTCCAT
CCAACACATCCAGAATGCAATTGATACGGAGAAGTCACAACAGGCACTGGTTTCAGAAGCGCCATTACCTTTTTGA
TGTGCAAAGGAATAACATTGCTATGGCTTTGGAAAGTTACTTACCGGGAACGACTGTATAGAGTATATAAGGAAGT
AAAGAATCGCCTGGACTATCATATATCTGTGCAGAACATGATGCGTCGAAAGGAACAAGAACACATGATAAATTG
GGTGGAGAAGCACGTGGTGCAAAGCATCTCCACACAGCAGGAAAAGGAGACAATTGCCAAGTGCATTGCGGACCT
AAAGCTGCTGGCAAAGAAGGCTCAAGCACAGCCAGTTATGTAAATGTATCTATCCCAATTGAGACAGCTAGAAAC
AGTTGACTGACTAAATGGAACTAGTCTATTTGACAAAGTCTTCTGTGTTGGTGTCTACTGAAGTTATAGTTTA
CCCTTCCTAAAAATGAAAAGTTTGTTTCATATAGTGAGAGAACGAAATCTCTATCGGCCAGTCAGATGTTTCTCA
TCCTTCTTGCTCTGCCTTTGAGTTGTTCCGTGATCACTTCTGAATAAGCAGTTTGCCTTTATAAAAACTTGCTGC
CTGACTAAAGATTAACAGGTTATAGTTTAAATTTGTAATTAATTCTACCATCTTGCAATAAAGTGACAATTGAAT
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

330/6881
FIGURE 309

MLSRVVL SAAATAAPSLKNA AFLGPGVLQATRTFHTGQPHLVPVPPLPEYGGKVR YGLIPEEFFQFLYPKTGVTG
PYVLGTGLILYALSKEIYVISAETFTALSVLGVMVYGIKKYGPFVADFADKLNEQKLAQLEEKQASIQHIQNAI
DTEKSQQALVQKRHYLFDVQRNNIAMALEVTYRERLYRVYKEVKNRLDYHISVQNMRRKEQEHMINWVEKHVQ
SISTQQEKETIAKCIADLKLLAKKAQAQPM

331/6881
FIGURE 310

GCGGGGAGCCGGCCCCGGAGCGCAGTTTCCAGTGGGGCCGGGGTTTCACCCGGGCCCTCTCTGTTTGAACCGAACC
CGACAAATGGGCGC**ATG**ACGATGGAGAGCAGGGAAATGGACTGCTATCTCCGTCGCCTCAAACAGGAGCTGATGT
CCATGAAGGAGGTGGGTGATGGCTTACAGGATCAGATGAACTGCATGATGGGTGCACTGCAAGAACTGAAGCTCC
TCCAGGTGCAGACAGCACTGGAACAGCTGGAGATCTCTGGAGGGGGTCCTGTGCCAGGCAGCCCTGAAGGTCCCA
GGACCCAGTGCGAGCACCCCTTGTTGGGAGGGTGGCAGAGGTCCTGCCAGGCCACAGTCTGTTCCCCCTCCAGTC
AACCTTCTCTTGGCAGCAGCACCAAGTTTCCATCCCATAGGAGTGTCTGTGGAAGGGATTTAGCCCCCTTGCCCA
GGACACAGCCACATCAAAGCTGTGCTCAGCAGGGGCCAGAGCGAGTGGAACCGGATGACTGGACCTCCACGTTGA
TGTCGCCGGGGCCGGAATCGACAGCCTCTGGTGTTAGGGGACAACGTTTTTGCAGACCTGGTGGGCAATTGGCTAG
ACTTGCCAGAACTGGAGAAGGGTGGGGAGAAGGGTGAGACTGGGGGGGCACGTGAACCCAAAGGAGAGAAAGGCC
AGCCCCAGGAGCTGGGCCGCAGGTTTCGCCCTGACAGCAAACATCTTTAAGAAGTTCTTGCGTAGTGTGCGGCCTG
ACCGTGACCGGCTGCTGAAGGAGAAGCCAGGCTGGGTGACACCCATGGTCCCTGAGTCCCGAACCGGCCGCTCAC
AGAAGGTCAAGAAAGCGGAGCCTTTCCAAGGGCTCTGGACATTTCCCCTTCCCAGGCACCGGGGAGCACAGGCGAG
GGGAGAATCCCCCACAAGCTGCCCCAAGGCCCTGGAGCACTCACCTCAGGATTTGATATTAACACAGCTGTTT
GGGTCT**TGA**ATCCTAGAGACAGAAAGTTGACTGAGCCTGAAAGGGCCAGGTCCCAGTGCTGGGCCCCCTGGGGAGGA
GGGAGGGTGGGCGGTATGGCTCTCGAAAGCCCAACTCCAAGTTCCTTTCCCCCAGAAAGCGGGGAGAAGCCAGAG
TTCTTGGCTCAGGACTGAAGGGAAGGTGGTTGGGAGAGGCTGTCTTGGGGGCTAGCTGGTGGAGGAGGTAAGAGT
AGCTGGAGAGTGAGCTGTGCGTGTGTGTGTGTGTGTGTCATGTGTGTGTCTGTCTGGCATGCATGCACTCACTT
TGGGGCTGGAGGTGACAGTAGGTGAGGGCAGAGGAGGAGATCAGAAAATCCCTCTGACATCTCCACTGCCCCCAA
AGACCTCCGTTGAACATTCTGTATGGAAAAGAGCCCTGGAGCATCAGGTTCCCCAGATAGGCCCCCAAATAAAGA
CCTGTCTATGGCTCTCCCAA

332/6881
FIGURE 311

MTMESREMDCYLRRLKQELMSMKEVGDGLQDQMNCMMGALQELKLLQVQTALQLEISGGGPVPGSPEGPRTQCE
HPCWEGGRGPAPRTVCSPSSQPSLGSSTKFP SHRSVCGRDLAPLPRTQPHQSCAQQGPERVEPDDWTSTILMSRGR
NRQPLVLGDNV FADLVGNWLDLPELEKGGEKGETGGAREPKGEKGQPQELGRRFALTANIFKKFLRSVRPDRDRL
LKEKPGWVTPMVPESRTGRSQVKKRSLSKGSGHFPPFGTGEHRRGENPPTSCPKALEHSPSGFDINTAVWV

333/6881

FIGURE 312A

GGCACGAGGCTGGGGCGCAGAGCAGCGCGGGAGGAGGCGGACACGTGGCAACAGCGGTAGCAGCCCGGGCGGGC
GCAGCAACAGCGGCGGGCGGCATCGGCCCCGAGCCGCGCGGCCCTCCACCCCTCCCGCCCCGCGGCAGCCCTAGC
TCCCTCCACTTGGCTCCCTGGTCCCGCTCGCTCGGCCGGGAGCTGCTCTGTGCTTTTCTCTCTGATTCTCCAGC
GACAGGACCCGGCGCCGGGCACTGAGCACCGCCACCATGGGGAAGGGGGTTGGACGTGATAAGTATGAGCCTGCA
GCTGTTTCAGAACAAAGGTGATAAAAAGGGCAAAAAGGGCAAAAAGACAGGGACATGGATGAACTGAAGAAAGAA
GTTTCTATGGATGATCATAAACTTAGCCTTGATGAACTTCATCGTAAATATGGAACAGACTTGAGCCGGGGGATTA
ACATCTGCTCGTGCAGCTGAGATCCTGGCGCGAGATGGTCCCAACGCCCTCACTCCCCCTCCCACTACTCCTGAA
TGGATCAAGTTTTGTGCGGCAGCTCTTTGGGGGGTTCTCAATGTTACTGTGGATTGGAGCGATTCTTTGTTTCTTG
GCTTATAGCATCCAAGCTGCTACAGAAGAGGAACCTCAAACGATAATCTGTACCTGGGTGTGGTGCTATCAGCC
GTTGTAATCATAACTGGTTGCTTCTCTACTATCAAGAAGCTAAAAGTTCAAAGATCATGGAATCCTTCAAAAAC
ATGGTCCCTCAGCAAGCCCTTGTGATTGCAAAATGGTGAGAAAATGAGCATAAATGCGGAGGAAGTTGTGGTTGGG
GATCTGGTGGAAGTAAAAGGAGGAGACCGAATTCCTGCTGACCTCAGAATCATATCTGCAAAATGGCTGCAAGGTG
GATAACTCCTCGCTCACTGGTGAATCAGAACCCAGACTAGGTCTCCAGATTTACAAAATGAAAACCCCTGGAG
ACGAGGAACATTGCCTTCTTTTCAACCAATTGTGTTGAAGGCACCGCACGTGGTATTGTTGTCTACACTGGGGAT
CGCACTGTGATGGGAAGAATTGCCACACTTGCTTCTGGGCTGGAAGGAGGCCAGACCCCATTGCTGCAGAAATT
GAACATTTTATCCACATCATCACGGGTGTGGCTGTGTTCTGGGTGTGTCTTTCTTCATCCTTTCTCTCATCCTT
GAGTACACCTGGCTTGAGGCTGTCACTCTCCTCATCGGTATCATCGTAGCCAATGTGCCGGAAGGTTTGCTGGCC
ACTGTCACGGTCTGTCTGACACTTACTGCCAAACGCATGGCAAGGAAAACTGCTTAGTGAAGAACTTAGAAGCT
GTGGAGACCTTGGGGTCCACATCCACCATCTGCTCTGATAAACTGGAACCTCTGACTCAGAACCGGATGACAGTG
GCCCACATGTGGTTTGACAATCAAATCCATGAAGCTGATACGACAGAGAATCAGAGTGGTGTCTCTTTTGACAAG
ACTTCAGCTACCTGGCTTGCTCTGTCCAGAATTGCAGGTCTTTGTAACAGGGCAGTGTTCAGGCTAACCAGGAA
AACCTACCTATTCTTAAGCGGGCAGTTGCAGGAGATGCCTCTGAGTCAGCACTCTTAAAGTGCATAGAGCTGTGC
TGTGGTTCCGTGAAGGAGATGAGAGAAAGATACGCCAAAATCGTCGAGATACCCTTCAACTCCACCAACAAGTAC
CAGTTGTCTATTTCATAAGAACCCCAACACATCAGAGCCCCAACACCTGTTGGTGATGAAGGGCGCCCCAGAAAGG
ATCCTAGACCGTTGCAGCTCTATCCTCCTCCACGGCAAGGAGCAGCCCTGGATGAGGAGCTGAAAGACGCCTTT
CAGAACGCCTATTTGGAGCTGGGGGGCCTCGGAGAACGAGTCCTAGGTTTCTGCCACCTCTTTCTGCCAGATGAA
CAGTTTCTGAAGGGTTCCAGTTTGACACTGACGATGTGAATTTCCCTATCGATAATCTGTGCTTTGTTGGGCTC
ATCTCCATGATTGACCTCCACGGGCGGCGCTTCTGATGCCGTGGGCAAATGTGCAAGTGCTGGAATTAAGGTC
ATCATGGTCACAGGAGACCATCCAATCAGCTAAAGCTATTGCCAAAGGTGTGGGCATCATCTCAGAAGGCAAT
GAGACCGTGGAAGACATTGCTGCCCCGCTCAACATCCCAGTCAGCCAGGTGAACCCAGGGATGCCAAGGCCTGC
GTAGTACACGGCAGTGATCTAAAGGACATGACCTCCGAGCAGCTGGATGACATTTTGAAGTACCACACTGAGATA
GTGTTTGCCAGGACCTCCCTCAGCAGAAGCTCATCATTGTGGAAGGCTGCCAAGACAGGGTGCTATCGTGGCT
GTGACTGGTGACGGTGTGAATGACTCTCCAGCTTTGAAGAAAGCAGACATTGGGGTTGCTATGGGGATTGCTGGC
TCAGATGTGTCCAAGCAAGCTGCTGACATGATTCTTCTGGATGACAACTTTGCCTCAATTGTGACTGGAGTAGAG
GAAGGTGCTCTGATCTTTGATAACTTGAAGAAATCCATTGCTTATACCTTAACCAGTAACATTCCCGAGATCACC
CCGTTCTTGATATTTATTATTGCAAACATTCCACTACCCTGGGGACTGTCACCATCCTCTGCATTGACTTGGGC
ACTGACATGGTTTCTGCCATCTCCCTGGCTTATGAGCAGGCTGAGAGTGACATCATGAAGAGACAGCCCAGAAAT
CCCAAACAGACAAACTTGTGAATGAGCGGCTGATCAGCATGGCCTATGGGCAGATTGGAATGATCCAGGCCCTG
GGAGGCTTCTTTACTTACTTTGTGATTCTGGCTGAGAACGGCTTCTCCCAATTCACCTGTTGGGCCCTCCGAGTG
GACTGGGATGACCGCTGGATCAACGATGTGGAAGACAGCTACGGGCAGCAGTGACCTATGAGCAGAGGAAAATC
GTGGAGTTCACCTGCCACACAGCCTTCTTCGTGAGTATCGTGGTGGTGCAGTGGGCCGACTTGGTCTATCTGTAAG
ACCAGGAGGAATTCGGTCTTCCAGCAGGGGATGAAGAACAAGATCTTGATATTTGGCCTCTTTGAAGAGACAGCC
CTGGCTGCTTTCTTTCTTCTACTGCCCTGGAATGGGTGTTGCTCTTAGGATGTATCCCTCAAACCTACCTGGTGG
TTCTGTGCCTTCCCTACTCTCTTCTCATCTTCGTATATGACGAAGTCAGAAAACCTCATCATCAGCGCAGCCCT
GGCGGCTGGGTGGAGAAGGAAACCTACTATTAGCCCCCGTCTGCACGCCGTGGAGCATCAGGCCACACACTCT
GCATCCGACACCCACCCCTCTTTGTGTACTTCAGTCTTGAGTTTGGAACTCTACCCTGGTAGGAAAGCACCGC
AGCATGTGGGGAAGCAAGACGTCTGGAATGAAGCATGTAGCTCTATGGGGGAGGGGGAGGGCTGCCTGAAAA
CCATCCATCTGTGGAATGACAGCGGGGAAGGTTTTTATGTGCCTTTTTGTTTTTGTAAAAAGGAACACCCGGA

334/6881
FIGURE 312B

AAGACTGAAAGAATACATTTTATATCTGGATTTTACAAATAAAGATGGCTATTATAATGGAAAAAAAAAAAAA
AAAAA

335/6881
FIGURE 313

MGKGVGRDKYEPAAVSEQGDKKGGKKGKDRDMDELKKEVSMDDHKLSLDELHRKYGTDL SRGLTSARAAEILARD
GPNALTPTPTTPEWIKFCRQLFGGFSMLLWIGAILCFLAYS IQAATEEEEPQNDNLYLGVVLSAVVIITGCF SY YQ
EAKSSKIMESFKNMVPPQALVIRNGEKMSINAEVVVVDLVEVKGGDRIPADLR IISANGCKVDNSSITGESE PQ
TRSPDFTNENPLETRNIAFFSTNCVEGTARGIVVYTGDR T VMGRIATLASGLEGGQTP IAAEIEHFIHIITGVAV
FLGVSFFILSLILEYTWLEAVIFLIGIIVANVPEGLLATVTVCLTLTAKR MARKNCLVKNLEAVETLGSTSTICS
DKTGTLTQNRMTVAHMFWDNQIHEADTTENQSGVSFDKTSATWLALSRIAGLCNRAVFQANQENLPILKRAVAGD
ASESALLKCIELCCGSVKEMRERYAKIVEIPFNSTNKYQLSIHKNPNTSEPQHLLVMKGAPERILDRCSSILLHG
KEQPLDEELKDAFQONAYLELGGLGERVLGFCHLFLPDEQFPEGFQFDTDDVNFPIDNLCFVGLISMIDPPRAAVP
DAVGKCRSAGIKVIMVTGDHPITAKAIAKGVGIISEGNETVEDIAARLNIPVSQVNPRDAKACVVHGS DLKDMTS
EQLDDILKYHTEIVFARTSPQKLIIVEGCQRQGAIVAVTGDGVNDSPALKKADIGVAMGIAGSDVSKQAADMIL
LDDNFASIVTGVEEGR LIFDNLKKSIA YTLTSNIPEITPFLIFIIANIPLPLGTVTILCIDLG TDMVPAISLAYE
QAESDIMKRQPRNPKTDKLVNERLISMAYGQIGMIQALGGFFTYFVILAENGFLPIHLLGLRVDWDDR WINDVED
SYGQQWTYEQRKIVEFTCHTAFFVSIVVVQWADLVICKTRRNSVFQQGMKNKILIFGLFEETALAAFLSYCPGMG
VALRMYPLKPTWWFCAFPYSL LIFVYDEV RKLIIRRRPGGWVEKETYY

336/6881
FIGURE 314A

TTCCAAAACGTGTTCTCTGGAGCTATAAGTGGATTGCCAGAAATGAGAGATTAGGAGCTGGGAGAAGAGGAAGCGC
CTTGTGTTGTGTCTCCTGGAGGCTGCCGACATGAAGTGCTTTTTCCCGGTGCTGAGCTGTCTGGCTGTGCTGGGT
GTGGTGTCTAGCACAGCGGCAGGTCACCGTTCAGGAAGGACCCCTGTACCGCACGGAGGGCTCCACATCACTATC
TGGTGCAATGTGAGTGGCTACCAGGGACCTTCTGAGCAGAATTTCCAGTGGTCCATTTACCTGCCTTCGTGCGCA
GAGCGAGAGGTGCAGATCGTCAGCACCATGGACTCTTCCTTCCCCTATGCCATCTACACCCAGCGCGTCCGCGGA
GGGAAGATCTTCATAGAAAGAGTCCAGGGGAACTCAACCCTATTGCACATCACAGATCTTCAGGCCCCGGGATGCC
GGGAGTATGAATGCCACACACCCAGCACTGATAAGCAATACTTTGGGAGTTACAGTGCAAAGATGAACCTAGTG
GTGATCCCAGACTCCCTGCAGACCACTGCCATGCCCCAGACTCTGCACAGAGTGGAGCAGGACCCGCTGGAGCTC
ACTTGTGAGGTGGCTCAGAGACCATTAGCACAGCCACCTGTCTGTGGCTGGCTCCGGCAGAAAGTTGGCGAG
AAGCCCGTGGAGGTCACTCTCCCTGAGCCGAGATTTTCATGCTTCACTCCAGCAGCGAATATGCCAGAGGCAGAGC
CTGGGGGAGGTGCGGCTGGACAAGCTGGGGAGGACCACCTTCCGCTCACCATCTTCCACCTGCAGCCTTCTGAC
CAGGGCGAATTCTACTGCGAGGCCGCCGAGTGGATCCAGGATCCGGATGGGTGCTGGTATGCTATGACCCGAAAG
CGTTCCGAGGGAGCCGTGGTCAACGTCCAGCCAAGTACAAAGAATTCAGTGTTCGGCTGGAGACAGAGAAGCGG
CTGCACACGGTGGGCGAGCCGGTGGAGTTCAGATGCATCCTGGAGGCTCAGAATGTTCCCGACCGTTACTTTGCT
GTCTCCTGGGCCTTCAACAGCTCGCTCATCGCCACCATGGGTCTAACGCTGTGCCTGTCTCAACAGCGAATTT
GCTCACCGGGAAGCCAGGGGACAGCTTAAGGTGGCCAAAGAGAGCGACAGTGTCTTTGTGCTGAAGATCTACCAC
CTCCGCCAGGAAGATAGCGGGAAATACAAGTCCCGGGTGAAGTGCAGAGAGAAAACCGTGACCGGGGAATTCATT
GATAAGGAGAGCAAGCGTCCCAAGAATCATCCCATCATAGTCTCTCCCTCAAGAGCAGCATCTCCGTGGAGGTG
GCCAGCAATGCCAGCGTCATCCTTGAGGGCGAGGACCTGCGCTTCTCCTGCAGTGTCCGCACGGCAGGCAGGCCG
CAGGGTTCGCTTCTCTGTCTCATCTGGCAGCTTGTGGACAGGCAGAACCGCCGAGCAATATCATGTGGCTAGACCGG
GATGGCACCGTGCAGCCAGGCTCGTCTACTGGGAGCGCAGCAGCTTTGGGGGCGTCCAGATGGAGCAGGTGCAG
CCCAACTCGTTAGCCTGGGCATCTTCAACAGCAGGAAGGAGGACGAGGGCCAGTATGAATGCCATGTGACTGAA
TGGGTGCGGGCAGTGGATGGCGAGTGGCAGATTGTTGGGGAGCGCCGGGCCAGCACTCCCATCTCCATCACAGCT
CTTGAAATGGGCTTCGCAGTCACAGCCATCTCCCGGACACCGGGGTGACCTACAGCGACTCCTTTGACTTGCAG
TGTATCATCAAACCCCACTACCTGCTGGGTCCCGTGTGCGGTGACATGGCGGTTCCAGCCGGTGGGCACGGTG
GAGTTCATGACTTTGGTGACCTTCACCCGGGACGAGGGGTCCAGTGGGGGGACAGGTCTCCAGCTTCCGAACC
CGAACTGCCATCGAGAAGGCTGAGTCCAGCAACAACGTCCGCCTAAGCATCAGCCGAGCCAGTGACACGGAAGCA
GGCAAGTACCAGTGTGTGGCAGAGCTGTGGCGGAAGAACTACAACAACACCTGGACGCGACTGGCGGAGAGGACC
TCCAACCTGCTGGAGATCAGGGTGTGTCAGCCAGTGACAAAGCTGCAGGTGAGCAAATCGAAGAGGACCCTCACC
CTGGTGGAAAACAAGCCATTGAGTTGAACTGCTCAGTCAAGTCTCAGACTAGCCAGAACTCCCACTTTGCGGTG
CTCTGGTATGTCCACAAGCCCTCGGATGCCGATGGCAAGCTTATCCTGAAGACCACCCACAACCTCCGCTTTGAA
TACGGTACTTACGCCGAGGAGGAGGGCCTGAGAGCCAGGCTCCAGTTTGAGAGGCATGTGTGCGGGGGCCTGTTC
AGCCTCACCGTCCAGAGAGCCGAGGTGACGACAGCGGCAGCTACTACTGCCACGTGGAGGAGTGGCTGCTGAGC
CCCAACTACGCCTGGTACAAGCTGGCAGAGGAGGTTTCTGGGCGCACAGAAGTCACTGTGAAACAGCCAGACAGC
CGCCTGAGGCTCAGCCAAGCCAGGGGAACCTGTGCGTTCTGGAGACCCGGCAGGTACAGCTGGAGTGTGTGGTT
CTCAACCGCACCCAGCATAACCTCCCAGCTCATGGTGGAAATGGTTTGTATGGAAGCCCAACCACCTGAGCGGGAG
ACTGTGGCCCGCTTGAGCCGTGACGCCACCTTCCACTATGGAGAGCAGGCAGCCAAGAACAATCTGAAGGGGCGG
CTGCATTTGGAGAGTCTTCCCCCGCGTGTACCGTCTCTTCATCCAGAACGTGGCTGTGTCAGGACAGCGGGACC
TACAGCTGCCATGTGGAGGAGTGGCTGCCAGCCCCAGTGGCATGTGGTATAAGCGGGCAGAGGACACCGCTGGG
CAGACAGCTCTGACAGTCATGCGACCAGATGCTTCCCTGCAGGTGGACACAGTGGTCCCCAATGCCACGGTCTCT
GAGAAGGCAGCTTTCCAGCTGGACTGTAGCATCGTGTCCGCTCCAGCCAGGACTCCCGCTTCGCTGTGGCCTGG
TATTCCTGAGGACTAAAGCTGGGGGGAAAAGGAGCAGCCCTGGCCTGGAAGAACAGGAAGAGGAAAGGGAGGAG
GAGGAGGAGGAGGACGACGACGACGACGACGACCCCAACAGAGCGGACGGCCCTGCTGAGCGTGGGCCCAGATGCT
GTCTTTGGCCCAGAGGGCAGTCTTGGGAGGGCAGGCTTCGCTTCCAGAGGCTCTCCCCGGTGTCTACCGGCTC
ACAGTGTGTCAGGCAAGCCCCCAAGATACAGGCAATTACTCCTGCCATGTGGAGGAGTGGCTGCCAGCCCTCAG
AAGGAATGGTACCGGCTGACGGAGGAGGAGTACGCCCCATCGGCATCCGTGTTCTAGATACAAGTCCCACCCCTC
CAGTCCATCATCTGCTCCAACGACGCACTCTTCTACTTCGTCTTCTTCTACCCCTTTCCCCATCTTTGGCATTCTT
ATCATCACCATCCTTCTGGTGCCTTTCAAGAGCCGGAACCTCCAGCAAGAACTCTGATGGGAAGAATGGGGTGCCT

337/6881
FIGURE 314B

CTGCTGTGGATCAAAGAGCCACACCTCAACTACTCCCCTACTTGCCTGGAGCCCCCTGTTCTCAGTATCCATCCA
GGGGCCATAGACTAAGCGGGTGATGCCCCAGCGGATGTTGGCCACGGAGGAGCTGAGGCTCTCCCTTTCTCTGTG
ATTGGACAGTTGACAGCACCCAACTCTGGGGTGTCATGTGTGTGGAAAGTTGTCAGACTTGAAAAGTTGCCAAG
TTCCCAGTCAGTCACAGAGACAGACTGCCTCTCGGTGGCAGTCTTGTTGGTTAGCTATTTGCGCGCAAATGTTG
TGATCCTGCCATTATAGATTTCTTGTTTCTGTTTTTAGTAATGTAGTGAGTAGCTCCAGGTGCCACATCTACTCA
CAGATTTATCTAGTATTCTCAGATAGATGTTACAGGGCTTCTTATTCTTTGTAATGTACTCTTTTTAAATCCCTT
TAGTTTACCCTTTTTTGATTCCCTTAATGTGGACGAATTTCTCTTACGTACAACTGACAGCAAAAGGAAGGGCGAA
CTTTCTAGTGACAAGGAATCTCTTCCAAGACTTTGTTTTTGCACATTTGAAAATGCCACCCATGGATCAAAATAT
ACCCAAACGTTTTTTACTTTCTTAACAAGACTTAAGAATTGTGTGTAGTGTGGGCAAAATTTGTATGTTGTCTTT
TCCCTCAGCTGGAGTTATTGGAACCACTTTGTAGTCAAGACGAAAGCACTGAATTTTGCTTCAAAGAAGTGTGTA
TGTACAAGAGAAATCCTGCATAACCCATTAGGAGTAGATGGTGCCCGGCCTATCTGTACAGGGAGGCAAAAAGG
CTTCATCCCATCCTTGCCAAAAATAAGAAAAGTGTCTTGAGAAATGGGTGAGAAGCCCCAAACGGGCACACACTT
TCCAAATTAAAGTGGGCAGGGGCTGCTTTTAGCAGCTGCTGACCTGCAGATTTGTCAAAGCCAGTGACTAGAGAA
GGAAGGGAGAAAGGCTGGCTGTTGGCTTGCTCTGAGCTGCAAGGATGGTCTCTAACTGATTAAGTGTGAGCAGGT
GGGCTGTGCTTCAGGTGCTTTGCCAACTCTTAAAGAAAGTGTCCAGTGAAGTTGGAAGTGGGCCCCCTGAGC
TGAGCACAGGGCCAAAGCAGCCATGGCAGACACCTGACGGAGGGCACGGGGCTGGCTGACACTAAGTTTGGTGGG
ACAGTGAGGGGTGGGAGGGGGGTTTCCAGGGCCTGGTGTTGGAGAGTGCAGAGAAATATCTACCTCCCTGGAGGT
GTGAAGACTAGGTTTTTCTTCTTCCCTTCCAATTAGATTTTCTTAAATTATAGTGATGTCTTCTTATTCATTTTT
CTCTCCCTGCCCTCTCAGTGCATAAGAATATCAGCCTGGGGGCAGTCCAGACGCAGCCCTTTGTATCCTTTCTG
TTTGCCCTAGTCTCAGCAGACTGTGATCACAAGGCATTGTCTGTGGGATTTTTTCTTTCCCTTTCTTGATCTCTCT
TGTGGTTCTAGGTTGTTTGGTTGTTTATTGTTATGGTGGCTTTTTTATTTTAAACGCCCTTGAGCCCCATGATGGC
TGGTGTACACCTGTTCTTTTACACTGTTGGGCCAGGTGCTGCTTGTCTTCTTAGGGCATCATCAATTGCAAATA
TTTTCTTTTGTCTCCCTTTATGAAGATGTTCTTATACCTTGCTTTCCCATATTTTTCTGECGAAGCATGCCATCT
CCTTTACTCTGGGAAGTTACATCCTGAATCCCAAGAGGGGGTGCAGTTTGGAAAAAGTCATCAGGGATTCTGGA
ACTAAGTCTGATAAAAGATTCCAGTGAAGCCCTGTTCTGAGAACGAGCAGACTGCAGGGGAGGCCATGGGATTCC
CCAGGCCAGTGCTGTGCTGATCCTTCAAGGGTCTGCAGGTATGCAGGTGGCCTGGGCTGCTCGGCAGATACTTT
GCTGATTCCCAGCTGAGGGGAGCATGGTGGCGATTGCTCAGCCATTTTCTGACAGACACACAGACCTGCCTTTTC
TCCCCCAAGTATACCGTACCCTCCTGTGAGACAGTGTGTGCAGGCACCACCCTTAATCCTGCTGTGCTGCTGAC
ATGCTGATTCTCATTTATTATGCTGCATCAACACATTAGAGGTACAGGAGCGGCTCAGTCATGAAAAAGAAGGT
CTTTTGCCCCATTTCTTTATTTTCAAGATGTGGGCTTTTCTAGTGGGAATTTGCTGACTCCTACTTTATAGGCTGAG
TCAATGAGGGAAGATGACTGGCGTTTCTCTGTCTAAATGGGAGGTTGCCAGAGCGCTGGCTGGGACTAGGATGT
GTAATAAGATTTTCAAGTTTGAATCTTAGATTTTCAAGTTTCAAGGCGATAAAGAAGTAGGTGCTGCACACAAATATG
TAAAGCAATTGTAGGAAATTTGAAAGGAAAAAAGAAACCGAAGCCAGTATTTTAAATAATTGCTTTTTTCTGTGTA
TTTTGTATTGGGCTGGGGGATAGCATCAAAGGTTGAAGTTTTTGTAGCTTTCTATGAAAAACCCAGGACCTTCTT
TCTTTGGCCATTTCTATGGAAATGCGATGTGAGATGGATGGTAATGGTGGCCTCCAGTGGCTGTGAGACCTCATT
GCGCATTGTCTACTGGAGCTTTAGTCTTCTGAGACGGAGGAAAACTGCTGAATACTCTGGATTTCATCTATGTCTA
CAATGTTGCATTTATGAAAACTACACTGTGCTAGGCGCATTCTAGGACATGAATATGACCACACCCCTCTTTCAC
CGGGTGTCTTCTGTAGCAAGTTTTTCTATTTCTTTTCAAACAATGGTTTCTCTGCGTTAATTATTGAGGAAAAA
AGATGGGGTAAGAAAACTACCCATGCATGATGTAGAGAGCTGTTGATTGTTTTCTGTTTTTTTAAAGGAAAACTA
TTTGTAAGATGTTGCACTAAAACATTTTATATACACTTCAGAGACCTGTAGTAAATTATGTTGAAAT

338/6881
FIGURE 315A

GCTCTTTGCCGAGGGCGTGTGGTGAGAGTCCCCACAGCGACCCCTGGTTTCGAGTGGTGGGCACTGAGCTGGTCATC
CCCTGCAACGTCAGTGA CTATGATGGCCCCAGCGAGCAAACTTTGACTGGAGCTTCTCATCTTTGGGGAGCAGC
TTTGTGGAGCTTGCAAGCACCTGGGAGGTGGGGTTCCCAGCCCAGCTGTACCAGGAGCGGCTGCAGAGGGGCGAG
ATCCTGTTAAGGCGGACTGCCAACGACGCCGTGGAGCTCCACATAAAGAACGTCCAGCCTTCAGACCAAGGCCAC
TACAAATGTTCAACCCCCAGCACAGATGCCACTGTCCAGGGAAA CTATGAGGACACAGTGCAGGTTAAAGTGCTG
GCCGACTCCCTGCACGTGGGCCCCAGCGCGCGGCCCCCGCCGAGCCTGAGCCTGCGGGAGGGGGAGCCCTTCGAG
CTGCGCTGCACCGCCGCTCCGCTCGCCGCTGCACACGCACCTGGCGCTGCTGTGGGAGGTGCACCGCGGGCCCG
GCCAGGCGGAGCGTCCCTCGCCCTGACCCACGAGGGCAGGTTCCACCCGGGCTGGGGTACGAGCAGCGCTACCAC
AGTGGGGACGTGCGCCTCGACACCGTGGGCAGCGACGCCTACCGCCTCTCAGTGTCCCGGGCTCTGTCTGCCGAC
CAGGGCTCCTACAGGTGTATCGTCAGCGAGTGGATCGCCGAGCAGGGCAACTGGCAGGAAATCCAAGAAAAGGCC
GTGGAAGTTGCCACCGTGGTGATCCAGCCATCAGTTCTGCGAGCAGCTGTGCCCAAGAATGTGTCTGTGGCTGAA
GGAAAGGAAGTGGACCTGACCTGTAACATCACAACAGACCGAGCCGATGACGTCCGGCCCCGAGGTGACGTGGTCC
TTCAGCAGGATGCTGACAGCACCTACCTGGCTCCCGCGTGTGTGGCGCGGCTTGACCGTGATTCCCTGGTGCAC
AGCTCGCCTCATGTTGCTTTGAGTCATGTGGATGCACGCTCCTACCATTTACTGGTTCGGGATGTTAGCAAAGAA
AACTCTGGCTACTATTACTGCCACGTGTCCCTGTGGGCACCCGACACAACAGGAGCTGGCACAAAGTGGCAGAG
GCCGIGTCTTCCCCAGCTGGTGTGGGTGTGACCTGGCTAGAACCACTACCAGGTGTACCTGAATGCTTCCAAG
GTCCCCGGGTTTGCGGATGACCCACAGAGCTGGCATGCCGGGTGGTGGACACGAAGAGTGGGGAGGCGAATGTC
CGATTACGGTTTCGTGGTACTACAGGATGAACCGGCGCAGCGACAATGTGGTGACCAGCGAGCTGCTTGCAGTC
ATGGACGGGGACTGGACGCTAAAATATGGAGAGAGGAGCAAGCAGCGGGCCAGGATGGAGACTTTATTTTTTCT
AAGGAACATACAGACACGTTCAATTTCCGGATCCAAAGGACTACAGAGGAAGACAGAGGCAATTATTACTGTGT
GTGTCTGCCTGGACCAAACAGCGGAACAACAGCTGGGTGAAAAGCAAGGATGTCTTCTCCAAGCCTGTTAACATA
TTTTGGGCATTAGAAGATTCCGTGCTTGTGGTGAAGGCGAGGCAGCCAAAGCCTTTCTTTGCTGCCGGAATAACA
TTTGAGATGACTTGCAAAGTATCTTCCAAGAATATTAAGTCGCCACGCTACTCTGTTCTCATCATGGCTGAGAAG
CCTGTGCGGACCTCTCCAGTCCCAATGAAACGAAGTACATCATCTCTCTGGACCAGGATTCTGTGGTGAAGCTG
GAGAATTGGACAGATGCATCACGGGTGGATGGCGTTGTTTTAGAAAAAGTGCAGGAGGATGAGTTCCGCTATCGA
ATGTACCAGACTCAGGTCTCAGACGCAGGGCTGTACCGCTGCATGGTGACAGCCTGGTCTCCTGTGAGGGGCAGC
CTTTGGCGAGAAGCAGCAACCAGTCTCTCCAATCCTATTGAGATAGACTTCCAACCTCAGGTCTATATTTAAT
GCTTCTGTGCATTACAGACACACCATCAGTAATTCGGGGAGATCTGATCAAATTGTTCTGTATCATCACTGTGCGAG
GGAGCAGCACTGGATCCAGATGACATGGCCTTTGATGTGTCTCTGGTTTGGCGGTGCACTCTTTTGGCCTGGACAAG
GCTCCTGTGCTCCTGTCTTCCCTGGATCGGAAGGGCATCGTGACCACCTCCCGGAGGGACTGGAAGAGCGACCTC
AGCCTGGAGCGCGTGAGTGTGCTGGAATTCTTGCTGCAAGTGCATGGCTCCGAGGACCAGGACTTTGGCAACTAC
TACTGTTCCGTGACTCCATGGGTGAAGTCACCAACAGGTTCTTGGCAGAAGGAGGCAGAGATCCACTCCAAGCCC
GTTTTTATAACTGTGAAGATGGATGTGCTGAACGCCTTCAAGTATCCCTTGCTGATCGGCGTCGGTCTGTCCACG
GTCATCGGGCTCCTGTCTCTCATCGGGTACTGCAGCTCCCACTGGTGTGTAAGAAGGAGGTTTCAAGAGACA
CGGCGGAGCGCGCAGGCTCATGTCGATGGAGATGGACTAGGCTGGCCCCGGGAGGGGAGTGACAGAGGGACGTT
CTAGGAGCAATTGGGGCAAGAAGAGGACAGTGATATTTTAAAACAAAGTGTGTTACACTAAAACAGTCCTCTC
TAATCTCAGGTGGGACTTGGCGCTCTCTCTTTTCTGCATGTCAAGTTCTGAGCGCGGACATGTTTACCAGCACAC
GGCTCTTCTTCCCACGGCACTTCTGTATGTAACAATCAGTGTGTGTTTTCCCAACTGCAGCTTTTAAATGGTTA
ACCTTCATCTAATTTTTTTTCTCCCACTGGTTTATAGATCCTCTGACTGTGTGTGTTTATAGCTTTTGTTCGC
GGGTTGTGGTGAGGAAGGGGTGATGGCATGCGGAGTTCTTTATCTTCAGTGAGAATGTGCCTGCCCGCCTGAGA
GCCAGCTTCCGCGTTGGAGGCACGTGTTAGAGAGCTGCTGAGCGCCACCCTCTACCCGGCTGACAGACAACACA
GACCTGTGCCGAAGGCTAATTTGTGGCTTTTACGACCCTACCCCAACCCCTGTTTTTCAAGGGTTTAGACTACATT
TGAAATCCAACTTGAGTATATACTTCTTATTGAGCCCACTGCTTTTTTTTTTTTTTTTTTGTCTCTCTGC
CCCTTTTCCATTTCTTTTGTATTTGTTTTCTGTGAGAGCACTGAAATGGCAGCCCTGGAATCTACAATTTGGCTC
TCCACTGAGCACCTTATCTTGCCACCTTAGCCTTAAGAATGAATATGAAGAAAAATACACAGCCACCTCTGTCCA
GGGCAGTAAGAAGGGCTGCAAGGAAGGGGAGGATGGGGACAAGGAAAGGATCAGATACCTGCTCCAGTAGTTGTG
AGGCCACTGTGTCTCAGGGGACTCCAGGAGGAGCAGAAGAGGGATCCACGAAGTTATTCTTACGCAGCTGGGGC
CAGGAGGGTCAGAGTGGTGCCAGGTGCAAGTTAGGCTAAGAAGCCACCCTATTCTCTCTTGGCCATTGTG

339/6881
FIGURE 315B

GGGGGCAAAGGCATTGGTCCACCAAGAGTCTTGCAAGGGGGACCCACAGATATGCCATGTCCTTCACACGTGCTTGG
GCTCCTTAACCTGAAGGCAAATTGCTACTTGCAAGACTGACTGACTTCAAGGAATCAGAAATTACCTAGAAGCAC
CATGTTTTTCTATGACCTTTTCAGTCCTTCAGGTCATTTTAAAGGTCCACTGCAGGGGGTTAGTGAGAAAGGGTA
TACTTTGTGGTATGTTTTGCTTTTCTAATAGGGACATGAAGGAAACCCAGCAATTTGCTGTTATGTGAATGGCCT
GTAGAGCAGAGTCAAGAGCGGTGTGCTTTGCCCCGACTGCTCCCATCAGGAATAGGAGAGTAGACAGAGATCTTCC
ACATCCCAGGCTTCTGCTGCTGCTTTAAAGCTCTGTCTTGGAGCCTCCCGCTCCCTGAAGTGTCTCGCCCCCT
GCACAGCACTGGCCTTTTCGGAAGCATCCAGTAGGGTTTTCTGAGGCTCGCTGGTGACTCATGCCCTAATTGCAA
TCCTCTGCTTTTATCTTGACTTTGAAGGATCTAACACTGCTCTCTCTTCCAAAGGGGAAAAAAGATTCAATTTGT
TTTGAGCAATAAACTAATAACAAATGATGGCCATTCAATGTGCAGCTCTTTGTACCATGGGCCGGATGAGTTGTG
CTCCTCCTGGCTCACCATTTCCCCCTGCTCCCCACAGCCGGTTCTGCACCTATCACCGAGTCGCCCCCTGGAAGC
AGATTCCCATTGAGTTTTCCCCACCAAGGGGACCATGCACATGGTAGAAACATTAGATTCTGCATTGACAGTAGC
CTTTCCTTGGCCCCGGCCCTGTGGTGGGAAGACGGGCAACAAGTATACCCACCAGGGCCTGAGTGACTAGAGGAA
GAGGACGAGGCCTTGTGGCACTAGATTTGGGTATTTTCTGCATGTCATAACATATCCTAACTGCTATTTTCAGAA
GAGGCAGCTTGTAGGTGATTGTACAAGTGAGAAATTAAGAGAGAAACAGATATTTAAACAGGTGCTGTATTAGTAA
CAGCCAGTGCCCTTTCAGCCCTTGCACTCTATTAAGAGGAGATTGAGGATTTTATTGGCACAGGCCCTTCTTAGTA
GGAAGAAAGGGTGCTTAGCTTTGGACCTGACCGGGTGTGTGTAAGACCATGGACTGAGTCACAGCAGACACTCGA
TGGTGGTAAATGTGATGGGTGCTTACACACTGTACCTTTTCTTTTCATACTGATGCTGCAGTTCAGGGCTGGAGT
TGTTAAGGCATTGACCTCCACCCACCTGCCCCATGTCCACTGGGCTGCCCAAGCTGCATGTCACCTGAGGGCTGG
CAGGAAGGGGCGAGAAATCCAGGGCATTGTACCAAGGACCTAGTTTCTTCTAGGGATATAAAATTTCCAGGAATG
TGTATTTTTAATGTGGTGAGATGCACTCTTTTGTGTACCAATAGGGCTCCCCACCCACCCCTGCGACAAGTG
CTCTTCTAGAACAGGTTTCTTACCAGCAGCACTGGTGTGAATGAAAGAGAGACCCAGCCGCTCTCACACAGGTGG
AATTGCACTTCTTAACAAAAGGAACCTTTATAAAAGTTTGGGATTTTTTTTCTTAATCATAAAAAATAGCCCCAGA
AAGAGCCTAAGCTATGTTTCAGATAGAAGCCTCGAAATTCCTGTAAATTGTTTACTTTATGATGTTTACATACAG
TTTCACTTTGAAAAAAATGCAAAATCGACTTTTAACTGTTGAGATGTTTCATGGGACAGTAGAACTCTGAC
TCACCAACTGGGCTAAATTTTAATTTAAAAATGTATTTATTTGAGTGTCTTTCCCCCCCCCACCCTCACCATCTG
AGGGGCTCCCTGAGATCTTGGTAGAGGAGGCCCTCCTGCCAGACCTTCGTTTGTTCCTCCGTTGGCCCTTGCT
TCTTGCTTTGCAGACTGCCTGCAGCCATGATTTTGTCACTGACATCTGTGAGCCAAAGACTGAGCCTTTTTGGCA
GGAATAATAAGCAATACTACACAACTTGCTACTTTTCAGAAAACCTTTTTTTTAGCTTCACCGATGACAACAGAGGA
AGAAGGGAAGTGGGATTTGGGTAAGTTCTCCTCCACTGTTTGACCAAATTCCTCAGTGATAAATATGTGTGCAGAT
CCCTAGAAGAGAAAACGCTGACTTTCTTTTAAAGTGTGGCACATAAGGATCTGCAGAATTTTCCGTAGACAAAGA
AAGGATCTTGTGTATTTTTGTCCATATCCAATGTTATATGAACATAATTGTATTGTTTTTACTGTGACCACAAAT
ATTATGCAATGCACCATTGTTTTTTTATTTTATTAAAGGAAGTTTAATTT

340/6881
FIGURE 316

MPDSTLPGSRVLARLDRDSLHSSPHVALSHVDARSYHLLVRDVSKENSGYYYCHVSLWAPGHNRSWHKVAEAVS
SPAGVGVTWLEPDYQVYLNASKVPGFADDPTELACRVVDTKSGEANVRFTVSWYYRMNRRSDNVVTSELLAVMDG
DWTLYGERSKQRAQDGDFFIFSKEHTDTFNFRIQRTTEEDRGNYCVVSAWTKQRNNSWVKS KDVF SKPVNIFWA
LEDSVLVVKARQPKPFFAAGNTFEMTCKVSSKNIKSPRYSVLIMAEKPVGDLSSPNETKYIISLDQDSVVKLENW
TDASRV DGVVLEKVQEDEF RYRMYQTQVSDAGLYRCMVTAWSPVRGSLWREAATSLSNPIEIDFQTSGPIFNASV
HSDTPSVIRGDLIKLFCIITVEGAALDPDDMAFDVSWFAVHSFGLDKAPVLLSSSLDRKGIVTTSRRDWKSDLSE
RVSVLEFLLQVHGSEDQDFGNYYCSVTPWVKSP TGSWQKEAEIHSKPVFITVKMDVLNAFKYPLLIGVGLSTVIG
LLSCLIGYCSSHWCCKKEVQETRERRRLMSMEMD

341/6881
FIGURE 317

GTCCATTTTGTTCGGTAGAGGCAGAAGGAGAAGGTCGGATTGTAGAAGCTGGGGTGGCCGGCAGCTCGCTCATCGG
TGTTTCGTGGGCTTTGTTCGGTCCGTGCCTCGTCTCTCCCTGGAAAGGGAGGGAGGCTTCAACGTCGAGAGGGAGCC
GCTGCCGCGTTAGTTCCGAGCTTGAAGTCACTAGGACTTCTCTCAAACCTTGAGTGCTGAGGAGACTCAGATGTTG
GCCTCAGCTCCTAGGCTGAACCTCAGCAGATCGGCCCATGAAAACCTTCTGTATTGAGACAAAGGAAGGGATCTGTC
AGAAAAGCAACACTTGTTATCTTGGGCTTGGCAGCAAGGAAGAGGACAGGTAGTGGAGATCCTGCAATCTGAAAAG
CAGACTGAAAGGTGACAAAGAAGCTGAAGATGGGTGGTAGAGAGAGGTATAACATTCCAGCCCCCTCAATCTAGAA
ATGTTAGTAAGAACCAACAACAGCTTAACAGACAGAAGACCAAGGAACAGAATTCCCAGATGAAGATTGTTTCATA
AGAAAAAAGAAAGAGGACATGGTTATAACTCATCAGCAGGTGCCTGGCAGGCCATGAAAAATGGGGGGAAGAACA
AAAATTTTCCAAATAATCAAAGTTGAATTCTAGCTTATCAGGTCCCAGCTTACTTTTTAAATCTCAAGCTAAAC
AGAACTATGCTGGTGCCAAATTTAGTGAGCCGCCATCACCAAGTGTTCTTCCCAAACCAAGCCACTGGGTCC
CTGTTTCCTTTAATCCTTCAGATAAGGAAATAATGACATTTCAACTTAAACCTTACTTAAAGTACAGGTATAAA
ATAAGACAAATGTTTAAAGTTTAGTTATGTTACAGATAGTTGTCAATTGGTCTGAAACAAATTTGCTAGGGAATC
TATTTGTGTAGAACTAATTAATGTAAAAAATAGACTTCATCTCGTGTTGTGTGCACTGTGATATAATGGTAGT
ATCAGTGCAACTTAACTAATGATTGTAATTGATATTAAGTGTTCTCAACTGAGTAACTTTTTAAGTGGAACCAA
GTTTAGATTTGGGGAGTGGTAAAGGAATCAGCTTTTTCTATTGTTAGGGGAAGATAGTAATTTATCATTTCATGGA
CCAGTAGATTGTTGAAAGTTGGTGAATCGGATTATAAGCTTCTGGCTAACACAAGGATTTCAGAATTAGGTAAACA
TCTGAAGGTTTAGTATATTAGAAACACCCAAACCAGTAATATGCTAACCTGATGCACTGCTGAAAGAAAAATGTGA
ATTTTTTCGTAATAATTGCATTTTAGTGAATTGTACAGTGGGTGGAAAGGGCATTGAGCTCATTAGAATGAGAC
ATAGTACACCCCAATGGCCCTGTTTATTAAATGTAGTGGATTAAGTGTCTGTCAACAAATACACCAAAACCATTT
TTTATAGAAACAGTATTTAATGGTCACTCAATAGCTTTCAAAAATACATTTTTGTATTACAGCACTGCACAAGCTA
TTCTAATAGTGATCTGGCCTCCTCATTCTGCCAAGCTTGCTTTGGGGAGTTGGATAATGTGAAAATTTTAAGTA
CCTAGGGGAGAAAGAGCCATGTAAATATCTGTAATAAACTTGTAGCATATGTAAAGTTTTCTTGCCCTTTATCTT
ACAAAAATGGAATATTTTAGTATGAATTTGCTGAATGTAAGACCGTGGACTGTTTTTTATAATATGGCCTAATTT
TAAAGGTCCAAAATAACTTGTTTTTAAAGTTTGCCCTTGCTGCTAAAGTGCCAGTGTATGTATGTTATACTTGATT
TGGTTGTAAACTATATTTCAAAGTAAACCCTAGTGTAAATAAGTTTTATAACTAAAAGGTTTAAGCTGCTAAAAC
TATTTTTAAGAGATGTGAAATGCAGTATGGGACTATCTTTTTTCTCCTCTAAGCCCAAAGATTAAGTAGAGTC
CCTCCAACCTTATAGATTTTTGGCTTTCACAATCTTATAACCTAGGATACAGGTAGTTTCGAGTATGGTGCCAGT
GATGTTTTGTTTTGTTTGGTCAAGGGGTAGGTGCAACCCCAATGGACCCTTATGCAAAAGATGTAACTCTTGC
ATAATACATCGATAACATGTTTTGCCAACTTTAAATGCTTAAACATAAGCGAAACCAGTAGCAAGTATGTGGGTC
AGTTTAAAAATTTGATTGTTAATGCCCTATTTTCTAATTTGGCACCTCTTTTGATGCCTAAGCAGGTAAGCAGA
TGCCTAAGCTGTATTTCTCAAATAAATCAAGAGGAAGTACTGCCCAAGTTAAATATTGATAGCCTAAAGACAAA
TTCATGTAGTACTTAATGTACATGATATGAATTTGAAGCATAAAATTAAATTTTTCCCCATTG

342/6881
FIGURE 318A

TTTCAGCCAAACTTCGGGCGGCGGCTGAGGCGGCGGCCGAGGAGCGGCGGACTCGGGGCGCGGGGAGTCGAGGCA
TTTGCGCCTGGGCTTCGGAGCGTAGCGCCAGGGCCTGAGCCTTTGAAGCAGGAGGAGGGGAGGAGAGAGTGGGGC
TCCTCTATCGGGACCCCTCCCCATGTGGATCTGCCAGGCGGCGGCGGCGGCGGCGGAGGAGGCGACCGAG
AAGATGCCCCGCTGCGCCCCGCTCTGCTGTGGGCGCTGCTGGCGCTCTGGCTGTGCTGCGCGGCCCCCGCGCAT
GCATTGCAGTGTGAGATGGCTATGAACCTGTGTAAATGAAGGAATGTGTGTTACCTACCACAATGGCACAGGA
TACTGCAAATGTCCAGAAGGCTTCTTGGGGGAATATTGTCAACATCGAGACCCCTGTGAGAAGAACCCTGCCAG
AATGGTGGGACTTGTGTGGCCCAGGCCATGCTGGGGAAAGCCACGTGCCGATGTGCCTCAGGGTTTACAGGAGAG
GACTGCCAGTACTCAACATCTCATCCATGCTTTGTGTCTCGACCCTGCCTGAATGGCGGCACATGCCATATGCTC
AGCCGGGATACCTATGAGTGCACCTGTCAAGTCGGGTTTACAGGTAAGGAGTGCCAATGGACGGATGCCTGCCTG
TCTCATCCCTGTGCAAATGGAAGTACCTGTACCCTGTGGCCAACCAGTTCTCCTGCAAATGCCTCACAGGCTTC
ACAGGGCAGAAATGTGAGACTGATGTCAATGAGTGTGACATTCCAGGACACTGCCAGCATGGTGGCACCTGCCTC
AACCTGCCTGGTTCCCTACCAGTGCCAGTGCCCTCAGGGCTTCACAGGCCAGTACTGTGACAGCCTGTATGTGCC
TGTGCACCCCTCACCTTGTGTCAATGGAGGCACCTGTGCGCAGACTGGTGACTTCACTTTTGAGTGCAACTGCCTT
CCAGGTTTTGAAGGGAGCACCTGTGAGAGGAATATTGATGACTGCCCTAACACAGGTGTGAGAATGGAGGGGTT
TGTGTGGATGGGGTCAACACTTACAACCTGCCGCTGTCCCCACAATGGACAGGACAGTTCTGCACAGAGGATGTG
GATGAATGCCTGCTGCAGCCCAATGCCTGTCAAAATGGGGGCACCTGTGCCAACCGCAATGGAGGCTATGGCTGT
GTATGTGTCAACGGCTGGAGTGGAGATGACTGCAGTGAGAACATTGATGATTGTGCCTTCGCTCCTGTACTCCA
GGCTCCACCTGCATCGACCGTGTGGCCTCCTTCTCTGCAATGTGCCAGAGGGGAAGGCAGGTCTCCTGTGTCTAT
CTGGATGATGCATGCATCAGCAATCCTTGCCACAAGGGGGCACTGTGTGACACCAACCCCTAAATGGGCAATAT
ATTTGCACCTGCCACAAGGCTACAAAGGGGCTGACTGCACAGAAGATGTGGATGAATGTGCCATGGCCAATAGC
AATCCTTGTGAGCATGCAGGAAATGTGTGAACACGGATGGCGCCTTCCACTGTGAGTGTCTGAAGGGTTATGCA
GGACCTCGTTGTGAGATGGACATCAATGAGTGCCATTACAGACCCCTGCCAGAATGATGCTACCTGTCTGGATAAG
ATTGGAGGCTTCACATGTCTGTGCATGCCAGGTTTCAAAGGTGTGCATTGTGAATTAGAAATAAATGAATGTCAG
AGCAACCCCTGTGTGAACAATGGGCAGTGTGTGGATAAAGTCAATCGTTTCCAGTGCCTGTGTCTCCTGGTTTC
ACTGGGCCAGTTTGCCAGATTGATATTGATGACTGTTCCAGTACTCCGTGTCTGAATGGGGCAAAGTGTATCGAT
CACCCGAATGGCTATGAATGCCAGTGTGCCACAGGTTTCACTGGTGTGTTGTGTGAGGAGAACATTGACAACCTGT
GACCCCGATCCTTGCCACCATGGTCAGTGTGAGGATGGTATTGATTCCCTACACCTGCATCTGCAATCCCGGGTAC
ATGGGCGCCATCTGCAGTGACCAGATTGATGAATGTTACAGCAGCCCTTGCTGAACGATGGTCGCTGCATTGAC
CTGGTCAATGGCTACCAGTGCAACTGCCAGCCAGGCACGTCAGGGGTTAATTGTGAAATTAATTTTGATGACTGT
GCAAGTAACCCCTGTATCCATGGAATCTGTATGGATGGCATTAAATCGCTACAGTTGTGTCTGCTCACCAGGATTC
ACAGGGCAGAGATGTAACATTGACATTGATGAGTGTGCCTCCAATCCCTGTCGCAAGGGTGCAACATGTATCAAC
GGTGTGAATGGTTTCCGCTGTATATGCCCCGAGGGACCCCATCACCCAGCTGCTACTCACAGGTGAACGAATGC
CTGAGCAATCCCTGCATCCATGGAACTGTACTGGAGGTCTCAGTGGATATAAGTGTCTCTGTGATGCAGGCTGG
GTTGGCATCAACTGTGAAGTGGACAAAATGAATGCCTTTCGAATCCATGCCAGAATGGAGGAACCTGTGACAAT
CTGGTGAATGGATACAGGTGTACTTGCAAGAAGGGCTTTAAAGGCTATAACTGCCAGGTGAATATTGATGAATGT
GCCTCAAATCCATGCCTGAACCAAGGAACCTGCTTTGATGACATAAGTGGCTACACTTGCCACTGTGTGCTGCCA
TACACAGGCAAGAATTGTGAGACAGTATTGGCTCCCTGTTCCCCAAACCCCTGTGAGAATGCTGCTGTTTGCAA
GAGTACCAAATTTTGAGAGTTTACTTGCTTGTGTGCTCCTGGCTGGCAAGGTCAGCGGTGTACCATTGACATT
GACGAGTGTATCTCCAAGCCCTGCATGAACCATGGTCTCTGCCATAACACCCAGGGCAGCTACATGTGTGAATGT
CCACCAGGCTTCAGTGGTATGGACTGTGAGGAGGACATTGATGACTGCCTTGCCAATCCTTGCCAGAATGGAGGT
TCCTGTATGGATGGAGTGAATACTTTCTCCTGCCTCTGCCTTCCGGGTTTCACTGGGGATAAGTGCCAGACAGAC
ATGAATGAGTGTCTGAGTGAACCTGTAAAGATGGAGGGACCTGCTCTGACTACGTCAACAGTTACACTTGCAAG
TGCCAGGCAGGATTTGATGGAGTCCATTGTGAGAACACATCAATGAGTGCAGTACAGAGCTCCTGTTTCAATGGT
GGCACATGTGTTGATGGGATTAACCTCTCTTGTGCTTGTGCCCTGTGGGTTTCACTGGATCCTTCTGCCTCCAT
GAGATCAATGAATGCAGCTCTCATCCATGCCTGAATGAGGGAAACGTGTGTTGATGGCCTGGGTACCTACCGCTGC
AGCTGCCCCCTGGGCTACACTGGGAAAACTGTGAGACCCCTGGTGAATCTCTGCAGTCGGTCTCCATGTAAAAAC
AAAGGTACTTGCCTTCAGAAAAAGCAGAGTCCCAGTGCCATATGTCCATCTGGATGGGCTGGTGCCTATTGTGAC
GTGCCCAATGTCTCTTGTGACATAGCAGCCTCCAGGAGAGGTGTGCTTGTGAACACTTGTGCCAGCACTCAGGT

343/6881
FIGURE 318B

GTCTGCATCAATGCTGGCAACACGCATTACTGTGTCAGTGCCCCCTGGGCTATACTGGGAGCTACTGTGAGGAGCAA
CTCGATGAGTGTGCGTCCAACCCCTGCCAGCACGGGGCAACATGCAGTGACTTCATTGGTGGATACAGATGCGAG
TGTGTCCAGGCTATCAGGGTGTCAACTGTGAGTATGAAGTGGATGAGTGCCAGAATCAGCCCTGCCAGAATGGA
GGCACCTGTATTGACCTTGTGAACCATTTCAGTGTCTTGTGCCACCAGGCACTCGGGGCTACTCTGTGAAGAG
AACATTGATGACTGTGCCCCGGGTCCCCATTGCCTTAATGGTGGTCAGTGCATGGATAGGATTGGAGGCTACAGT
TGTGCTGCTTGCCTGGCTTTGCTGGGGAGCGTTGTGAGGGAGACATCAACGAGTGCCTCTCCAACCCCTGCAGC
TCTGAGGGCAGCCTGGACTGTATACAGCTCACCAATGACTACCTGTGTGTTTGCCGTAGTGCCTTTACTGGCCGG
CACTGTGAAACCTTCGTCGATGTGTGTCCCCAGATGCCCTGCCTGAATGGAGGGACTTGTGCTGTGGCCAGTAAC
ATGCCTGATGGTTTCATTTGCCGTTGTCCCCCGGGATTTTCCGGGGCAAGGTGCCAGAGCAGCTGTGGACAAGTG
AAATGTAGGAAGGGGGAGCAGTGTGTGCACACCGCCTCTGGACCCCGCTGCTTCTGCCCCAGTCCCCGGGACTGC
GAGTCAGGCTGTGCCAGTAGCCCTGCCAGCACGGGGGAGCTGCCACCCTCAGCGCCAGCCTCCTTATTACTCC
TGCCAGTGTGCCCCACCATTTCTCGGGTAGCCGCTGTGAACTCTACACGGCACCCCCCAGCACCCCTCCTGCCACC
TGTCTGAGCCAGTATTGTGCCGACAAAGCTCGGGATGGCGTCTGTGATGAGGCCTGCAACAGCCATGCCCTGCCAG
TGGGATGGGGGTGACTGTTCTCTCACCATGGAGAACCCCTGGGGCAACTGCTCCTCCCCACTTCCCTGCTGGGAT
TATATCAACAACCAGTGTGATGAGCTGTGCAACACGGTCGAGTGCCTGTTTGACAACTTTGAATGCCAGGGGAAC
AGCAAGACATGCAAGTATGACAAATACTGTGCAGACCACTTCAAAGACAACCACTGTGACCAGGGGTGCAACAGT
GAGGAGTGTGGTTGGGATGGGCTGGACTGTGCTGCTGACCAACCTGAGAACCTGGCAGAAGGTACCCCTGGTTATT
GTGGTATTGATGCCACCTGAACAACCTGCTCCAGGATGCTCGCAGCTTCTTGCGGGCACTGGGTACCCCTGCTCCAC
ACCAACCTGCGCATTAAAGCGGGACTCCCAGGGGGAACTCATGGTGTACCCCTATTATGGTGAGAAGTCAGCTGCT
ATGAAGAAACAGAGGATGACACGCAGATCCCTTCTGGTGAACAAGAACAGGAGGTGGCTGGCTCTAAAGTCTTT
CTGGAAATTGACAACCGCCAGTGTGTTCAAGACTCAGACCACTGCTTCAAGAACACGGATGCAGCAGCAGCTCTC
CTGGCCTCTCAGCCATACAGGGGACCCTGTCAACCCCTCTTGTGTCTGTGTCAGTGAATCCCTGACTCCAGAA
CGCACTCAGCTCCTCTATCTCCTTGCTGTTGCTGTTGTCAATCTGTTTATTATTCTGCTGGGGGTAATCATG
GCAAAACGAAAGCGTAAGCATGGCTCTCTCTGGCTGCCTGAAGGTTTCACTCTTCGCCGAGATGCAAGCAATCAC
AAGCGTCGTGAGCCAGTGGGACAGGATGCTGTGGGGCTGAAAAATCTCTCAGTGCAAGTCTCAGAAGCTAACCTA
ATTGGTACTGGAACAAGTGAACACTGGGTGATGATGAAGGGCCCCAGCCAAAGAAAGTAAAGGCTGAAGATGAG
GCCTTACTCTCAGAAGAAGATGACCCCATTGATCGACGGCCATGGACACAGCAGCACCTTGAAGCTGCAGACATC
CGTAGGACACCATCGCTGGCTCTCACCCTCCTCAGGCAGAGCAGGAGGTGGATGTGTTAGATGTGAATGTCCGT
GGCCCAGATGGCTGCACCCCATTGATGTTGGCTTCTCTCCGAGGAGGCAGCTCAGATTTGAGTGATGAAGATGAA
GATGCAGAGGACTCTTCTGCTAACATCATCACAGACTTGGTCTACCAGGGTGCCAGCCTCCAGGCCCAGACAGAC
CGGACTGGTGAGATGGCCCTGCACCTTGACGCCCCGCTACTCACGGGCTGATGCTGCCAAGCGTCTCCTGGATGCA
GGTGCAGATGCCAATGCCAGGACAACATGGGGCCGCTGTCCACTCCATGCTGCAGTGGCAGCTGATGCCAAGGT
GTCTTCCAGATTCTGATTGCAACCGAGTAACTGATCTAGATGCCAGGATGAATGATGGTACTACACCCCTGATC
CTGGCTGCCCGCCTGGCTGTGGAGGGAATGGTGGCAGAATGATCAACTGCCAAGCGGATGTGAATGCAGTGGAT
GACCATGGAAAATCTGCTCTTCACTGGGCAGCTGCTGTCAATAATGTGGAGGCAACTCTTTTGTGTTGAAAAAT
GGGGCCAACCGAGACATGCAGGACAACAAGGAAGAGACACCTCTGTTTCTTGCTGCCCCGGGAGGGGAGCTATGAA
GCAGCCAAGATCCTGTTAGACCATTTTGCCAATCGAGACATCACAGACCATATGGATCGTCTTCCCCGGGATGTG
GCTCGGGATCGCATGCACCATGACATTGTGCGCCTTCTGGATGAATACAATGTGACCCCAAGCCCTCCAGGCACC
GTGTTGACTTCTGCTCTCTCACCTGTCTCTGTGGGCCCAACAGATCTTTCCTCAGCCTGAAGCACACCCCAATG
GGCAAGAAGTCTAGACGGCCAGTGCCAAGAGTACCATGCCTACTAGCCTCCCTAACCTTGCCAAGGAGGCAAG
GATGCCAAGGGTAGTAGGAGGAAGAAGTCTCTGAGTGAGAAGGTCCAACCTGTCTGAGAGTTCAGTAACCTTTATCC
CCTGTTGATTCCCTAGAATCTCCTCACACGTATGTTTCCGACACCACATCCTCTCCAATGATTACATCCCCTGGG
ATCTTACAGGCCTCACCCAACCTATGTTGGCCACTGCCGCCCTCCTGCCCCAGTCCATGCCAGCATGCACTA
TCTTTTCTAACCTTCATGAAATGCAGCCTTTGGCACATGGGGCCAGCACTGTGCTTCCCTCAGTGAGCCAGTTG
CTATCCCACCACCACATTGTGTCTCCAGGCAGTGGCAGTGTGGAAGCTTGAGTAGGCTCCATCCAGTCCCAGTC
CCAGCAGATTGGATGAACCGCATGGAGGTGAATGAGACCCAGTACAATGAGATGTTTGGTATGGTCCTGGCTCCA
GCTGAGGGCACCCATCCTGGCATAGCTCCCCAGAGCAGGCCACCTGAAGGGAAGCACATAACCACCCCTCGGGAG
CCCTTGCCCCCATTGTGACTTTCCAGCTCATCCCTAAAGGCAGTATTGCCCAACCAGCGGGGGCTCCCCAGCCT

344/6881
FIGURE 318C

CAGTCCACCTGCCCTCCAGCTGTTGCGGGCCCCCTGCCACCATGTACCAGATTCCAGAAATGGCCCGTTTGCCC
AGTGTGGCTTTTCCCCACTGCCATGATGCCCCAGCAGGACGGGCAGGTAGCTCAGACCATTCTCCCAGCCTATCAT
CCTTTCCAGCCTCTGTGGGCAAGTACCCACACCCCCCTTCACAGCACAGTTATGCTTCCTCAAATGCTGCTGAG
CGAACACCCAGTCACAGTGGTCACCTCCAGGGTGAGCATCCCTACCTGACACCATCCCCAGAGTCTCCTGACCAG
TGGTCAAGTTCATCACCCCACTCTGCTTCTGACTGGTCAGATGTGACCACCAGCCCTACCCCTGGGGGTGCTGGA
GGAGGTCAGCGGGACCTGGGACACACATGTCTGAGCCACCACACAACAACATGCAGGTTTATGCGTGAGAGAGT
CCACCTCCAGTGTAGAGACATAACTGACTTTTGTAAATGCTGCTGAGGAACAAATGAAGGTCATCCGGGAGAGAA
ATGAAGAAATCTCTGGAGCCAGCTTCTAGAGGTAGGAAAGAGAAGATGTTCTTATTAGATAATGCAAGAGAAAGC
AATTGCTCAGTTTCACTGGGTATCTGCAAGGCTTATTGATTATTCTAATCTAATAAGACAAGTTTGTGGAAATGC
AAGATGAATACAAGCCTTGGGTCCATGTTTACTCTCTTCTATTGAGAAATAAGATGGATGCTTATTGAAGCCCA
GACATTCTTGACGCTTGGACTGCATTTTAAGCCCTGCAGGCTTCTGCCATATCCATGAGAAGATTCTACACTAGC
GTCTGTTGGGAATTATGCCCTGGAATTCGCTGAATTGACCTACGCATCTCCTCCTTGGACATTCTTTTG
TCTTCATTTGGTGCTTTTGGTTTTGCACCTCTCCGTGATTGTAGCCCTACCAGCATGTTATAGGGCAAGACCTTT
GTGCTTTTGATCATTCTGGCCCATGAAAGCAACTTTGGTCTCCTTTCCCTCCTGTCTTCCCGGTATCCCTTGA
GTCTCACAAGGTTTACTTTGGTATGGTTCTCAGCACAAACCTTTCAAGTATGTTGTTTCTTTGGAAAATGGACAT
ACTGTATTGTGTTCTCCTGCATATATCATTCTGGAGAGAGAAGGGGAGAAGAATACTTTTCTTCAACAAATTTT
GGGGCAGGAGATCCCTTCAAGAGGCTGCACCTTAATTTTTCTTGCTGTGTGTCAGGTCTTCATATAAACTTTAC
CAGGAAGAAGGGTGTGAGTTTGTGTTTTCTGTGTATGGGCCTGGTCAGTGTAAGTTTTATCCTTGATAGTCT
AGTTACTATGACCCTCCCCACTTTTTTAAACCAGAAAAGGTTTGAATGTTGGAATGACCAAGAGACAAGTTA
ACTCGTGCAAGAGCCAGTTACCCACCCACAGGTCCCCCTACTTCTGCCAAGCATTCCATTGACTGCCTGTATGG
AACACATTTGTCCCAGATCTGAGCATTCTAGGCCTGTTTCACTCACTCACCAGCATATGAACTAGTCTTAACT
GTTGAGCCTTTCTTTTCATATCCACAGAAGACACTGTCTCAAATGTTGTACCCTTGCCATTTAGGACTGAACTTT
CCTTAGCCCAAGGGACCCAGTGACAGTTGTCTTCCGTTTGTGATGATCAGTCTCTACTGATTATCTTGCTGCT
TAAAGGCCTGCTCACCAATCTTTCTTTCACACCGTGTGGTCCGTGTTACTGGTATACCCAGTATGTTCTCACTGA
AGACATGGACTTTTATATGTTCAAGTGCAGGAATTGGAAAGTTGGACTTGTTTTCTATGATCCAAAACAGCCCTAT
AAGAAGGTTGGAAAAGGAGGAACATATAGCAGCCTTGTCTATTTTCTGCTACCATTTCTTTTCTCTGAAGCGG
CCATGACATTCCCTTTGGCAACTAACGTAGAACTCAACAGAACATTTTCTTTTCTAGAGTCACCTTTTAGATG
ATAATGGACAACATATAGACTTGCTCATTGTTGAGACTGATTGCCCTCACCTGAATCCACTCTCTGTATTATGC
TCTTGGAATTTCTTTGACTTTCTTTTAAAGGCAGAAAGCATTTTAGTTAATTGTAGATAAAGAATAGTTTTCTTC
CTCTTCTCCTTGGGCCAGTTAATAATTGGTCCATGGCTACACTGCAACTTCCGTCCAGTGCTGTGATGCCCATGA
CACCTGCAAAATAAGTTCTGCCTGGGCATTTGTAGATATTAACAGGTGAATTCCCGACTCTTTTGGTTTGAATG
ACAGTTCTCATTCTTCTATGGCTGCAAGTATGCATCAGTGCTTCCCACTTACCTGATTGTCTGTGCGGTGGCCC
CATATGGAAACCCCTGCGTGTCTGTTGGCATAATAGTTTACAAATGGTTTTTTTTCAGTCTATCCAAATTTATTGAA
CCAACAAAAATAATTACTTCTGCCCTGAGATAAGCAGATTAAAGTTTGTTCATTCTCTGCTTTATTCTCTCCATGT
GGCAACATTCTGTGACGCTCTTTTCATAGTGTGCAACATTTTATCATTCTAAATGGTGACTCTCTGCCCTTGGAC
CCATTTATTATTACAGATGGGGAGAACCTATCTGCATGGACCTCTGTGGACCACAGCGTACCTGCCCTTTCTG
CCCTCCTGCTCCAGCCCCACTTCTGAAAGTATCAGCTACTGATCCAGCCACTGGATATTTTATATCCTCCCTTTT
CCTTAAGCACAAATGTCAGACCAAATTGCTTGTTCTTTTCTTGGACTACTTTAATTTGGATCCTTTGGGTTTGG
AGAAAGGGAATGTGAAAGCTGTCAATTACAGACAACAGGTTTCAGTGATGAGGAGGACAACACTGCCTTTCAAAC
TTTTACTGATCTCTTAGATTTTAAAGAACTCTTGAATTGTGTGGTATCTAATAAAAGGGAAGGTAAGATGGATAAT
CACTTTCTCATTGGGTTCTGAATTGGAGACTCAGTTTTTATGAGACACATCTTTTATGCCATGTATAGATCCTC
CCCTGCTATTTTTGGTTTTATTTTTATTGTTATAAATGCTTTCTTTCTTGACTCCTCTCTGCCTGCCTTTGGGG
ATAGGTTTTTTGTTTGTGTTATTTGCTTCTCTGTTTTGTTTAAGCATCATTTTCTTATGTGAGGTGGGGAAAGG
GAAAGGTATGAGGGAAAGAGAGTCTGAGAATTAAATATTTAGTATAAGCAATTGGCTGTGATGCTCAAATCCA
TTGCATCCTCTTATTGAATTTGCCAATTTGTAATTTTGCATAATAAAGAACCAAAGGTGTAATGTTTTGTTGAG
AGGTGGTTTAGGGATTTTGGCCCTAACCAATACATTGAATGTATGATGACTATTTGGGAGGACACATTTATGTAC
CCAGAGGCCCCCACTAATAAGTGGTACTATGGTTACTTCTTGTGTACATTTCTCTTAAAGTGATATTATATCT
GTTTGTATGAGAAACCCAGTAACCAATAAATGACCGCATATTCCTGACTAAACGTAGTAAGGAAAATGCACACT

345/6881
FIGURE 318D

TTGTTTTTACTTTTCCGTTTCATTCTAAAGGTAGTTAAGATGAAATTTATATGAAAGCATTTTTATCACAAAATA
AAAAAGGTTTGCCAAGCTCAGTGGTGTGTATTTTTTATTTTCCAATACTGCATCCATGGCCTGGCAGTGTTACC
TCATGATGTCATAATTTGCTGAGAGAGCAAATTTTCTTTTCTTTCTGAATCCCACAAAGCCTAGCACCAAAC TTC
TTTTTTTCTTCCTTTAATTAGATCATAAATAAATGATCCTGGGGAAAAAGCATCTGTCAAATAGGAAACATCACA
AAACTGAGCACTCTTCTGTGCACTAGCCATAGCTGGTGACAAACAGATGGTTGCTCAGGGACAAGGTGCCTTCCA
ATGGAAATGCGAAGTAGTTGCTATAGCAAGAATTGGGAAGTGGGATATAAGTCATAATATTAATTATGCTGTTAT
GTAAATGATTGGTTTGTAACATTCCTTAAGTGAATTTGTGTAGAACTTAATATACAGGATTATAAAATAATATT
TTGTGTATAAATTTGTTATAAGTTCACATTCATACATTTATTTATAAAGTCAGTGAGATATTTGAACATG

346/6881
FIGURE 319

GAGGAGGAGGAGGAGATGACTGGGGAGCGGGAGCTGGAGAATACTGCCCAGTTACTCTAGCGCGCCAGGCCGAAC
CGCAGCTTCTTGGCTTAGGTACTTCTACTCACAGCGGCCGATTCCGAGGCCAACTCCAGCAATGGCTTTTGCAAA
TCTGCGGAAAGTGCTCATCAGTGACAGCCTGGACCCTTGCTGCCGGAAGATCTTGCAAGATGGAGGGCTGCAGGT
GGTGGAAAAGCAGAACCTTAGCAAAGAGGAGCTGATAGCGGAGCTGCAGGACTGTGAAGGCCTTATTGTTTCGCTC
TGCCACCAAGGTGACCGCTGATGTCATCAACGCAGCTGAGAACTCCAGGTGGTGGGCAGGGCTGGCACAGGTGT
GGACAATGTGGATCTGGAGGCCGCAACAAGGAAGGGCATCTTGTTATGAACACCCCCAATGGGAACAGCCTCAG
TGCCGCAGAACTCACTTGTGGAATGATCATGTGCCTGGCCAGGCAGATTCCCCAGGCGACGGCTTCGATGAAGGA
CGGCAAAATGGGAGCGGAAGAAGTTTCATGGGAACAGAGCTGAATGGAAAGACCCTGGGAATTCTTGGCCTGGGCAG
GATTGGGAGAGAGGTAGCTACCCGGATGCAGTCCTTTGGGATGAAGACTATAGGGTATGACCCCATCATTTCCCC
AGAGGTCTCGGCCCTCTTTGGTGTTCAGCAGCTGCCCCCTGGAGGAGATCTGGCCTCTCTGTGATTTTCATCACTGT
GCACACTCCTCTCCTGCCCTCCACGACAGGCTTGCTGAATGACAACACCTTTGCCAGTGCAAGAAGGGGGTGC
TGTGGTGAAGTGTGCCCGTGGAGGGATCGTGGACGAAGGCGCCCTGCTCCGGGCCCTGCAGTCTGGCCAGTGTGC
CGGGGCTGCACTGGACGTGTTTACGGAAGAGCCGCCACGGGACCGGGCCTTGGTGGACCATGAGAATGTCATCAG
CTGTCCCCACCTGGGTGCCAGCACCAAGGAGGCTCAGAGCCGCTGTGGGGAGGAAATTGCTGTTTCAGTTCGTGGA
CATGGTGAAGGGGAAATCTCTCACGGGGGTGTGAATGCCAGGCCCTTACCAGTGCCTTCTCTCCACACACCAA
GCCTTGGATTGGTCTGGCAGAAGCTCTGGGGACACTGATGCGAGCCTGGGCTGGGTCCCCCAAAGGGACCATCCA
GGTGATAACACAGGGAACATCCCTGAAGAATGCTGGGAATGCCTAAGCCCCGAGTCATTGTGGCCTCCTGAA
AGAGGCTTCCAAGCAGGCGGATGTGAACCTGGTGAACGCTAAGCTGCTGGTGAAGAGGCTGGCCTCAATGTCAC
CACCTCCCACAGCCCTGCTGCACCAGGGGAGCAAGGCTTCGGGGAATGCCTCCTGGCCGTGGCCCTGGCAGGCGC
CCCTTACCAGGCTGTGGGCTTGGTCCAAGGCACTACGCCTGTACTGCAGGGGCTCAATGGAGCTGTCTTCAGGCC
AGAAGTGCCTCTCCGCAGGGACCTGCCCCTGCTCCTATTCCGGACTCAGACCTCTGACCCTGCAATGCTGCCTAC
CATGATTGGCCTCCTGGCAGAGGCAGGCGTGCGGCTGCTGTCTACCAGACTTCACTGGTGTGAGATGGGGAGAC
CTGGCACGTGATGGGCATCTCCTCCTTGCTGCCCAGCCTGGAAGCGTGGAAGCAGCATGTGACTGAAGCCTTCCA
GTTCCACTTCTAACCTTGGAGCTCACTGGTCCCTGCCTCTGGGGCTTTTCTGAAGAAACCCACCCACTGTGATCA
ATAGGGAGAGAAAAATCCACATTCTTGGGCTGAACGCGGGCCTCTGACACTGCTTACACTGCACTCTGACCCTGTA
GTACAGCAATAACCGTCTAATAAGAGCCTACCCCC

347/6881
FIGURE 320

MAFANLRKVLISDSLDPCCRKILQDGGGLQVVEKQNLKSKEELIAELQDCEGLIVRSATKVTADVINA AEKLQVVGR
AGTGVDNVDLEAATRKGILVMNTPNGNSLSAAELTCGMIMCLARQIPQATASMKGKWERKKFMGTELNGKTLGI
LGLGRIGREVATRMQSFGMKTIGYDPIISPEVSASFVQQLPLEEIIWPLCDFITVHTPLLPSTTGLLNDNTFAQC
KKGVRVVNCARGGIVDEGALLRALQSGQCAGAAALDVFTTEPPRDALVDHENVISCPHLGASTKEAQSRCGEEIA
VQFVDMVGKSLTGTVNAQALTSASFSPHTKPWIGLAEALGTLRAWAGSPKGTIQVITQGTSLKNAGNCLSPAVI
VGLLKEASKQADVNLVNAKLLVKEAGLNVTTSHSPAAPGEQGFGECLLAVALAGAPYQAVGLVQGTTPVLQGLNG
AVFRPEVPLRRDLPLLLFRTQTS DPAMPLPTMIGLLAEAGVRLLSYQTSLSVSDGETWHVMGISSLLPSLEAWKQHV
TEAFQFHF

348/6881
FIGURE 321

GGGCAGGGGTGCGGAGGGACCGACGGACGCACGGGCGGGCGGCCGGGAGCCATGGAGCGCGGCCCTGGGGCCCGG
GGGCGCGGGCCGGGTGGGCTTCCACGGCACGACATGGAGACCTGTGGTTGCGAGGCTCCCTGGGGCTCGGCTT
GGACCGCGATGGGGCTGGGCCCTGGCCTCCTAACGGGGCTGCTGTCTGGGGCGGTAGCTGGGGGGGCGCTCTCCC
CCCTGCCCCGCGACTCGGAGCACCCACCCCTCCCCTGCCGGGCCAGGCCGGGCGGCCTTGTGGCGGGGGCCCCG
GTGGAGGGCCCGGCCGGGCGGCGCCCGCCATGAACGGGCTGTGCTGAGTGAGCTCTGCTGCCTCTTCTGCTGCC
CTCCCTGCCCCGGCCGCATCGCTGCCAAGCTCGCCTTCCTGCCGCCGGAGGCCACCTACTCCCTGGTGCCTGAGC
CCGAGCTGGGGCCTGGTGGGGCCGGGGCCGCCCCCTTGGGGACCCCTGAGAGCCTCCTCGGGCGCACCCGGGCGCT
GGAAGCTGCACCTGACGGAGCGTGCCGACTTCCAGTACAGCCAGCGCGAGCTGGACACCATCGAGGTCTTCCCCA
CCAAGAGCGCCCGCGGCAACCGTGTCTCCTGCATGTATGTTTCGCTGCGTGCCCTGGTGCCAGGTACACGGTCCCTCT
TCTCGCACGGCAATGCCGTGGACCTGGGCCAGATGAGCAGCTTCTACATTGGCCTGGGCTCCCGCCTCCACTGCA
ACATCTTCACCTACGACTCCTCCGGCTACGGTGCCAGCTCGGGCAGGCCTTCCGAGAGGAACCTCTATGCCGACA
TCGACGCCACCTGGCAGGCCCTGCGCACCAGGTACGGCATCAGCCCCGACAGCATCATCCTGTACGGGCAGAGCA
TCGGCACGGTGCCCAACATGGACCTGGCCTCGCGCTACGAGTGTGCCGCGGTGGTGCTGCACTCGCCGCTCACCT
CGGGCATGCGCGTGCCTTCCGCGACACCAAGAAGACCTACTGCTTCGACGCCTTCCCTAACATCGAGAAGGTGT
CCAAGATCACGTCTCCCGTGCTCATCATCCACGGCAGGGAGGACGAGGTGATCGACTTCTCGCACGGGCTGGCGC
TCTACGAGCGCTGCCCCAAGGCGGTGGAGCCGCTGTGGGTGGAGGGCGCCGGGCACAACGACATCGAGCTCTACA
GCCAGTACCTGGAGCGCCTGCGTTCGCTTCATCTCCCAGGAGCTGCCCAGCCAGCGCGCTTAGCGGGCGGCCCAAC
CAGCCGGACCTCAGCAATAAGGCGGCCCCCGGACCTCACCCCGCGCCGGCCCCCACCAGGGGCTGCATGTGGAC
CCCCCGGGCGGCCAGGGGACCCGCCCCGACCCAGGGGCTGTGGACGATGTACAGGCAACAGAGCTACGCACT
CCTTTCCTTTTGAAGCAAGAAGAAAATACGTGAAAACGGAAATTAAAGATTAAAATT

349/6881
FIGURE 322

MNGLSLSELCCCLFCCPPCPGRIAAKLAFLPPEATYSLVPEPELGPGGAGAAPLGTLRASSGAPGRWKLHLTERAD
FQYSQRELDTIIEVFPTKSARGNRVSCMYVRCVPGARYTVLF SHGNAVDLGQMSSFYIGLGSRLHCNIFTYDSSGY
GASSGRPSEARNLYADIDATWQALRTRYGISPDSIIILYGQSIGTVPTMDLASRYECAAVVLHSPLTSGMRVAFRDT
KKTYCFDAFPNIEKVSKITSPVLI IHGREDEVIDFSHGLALYERCPKAVEPLWVEGAGHNDIELYSQYLERLRRE
ISQELPSQRA

350/6881
FIGURE 323A

AGCGTGAACCTGGGAGGCAGAGCTTGCAGTGAGCCTAGATCGCGTCACTGCACTCCAGCCTGGGAGACAGAGTGA
GACTCTGTCTCAAAAAAAAAAAAAAGTCAAAACAAGAGAACATACTAAATGATTCCATTTTTTTTATTTATGACTT
CATGACTACCATTAAAGAAAATATAACCTGTTGGGAAACTGTTTCTGCCTTGATGATGTTGTACAGACAAGAGATA
AACAGTGAGGAATGTGCTTAGATGTATTGGGAAAGACACGGGTCTGTGGCATTGTCACAAGGTACACGAATACT
GAGAGTGAATGCTGAAGGAATGATCCCCATTGGTGGTGACCTCAGGTGAGACTAGGGTGCCTGTGTTTCAGCAA
AGCCTGGGCAATTGGAATGCAGGGCTCCTAAGATTCCATGACACCCCCACCTTCTAATTCTGTTATTGCAACTGC
AGACCGTTACCTGGCACGCTGGCCACAATCTACCTCACTCTTATCAGAGTCTGAGCTACTGGCAGTGCTTTTCAGC
TCTGAGTTGAGGCACCTCGAACCTTGTGTTTGTGGTGAAGGATCCTAAAGTGCTGTGGGAGTGATCACATTTTTTC
ACAACAGTAAGTCCCTGACTCCACCTCTTCTGCCACAAACGTGAGCATGGTGGTATCAGCCGGCCCTTGGTCCAG
CGAGAAGGCAGAGATGAACATTCTAGAAATCAACGAGAAATTGCGCCCCCAGTTGGCAGAGAACAAACAGCAGTT
CGTAAACCTCAAAGAGATGTTTCTAACTCAACTGGCCGGCTTCTGGCCAACCGACAGAAGAAATACAGCAATA
TAAAGTCTTGGTTCACTCTCAGGAACGAGAGCTGACGCAGTTAAAGGAGAAAGTTACAGGAAGGGAGAGATGCCTC
CCGCTCATTGAATGAGCATCTCCAGGCCCTCTCACTCTGGATGAGCCGGACAAAGTCCCAGGGGCAGGACCTCCA
AGAACAGCTGGCTGAGGGGTGTAGACTGGCACAGCACCTTGTCCAAAAGCTCAGCCCAGAAAATGACGAAGATGA
GGATGAAGATGTTCAAGTTGAGGAGGATGAGAAAGTGCAGAAATCATCTGCCCCCAGGGAGGTGCAGAAGGCTGA
AGTGAGCAAAGTCCCTGAGGACTCACTGGAGGAATGTGCCATCACTTGTTCAAATAGCCACGGCCCTTGTGACTC
CAACCAGCCTCACAGAACATCAAAATCACATTTGAGGAAGACGAAGTCAACTCAACTCTGGTTGTAGACAGAGA
ATCCTCTCATGATGAATGTGAGGATGCTCTAAACATTCTCCAGTCCCTGGCCCCACCTCTTCTGCCACAAACGT
CAGCATGGTGGTATCAGCCGGCCCTTTGTCCAGCGAGAAGGCAGAGATGAACATTCTAGAAATCAATGAGAAATT
GCACCCCCAGCTGGCAGAGAAGAAACAGCAGTTCAGAAACCTCAAAGAGAAATGTTTTCTAACTCAACTGGCCGG
CTTCTTGGCCAACCAGCAGAACAAATACAAGTATGAAGAGTGTAAAGACCTCATAAAATTTATGCTGAGGAATGA
GCGACAGTTCAAGGAGGAGAAGCTTGCAGAGCAGCTGAAGCAAGCTGAGGAGCTCAGGCAATATAAAGTCTTGGT
TCACGCTCAGGAACGAGAGCTGACCCAGTTAAGGGAGAAGTTGCGGGAAGGGAGAGATGCCTCCCGCTCATTGAA
TGAGCATCTCCAGGCCCTCCTCACTCCGGATGAGCCGGACAAGTCCCAGGGGCAGGACCTCCAAGAACAGCTGGC
TGAGGGGTGTAGACTGGCACAGCACCTTGTCCAAAAGCTCAGCCCAGAAAATGACAACGATGACAATGAAGATGT
TCAAGTTGAGGTGGCTGAGAAAGTGCAGAAATCGTCTGCCCCCAGGGAGATGCAGAAGGCTGAAGAAAAGGAAGT
CCCTGAGGACTCACTGGAGGAATGTGCCATCACTTATTCAAATAGCCATGGCCCTTATGACTCCAACCAGCCACA
TAGGAAAACCAAATCACATTTGAGGAAGACAAAGTCGACTCAACTCTCATTGGCTCATCCTCTCATGTTGAACG
GGAAGATGCTGTACACATTATTCCAGAAAATGAAAGTGATGATGAGGAAGAGGAAGAAAAAGGGCCAGTGTCTCC
CAGGAATCTGCAGGAGTCTGAAGAGGAGGAAGTCCCCCAGGAGTCTGGGATGAAGGTTATTGACTCCCTCAAT
TCCTCCTGAAATGTTGGCCTCGTACAAGTCTTACAGCAGCACATTTCACTCATTAGAGGAACAGCAAGTCTGCAT
GGCTGTTGACATAGGCAGACATCGGTGGGATCAAGTGAAAAAGGAGGACCAAGAGGCAACAGGTCCCAGGCTCAG
CAGGGAGCTGCTGGATGAGAAAGGGCCTGAAGTCTTGCAGGACTCACTGTATAGATGTTATTCAACTCCTTCAGG
TTGTCTTGAACGACTGACTCATGCCAGCCCTACAGAAGTGCCTTTTACGTATTGGAGCAACAGCGTGTGGCTT
GGCTGTTGACATGGATGAAATTGAAAAGTACCAAGAAGTGGAAGAAGACCAAGACCCATCATGCCCCAGGCTCAG
CAGGGAGCTGCTGGATGAGAAAGAGCCTGAAGTCTTGCAGGACTCACTGGGTAGATGGTATTGACTCCTTCAGG
TTATCTTGAACGCTGACTTAGGCCAGCCCTACAGCAGTGCTGTTTACTCATTGGAGGAACAGTACCTTGGCTT
GGCTCTTGAACGCTTGGACAGAATTAAAAAGGACCAAGAAGAGGAAGAAGACCAAGGCCACCATTGCCCCAGGCTCAG
CAGGGAGCTGCTGGAGGTAGTAGAGCCTGAAGTCTTGCAGGACTCACTGGATAGATGTTATTCAACTCCTTCAG
TTGTCTTGAACAGCCTGACTCCTGCCAGCCCTATGGAAGTTCCTTTTATGCATTGGAGGAAAAACATGTTGGCTT
TTCTCTTGACGTGGGAGAAATTGAAAAGAAGGGGAAGGGGAAGAAAGAAGGGGAAGAAGATCAAAGAAGGAAAG
AAGAAGGGGAAGAAAAGAAGGGGAAGAAGATCAAAACCCACCATGCCCCAGGCTCAACGGCGTGCTGATGGAAGT
GGAAGAGCCTGAAGTCTTGCAGGACTCACTGGATGGATGTTATTCTACTCCGTCAATGTACTTTGAACTACCTGA
CTCATTCCAGCACTACAGAAGTGTGTTTTACTCATTTGAGGAACAGCACATCAGCTTCGCCCTTTACGTGGACAA
TAGGTTTTTTTACTTTGACGGTGACAAGTCTCCACCTGGTGTTCAGATGGAAGTCATATTTCCACAATAAGCAGC
CCTTACTAAGCCGAGAGATGTCATTCTGCAGGCAGGACCTATAGGCACGTGAAGATTTGAATGAACTACAGTT
CCATTGGAAGCCCAGACATAGGATGGGTGAGTGGGCATGGCTCTATTCTCTCAAACCATGCCAGTGGCAA
CCTGTGCTCAGTCTGAAGACAATGGACCCACGTTAGGTGTGACACGTTACATAACTGTGCAGCACATGCCGGGA

351/6881
FIGURE 323B

GTGATCAGTCAGACATTTTAATTTGAACCACGTATCTCTGGGTAGCTACAAAATTCCTCAGGGATTTTCATTTTGC
AGACATGTCTCTGAGCTTCTATACCTGCTCAAGGTCATTGTCATCTTTGTGTTTAGCTCATCCAAAGGTGTTACC
CTGGTTTCAATGAACCTAACCTCATTCTTCGTGTCTTCAGTGTGGCTTGTTTTAGCTGATCCATCTGTAACACA
GGAGGGATCCTTGGCTGAGGATTGTATTTCAGAACCACCAACTGCTCTTGACAATTGTTAACCCGCTAGGCTCCT
TTGGTTAGAGAAGCCACAGTCCTTCAGCCTCCAATTGGTGTCACTTAGGAAGACCACAGCTAGATGGACAAA
CAGCATTGGGAGGCCTTAGCCCTGCTCCTCTCAATTCCATCCTGTAGAGAACAGGAGTCAGGAGCCGCTGGCAGG
AGACAGCATGTCACCCAGGACTCTGCCGGTGCAGAATATGAACAATGCCATGTTCTTGCAGAAAACGCTTAGCCT
GAGTTTCATAGGAGGTAATCACCAGACAACCTGCAGAATGTAGAACAACCTGAGCAGGACAACCTGACCTGTCTCCTTC
ACATAGTCCTTATCACCACAAATCACACAACAAAAAGGAGAAGAGATATTTTGGGTTCAAAAAAGTAAAAAGAT
AATGTAGCTGCATTTCTTTAGTTATTTTGAACCCCAAATATTTCTCATCTTTTTGTTGTTGTCTGGAATGGTGG
TGACATGGACTTGTTTATAGAGGACAGGTCAGCTGTCTGGCTCAATGATCTACATTCTGAAGTTGTCTGAAAATG
TCTTCATGATTAAATTCAGCCTAAACGTTTTGCCGGGAACACTGCAGAGACAATGCTGTGAGTTTCCAACCTCAG
CCCATCTGCGGGCAGAGAAGGTCTAGTTTGTCCATCACCATTATGATATCAGGACTGGTTACTTGGTTAAGGAGG
GGTCTAGGAGATCTGTCCCTTTTAGAGACACCTTACTTATAATGAAGTACTTGGGAAAGCGTTTTCAAGAGTAT
AAATATCCTGTATTCTAATGATCATCCTCTAAACATTTTATCATTATTAATCCTCCCTGCCTGTGTCTATTATT
ATATTCATATCTCTACGCTGCAAATTTTGGGTCTCAATTTTACTGTGCCTTTGTTTTTACTAGTGTCTGCTGTT
GCAAAAAGAAGAAAACATTCTCTGCCTGAGTTTTAATTTTGTCCAAAGTTAATTTTAATCTATACAATTAAC
CTTTTGCCTATCACTCTGGACTTTTGGATTGTTTTTTACATTCAGTGTATAATATTTGATTATGCTGATTGGTT
TTGGTGGGTACTGATGCGAATTAATAAAAACATTTTCATTTCC

352/6881
FIGURE 324A

GTTTTGTAACCTCAACTGGCCGGCTTCCTGGCCAAGCAGCAGAACAATACAAATATGAAGAGTGCAAAGACCTCA
TAAATCTATGCTGAGGAATGAGCTACAGTTCAAGGAGGAGAAGCTTGCAGAGCAGCTGAAGCAAGCTGAGGAGC
TCAGGTGAGGGGACCCCATGGGGGCAGGCAGGGGGGCAGGTGTGTAAATCTCTGAAGTACAACAGCTCGGTGGGG
AGACTTAAGAGCTAAGCTGGGCCAGGGGAAGGGCAGGAATTGCCATGGCAGGCTCGCTACACACAAATATTTATC
AAACAGAGAAGAAGGATAATAAAAATTTATGGGTTGCAGTGTTTCTCAGAGCCTGTTTTCTTTTTTCAAACAAGT
AATGTTGATGTGAAATTTACATAACACAAAATTAACCAAGGAGTGTGAACCACACAGCAGCATTCAGTATACTC
AAAATGGTGTGCCATCACCACCCCACTTACCCTAGTGAGAATCACCTCCTGACTGACTGCGGCTTCTCATTCTTT
CACTCAATCAATGTTGCCCTTCTCGACCCTGTCAATCTTTTCTTCTTTCGTCTTTTCAATTGCGCCCTATCTGCATC
TGGCCTCATTCTGTACATGGCTTTGTATCTAATGGCCGCAAGATGCACTATGTGTATTTTACATGGAAATGTC
CATGGCCAGAGTGAGGAACCTGAAAGGATGTCTTTTGAACGGAATTAGGAAGACACCTACTTTTGTTTACAGAG
GGGAAAGATGAATGGAACATCATCGAGGATCTTGCAGGAGCCCTCTCTGATACAGAGGAAGCCTGTAAACCATT
TCTATTCTTTCTCTTGGCCACAGACATTCCTTTCAACATGTGCTGACCTTCTGCTTGGAGGTCTCCTTGAGGACA
TTGTCTCAGAAATCTCTGTTGCAATATTTGAACGGATCACTCAACCCTTTCCTACTCTTAAATTTTCTCTACCGTC
TCACCTTAGGCAATATAAAGTCCTGGTTCACTCTCAGGAACGAGAGCTGACCCAGTTAAGGGAGAAGTTACGGGA
AGGGAGAGATGCCTCCCGCTCATTGAATGAGCATCTCCAGGCCCTCCTCACTCCGGATGAGCCGGACAAGTCCCA
GGGGCAGGACCTCCAAGAACAGCTGGCTGAGGGGTGTAGACTGGCACAACACCTTGTCCAAAAGCTCAGCCCAGA
AAATGATAACGATGACGATGAAGATGTTCAAGTTGAGGTGGCTGAGAAAGTGCAAGAAATCGTCTTCCCCCAGGGA
GATGCAGAAGGCTGAAGAAAAGGAAGTCCCTGAGGACTCACTGGAGGAGTGTGCCATCACTTGTTCAAATAGCCA
TGGCCCTTATGACTCCAACCAGCCACATAGGAAAACCAAAATCACATTTGAGGAAGACAAAGTCGACTCAACTCT
CATTGGCTCATCCTCTCATGTTGAATGGGAGGATGCTGTACACATTATCCCAGAAAATGAAAGTGATGATGAGGA
AGAGGAAGAAAAAGGGCCAGTGTCTCCCAGGAATCTGCAGGAGTCTGAAGAGGAGGAAGTCCCCCAGGAGTCTG
GGATGAAGGTTATTGACTCTCTCAATTCCTCCTGAAAGGTTGGCCTCATACCAAGTCTTACAGCAGCACATTTCA
CTCATTAGAGGAACAGCAAGTCTGCATGGCTGTTGACATAGGCAGACATCGGTGGGATCAAGTGAAAAAGGAGGA
CCAAGAGGCAACAGGTCCAGGCTCAGCAGGGAGCTGCTGGCTGAGAAAGAGCCTGAAGTCTTGCAGGACTCACT
GGATAGATGTTATTCAACTCCTTCAGTTTATCTTGGACTGACTGACTCATGCCAGCCCTACAGAAGTGCCTTTTA
CGTATTGGAGCAACAGCGTGTGGCTTGGCTGTTGACATGGATGAAATTGAAAAGTACCAAGAAAGTGAAGAAGA
CCAAGACCCATCATGCCCCAGGCTCAGCAGGGAGCTGCTGGCTGAGAAAGAGCCTGAAGTCTTGCAGGACTCACT
GGATAGATGTTATTGACTCCTTCAGGTTATCTTGAAGTGCCTGACTTAGGCCAGCCCTACAGAAGTGCCTGTTTA
CTCATTGGAGGAACAGTACCTTGGCTTGGCTCTTGACGTGGACAGAATTAAGAAAGGACCAAGAAAGAGGAAGA
CCAAGGCCCACCATGCCCCAGGCTCAGCAGGGAGCTGCTGGAGGTAGTAGAGCCTGAAGTCTTGCAGGACTCACT
GGATAGATGTTATTCAACTCCTTCAGTTGTCTTGAACAGCCTGACTCCTGCCAGCCCTACAGAAGTTCCTTTTA
TGCATTGGAGGAAAAACATGTTGGCTTTTCTCTTGACGTGGGAGAAATTGAAAAGAAGGGGAAGGGGAAGAAAAG
AAGGGGAAGAAGATCAAAGAAGAAAAGAAGAAGGGGAAGAAAAGAAGGGGAAGAAGATCAAACCCACCATGCCC
CAGGCTCAACAGCGTGCTGATGGAAGTGGAAGAGCCTGAAGTCTTGCAGGACTCACTGGATAGATGTTATTGAC
TCCATCAATGTACTTTGAACTACCTGACTCATTCCAGCACTACAGAAGTGTGTTTTACTCATTGAGGAACAGCA
CATCACCTTTGCCCTTGACATGGACAATAGCTTTTTTACTTTGACGGTGACAAGTCTCCACCTGGTCTTCCAGAT
GGGAGTCATATTCCCACAATAAGCAGCCCTTACTAAGCCGAGAGGTGTCATTCTGCAGGCAGGACCTATAGGCA
CCTGAAGATTTGAATGAACTATAGTTCCATTTGGAAGCCAGACATAGGATGGGTGAGTGGGCATGGCTCTATT
CCTATTCTCAGAGCATGCCAGTGGCAACCTGTGCTCAGTCTGAAGACAATGGACCCACGTTAGGTGTGACACGTT
CACATAACTGTGCAGCACATGCCGGGAGTGATCAGCCGGACATTTTAAATTTGAACCATGTATCTCTGGGTAGCTA
CAAAATTCCTCAGGGATTTCAATTTGCAGGCATGTCTCTGAGCTTCTATACCTACTCAAGGTGAGTGTATCTTT
GTGTTTAGTTTATCCAAAGGTGTTACCCTGGTTTCAATGAACCTAACCTCATTATTTGTGTCTTCAAGTGTGGCT
TGTTTTAGCTGATCCATCTGTAACACAGGAGGGATCCTTGGCTGAGGATTGTATTTGAGAACCACTGCTCT
TGACAATTGTTAACCCTGCTAGGCTCCTTTGGTTAGAGAAGCCACAGTCCTTCAGCCTCCAATTGGTGTGAGTACT
TAGGAAGACCACAGCTAGATGGACAAACAGCATTGGGAGGCCCTTAGCCCTGCTCCTCTCAATTCCATCCTGTAGA
GAACAGGAGTCAGGAGCCGCTGGCAGGAGACAGCATGTCAACCAGGACTCTGCCGGTGCAGAAATATGAGCAATGC
CATGTTCTTGCAGAAAACGCTTAGCCTGAGTTTCATAGGAGGTAATCACCAGACAAGTGCAGAAATGTAGAACACT
GAGCAGGACAACCTGACCTGTCTCCTTCACATAGTCCATATCACCACAAATCACACAACAAAAGGAGAAGAGATA

353/6881
FIGURE 324B

TTTTGGGTTGAAAAAAGTAAAAAGATAATTAGCTGCATTTCTTTAGTTATTTTGAACCCCAAATATTTCCCTCAT
CTTTTTGTTTGTTCATTGATGGTGGTGACATGGACTTGTTTATAGAGGACAGGTCAGCTCTCTGGCTCAATGAT
CTACATTCTGAAGTTGTCTGAAAATGTCTTCATGATTAAATTCAGCCTAAACTTTTTGCTGGGAACACTGCAGAG
ACAATGCTGTGAGTTTCCAACCTCAGCCCATCTGCGGGCAGAGAAGGTCTAGTTTGTCCATCACCATTATGATAT
CAGGACTGGTTACTTGTTAAGGAGGGGTCTAGGAGATCTGTCCCTTTTAGAGACACCTTACTTATAATGAAGTA
CTTGGGAAAGCGGTTTTCAAGAGTATAAATATCCTGTATTCTAATGATCATCCTCTAAACATTTTATCATTATT
AATCCTCCCTGCCTGTGTCTATTATTATATACATATCTCTACGCTGCAAATTTTGGGTCTCAATTTTACTGTGC
CTTTGTTTTTACTAGTGTCTGCTGTTGCAAAAAGAAGAAAACATTCTCTGCCTGAGTTTTAATTTTTGTCCAAAG
TTAATTTTAATCTATACAATTAAACCTTTTGCCTATC

354/6881
FIGURE 325

MLRNELQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLNEHLQALLTPDEPKSQGGDL
QEQLAEGCRLAQHLVQKLSPENDNDDDEDVQVEVAEKVQKSSSPREMQAEEKEVPEDSLEECAITCSNSHGPYD
SNQPHRKTKitFEEDKVDSTLIGSSSHVEWEDAVHIIPENESDDEEEEKGPVSPRNLQESEEEVVPQESWDEGY
STLSIPPERTSVGSSEKGGPRGNRSQAQQAAG

355/6881
FIGURE 326

CTCCGCGGTCTTCTGAGCGGTACAGTGAACGGCTTCCTGCAGGCTGGCCATGGCGCTTCAAGTTCCCAAGGCTCC
GGGCTTCGCCCAGATGCTCAAGGAGGGAGCGAAACACTTTTCAGAATTAGAAGAGGCTGTGTATAGAAACATACA
AGCTTGCAAGGAGCTTGCCCAAACCACTCGTACAGCATATGGACGAAATGGAATGAAAAAATGGTTATCAACTA
CTTGGAGAAGTTGTTTGTGACAAATGATGCAGCGACTATTTTAAGAGAAGTACAAGTACAGCATCCTGCTGCAAA
AATGACTGTAATGGCTTCTCATATGCAAGAGCAAGAAGTTGGAGATGGCACAAACATTGTTCTGGTATTTGCTGG
AGCTCTCCTGGAATTAGCTGAAGAAGTTCTGAGGATTGGCCTGTCAGTTTCAGAGGTCATAGAAGGTTATGAAAT
AGCTTGCAAGGAGCTCATGAGATTCTTCTAATTTGGTACGTTGTTCTGCAAAAAACCTTCGAGATGTTGATGA
AGTCTCATCTCTACTTCGTACCTCTGTAATGTGTAAACAATATGGTAATGAAGTATTTCTGGCCAAGCTTATTGT
TCAGGCATGCGTATCTATTTTTCTGATTCTGGCCATTTCAAAGTTGATAACATCAGAGTTTGTAATAATCTGGG
CTGTGGTATCACTTCCTCTTCAGTATTGCATGGCATGGTTTTTAAGAAGGAAACAGAAGGTGATGTACATCTGTC
AAAGATGCAAAAAATAGCAGTGTACTCTTGTCTTTTGTATGGCATGATAACAGAACTAAGGGAACAGTGTTGATA
AAGACTGATGAAGAATTGATGAATTTAAGTAAGGGAGAAGAAAATCTCATGGATGCATAAGTCAAAGCTATTGCT
GATACTGGTGCAAAATGTTGTAGTAACAGGTGGCAAAGTGGCAGACATGGCTCTTCATTATGCAACAAATATAAT
ATGATGTTAGTGAAGCTAAACTCAAATGGGATGTCTGAAGACTCTGTAAAACAGTTGGTGCTACAGCTCTTCCT
AGATTGACACCTCCTGTCTTGAAGAAATGGGACACTGAGACAGTGTTCCTCTCAGAAGTTGGAGATACTCAG
GTGGTGGTTTTTAAGCATGAAAAGGAAGATGGCATCATTTCTACCATAGTACTTCAGGGCTCTACAGACAATCTG
ATGGATGACATAGAAAGGGCAGTAGATGATGGTGTTAATACTTTCAAAGTTCTTACAAGGGATAAACGTCTTGTA
CCCGGAGGTGGAGCAACAGAAATTGAATTAGCCAAACAGATCACATCATATGGAGAGACATGTCTGGACTTGAA
CAGTACGCTATTAAGAAGTTTGCTGAGGCGTTTGAAGCTATTCCCCGTGCACTGGCAGAAATACTCTGGAGAAAA
CTCTGGAGTTAAGGCCAATGAAGTAATCTCTAAACTTTATGCAGTACCTCAAGAAGGAAATAAAAAATGTTGGATT
AGATACTGAGGCTGTAGTCCCTGCTGTAAACGGACATGTTGGAAGCTGGTGTTCTAGATACTTACCTGGGAAAACA
CTGGTCTATCAAACCTCGCTGCTAATGCTGCAGTCACTGTACTTAGAGTGGGTCAGGTAATCATGGCAAAACCAGA
TGGTGGGCCCCAAGCCTCCAAGTGGGAAGAAAGACTGGGATGATGACCAAAATGATTGAAATTGGCTTAATTTT
CTGTAGGTGAAGGCTGTATTTGTAGTAGTATTCTAAGAATCGCGTGATGTTTTCTTATTCTCCTTACATTAAGAG
GTATTTTGTGTTTGTATTCTTGGCTGGATGTTATAATAACATATTGTTACTGTC

356/6881
FIGURE 327

GGGCTTCGCCCAGATGCTCAAGGAGGGAGCGAAACACTTTTCAGAATTAGAAGAGGCTGTGTATAGAAACATACA
AGCTTGCAAGGAGCTTGCCCAAACCACTCGTACAGCATATGGACGAAATGGAATGAAAAAATGGTTATCAACTA
CTTGAGAGAAGTTGTTTGTGACAAATGATGCAGCGACTATTTTAAGAGAACTAGAAGTACAGCATCCTGCTGCAAA
AATGACTGTAATGGCTTCTCATATGCAAGAGCAAGAAGTTGGAGATGGCACAAACATTGTTCTGGTATTTGCTGG
AGCTCTCCTGGAATTAGCTGAAGAACTTCTGAGGATTGGCCTGTCAGTTTCAGAGGTCATAGAAGGTTATGAAAT
AGCTTGCAAGAAAGCTCATGAGATTCTTCCTAATTTGGTACGTTGTTCTGCAAAAAACCTTCGAGATGTTGATGA
AGTCTCATCTCTACTTCGTACCTCTGTAATGTGTAAACAATATGGTAATGAAGTATTTCTGGCCAAGCTTATTGT
TCAGGCATGCGTATCTATTTTTCCTGATTCTGGCCATTTCAAAGTTGATAACATCAGAGTTTGTAATAATTCTGGG
AACAGTGTTGATAAAGACTGATGAAGAATTGATGAATTTAAGTAAGGGAGAAGAAAATCTCATGGATGCATAAGT
CAAAGCTATTGCTGATACTGGTGCAAATGTTGTAGTAACAGGTGGCAAAGTGGCAGACATGGCTCTTCATTATGC
AAACAAATATAATATGATGTTAGTGAAGCTAAACTCAAATGGGATGTCTGAAGACTCTGTAAACAGTTGGTGC
TACAGCTCTTCCTAGATTGACACCTCCTGTCCTTG

357/6881
FIGURE 328

GTGGGTAGGAGCTTGCTTATAGAAAAGTGAATCGAGTAGTCCTTGCTGGTGGAGCCGCTGCCGCCAGGGAACTC
AGGGCCGGCTCCTGTTCCCTTCAAGAGTGCTGGAGGCCAAACTTGAAATACAAGTTTAATGTTTCCTCGTCGGGCAA
AAGATAAGGATCCGATCTCCCCGGCCCCGGTGTGCAGCAGGAGCGACCAACCCCGACCCGGGTAAAACTCCCAG
GGACTCTTCGCTGCTGCCACCTCTTGTTCTCTCCCCGTTCCCACTCGGGGTCTCCCTCAGGGCCGGGAGGCACA
GCGGTCCCTGCTTGCTGAGGGGCTGGATGTACGCATCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCC
CGGCGCCCGCAGAAGACTTGTTGTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCA**ATG**ATC
ACTGGTGTGTTACAGCATGCGCTTGTTGGACCCCACTGGGGCGTCTGACCTCGCTGGCGTACTGCCTGCACCAGCGG
CGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGCCTGCTGAAGTTGAAAATG
GTGCAGGTGCTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCCGCTCCCGCTGGAGGAGCAGGTAGAGTGGAAC
CCCCAGCTATTAGAGGTCCCACCCCAAACCTCAGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCA
TATTCTCCTTACGACTCTCAATACCATGAGACCACCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTG
GGCATGCAGCAAAATGTTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTCTTTCACCA
ACCTTCAACCCACAGGAGGTCTTTATTTCGTTCCACTAACATTTTTTCGGAATCTGGAGTCCACCCGTTGTTTGCTG
GCTGGGCTTTTCCAGTGTGAGAAAGAAGGACCCATCATCATCCACACTGATGAAGCAGATTGAGAAGTCTTGAT
CCCAACTACCAAAGCTGCTGGAGCCTGAGGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGA
ATCTCAGAGGATTTGAAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTC
CTGGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTGCACGGATGATC
GAACAGAGAGCTGTGGACACATCCTTGTTACATACTGCCCAAGGAAGACAGGGAAAGTCTTCAGATGGCAGTAGGC
CCATTCTCCACATCCTAGAGAGCAACCTGCTGAAAGCCATGGACTCTGCCACTGCCCCGACAAGATCAGAAAG
CTGTATCTCTATGCGGCTCATGATGTGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTTTGACCACAAATGG
CCACCGTTTGCTGTTGACCTGACCATGGAACCTTTACCAGCACCTGGAATCTAAGGAGTGTTTTGTGCAGCTCTAT
TACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGTTCTTGAATGCCATG
TCAGTTTATACCTTAAGCCCAGAAAAATACCATGCACCTCTGCTCTCAAACCTCAGGTGATGGAAGTTGGAAATGAA
GAG**TAA**CTGATTTATAAAAGCAGGATGTGTTGATTTTAAAATAAAGTGCCTTTATACAATGCCAAAAAAAAAAAA
AAAAAAAAAAAA

358/6881
FIGURE 329

MITGVFSMRLWTFVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLMVQVVFRHGARSPLKPLPLEEQVE
WNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQLTKVGMQQMFALGERLRKNYVEDIPFL
SPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKEGPIIIHTDEADSEVLYPNYQSCWSLRQRTGRRTASLQ
PGISEDLKVKVDRMGIDSSDKVDFFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMA
VGPFLHILESNNLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEWFVQ
LYYHGKEQVPRGCPDGLCPDLMFLNAMS VYTLSP EKYHALCSQTQVMEVGNEE

359/6881
FIGURE 330

CTTAAAGTGAAATAATTTTTTGCAAAGGGGTTTCCTCGATTGAGCTTTTTTTTTCTTCCACCGTCATTTCTAA
CTCTTAAAACCAACTCAGTTCCATCATGGTGATGTTCAAGAAGATCAAGTCTTTTGAGGTGGTCTTTAACGACCC
TGAAAAGGTGTACGGCAGTGGCGAGAAGGTGGCTGGCCGGGTGATAGTGGAGGTGTGTGAAGTTACTCGTGTCAA
AGCCGTTAGGATCCTGGCTTGCGGAGTGGCTAAAGTGCATCCTCAACAACAATGTGCAGTGAGCATGTGGAAGAA
AAGAAGCAGCTTTACCTACTTGTTTTCTTTTTGTCTCTCTTCCTGGACACTCACTTTTTCAGAGACTCAACAGTCT
CTGCAATGGAGTGTGGGTCCACCTTAGCCTCTGACTTCCTAATGTAGGAGGTGGTCAGCAGGCAATCTCCTGGGC
CTTAAAGGATGCGGACTCATCCTCAGCCAGCGCCCATGTTGTGATACAGGGGTGTTTGTGGATGGGTTTAAAAA
TAACTAGAAAAACTCAGGCCCATCCATTTTCTCAGATCTCCTTGAAAATTGAGGCCTTTTCGATAGTTTCGGGTC
AGGTAAAAATGGCCTCCTGGCGTAAGCTTTTCAAGGTTTTTGGAGGCTTTTGTAAATTGTGATAGGAACTTTG
GACCTTGAAC TTATGTATCATGTGGAGAAGAGCCAATTTAACAACTAGGAAGATGAAAAGGGAAATTGTGGCCA
AACTTTGGGAAAA

360/6881
FIGURE 331

TGACTTGCTCACTATCATGAACTCAAAAGAACTAGCAATTTTTTAGACTTCTTTTGGGATCCTTGTACCGCATC
CTATACTGCTTTTATGTTTCATGTGTGCATTTGTGTACATGTATACACATATTACTCCATAACGAAGCACAGTCTT
CTTTTATACCTTTCCCTGGTTGGGGTAGTAGAGGAATTTTACAGCCTACAATCAGACACATCCAGAAGAAGAGTGG
AATATGTATGATACCTTAAAAATCAGCACATTTAACAAAGTATAAATTACTCATGGTTACAATAAGTTAATGTT
TTTTCCCTTTATTTTTCAAAAGGCTCATTTTTCTCCATTTCTCTACTATCAAAGTCAAGAACTGCCCCAATGGCTC
TGTC AAGGAGGCTCCAGCTCCTACTCCCACTTCTCTGGAAGTCTCAAGTCCACCAGATACTACAGAGGAAGAAGA
TCATAAGCCTAAACTCTGCAGGCTGGCTAAAGGTGAAAATGGCTATGGCTTTCACTTAAATGCGATTTCGGGGTCT
GCCAGGCTCATTCATCAAAGAGGTACAGAAGGGCGGTCCTGCTGACTTGGCTGGGCTAGAGGATGAGGATGTCAT
CATTGAAGTGAATGGGGTGAATGTGCTAGATGAACCTATGAGAAGGTGGTGGATAGAATCCAGAGCAGTGGGAA
GAATGTCACACTTCTAGTCTGTGGAAAGAAGGCCTATGATTATTTCCAAGCTAAGAAAATCCCTATTGTTTCCTC
CCTGGCTGATCCACTTGACACCCCTCCAGATTCTAAAGAAGGAATAGTGGTGGAGTCAAAGCATGACTCGCACAT
GGCAAAAGAACGGGCCACAGTACAGCCTCACATTCTTCTTCCAATTCTGAAGATACAGAGATGTGATGAAAACA
AGCGGCTATTGCAGACGGCTAATTTATGCTTAACTTAGGAAGAGATAAGGTTTCCTTGAGCACCAAAGATGATTCA
TAACTCTGTATAGGTGACAGCTGCTTATAAAAGCATCTTAGCAGATAAGCCTATTAAAATTGTGCTTTTGTAAACA
ATGTTGTGGTTGCTAGATAAATAACCATTAACAAA

361/6881
FIGURE 332

GTCCCAACTCTTGGACTCCATTTGCTATTCTCTTCTTTCTCCCCACACCTATCTGGTGGTGGTAGTGGGCGTTT
ATATTTGCGTTCCTTTTCATTCATTTCTAAATCTCTTAAAAATTTTGGGTTGGGGGTATTGGGGAAGGCAGGAAA
GGGAAAAGGAGAGTAGTAGCTGAAGAGCAAGAGGAGGACATGGAGATGAAGAAGAAGATTAACCTGGAGTTAAGG
AACAGATCCCCGGAGGAGGTGACAGAGTTAGTCCTTGATAATTGCCTGTGTGTCAATGGGGAAATTGAAGGCCTG
AATGATACTTTCAAAGAACTAGAATTTCTGAGTATGGCTAATGTGGAACCTAAGTTCGCTGGCCCGGCTTCCCAGC
TTAAATAAACTTCGAAAATTGGAGCTTAGTGATAATATAATTTCTGGAGGCTTGGAAGTCCTGGCAGAGAAATGT
CCAAATCTTACCTACCTCAATCTGAGTGGAAACAAAATAAAAGATCTCAGTACAGTAGAAGCTCTGCAAAATCTT
AAAAATTTGAAAAGTCTTGACCTGTTTAACTGTGAGATCACAAACCTGGAAGATTATAGAGAAAGTATTTTGA
CTACTGCAGCAAATCACATACTTAGATGGATTGATCAGGAGGATAATGAAGCGCCGGACTCTGAAGAGGAGGAT
GATGAGGATGGAGATGAAGATGATGAAGAGGAAGAGGAAAATGAAGCTGGTCCACCGGAAGGATATGAGGAAGAG
GAGGAGGAAGAGGAAGAGGAGGATGAGGATGAGGATGAAGATGAAGATGAAGCAGGTTGAGAGTGGGAGAGGGA
GAAGAGGAAGTGGGCCTCTCATACTTAATGAAAGAAGAAATTCAGGATGAAGAAGATGATGATGACTATGTTGAA
GAAGGGGAAGAAGAGGAAGAAGAGGAAGAAGGAGGTCTTCGAGGGGAGAAGAGGAAACGAGATGCTGAAGACGAT
GGAGAGGAAGAAGATGACTTAGATCATTCTAAGACCAGATTCTCTAATGTTTCTGGGTGTGCAATAGAGTGATCAC
ATCTTTGTTTCTTCATGTACGATAGCTATCCCTACAGAAGATAATGTGTAACTTTTTATAGGAAAAGTGTGGTTT
TACTATTTTTGCCTTATCATTCCAAATAAGAACTAGTCTGTTAATGATCATATTGTATGTAGAGAAAAATTTCA
TTGACTCCCATTTGTGGAATTCCTAGCAATTTATTTAGACTTAATTTTTTAAATTCAAGCTTACTGTATTAGTCA
TTTTTAGCCATAATTAAACATGATCACTTTTAAAAAAAAAAAAAAAAAAAAA

362/6881
FIGURE 333

MEMKKKINLELRNRSPEEVTELVLDNCLCVNGEIEGLNDTFKELEFLSMANVELSSLARLP SLNKL RKLELS DNI
ISGGLEVLA EKCPNLTYLNLSGNKIKDLSTVEALQNLK NLKSLDLFNCEITNLEDYRESIFELLQQITYLDGFDQ
EDNEAPDSEEEDEDEDGDEDEDEEEENEAGPPEG YEEEEEEEEDEDEDEDEDEDEAGSELGEGEEVGLSYLMKEE
IQDEEDDDDYVEEGEEEEEEEEEGGLRGEKRKRDAEDDGEEEDD

363/6881
FIGURE 334

GTGGGGTCGCGTTGCCACCCACGCGGACTCCCCAGCTGGCGCGCCCCCTCCCATTTGCCTGTCCTGGTCAGGCCC
CCACCCCCCTTCCCACCTGACCAGCCATGGGGGGCTGCGGTGTTTTTCGGCTGCACTTTTCGTGCGGTTCCGGCCCGG
CCTTCGCGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCAGGGGCATTTTTCT
GGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTTCATCTTGGTCCATGTGACCGACCGGTCAGATGCCCGGC
TCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTCTGTCTTCTACAGGAGGTGTTCCGCTTTGCCTACTACA
AGCTGCTTAAGAAGGCAGATGAGGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGA
TGGCCTATGTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCTGATGCAC
TTGGGCCAGGTGTGGTTGGGATCCATGGAGACTCACCTATTACTTCCCTGACTTCAGCCTTTCTGACAGCAGCCA
TTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATGCCTGTGAGAGGAGACGGTACTGGGCTTTGGGCC
TGGTGGTTGGGAGTCACCTACTGACATCGGGACTGACATTCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCCA
TCTATGCAGTCACTGTTTCCATGGGGCTCTGGGCCTTCATCACAGCTGGAGGGTCCCTCCGAAGTATTACAGCGCA
GCTCTTGTAAGGACTGACTACCTGGACTTGATCGCCTGACAGATCCCACCTGCCTGTCCACTGCCCATGACTGA
GCCAGCCCCAGCCCGGGGTCCATTGCCACATTCTCTGTCTCCTTCTCGTCGGTCTACCCCACTACCTCCAGGG
TTTTGCTTTGTCTTTTGTGACCGTTAGTCTCTAAGCTTTACCAGGAGCAGCCTGGGTTACGCCAGTCAGTGACT
GGTGGGTTTGAATCTGCACTTATCCCCACCACCTGGGGACCCCTTGTGTGTGCCAGGACTCCCCCTGTGTCAGT
GCTCTGCTCTCACCTGCCCAAGACTCACCTCCCTTCCCTCTGCAGGCCGACGGCAGGAGGACAGTCGGGTGAT
GGTGTATTCTGCCCTGCGCATCCCACCCGAGGACTGAGGGAACCTAGGGGGACCCCTGGGCCTGGGGTGCCCTC
CTGATGTCTCTGCCCCGTATTTCTCCATCTCCAGTTCTGGACAGTGCAGGTTGCCAAGAAAAGGGACCTAGTTTA
GCCATTGCCCTGGAGATGAAATTAATGGAGGCTCAAGGATAGATGAGCTCTGAGTTTCTCAGTACTCCCTCAAGA
CTGGACATCTTGGTCTTTTTCTCAGGCCTGAGGGGGAACCATTTTTGGTGTGATAAATACCCTAAACTGCCTTTT
TTTCTTTTTTTGAGGTGGGGGGAGGGAGGAGGTATATTGGAACCTTCTAACCTCCTTGGGCTATATTTTCTCTCC
TCGAGTTGCTCCTCATGGCTGGGCTCATTTCGGTCCCTTTCTCCTTGGTCCCAGACCTTGGGGGAAAGGAAGGAA
GTGCATGTTTGGGAACCTGGCATTACTGGAATAATGGTTTTTAACCTCCTTAACCACCAGCATCCCTCCTCTCCCC
AAGGTGAAGTGGAGGGTGTCTGGTGAGCTGGCCACTCCAGAGCTGCAGTGCCACTGGAGGAGTCAGACTACCAT
GACATCGTAGGGAAGGAGGGGAGATTTTTTTGTAGTTTTTAATTGGGGTGTGGGAGGGGCGGGGAGGTTTTTCTAT
AAACTGTATCATTTTCTGCTGAGGGTGGAGTGTCCCATCCTTTTAATCAAGGTGATTGTGATTTTGACTAATAAA
AAAGAATTTGTAAAAAA

364/6881
FIGURE 335

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIILVAGAFFWLVSLLLASVVWFILVHVTD RSDARLQYGLLIFG
AAVSVLLQEVFRFAYYKLLKKADEGLASLSE DGRSPISIRQMAYVSGLSFGIISGVFSVINILADALGPGVVG I H
GDSPYYFLTSAFLTAAILLHTFWGVVFFDACERRRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMG
LWAFITAGGSLRSIQRSSCVRTDYLD

365/6881
FIGURE 336

TTCCGGTGGGCTAGGTACTGAGCGCGCGAGGCTCTACAGAGTGAAGGTTTAAATCCAAGGTCATGGCAAAACATC
TGAAGTTCATCGCCAGGACTGTGATGGTACAGGAAGGGAACGTGGAAAGCGCATAACAGGACCCTAAACAGAATCC
TCACTATGGATGGGCTCATTGAGGACATTAAGCATCGGCGGTATTATGAGAAGCCATGCCGCCGGCGACAGAGGG
AAAGCTATGAAAGGTGCCGGCGGATCTACAACATGGAAATGGCTCGCAAGATCAACTTCTTGATGCGAAAGAATC
GGGCAGATCCGTGGCAGGGCTGCTTGAGGCCTGTGGGTGGGACACCCAGTGCGAAACCCTCATCCAGTTTTCTCTC
CATCTCTTTTCTTTGTACAATCCCATTTCTATTACCATTTCTCTGCAATAAACTCAAATCACATGTCTGCAAAAA

366/6881
FIGURE 337

MAKHLKFIARTVMVQEGNVESAYRTLNRILTM DGLIEDIKHRRYYEKPCRRRQRESYERCRIYNMEMARKINFL
MRKNRADPWQGC

367/6881
FIGURE 338A

ATGTCTCCACTTCTGAGAAGCATCTGTGACATCACTGAAATTTTCAATCAGTATGTCTCTCATGATTGTGATGGA
GCAGCATTAACCTAAGAAAGACCTGAAGAACTCCTTGAAAGGGAATTTGGAGCTGTGCTTCGGAGACCACATGAC
CCTAAGACGGTAGATCTGATCCTGGAACCTTCTGGATCTTGACAGTAATGGGCGTGTGATTTCAACGAATTCCTC
CTATTTATTTTCAAAGTGGCTCAAGCTTGTTACTATGCTCTCGGCCAGGCCACGGGACTGGATGAGGAGAAGCGA
GCCCCGGTGTGACGGAAGGAGAGCCTGTTACAAGATCGCAGGCAAGAAGAAGACCAAAGGAGATTTCGAGCCCCGG
GACAGACAACCTGGAAGAAGAACCTGGGCAACGACGCAGGCAGGAAGAGGCAGGAACAGGAGAGGGAGCTAGCTGAG
GGAGAGGAGCAAAGTGAGAAACAAGAGCGACTTGAACAGCGCGACAGGCAGCGCCGCGACGAGGAGCTGTGGCGG
CAAAGGCAAGAATGGCAAGAACGGGAAGAGCGCCGTGCAGAGGAAGAGCAGCTGCAGAGTTGCAAAGGTCACGAA
ACTGAGGAGTTTCCAGACGAAGAGCAACTGCGAAGGCGGGAGCTGCTGGAGCTGAGGAGGAAGGGCCGCGAGGAG
AAACAGCAGCAAAGGCGAGAGCGGCAAGACAGAGTGTTCCAGGAGGAAGAAGAGAAAGAGTGAGGAAGCGCGAG
ACAGTGCTCCGGAAGGAAGAAGAGAAGCGCAACGTTGGCTGAAGCTCGAGGAGGAGGAGAGGCGCGAGCAGCAG
GAGAGGCGCGAGCAGCAACTAAGGCGGGAGCAAGAGGAGAGGCGCGAGCAGCGGCTGAAGCGCCAGGAGGAGGAA
GAGAGGCTCCAGCAGCGGTTGAGGAGCGAGCAACAATAAGACGCGAGCAGGAGGAGAGGCGCGAGCAGCTGCTG
AAGCGCGAGGAGGAGAAGAGGCTCGAGCAGGAGAGGCGAGAGCAGCGGCTGAAGCGCGAGCAGGAGGAGAGGCGC
GATCAGCTGCTGAAGCGCGAGGAGGAGAGGCGCCAGCAGCGGCTGAAGCGCGAGCAGGAAGAGAGGCTCGAGCAG
CGACTGAAGCGCGAGGAGGTGGAGAGACTCGAGCAGGAGGAGAGGCGCGAGCAGCGGCTGAAGCGCGAGGAGCCG
GAGGAAGAGAGGCGCCAGCAGCTGCTGAAGAGCGAGGAGCAGGAGGAGAGGCGCCAGCAGCAACTAAGGCGCGAG
CAGCAGGAAGGCGCGAGCAGCGGCTGAAGCGCGAGGAGGAGGAAGAGAGGCTCGAGCAGCGGCTGAAGCGCGAG
CATGAGGAAGAGAGGCGCGAGCAGGAGCTAGCTGAGGAGGAGCAGGAACAGGCCCGGAGCGGATTAAGAGCCGC
ATCCCGAAGTGGCAGTGGCAGCTAGAAAAGCGAGGCCGACGCACGGCAAAGCAAAGTCTACTCGAGGCCCGCGCAAG
CAGGAAGGGCAGAGGCGCCGCCAAGAGCAGGAGGAAAAGAGGCGGCGCGGGAGAGTGAGCTGCAATGGCAGGAG
GAGGAACGGGCTCACCGGCAGCAGCAGGAAGAGGAGCAGCGCCGGGACTTCACATGGCAGTGGCAGGCGGAGGAA
AAGAGCGAGAGGGGCGCTCAGAGGCTGTGCGCCAGGCCCCATTGCGGGAGCAGCGGGAGAGGCAGCTGAGGGCC
GAGGAGCGCCAGCAGCGGGAACAACGGTTTTCTCCCGAGGAGGAGGAGGAAGGAGCAGCGGCGCCGCCAGCGACGC
GAGAGGGAGAAAGAGCTGCAGTTCTTGAGGAAGAGGAGCAGCTCCAGCGGCGGGAGCGTGCCCAACAGCTCCAG
GAGGAGGAGGACGGCTCCAGGAGGATCAGGAGAGGAGGCGAAGCCAGGAGCAGCGCCGCGACCAAAAATGGAGG
TGGCAACTAGAAGAAGAAAGGAAGAGACGCCGCCACACGCTGTACGCCAAGCCAGCCCTACAAGAGCAGCTGAGG
AAGGAACAGCAGCTGTGTCAGGAGGAGGAGGAGGAGCTACAGAGAGAGGAGCGCGAGAAGAGAAGGCGCCAAGAA
CAGGAGAGACAATACCGCGAGGAAGAGCAGCTGCAGCAGGAGGAAGAGCAGCTGCTGAGAGAGGAACGGGAGAAA
AGAAGACGCCAGGAGCGGGAAAGGCAATATCGGAAGGATAAGAAGCTGCAGCAGAAGGAAGAGCAGCTGCTGGGA
GAGGAACCGGAGAAGAGAAGGCGCCAGGAGCGGGAGAAAAAATACCGCGAGGAAGAGGAGTTGCAGCAGGAGGAA
GAGCAGCTGCTGAGAGAGGAACGGGAGAAGAGAAGGCGCCAGGAGTGGGAGAGGCACTACCGCAAAAAGACGAG
CTGCAGCAGGAAGAAGAGCAGCTGCTGAGAGAGGAACGGGAGAAAAGAAGACTCCAGGAGCGGGAGAGGCAATAT
CGGGAGGAAGAGGAGCTGCAGCAGGAGGAAGAGCAGCTGCTGGGAGAGGAACGGGAGACGAGAAGGCGCCAGGAG
CTGGAGAGGCAATATCGGAAGGAAGAGGAGCTGCAGCAGGAGGAAGAGCAGCTGCTGAGAGAGGAACGGGAGAAG
AGAAGGCGCCAGGAGCGGGAGAGGCAATGCAGAGAGAATGAACAGTTCCGGCAGTTGGAAGATTCCCAGCTGCGC
GACAGACAATCCCAGCAAGATCTGCAGCACCTGCTGGGTGAACAGCAAGAGCGAGATCGTGAGCAAGAGAGGAGG
CGCTGGCAGCAGCGCGACAGGCATTTCCAGAGGAAGAACAGCTGGAGCGAGAAGAGCAAAAGGAAGCCAAAAGG
CGCGACAGGAAGTCCCAAGAGGAAAAGCAGTTGCTGAGAGAGGAAGAGAAGAGAAGAGACGCCGTCAAGAGACA
GACAGAAAAATTCCGCGAGGAGGAACAGCTGCTCCAGGAAGGGAGGAACAGCCGCTGCGCCGCCAAGAGCGTGAC
AGAAAAATTCCGCGAAGAGGAACTGCGCCATCAGGAACAAGGGAGAAAATTCTCGAGGAGGAACAGCGGCTGCGC
CGCCAGGAACGGGAGAGAAAATTCTTAAGGAGGAACAGCAGCTGCGCTGCCAGGAGCGCGAGCAACAGCTGCGT
CAGGACCGCGACAGAAAATTCCGCGAGGAGGAACAGCAGCTGAGCCGCCAAGAGCGTGACAGAAAATTCCGTGAA
GAGGAACAGCAGGTGCGCCGCCAGGAACGAGAGAGAAAATTCTTGAGGAGGAACAGCAGCTGCGCCAGGAGCGT
CACAGAAAATTCCGCGAAGAGGAACAGCTGCTCCAGGAAGGGAGAAGAACAGCAGCTGCACCGCCAAGAGCGTGAC
AGAAAATTCTTGAGGAGGAACAACAGCTGCGCCGCCAAGAGCGTGACAGAAAATTCCGCGAACAGGAACCTGCGC
AGTCAGGAACAGAGAGAAAATTCTCGAGGAGGAACAGCAGCTGCACCGCCAGCAACGGCAGAGAAAATTCTCTC
CAGGAGGAACAGCAGCTGCGCCGCCAGGAGCGCGGGCAACAGCGGCGTCAGGACCGTGACAGAAAATTCCGCGAG

368/6881
FIGURE 338B

GAGGAACAGCTGCGCCAGGAGAGGGAGGAACAGCAGCTGAGCCGCCAAGAGCGTGACAGAAAATTCCGTTTAGAG
GAACAGAAAGTGCGCCGCCAGGAACAAGAGAGAAAATTCATGGAGGACGAACAGCAGCTGCGCCGCCAGGAGGGC
CAACAACAGCTGCGCCAGGAGCGCGACAGAAAATTCGCGAAGACGAACAGCTGCTCCAGGAAAGGGAAGAACAG
CAGCTGCACCGCCAAGAGCGTGACAGAAAATTCCTCGAGGAGGAACCGCAGCTGCGCCGCCAGGAGCGCGAACAA
CAGCTGCGTACGACCGCGACAGAAAATTCGCTGAAGAGGAACAGCTGCTCCAGGAAGGGGAGGAACAGCAGCTG
CGCCGCCAAGAGCGTGACAGAAAATTCGCGAAGAGGAACAGCAGCTCCGCCGTCAGGAACGAGAGAGAAAATTC
CTCCAGGAGGAACAGCAGCTGCGCCGCCAGGAACCTGGAGAGAAAATTCGCTGAGGAGGAACAGCTGCGCCAAGAA
ACGGAGCAAGAGCAGCTGCGCCGCCAAGAACGCTACAGAAAAATCCTAGAGGAAGAGCAGCTCCGTCCGGAAAGG
GAAGAACAGCAGCTGCGCCGCCAGGAGCGCGACAGAAAATTCGCGAGGAGGAACAGCTCCGCCAGGAGAGGGAG
GAACAGCAGCTGCGCAGCCAAGAGTCTGACAGAAAATTCGCGAGGAGGAACAGCTACGCCAGGAGAGGGAAGAA
CAGCAGCTGCGCCCCCAACAGCGTGACGGAAGTATCGCTGGGAAGAAGAGCAGCTCCAATTGAGGAACAAGAG
CAGAGGCTGCGGCAGGAGCGAGACCGGCAGTACCGGGCGGAGGAGCAGTTTGCCACGCAGGAGAAGAGTCGTCTG
GAGGAACAAGAACTATGGCAAGAAGAGGAGCAGAAACGTGCGCAGGAACGGGAAAGGAAATTACGGGAAGAACAC
ATCCGCCGCCAGCAGAAGGAGGAACAGAGGCACCGCCAAGTCGGGGAGATAAAATCCCAAGAAGGGAAGGGCCAT
GGGCGGCTTCTGGAGCCCGGCACTCATCAGTTTGCCAGTGTCCAGTGCGCTCCAGCCCTCTCTATGAGTACATC
CAAGAGCAGAGATCTCAATACCGCCCTTAA

369/6881
FIGURE 339

MSPLLRSIDITEIFNQYVSHDCDGAALTKKDLKNLLEREFGAVLRRPHDPKTVDLILELLDLDSDNGRVDFNEFL
LFIFKVAQACYALGQATGLDEEKRARCDGKESLLQDRRQEEDQRRFEPDRDRQLEEEPGQRRRQKRQEQERELAE
GEEQSEKQERLEQRDRQRDEELWRQRQEWQEREERRAEELQSQCKGHETEEFPDEEQLRRELLELRKRGREE
KQQQRREQRDRVFQEEEEKEWRKRETVLRKEEEKRERWLKLEEEERREQQERREQQLRREQEERREQRKLRQEEE
ERLQQRRLRSEQQLRREQEERREQLLKREEEKRLQEERREQRKLRQEERDQLLKREEERROQLKREQEERLEQ
RLKREEVERLEQEERREQRKLRREEPEERRQQLLKSEEQEERRQQLRREQQERREQRKLRREEEEERLEQRKRE
HEEERREQELAEELQEQARERIKSRIPKWQWQLESEADARQSKVYSRPRKQEGQRRRQEQEEKRRRRESELQWQE
EERAHRRQQEEEQRRDFTWQWQAEKSERGRQRLSARPPLEQRERQLRAEERQQREQRFLPEEEEEKEQRRRQRR
EREKELQFLEEEELQRRERAAQQLQEEEDGLQEDQERRRSQEQRRDQKWRWQLEEEERKRRRHTLYAKPALQEQLR
KEQQLLQEEEEEELQREEREKRRRQEQERQYREELQEQEEEQLLREEREKRRRQERERQYRKDKKLQKKEEQLLG
EEPEKRRRQERREKKYREELQEQEEEQLLREEREKRRRQEWERQYRKDELQEQEEEQLLREEREKRRRLQERERQY
REEEELQEQEEEQLLGEERETRRRQELERQYRKEEELQEQEEEQLLREEPEKRRRQERERQCRENEQFRQLEDSQLR
DRQSQQDLQHLLEGEQQERDRERRRWQQRDRHFPFEEQLEREEQKEAKRRDRKSQEEKQLLREEREKRRRQET
DRKFREEEQLLQEREEQPLRRQERDRKFREELRHQEQGRKFLEEEQLRRLRQERERKFLKEEQQLRCQEREQQLR
QDRDRKFREEEQQLSRQERDRKFREEEQVRRQERERKFLEEEQQLRQERHRKFREEEQLLQEREEQQLHRQERD
RKFLLEEEQQLRRQERDRKFREELRSQEPERKFLEEEQQLHRQQRQRKFLOEEQQLRRQERGGQRRQDRDRKFRE
EEQLRQEREEQQLSRQERDRKFRLQEKVRRQEQERKFMEDEQQLRRQEGQQQLRQERDRKFREDEQLLQEREEQ
QLHRQERDRKFLEEEQQLRRQEREQQLRHDRDRKFREEEQLLQEGEEQQLRRQERDRKFREEEQQLRRQERERKF
LQEEQQLRRQELERKFREEEQLRQETEQEQQLRRQERYRKILEEQQLRPEREQQLRRQERDRKFREEEQLRQERE
EQQLRSQESDRKFREEEQLRQEREQQLRPQQRDGKYRWEEELQLEEQEQRLRQERDRQYRAEEQFATQEKSR
EEQELWQEEEQKRRQERERKLRREHIRRQKEEQRRHQVGEIKSQEGKGHGRLLEPGTHQFASVPVRSSPLYEYI
QEORSQYRP

370/6881
FIGURE 340

GGGCAAGGCTGGGCGGGAAGGGCGTGGGTTGAGGAGAGGCTCCAGACCCGCACGCCGCGCGCACAGAGCTCTCA
GCGCCGCTCCCAGCCACAGCCTCCCGCGCCTCGCTCAGCTCCAACATGGCAAAAATCTCCAGCCCTACAGAGACT
GAGCGGTGCATCGAGTCCCTGATTGCTGTCTTCCAGAAAGTATGCTGGAAAGGATGGTTATAACTACACTCTCTCC
AAGACAGAGTTCCTAAGCTTCATGAATACAGAACTAGCTGCCTTCACAAAGAACCAGAAGGACCCTGGTGTCTCTT
GACCGCATGATGAAGAACTGGACACCAACAGTGATGGTCAGCTAGATTTCTCAGAATTTCTTAATCTGATTGGT
GGCCTAGCTATGGCTTGCCATGACTCCTTCCTCAAGGCTGTCCCTTCCCAGAAGCGGACCTTGAGGACCCCTTGGC
CCTGGCCTTCAAACCCACCCCTTTTCCTTCCAGCCTTTCTGTTCATCATCTCCACAGCCCACCCATCCCCTGAGCA
CACTAACCACCTCATGCAGGCCCCACCTGCCAATAGTAATAAAGCAATGTCACTTTTTTAAACATGAAA

371/6881
FIGURE 341

MAKISSPTETERCIESLIAVFQKYAGKDGNYTILSKTEFLSFMNTELAAF~~T~~KNQKDPGVLD~~R~~MMKKLD~~T~~NSDGQL
DFSEFLNLIGGLAMACHDSFLKAVPSQKRT

372/6881
FIGURE 342

CCGGTGGGGCGGGAAGCCCGGCTTCTGGGGAGGTGCCGCCCCTCCACTGGCGCAGGCCGCCGAGACCCCCAGACG
GACCTCCTAGGGCTAATCTGATAGTGCTTCTGAGGTCGATAGGACTCCACGTGCCACTCCCTGCAGGGTCATCCA
GCAAGTAATTCTAGACCCGTAGGTGGCCGCAGAGCCGTTACCTCTGGTTCTGCGCCAGCGTGCCCCACCCGCA
GGACGGCCGGGTTCTTTGATTTGTACACTTTCTAAAACCAAACCCGAGAGGAAGGGCAGGCTCAGGGTGGGGATG
CCCTGAAATATTCTGAGAGCAGGACCGTTTCTACTGAAGAGAAGTTTACAAGAACGCTCTGTCTGGGGCGGGCGAG
GCTTCTGCGAGGCGGGTCCGGGAGCGAGGGCAGGGCGTGGGGCCGCGCGCCCGGGGTCGGGGGAGTCGGGGGCAGG
AAGAGGGGGAGGAGACAGGGCTGGGGGAGCGCCCTGCCGAGCGCCCGCCAGGCTCCTCCCGCTCCCGCGCCGCT
CCCTCTACCCACCCGCCGCACGTACTAAGGAAGGCGCACAGCCCGCCGCGCTCGCCTCTCCGCCCCGCGTCCAGC
TCGCCCAGCTCGCCAGCGTCCGCCGCGCTCGGCCAAGGCTTCAACGGACCACACCAAAATGCCATCTCAAATG
GAACACGCCCATGGAAACCATGATGTTTACATTTACAAATTCGCTGGGGATAAAGGCTACTTAACAAAGGAGGAC
CTGAGAGTACTCATGGAAAAGGAGTTCCCTGGATTTTTGGAAAATCAAAAAGACCCCTCTGGCTGTGGACAAAATA
ATGAAGGACCTGGACCAGTGTAGAGATGGCAAAGTGGGCTTCCAGAGCTTCTTTTCCCTAATTGCGGGCCTCACC
ATTGCATGCAATGACTATTTTGTAGTACACATGAAGCAGAAGGGAAAGAAGTAGGCAGAAATGAGCAGTTCGCTC
CTCCCTGATAAGAGTTGTCCCAAAGGGTCGCTTAAGGAATCTGCCCCACAGCTTCCCCCATAGAAGGATTTTCATG
AGCAGATCAGGACACTTAGCAAATGTAAAAATAAAATCTAACTCTCATTTGACAAGCAGAGAAAGAAAAGTTAAA
TACCAGATAAGCTTTTGATTTTTGTATTGTTTGCATCCCCTTGCCCTCAATAAAATAAAGTTCTTTTTTAGTTCC

373/6881
FIGURE 343

MPSQMEHAMETMMFTFHKFAGDKGYLTKEDLRVLMEKEFPGFLENQKDPLAVDKIMKDLDQCRDGKVGFSFFSL
IAGLTIIACNDYFVVHMKQKGKK

374/6881
FIGURE 344

CGGCTGAAGCGCCGCCGGCGGGGCTCACTGTGGTGGTGTGAGTGGGAGGCGGCGGCGCTGGTGGCTGCAGCTGGG
GTGAGGCGCGAGGCGGCGCACTCGACGGCTGACTGGAGCAGCGGTAAAGGCGAGGATGGAGACCGAAGGATATAA
GTCAAAGAGTACAGCAGAAAATGCTCTACTGAACGGACTTCTTGGACAAGCCTGTCCACCATTTCAGAAAATAGCCC
TGGGCCTTGGGATCCCAAGCAGTGCAACAGTTGCCTATATCCTATACCGCAGGTATAGGGAAAGCAGAGAAGAGC
GGCTGACATTTGTTGGGGAAGATGACATTGAGATAGAGATGCGGGTTCCCCAGGAGGCTGTGAAACTCATCATTG
GCCGGCAAGGAGCCAATATTAAACAGCTGCGGAAACAGACAGGTGCTCGGATTGATGTGGACACAGAGGATGTAG
GCGATGAGCGAGTGCTGCTTATCAGTGGTTTTCTGTTCAGGTGTGCAAGGCCAAAGCAGCAATCCATCAGATCC
TGACAGAGAATACCCAGTGTCTGAGCAGCTTTCAGTTCCCCAGAGATCTGTGGGCAGAATCATAGGGGAGAGGCG
GCGAGACAATTCGTTCTATCTGTAAGGCATCTGGAGCCAAAATTACCTGTGACAAAGAATCAGAAGGGACATTAC
TACTATCAAGACTTATAAAAATCTCAGGAACACAGAAGGAAGTGGCAGCAGCCAAGCATTGTGATACTGGAGAAAG
TTTCAGAAGATGAAGAACTTCGGAAGAGAATTGCTCATTCTGCAGAAACCAGGGTCCCACGCAAACAGCCAATCA
GTGTGAGAAGAGAAGACATGACAGAGCCAGGTGGAGCTGGAGAGCCAGCATTATGGAAAAACACCAGTTCTAGCA
TGGAGCCGACTGCACCCCTGGTGACTCCTCCACCCAAAGGAGGAGGCGACATGGCTGTGGTAGTGTCAAAGGAAG
GTTCTTGGGAGAAACCTAGTGATGACAGCTTTCAGAAGTCTGAAGCCCAGGCCATCCAGAGATGCCCATGTTTG
AAATCCCCAGTCTGACTTCAGTTTTCATGCTGATGAGTACCTAGAAGTCTACGTTTCTGCTTCTGAGCACCTTA
ACCACTTCTGGATCCAGATCGTTGGCTCCCGCAGCCTGCAATTGGATAAGCTTGTCAATGAGATGACCCAGCACT
ATGAGAATAGTGTGCCTGAAGACTTGACTGTGCATGTAGGAGACATTGTAGCAGCACCTTTACCTACAAATGGTT
CCTGGTATCGAGCCCCGGTCTCCTCGGCACCTTGGAGAATGGGAACCTTGACCTCTATTTTGTGACTTTGGAGATA
ATGGAGATTGCCCACTGAAGGACCTCAGGGCTCTCAGGAGTGACTTCCTAAGCCTTCCATTTCAAGCAATAGAAT
GTAGTCTGGCACGGATTGCTCCCTCAGGTGACCAGTGGGAAGAGGAAGCTTTGGATGAGTTTGATAGACTCACTC
ATTGTGCTGACTGGAAGCCTCTGGTAGCCAAGATCTCTAGCTATGTCCAGACTGGGATCTCAACTTGGCCAAAGA
TCTACTTATATGATACTAGCAATGGGAAGAACTTGATATTGGGCTAGAATTAGTACACAAAGGATACGCAATTG
AGCTTCCTGAAGACATAGAAGAAAACAGAGCTGTCCAGACATGTTGAAGGACATGGCCACAGAAACAGATGCCT
CTCTCAGCACGTTGCTCACTGAGACCAAAAAGAGCTCTGGAGAGATAACACATACCCTGTCCTGCCTCAGCTTAT
CAGAAGCTGCTTCCATGTCTGGTGATGATAACCTGAAGATGACTACTTACTCGGAAGTCTGGGCTTCAGTTTGC
TCAGCCATCTGCTTTGCTGTATGTTGCCTGCAATGAACTCGCTGAAGCATGCTCAGCCCTGGAACCTGGTGCTACC
AGAGTTCCGTAGGGAACCTTTACTCTTTAGAGGTTCCCTTGATATAAAATCATTTCATAAGACTTCCTACCCTGGAAA
ATGAGTAATGTCTCATTCTTACCTGCAGTTTGTTACTATGTATAAAAGTCTTTTTCTTTAATATGCCTTTAAGTC
TTACCTGTTTACAGCCCATTCTGATGGGTTCTTTGTCACTTCTGTTAGTATAACCCAGTACTTTTCTGCTGCCTG
GAATGCCCTCTTCTATGTTACCTATTCTGTCCGTTGAGATGCCCCAAGTTGGGCCAAAGCCAAGAGATCTATGTG
CCTTCTCTGGTTTTCTCCACATCTATAGCACCTCAACTGAAATATATGGATAAAAACAGCCTAACAAAAA
AAAAA

375/6881
FIGURE 345

MSTERTSWTSLSTIQKIALGLGIPASATVAYILYRRYRESREERLTFVGEDDIEIEMRVPQEAVKLIIGRQGANI
KQLRKQTGARIDVDTEDVGDERVLLISGFPVQVCKAKAAIHQILTENTPVSEQLSVPQRSVGRIIGRGETIRSI
CKASGAKITCDKESEGTLTLLSRLIKISGTQKEVAAAKHLILEKVSEDEELRKRIAHSAETRVPRKQPISVRREDM
TEPGGAGEPALWKNTSSSMEPTAPLVTPPPKGGGDMAVVVSKEGSWEKPSDDSFQKSEAQAIPEMPMFEIPSPDF
SFHADEYLEVYVSASEHPNHFQIIVGSRSLQLDKLVNEMTQHYENSVPEDLTVHVGDIVAAPLPTNGSWYRARV
LGTLENGNLDLYFVDFGDNGDCPLKDLRALRSDFLSLPFQAIECSLARIAPSGDQWEEELDEFDRLTHCADWKP
LVAKISSYVQTGISTWPKIYLYDTSNGKKLDIGLELVHKGYAIELPEDIEENRAVPDMLKDMATETDASLSTLLT
ETKKSSGEITHTLSCSLSEAAASMSGDDNLEDDYLLGSLGFSLLSHLLCCMLPAMNSLKHAQPWNWCYQSSVGNL
YSLEVP

376/6881
FIGURE 346

TTTTTCTGCTACCGTGACTAAGATGGGAAGCGTTTTTGGGGTCGCGGTCCGGACTTTGGGCGGGGGGTCCGGCCC
CAGGACAGTTTTTACCGCATTCCGTCCACTCCCGATTCTTCATGGATCCGGCGTCTGCACTTTACAGAGGTCCAA
TCACGCGGACCCAGAACCCCATGGTGACCGGGACCTCAGTCCTCGGCGTTAAGTTCGAGGGCGGAGTGGTGATTG
CCGCAGACATGCTGGGATCCTACGGCTCCTTGGCTCGTTTTCCGCAACATCTCTCGCATTATGCGAGTCAACAACA
GTACCATGCTGGGTGCCTCTGGCGACTACGCTGATTTCCAGTATTTGAAGCAAGTTCTCGGCCAGATGGTGATTG
ATGAGGAGCTTCTGGGAGATGGACACAGCTATAGTCCTAGAGCTATTCATTCATGGCTGACCAGGGCCATGTACA
GCCGGCGCTCGAAGATGAACCCCTTTGTGGAACACCATGGTCATCGGAGGCTATGCTGATGGAGAGAGCTTCCTCG
GTTATGTGGACATGCTTGGTGTAGCCTATGAAGCCCCCTTCGCTGGCCACTGGTTATGGTGCATACTTGGCTCAGC
CTCTGCTGCGAGAAGTTCTGGAGAAGCAGCCAGTGCTAAGCCAGACCGAGGCCCGCGACTTAGTAGAACGCTGCA
TGCGAGTGCTGTACTACCGAGATGCCCGTTCTTACAACCGGTTTCAAACCGCCACTGTCACCGAAAAAGGTGTTG
AAATAGAGGGACCATTTGTCTACAGAGACCAACTGGGATATTGCCACATGATCAGTGGCTTTGAATTGAAAATACAG
ATGCATTATCCAGAACTGAAGTTGCCCTACTTTTAACTTTGAACTTGGCTAGTTCAAAGATAGACTCTTCTTTTG
TAAAGTAAATAAATTCTTCAAAATG

377/6881
FIGURE 347

MEAFLGSRSGLWAGGPAPGQFYRIPSTPDSFMDPASALYRGPIIRTRQNPMVTGTSVLGVKFEGGVVIAADMLGSY
GSLARFRNISRIMRVNNSTMLGASGDYADFQYLKQVLGQMVIDEELLGDGHSYSPRAIHSWLTRAMYSRRSKMNP
LWNTMVIIGGYADGESFLGYVDMLGVAYEAPSLATGYGAYLAQPLLREVLEKQPVLSQTEARDLVERCMRVLYYRD
ARSYNRFQTATVTEKGVEIEGPLSTETNWDIAHMISGFE

378/6881
FIGURE 348

AATTGGAGGAGTTGTTGTTAGGCCGTCCCGGAGACCCGGTCCGGGAGGGAGGAAGGTGGCAAGATCGGTGTTGGAAA
GCACTATGGTGTGTGTGGACAACAGTGAGTATATGCGGAATGGAGACTTCTTACCCACCAGGCTGCAGGCCCCAGC
AGGATGCTGTCAACATAGTTTGTTCATTCAAAGACCCGCAGCAACCCTGAGAACAACGTGGGCCTTATCACACTGG
CTAATGACTGTGAAGTGCTGACCACACTCACCCCAGACACTGGCCGTATCCTGTCCAAGCTACATACTGTCCAAC
CCAAGGGCAAGATCACCTTCTGCACGGGCATCCGCGTGGCCCATCTGGCTCTGAAGCACCGACAAGGCAAGAATC
ACAAGATGCGCATCATTGCCCTTTGTGGGAAGCCCAGTGGAGGACAATGAGAAGGATCTGGTGAAACTGGCTAAAC
GCCTCAAGAAGGAGAAAAGTAAATGTTGACATTATCAATTTTGGGGAAGAGGAGGTGAACACAGAAAAGCTGACAG
CCTTTGTAAACACGTTGAATGGCAAAGATGGAACCGGTTCTCATCTGGTGACAGTGCCTCCTGGGCCCCAGTTTGG
CTGATGCTCTCATCAGTTCTCCGATTTTGGCTGGTGAAGGTGGTGCCATGCTGGGTCTTGGTGCCAGTGACTTTG
AATTTGGAGTAGATCCCAAGTGCTGATCCTGAGCTGGCCTTGGCCCTTCGTGTATCTATGGAAGAGCAGCGGCAGC
GGCAGGAGGAGGAGGCCCGGGCGGCAGCTGCAGCTTCTGCTGCTGAGGCCGGGATTGCTACGACTGGGACTGAAG
ACTCAGACGATGCCCTGCTGAAGATGACCATCAGCCAGCAAGAGTTTGGCCGCACTGGGCTTCCTGACCTAAGCA
GTATGACTGAGGAAGAGCAGATTGCTTATGCCATGCAGATGTCCCTGCAGGGAGCAGAGTTTGGCCAGGCGGAAT
CAGCAGACATTGATGCCAGCTCAGCTATGGACACATCTGAGCCAGCCAAGGAGGAGGATGATTACGACGTGATGC
AGGACCCCGAGTTCCTTCAGAGTGTCTTAGAGAACCTCCCAGGTGTGGATCCCAACAATGAAGCCATTGAAATG
CTATGGGCTCCCTGGCCTCCAGGCCACCAAGGACGGCAAGAAGGACAAGAAGGAGGAAGACAAGAAGTGAGACT
GGAGGGAAAGGGTAGCTGAGTCTGCTTAGGGGACTGCATGGGAAGCACGGAATATAGGGTTAGATGTGTGTTATC
TGTAACCATTACAGCCTAAATAAAGCTTGGCAACTTTT

379/6881
FIGURE 349

MVLESTMVCVDNSEFYMRNGDFLPTRLQAQQDAVNIVCHSKTRSNPENNVGLITLANDCEVLTTLTPTDTGRILSKL
HTVQPKGKITFCTGIRVAHLALKHRQGKNHKMRIIAFVGSPVEDNEKDLVKLAKRLKKEKVNVDIINFGEEEVNT
EKLTAFVNTLNGKDG TGSHLVTVP GP SLADALISSPILAGEGGAMLGLGASDFEFGVDP SADPELALALRVSM
EQRQRQEEEEARRAAAAASAAEAGIATTGTEDSDDALLKMTISQQEFGR TGLPDLSSMTEEEQIAYAMQMSLQGAEF
GQAESADIDASSAMDTSEPAKEEDDYDVMQDPEFLQSVLENLPGVDPNNEAIRNAMGSLASQATKDGKKDKKEED
KK

380/6881
FIGURE 350

CTGGTGAGGGGCTGCAGGTGGCGGCGCAGTCTCGGTAGGCGGTATGAGTTTGGCTGGGGGCCGGGCACCCCGGAA
GACCGCTGGGAACCGGCTTTCTGGGCTTTTGGAGGCAGAGGAGGAAGATGAGTTCTACCAGACGACTTATGGGGG
TTTACAGAGGAATCCGGAGATGATGAGTATCAAGGGGACCAGTCAGACACAGAGGACGAAGTGGACTCTGACTT
TGACATTGATGAAGGGGATGAACCATCCAGTGATGGAGAAGCAGAAGAGCCAAGAAGGAAGCGCCGAGTAGTCAC
CAAGGCCTATAAGGAACCTCTCAAGAGCTTAAGGCCTCGAAAGGTCAACACCCCGGCTGGTAGCTCTCAGAAGGC
GCGAGAAGAGAAGGCACTACTGCCATTAGAACTACAAGATGACGGCTCTGACAGTCGGAAGTCTATGCGTCAGTC
TACAGCTGAGCATACACGACAAACGTTTCCTTCGGGTACAGGAGAGGCAGGGCCAGTCAAGACGGCGAAAGGGGCC
CCACTGTGAGCGGCCACTAACCCAGGAGGAAGTCTCCGGGAGGCCAAGATCACAGAAGAGCTTAATTTACGGTC
ACTGGAGACATATGAGCGGCTCGAGGCTGATAAAAAGAAGCAGGTTTCATAAGAAGCGGAAGTGCCCCGGGCCCCAT
AATCACCTATCATTGAGTGACAGTGCCACTTGTTGGGGAGCCAGGCCCAAGGAAGAGAACGTTGACATAGAAGG
ACTTGATCCTGCTCCCTCGGTGTCTGCATTGACTCCTCATGCTGGGACTGGACCCGTCAACCCCCCTGCTCGCTG
CTCACGTACCTTCATCACTTTTAGTGATGATGCAACTTTTCGAGGAATGGTTCCCCCAAGGGCGGCCCCCAAAGT
CCCTGTTTCGTGAGGTCTGTCCAGTGACCCATCGTCCAGCCCTATACCGGGACCCTGTTACAGACATACCCTATGC
CACTGCTCGAGCCTTCAAGATCATTCGTGAGGCTTACAAGAAGTACATTACTGCCCATGGACTGCCGCCCCACTGC
CTCAGCCCTGGGCCCCGGCCCCGCCACCTCCTGAGCCCTCCCTGGCTCTGGGCCCCGAGCCTTGCGCCAGAAAAT
TGTCATTAAATGAAGAGATGTCTAGTCCTCAGAACTTCTTTCCCTGCCCTGATTGGGGCTCTTGCTGTTCCGTTT
CTTCTCCCTGCTTCTCCCTTTGTCATCTCTGATCTTTCCTAATCTGTTTCTTTTCCCTTTTCCCTAGTTCTT
ACAGGTTTCGTTGTGTTTTTTAATCTAATAAAATAGAAAGATCCCTTTT

381/6881
FIGURE 351

MSLAGGRAPRKTAGNRLSGLLEAEEEDFYQTTYGGFTEESGDDEYQGDQSDTEDEVDSDFDIDEGDEPSSDGEA
EEPRRKRRVVTKAYKEPLKSLRPRKVNTAGSSQKAREEKALLPLELQDDGSDSRKSMRQSTAEHTRQTFLRVQE
RQGQSRRRKGPHCERPLTQEELLREAKITEELNLRSLTYERLEADKKQVHKKRKCPGPIITYHSVTVPVLPVGE
GPKEENVNDIEGLDPAPSVSALTPHAGTGPNPFPARCSRTFITFSDDATFEWFPPQGRPPKVPVREVCVTHRPAL
YRDPVTDIPYATARAFKIIREAYKKYITAHGLPPTASALGPGPPPPEPLPGSGPRALRQKIVIK

382/6881
FIGURE 352

CCTGGCTTTGTGCATTGGGTTCTGGTGCCTGATGGACACATTTTTCCAGTTACAGGCCGAATGGTCTCAATGTAG
CTGAAGAAGTGTGCCACTGATCAGTATTACGTATTGCAAATGCAGGAGGTGGCTGTATCTGACAGACCCAGGCC
TTCCAGCTCCGACAGATCCAGTTCTGGGATGGGCATCCTCCAGAAAAGAAAGGAAGTGTACTGGCTACTCACAGG
GTCCCTCATAGCTTCTTAGAAAGAAACCACTTGTGCTCCTCATGCTACAGCAACTTCTTTGTGGCCCATGGCCT
TTCCTTGCTTAGATACTCCACATACTGTTCTCCCCGCAGGGGCGGCGGCCTTGAGGGGCTGCAGAGGCACCCTCC
CACGTCCCGCGCAGTGCAGTGCCTCCGCAGTCCAGAGGGGAGCAGTGCGCCGGGCTCCGAGCCGGACGGGTTTCG
TAATCGCGTCGCCGCCGCTTCCGCCCTCAGCCGGCCCCACCTCTGCCGGCTCGTACTCGGCTCCCCACCTCGCC
GCAGAGCTAGCCCGGGAAGCCACACTGGCGGCCACGGAGCAGAGTCCCTCACCCCCACCAGCTGTAGCTGAACG
TCTGGATGGTGGAGAAGAGCAGGTGAGGCCGTGCAGTTGGTCCCCTGGCCCGCCTGCCGCGCCGGCCGGGCCAGG
CGGAGACACACCGGATGCGGGGTGTGGGGGAGGCGGGTGTCTGGGCTGCAGAGATGCTGGGGTGGTGGGAAAGG
GGTGC CGCCCGGGGTGGCCGTAGTCATCCACGCTCCTGGGGTGCAGGCTGAGGCCGCTGAAGAGTAGAAGGA
AAAGAAGGAAGTGAATGTTGGGGGAGGTGGGAGGGAGAGGGTCCGAAAGATTCCAGAGAGGTCCAGTCCGGT
TAAGGGTTGAGAACAGCAGAGAACTTCTAGGTAGAGTTGTGTAGTGGGGGAGACAGATACGGAATCTGTGTGAT
TGAATATATTTGGGGAGGGGAGGCTTAGGGCCTAGCCCTCTTTCCTCTTAAGCCCCCAGAAGACCTTTCCTGGGG
AAGGGAAGGTTGGTGTGGGCCCTGTCACTTGGCTGAAAATATGGAGTCCACACCGCTTCTCCAGAGTCCCTCAGCA
GCCCTCCATGTCTCGGGGTCTCCACACAGGGACCAGCTGCTGCCCGGGCTTCTAGCCAGAATTGCCCATGCCAT
TCTCTCGATTCTTTCTTCTCTCCAGCTGCTTCATGTGAGGGCTTGTGAGGCCGCGGGTTGGAGGCCCTAGGGCC
AGAGGCCGGTGGGACCGGGAGAACCGGTTTGGGGCCCCGAACAGGACCAGAGAACTAGCCTGTACATCCTTCCCTCC
TGGCACCTCTTTCCCATCCCTTCTGCTCACCTCCCAACAGCTCTGAGACCCTCAAGTCCTAGTATGATCTTGGTG
GGGGCGGGGGGTGGCTTTCCCGGTTCCATATTTCACTCTTGCCATTTGGAAGTCAAGAGAGGTTCGAGTTCTGAGCA
CCACTTGGCTCTCAGGACGTGGCCTTATGAGGTCTAATCCTCATCCCTCCTGTTGTTTTCTCAGCCCTTCCCTA
TTCAGTGTGGGGTTGGATTGGGTGGCTCTTCCGCCCTGGGCTGACCAGCTCAGGACTTCATTTTCTCAACCCA
CTCTCTTCTGGCTGCTTTAAAGAAGAGTGGCCGCCAGTGGCTCTTACTTCTTTCTGGCTTTGTTCCTCATCCCC
CACTGCCCTGCGCTACCATCACATTACCTGACCTGTCTTCTTACACTCTGACCCACCCCTCAAGTTTCAGAG
ACCCTAATGTCCTAGGGAATGGAATTTCTGGTCACTTCTCGTCATCATTGGTCAATTCATGCCAAGTCCACAC
ACACGCTTTCCCTCCACCCAGCTCTGGTCAGGTCCCTGGAAGAAAGAAAGAAATGGCCTTGTCTCTCCACTGCC
CCTTTCCCTCTCTCCTTCTCCTCCCCCTCTCTTCTCTTCCCTCCCAGCACTATCCACCTCTGTCCCTCAGCTTG
AGCAGAGTGGGGGATGTTGAGGGAGAGTCCAGTCACAGTACAGCCTGCCTGCTGGTGTGGGGGTTTCTCTAAT
TCTTCATTTTCCCCAACCCTTACCACCTGCCACCACCACCATCAGGACAAACCCTATGACTGACTCACTGACGT
CCCAGTACCACAGCTCCCTCTCTGGACAGCGTGTTTAGCTTCCGCTCCTTCTGGTTACTCCTCCCTTCCAGT
GGTGAGAAGAGAAGAGAAAGCCAGCCTCCTGGGTTCTCCCCTCCCCTAGAAGCTACATTTGAGTGTGTTGTGTA
TCTCATCTCAAGGCTGTT

383/6881
FIGURE 353

AGTCAGCACGGGGGTGCTGGAAGAGATCGGGAATAATAGCGCAGACCAATGAGCCTAGGGAGATGCTTTCATCGT
CTCTCCTTCCCTCAAGTGTTCTGGAACCTATCATTGGAATTAGCCGAGTCAGGCAGGAGGGGGCGGGGAATCCTT
CCGCCCTTCTTAGGAGGGGCTGCATTGCAGGGGGAGAGTGAACTGACAGACTCAGTCACTGAAGAGGGAAAAAGGA
GTGAGAAGACAAAGCCGTCAAAGCCCCAACAGCTTTGTATTTCTCCAGCCCGGCGCAGACCCCGGAGCTCCCGAG
GCACTCCCTCCATCTTTGGAACACGCCAGTAATTGATTGATAACAGGAAGCTATGAGGGACCCTGTGAGTAGCCA
GTACAGTTCCTTTCTTTCTGGAGGATGCCATCCAGAACTGGATCTGTCGGAGCTGGAAGGCCTGGGTCTGTC
AGATACAGCCACCTACAAGGTCAAAGACAGCAGCGTTGGCAAAATGATCGGGCAAGCAACTGCAGCAGACCAGGA
GAAAAACCCTGAAGGTGATGGCCTCCTTGAGTACAGCACCTTCAACTTCTGGAGAGCTCCCATTTGCCAGCATCCA
CTCCTTCGAACTGGACTTGCTCTAAGGCCAAGACTTCTCTCTCCCATCACCTTGCCCTCATTGTCTTCCCTCTCA
AGCCCCCTCCTTTCCACTCCTTTCCCATTTTAACTTGTCTCTCCCTACTGTGTTGGTGGTGCTGATGAATCTG
CCAGAGTTGAGTTCTATGTATTTATTTATCTATCTGTCTACTCCATTTCTCTCAAAGCCCTCAAGTCACAAAGT
AAATGGTTCAAGCAATGGAGTACTGGGTACAGGGATTCTCCTTTCCCCCCCCAAATATTAAGTCCAGAAACTAG
GCCTGACTGGGGACACCTGAGAGTAGTATAGTAGTGCAAAATGGAAGACTGATTTTTGACTCTATTATAATCAGC
TTCAGAGATTCTTAAACCTTCCTAATTTCTGCTCCAGGGCAGTAAACACAAATATTTCTTCAAGGGGTGATGA
AAACCTCGGAAGTTTTAATTTGAGGTTATCTGCTACGAAACAGTATTTCTAAAAGGCTAAAGTGATAAGTCTCTT
GCTTTTTTTTTGATCCTGCTCTTATATTCTTTTTTTTTTCTCAGAGAAATCAGGAGGGTAGTTAGAGGTATAAAACA
GGAGGAAATATTATGGAATAAGGAAATAGGGAAATAATTGAATCATTTTAGAAGTAGCTAATTTCTTTTCTCAA
AAGAGTGTCCCTTCTTCACACCTACTCACTTTACAACCTTTGCTCCTAACTGTGGGTTGAAAACCTCTAGCTAAAGA
AAGTTATCAAATCTTAACATGCATTCCCTACTATTATGATAGTTTTTAAGGTTTCAATTCAATCTTCTGAACGGCA
TAAGTCCTATTTTAGCCTTACCTCCTGCATTTGCAATACGTAATACTGATCAGTGGGCACAGTTCTTCAGCTACA
TTGAGACCCTGAAATGAACAATTATTTCTGACTCGACATCTTGTCCCCAATCCTTCCAAAAATATTGATGGTGA
TTTGTGCTACCATTTACTCGTTTATTTAATAAAGACATTCAATCCC

384/6881
FIGURE 354

GGGGGCGGGGCGACGCCGACTCCGGAGCGCCCGCTTACGCAGTTCCCTCCCGGGGTCCGGAGGCCGATTCCGCCGTG
TGGCGGGTTCGAGTCCCGCCTCCTGACTCTGGCCTCTAGTCCCTGAGTCCCGGGCGGGCTGCATTCTGTCGGGGAA
ACCTCTCCTCGACCAGGGGACCTCTACTCGACCAGGGGCGACGGCGTACTTTGGGCTTCATCATGGAGGACTAC
CTGCAGGGTTGTGAGCTGCTCTGCAGGAGTCCCGACCTCTACATGTTGTGCTGGGAAATGAAGCCTGTGATTTG
GACTCCACAGTGTCTGCTCTTGCCCTGGCTTTTTACCTAGCAAAGACAACCTGAGGCTGAGGAAGTCTTTGTGCCA
GTTTTAAATATAAAACGTTCTGAACCTCTGCGAGGTGACATTGTCCTTCTTTCTTCAGAAGGTTTCATATTCCA
GAGAGTATCTTGATTTTTTCGGGATGAGATTGACCTCCATGCATTATACCAGGCTGGCCAACTACCCCTCATCCTT
GTCGACCATCATATCTTATCCAAAAGTGACACAGCCCTAGAGGAGGCAGTAGCAGAGGTGCTAGACCATCGACCC
ATCGAGCCGAAACACTGCCCTCCCTGCCATGTTTTAGTTGAGCTGGTGGGGTCTGTGCTACCCTGGTGACCGAG
AGAATCCTGCAGGGGGCACCAGAGATCTTGACAGGCAAACCTGCAGCCCTTCTGCATGGAACCATCATCCTGGAC
TGTTGTCAACATGGACCTTAAATTTGGAAAGGCAACCCCAAAGGACAGCAAATATGTGGAGAACTAGAGGCCCTT
TTCCCAGACCTACCCAAGAGAAATGATATATTTGATTCCCTACAAAAGGCAAAGTTTGATGTATCAGGACTGACC
ACTGAGCAGATGCTGAGAAAAGACCAGAAGACTATCTATAGACAAGGCGTCAAGGTGGCCATTAGTGCAATATAT
ATGGATTTGGAGGCCCTTCTGCAGAGGTCTAACCTCCTTGAGATCTCCATGCTTTCTGCCAGGCTCACAGCTAT
GATGTCCTGGTTGCCATGACTATCTTTTTCAACACTCACAATGAGCCAGTGCGGCAGTTGGCTATTTTCTGTCCC
CATGTGGCACTCCAAACAACGATCTGTGAAGTCTGGAACGCTCCCACTCTCCACCCCTGAAGCTGACCCCTGCC
TCAAGTACCCACCCTAACCTCCATGCCTATCTTCAAGGCAACACCCAGGTCTCTCGAAAGAACTTCTGCCCTG
CTCCAGGAAGCCCTGTCAGCATATTTTGAATCCATGAAGATCCCTTCAGGACAGCCTGAGACAGCAGATGTGTCC
AGGGAGCAAGTGGACAAGGAATTGGACAGGGCAAGTAACTCCCTGATTTCTGGCCTGAGTCAAGATGAGGAGGAC
CCTCCGCTGCCCCCGACGCCCATGAACAGCTTGGTGGATGAGTGCCCTCTAGATCAGGGGCTGCCTAAACTCTCT
GCTGAGGCCGTCTTCGAGAAGTGCAGTCAGATCTCACTGTCACAGTCTACCACAGCCTCCCTGTCCAAGAAGTGA

CTGTTGAGAGGCGAGGAGGTAGTGGGTGAGGCTACCTGACTCACTTCAAATGCATGTTTTGAGATGTTTGGAGAT
TCAGCAATTCTGTCTTCATTGCTCCAGGATCTGGTATACTGTTCTCATAAACTGAGAGGAGAAAAAAGTGAAA
GAAAGCAGCTGCTTTAAGAATGGTTTTCCACCTTTTTCCCCCTAATCTCTACCAATCAGACACATTTTATTATTTA
AATCTGCACCTCTCTCTATTTTATTTGCCAGGGGACGATGTGACATATCTGCAGTCCCAGCACAGTGGGACAAA
AAGAATTTAGACCCCAAAAGTGTCTCGGCATGGATCTTGAACAGAACCAGTATCTGTGATGGAACCTGAACATTC
ATCGATGGTCTCCATGTATTTCATTTATTCACCTTGTTCAATTCAAGTATTTATTGAATACCTGCCTCAAGCTAGAGA
GAAAAGAGAGTGCCTTTGGAAATTTATTCCAGTTTTTCCAGCTACAGCAGATTATCAGCTCGGTGACTTTTTCTTT
CTGCCACCATTAGGTGATGGTGTGTTGATTGAGAGATGGCTGAATTTCTATTCTTAGCTTATTGTGACTGTTTCA
GATCTAGTTTGGGAACAGATTAGAGGCCATTGTCTTCTGTCTGATCAGGTGGCCTGGCTGTTTCTTTGGATCCC
TCTGTCCCAGAGCCACCCAGAACCCTGACTCTTGAGAATCAAGAAAACACCCAGAAAGGCCCTTAATGACCTCATA
GGCACTCTTCCAAAAAGACAACAGAACCTGGAATGAGAGGCCTGGGTCTGTCTCCTGCCTTAGCAGGCCTATCAAT
TTCTTGTCAATCTCTTTTTTTTCTTGCTCACATTAAGGAAGCATGGAGTTCTAATGCTCCCATAACTATGTA
TTTTGGCAAGACACTTCACTACTCCAGGTCTCACTTTCCCCATCTGTAAAACAGGGTTTGGACTAGGTGTTCCCT
GGTATTCTGTGATCTGCCTCTTGCTGCCATTCTTTCTCTCCTCTGCTTCTCTGTATTTTTCTTCTGTTATCCCTG
GGGGTGTGAGTTCACTTGATTGTCTGTATTTCTGTGTGGTTGTAGCAAGGACTCAGCCTCATGTAGCACGAAT
AGGGGTGTGGTTTCATGGCGTGTGACCCAGCAGAGCACTCCCTCCCACTAAGTTGTTCTGCATGTGTAGAGTCTC
CCATTTTTTTTTAACGCAACCCTTTCCCTTTTTTCTACCCACAGCTCTGTTCCATGTAAGTTGCCAACAGTTT
CACTGAACAGTGGGGTATGTGATGGTTTTGGCATGACATCTTCAGTATGAGGGGGACAGTTTGAAGTTTCACTTTGA
GGGTGTGATGTCTGTAGCTATGTGGAAGGTAAAAATAGTGGTGTGATCATGAACCAAAGGAATTTATGTTTTGTA
ACTTGGGTACTTTATTTTGCAATTTTGTATATACTATTAAATAATTTTTTCTGTT

385/6881
FIGURE 355

MEDYLQGCRAALQESRPLHVVLGNEACDLDSTVSALALAFYLAKTTEAEVFVPVLNKRSELPLRGDIVFFLQK
VHIPESILIFRDEIDLHALYQAGQLTLILVDHHILSKSDTALEEAVAELDHRPIEPKHCPPCHVSVELVGSCAT
LVTERILQGAPEILDRQTAALLHGTTIILDCVNMDLKIGKATPKDSKYVEKLEALFPDLPKRNDIFDSLQAKFDV
SGLTTEQMLRKDQKTIYRQGVKVAISAIYMDLEAFLQRSNLLADLHAFCAHSYDVLVAMTIFFNTHNEPVRQLA
IFCPHVALQTTICEVLERSHSPPLKLTPASSTHPNLHAYLQGNQVSRKKLLPLLQEALSAYFDSMKIPSGQPET
ADVSREQVDKELDRASNLSGLSQDEEDPPLPPTPMNSLVDECPLDQGLPKLSAEAVFEKCSQISLSQSTTASL
SKK

386/6881
FIGURE 356

GAAACAAGCACTGGATTCCATATCCCACTGCCAAAACCGCATGGTTCAGATTATCGCTATTGCAGCTTTCATCAT
AATACACACCTTTGCTGCCGAAACGAAGCCAGACAACAGATTTCCATCAGCAGGATGTGGGGGCTCAAGGTTCTG
CTGCTACCTGTGGTGAGCTTTGCTCTGTACCCTGAGGAGATACTGGACACCCACTGGGAGCTATGGAAGAAGACC
CACAGGAAGCAATATAACAACAAGGTGGATGAAATCTCTCGGCGTTTAATTTGGGAAAAAACCTGAAGTATATT
TCCATCCATAACCTTGAGGCTTCTCTTGGTGTCCATACATATGAACTGGCTATGAACCACCTGGGGGACATGACC
AGTGAAGAGGTGGTTCAGAAGATGACTGGACTCAAAGTACCCCTGTCTCATTCCCGCAGTAATGACACCCTTTAT
ATCCCAGAATGGGAAGGTAGAGCCCCAGACTCTGTGCACTATCGAAAGAAAGGATATGTTACTCCTGTCAAAAAT
CAGGGTCAGTGTGGTTCCTGTTGGGCTTTTAGCTCTGTGGGTGCCCTGGAGGGCCAACTCAAGAAGAAAACCTGGC
AAACTCTTAAATCTGAGTCCCCAGAACCTAGTGGATTGTGTGTCTGAGAATGATGGCTGTGGAGGGGGCTACATG
ACCAATGCCTTCCAATATGTGCAGAAGAACCGGGGTATTGACTCTGAAGATGCCTACCCATATGTGGGACAGGAA
GAGAGTTGTATGTACAACCCAACAGGCAAGGCAGCTAAATGCAGAGGGTACAGAGAGATCCCCGAGGGGAATGAG
AAAGCCCTGAAGAGGGCAGTGGCCCGAGTGGGACCTGTCTCTGTGGCCATTGATGCAAGCCTGACCTCCTTCCAG
TTTTACAGCAAAGGTGTGTATTATGATGAAAGCTGCAATAGCGATAATCTGAACCATGCGGTTTTTGGCAGTGGGA
TATGGAATCCAGAAGGGAAACAAGCACTGGATAATTA AAAACAGCTGGGGAGAAAACCTGGGGAAACAAAGGATAT
ATCCTCATGGCTCGAAATAAGAACAACGCCTGTGGCATTGCCAACCTGGCCAGCTTCCCCAAGATGTGACTCCAG
CCAGCCAAATCCATCCTGCTCTTCCATTTCTTCCACGATGGTGCAGTGTAAACGATGCACTTTGGAAGGGAGTTGG
TGTGCTATTTTGAAGCAGATGTGGTGATACTGAGATTGTCTGTTCAGTTTCCCATTGTGTTGTGCTTCAAATG
ATCCTTCCTACTTTGCTTCTCTCCACCCATGACCTTTTTCACTGTGGCCATCAGGACTTTCCCTGACAGCTGTGT
ACTCTTAGGCTAAGAGATGTGACTACAGCCTGCCCCTGACTGTGTTGTCCCAGGGCTGATGCTGTACAGGTACAG
GCTGGAGATTTTCACATAGGTTAGATTCTCATTACGGGACTAGTTAGCTTTAAGCACCCCTAGAGGACTAGGGTA
ATCTGACTTCTCACTTCCTAAGTTCCCTTCTATATCCTCAAGGTAGAAATGTCTATGTTTTCTACTCCAATTCAT
AAATCTATTTCATAAGTCTTTGGTACAAGTTTACATGATAAAAAGAAATGTGATTGTCTTCCCTTCTTTGCACTT
TTGAAATAAAGTATTTATC

387/6881
FIGURE 357

MWGLKVLLLPVVSFALYPEEILDTHWELWKKTHRKQYNNKVDEISRRLIWEKNLKYISIHNLASLGVHTYELAM
NHLGDMTSEEVVQKMTGLKVPLSHSRSDTLYIPEWEGRAPDSVDYRKKGYVTPVKNQGQCGSCWAFSSVGALEG
QLKKKTGKLLNLSPQNLVDCVSENDGCGGGYMTNAFQYVQKNRGIDSEDAYPYVGQEESCMYNPTGKAAKCRGYR
EIEPEGNEKALKRAVARVGPVSVAIDASLTSFQFYSGVYYDESCNSDNLNHAVLAVGYGIQKGNKHWI IKNSWGE
NWGNKGYILMARNKNNACGIANLASFPKM

388/6881
FIGURE 358

GGCACGAGGAAGGAACATGGGCCCTGTATCAGAGGTGGCGGTGTCTCCGGCTCCAAGGTTTACAGGCTTGCAGGCT
ACACACGGCAGTTGTGTCGACCCCTCCACGCTGGTTGGCAGAGCGGCTTGGCCTTTTTGAGGAGCTGTGGGCTGC
TCAGGTAAAGAGATTAGCAAGCATGGCACAGAAGGAACCCCGGACTATTAAGATATCACTTCTTGGAGGCCAGAA
AATTGATGCTGTGGCATGGAACACAACCCCTACCAACTAGCCCGGCAGATCAGTTCAACACTGGCAGATACTGC
AGTGGCTGCTCAAGTGAATGGAGAACCTTATGATCTGGAGCGGCCCTTGGAGACAGATTCTGACCTCAGATTTCT
GACATTTCGATTCCCCAGAGGGGAAAGCAGTGTTCTGGCACTCCAGCACCCATGTCCTGGGGGCAGCAGCTGAACA
ATTCTAGGTGCTGTTCTCTGCAGAGGTCCAAGTACAGAAATATGGCTTTTACCATGATTTCTTCTTGGGAAAGGA
GAGGACAATCCGGGGCTCAGAGCTGCCTGTTTTGGAGCGGATTTGCCAGGAACCTTACAGCTGCTGCTCGACCCCT
CCGGAGGCTAGAGGCTTACGGGATCAGCTTCCGCAGTTGTTCAAGGATAACCCCTTTAAGCTTCACTTGATTGA
GGAGAAAGTGACAGGTCCAACAGCAACAGTATATGGGTGTGGCACATTGGTTGACCTTTGCCAGGGCCCCCACCT
TCGGCATACTGGACAGATTGGAGGACTGAAGCTGCTATCGAACTCATCATCCTTATGGAGGTCTTCAGGGGGCCCC
AGAGACACTGCAGAGAGTGTTCAGGGATTTTCCTTCCCCACAACAGAATTGCTGAGGGTCTGGGAAGCATGGAGGGA
GGAAGCAGAATTGCGGGACCACCGGCGCATTGGGAAGGAACAGGAGCTCTTCTTCTTCCATGAACTGAGCCCTGG
GAGCTGCTTCTTCTTCCGACGAGGGACAAGGGTGTATAATGCACTAGTGGCGTTTATCAGGGCTGAGTATGCCCA
TCGTGGTTTTCTCCGAGGTGAAAACCTCCACACTGTTTTCTACGAAGCTCTGGGAACAGTCAGGGCACTGGGAGCA
TTATCAGGAAGACATGTTTGGCGTGCAGCCCCAGGCTCTGACAGGCCTCCAGCTCCCAGAGTGACGATTCTAC
CAGGCATATCACAGATACTCGCCCTCAAGCCTATGAACTGCCCTGCACACTGCCTGATGTTGCCCCACCGGCC
CAGATCCTGGCGGGAACCTGCCCTGCGACTAGCTGACTTTGGGGCTCTACACCGGGCCGAAGCCTCTGGTGGTCT
GGGGGGACTGACCCGACTGCGGTGCTTCCAGCAGGATGACGCTCACATCTTCTGTACAACAGATCAGCTGGAAGC
AGAGATCCAAAGCTGTCTTGATTTCTTCCGTTCCGTCTATGCCGTTCTTGGCTTCTCCTTCCGCTGGCACTGTC
CACCCGGCCATCTGGCTTCTTGGGGACCCCTTGCCCTTGGGACCAGGCCGAACAGGTCCCTTAAACAGGCCCTGAA
GGAATTTGGAGAACCCTGGGACCTCAACTCTGGAGATGGTGCCTTCTATGGACCTAAGATTGACGTGCACCTCCA
CGATGCCCTGGGCCGGCCACATCAGTGTGGGACAATTCAGCTTGACTTCCAACCTGCCCCTGAGATTTGACCTCCA
GTATAAGGGGCAGGCGGGTGGCCTGGAGCGTCCAGTCCCTCATTACCGAGCAGTGCTCGGTTCTGTGGAAAGACT
GTTGGGAGTGCTGGCAGAAAGCTGCGGGGGGAAATGGCCACTGTGGCTGTCCCCGTTCCAGGTGGTGGTCATCCC
TGTGGGGAGTGAGCAAGAGGAATACGCCAAAGAGGCACAGCAGAGCCTGCGGGCTGCAGGACTGGTCAGTGACCT
GGATGCAGACTCTGGACTGACCCTCAGCCGGAGAATCCGCCGGGGCCAGCTTGCCCACTACAATTTTTCAGTTTGT
GGTTGGCCAGAAAGAGCAAAGTAAGAGAACAGTGAACATTTCGACTCGAGATAATCGTCGCCTTGGGGAGTGGGA
CTTGCCCTGAGGCTGTGCAGCGACTGGTGGAGCTACAGAACACGAGGGTCCCAAATGCCGAAGAAAATTTCTGAGC
CTTTGTACATAGATGAGGCAAAAACCTGCGAGTGCCATCAGCCTCCCTCACATGGGAGACCCCCAACCCAGCTGAC
AATGTGGAGCCCCCAGAACTTCAGAACTGTGTGGAGGCACATGTCTGCTCTCCTGAAAAGAGACTTGGTTTGGGG
ACCCACAAAAAGGAGGGAAGCTGTAGCTGTTTGGATGTGAGGAGAATGAACTACAAAAAAAAAAAAAAAAAAAA

389/6881
FIGURE 359

MALYQRWRCLRLQGLQACRLHTAVVSTPPRWLAERLGLFEELWAAQVKRLASMAQKEPRTIKISLPGGQKIDAVA
WNTTPYQLARQISSTLADTAVAAQVNGEPYDLERPLETDSDLRFLTFDSPEGKAVFWHSSTHVLGAAAEQFLGAV
LCRGPSTEYGFYHDFFLGKERTIRGSELPVLERICQELTAAARPFRRLEASRDQLRQLFKDNFFKLHLIEEKVTG
PTATVYGCGLVLDLCQGPHLRHTGQIGGLKLLSNSSSLWRSSGAPETLQRVSGISFPTTELLRVWEAWREEAELR
DHRRIGKEQELEFFFHELS PGSCFFLPRGTRVYNALVAFIRAEYAHRGFSEVKTPTLFSTKLWEQSGHWEHYQEDM
FAVQPPGSDRPPSSQSDDSTRHITDTLALKPMNCPAHCLMFAHRPRSWRELPLRLADFGALHRAEASGGLGGLTR
LRCFQQDDAHIFCTTDQLEAEIQSCLDFLRSVYAVLGF SFR LALSTRPSGFLGDPCLWDQAEQVLKQALKEFGEP
WDLNSGDGAFYGP KIDVHLHDALGRPHQCGTIQLDFQLPLRFDLQYKGQAGALERPVLIHRAVLGSVERLLGVLA
ESCGGKWPLWLSPFQVVVIPVGSEQEEYAKEAQQSLRAAGLVSDLDADSGLTLSRRIRRAQLAHYNFQFVVGQKE
QSKRTVNIRTRDNRRRLGEWDLPEAVQRLVELQNTRVPAEEIF

390/6881
FIGURE 360

ACCAGATCCCAGAGGCTGAACACCTCGACCTTCTCTGCACAGCAGGTCCAGCATCCTTTGAAGCATGAGTTCTTA
CCAGCAGAAGCAGACCTTTACCCACACCTCAGCTTCAACAGCAGCAGGTGAAACAACCCAGCCAGCCTCCACC
TCAGGAAATATTTGTTCCCAACAACCAAGGAGCCATGCCACTCAAAGGTTCCACAACCTGGAAACACAAAGATTCC
AGAGCCAGGCTGTACCAAGGTCCCTGAGCCAGGCTGTACCAAGGTCCCTGAGCCAGGCTGTACCAAGGTCCCTGA
GCCAGGTTGTACCAAGGTCCCTGAGCCAGGCTGTACCAAGGTCCCTGAGCCAGGTTGTACCAAGGTCCCTGAGCC
AGGCTACACCAAGGTCCCTGAACCAGGCAGCATCAAGGTCCCTGACCAAGGCTTCATCAAGTTTCCTGAGCCAGG
TGCCATCAAAGTTCCTGAGCAAGGATACACCAAAGTTCCTGTGCCAGGCTACACAAAGCTACCAGAGCCATGTCC
TTCAACGGTCACTCCAGGCCCAGCTCAGCAGAAGACCAAGCAGAAGTAATTTGGTGCACAGACAAGCCCTTGAGA
AGCCAACCACCAGATGCTGGACACCCTCTTCCCATCTGTTTCTGTGTCTTAATTGTCTGTAGACCTTGTAATCAG
CACATTGTACCCCCAAGCCATAGTCTCTCTCTTATTTGTATCCTAAAAATACGTACTATAAAGCTTTTGTTTACA
CACACTCTGAAGAATCCTGTAAGCCCCTGAATTAAGCAGAAAGTCTTCATGGCTTTTCTGGTCTTCGGCTGCTCA
GGGTTTCATCTGAAGATTCGAATGAAAAGAAATGCATGTTTCCTGCTCTTCCCTCATTAAATTGCTTTTAATTCCA

391/6881
FIGURE 361

CAGTTCTAAGGGACCATACAGAGTATTCTCTCTTCACACCAGGACCAGTCACTGTTGCAGCATGAGTTCCCAGC
AGCAGAAGCAGCCTTGACCCCCACCCCTCAGCTTCAGCAGCAGCAGGTGAAACAGCCTTGCCAGCCTCCACCTC
AGGAACCATGCATCCCCAAAACCAAGGAGCCCTGCCACCCAAGGTGCCTGAGCCCTGCCACCCCAAAGTGCCCG
AGCCCTGCCAGCCCAAGGTTCCAGAGCCATGCCACCCAAGGTGCCTGAGCCCTGCCCTTCAATAGTCACTCCAG
CACCAGCCCAGCAGAAGACCAAGCAGAAGTAATGTGGTCCACAGCCATGCCCTTGAGGAGCCGGCCACCAGATGC
TGAATCCCCTATCCCATTCTGCGTATGAGTCCCATTGCCTTGCAATTAGCATTCTGTCTCCCCAAAAAAGAAT
GTGCTATGAAGCTTTCTTTCCTACACACTCTGAGTCTCTGAATGAAGCTGAAGGTCTTAGTACCAGAGCTAGTTT
TCAGCTGCTCAGAATTCATCTGAAGAGAGACTTAAGATGAAAGCAAATGATTTCAGCTCCCTTATACCCCCATTAA
ATTCACTTTCAATTCCA

392/6881
FIGURE 362

MSSQQQKQPCITPPQLQQQVKQPCQPPQEPICPKTKEPCHPKVPEPCHPKVPEPCQPKVPEPCHPKVPEPCPS
IVTPAPAQQKTKQK

393/6881
FIGURE 363

ATGACAATTGCAAAGGTGGTAGAAGCTCATGACCAGGTGACAGACAGACACAGAACACATCAACAGAATTGTCTG
ATGGTTCCCAGGGAGAGAGCTGCTGCTCTTTCTTCCGAAGCTCTGGGAGCTGGCACAGCTGAGGACTTCCTTTTC
TTAGCTCCACCTGGACAGTGGCAGTATGGCAGCCTCAGAAAGGGAATCTTTTGCTGTCACAGATCATCACAGGCA
GGCCACAGGTTAAGGAGAAAGAAGCTCCCTGTGCATCCATGGAAGGCTTTGGTGAGAAGATGCAAGTGGAGCTGT
GGAACGAGGGAGAGAGCTGCTGCTCTTTCTTCCGAAGCTCTGGGAGCTGGCACAGCCCAGGACTTCCTTTGCTCA
GTCTCCACCTGGACAGTGGCAGTATGGCAGCCTCAGAAAAGAACTTTTGCTGTCAGGGATCATCATGGGCAGA
TTACTGGCTAAGGAGAAAGAAGCTCCCTGTGTATCCATGGTAGGCTTTGATGAGAAGATGAAGGTGGAGCTGTGG
AACGAGATACTTTATTTCAGGGAGTGAAAGAAAAGTGACAATTGCACAGGTGGTAGAAGCTCATGCCCAGGTGAAA
GACAGACACAGAACACATCAACAGAATTCTCTGATGGTTCCCAGGCACACAGCTGCAGCTCTTTCTGCTGAAGCT
CTGGGAACTGACAAAGCCAAGGTTCTTTGCTCAGTCTCCACCTGGACAGTGGCATCTCCACCTGGACAGTGGCA
ATATGGCAGCCTCAGAAAGGAAACCTTTTGCTATCAGGGATCATCATGGGCAGATCACTGGCTAAGAGGAAAGAA
GCTAACTGTGTATCCATGGTAGGCTTTGATGAGAAGATGCAGGTGAAGCTGTGGAACAAGTGCAGGCACCAGAGC
AGCAGCAGCCCTAGTGCCCCCAGCATCTCAGACAGGCTCACTTTACAAGTTGAGGTGATGAAGTTGAAGCTAAGA
GTTCTTCACAGTCCAGGGAGTGAAAGGAAAGTGACAACTGCACAGGTGGTGGAAAGCTCATGCCCAGGGGACAGAC
AGACACAGAAAACATCAACAGAATTCTCTAATGGTTCCCAGGGAGAGAGCTGCTCTTTCTTCTGAAGCTCTGGGA
GCTGGCACAGCCCAGGACTTCCTTTGCTCAGTCTCCACCTGGACAGTGGCAGTATGGCAGCCTCAAAAAGAAAAC
CTTTTGCTATCAGAGATCATCACAGGCCGATCACAGGCTAAGAGGAAAGAAGCTCCCTGTGTATCCCTGGATGGC
TTTGATGAGAAGATGCAGGTGGAGCTGTGGAACGAGCATCAAATCAACATTCATAGGATTGGATCAACCAAACCTT
GCTGTATTTCAGATTAAATTCAACATTTTCAGGGCACAAAGAACAGAGGAACCTCAGGAAGCCGACTCACCAGGTTT
TCCAAGGCAGATCGGTGCTTAGGAGACTATAATCCGTGTGGACAGCCACCTAGAAGCAAACCTTCTGGCCATGGTA
GCACAGACTGTGTATCATATTCCAGGTTCTGTGGCCAAGCCCCCAAACAGGAATCACGTAGTGAAGTTCAAAGAA
ACTTCCAAAAGGTGCAGCAAAAGAAAGAAAAGAAAACATAA

394/6881
FIGURE 364

AAACACTCTGTGTGGCTCCTCGGCTTTGGGACAGAGTGCAAGACGATGACTTGCAAAATGTCGCAGCTGGAACGC
AACATAGAGACCATCATCAACACCTTCCACCAATACTCTGTGAAGCTGGGGCACCCAGACACCCTGAACCAGGGG
GAATTCAAAGAGCTGGTGCGAAAAGATCTGCAAAATTTTCTCAAGAAGGAGAATAAGAATGAAAAGGTCATAGAA
CACATCATGGAGGACCTGGACACAAATGCAGACAAGCAGCTGAGCTTCGAGGAGTTCATCATGCTGATGGCGAGG
CTAACCTGGGCCTCCCACGAGAAGATGCACGAGGGTGACGAGGGCCCTGGCCACCACCATAAGCCAGGCCTCGGG
GAGGGCACCCCTTAAGACCACAGTGGCCAAGATCACAGTGGCCACGGCCATGGCCACAGTCATGGTGGCCACGGC
CACAGGCCACTAATCAGGAGGCCAGGCCACCCTGCCTCTACCCAACCAGGGCCCCGGGGCCTGTTATGTCAAAC
GTCTTGGCTGTGGGGCTAGGGGCTGGGGCCAAATAAAGTCTCTTCCTCCAA

395/6881
FIGURE 365

MTCKMSQLERNIETIINTFHQYSVKLGHPDTLNQGEFKELVRKDLQNFLKKENKNEKVIEHIMEDLDTNADKQLS
FEEFIMLMARLTWASHEKMHEGDEGPGHHHKPGLGEGTP

396/6881
FIGURE 366

GAGCAGCCTTCCTGAGAGAGGAGAGAGAGAAAGCTCAGGGAGGTCTGGAGCAAAGATACTCCTGGAGGTGGGGAGTG
AGGCAGGGATAAGGAAGGAGAGTATCCTCCAGCACCTTCCAGTGGGTGGGGCAAGTCCGTGGGCATCATGTTGAC
CGAGCTGGAGAAAGCCTTGAAGTCTATCATCGACGTCTACCACAAGTACTCCCTGATAAAGGGGAATTTCCATGC
CGTCTACAGGGATGACCTGAAGAAATTGCTAGAGACCGAGTGTCTCAGTATATCAGGAAAAAGGGTGCAGACGT
CTGGTTCAAAGAGTTGGATATCAACACTGATGGTGCAGTTAACTTCCAGGAGTTCCTCATTCTGGTGATAAAGAT
GGGCGTGGCAGCCACAAAAAAGCCATGAAGAAAGCCACAAAGAGTAGCTGAGTTACTGGGCCCAGAGGCTGGG
CCCCTGGACATGTACCTGCAGAATAATAAAGTCATCAATACCTC

397/6881
FIGURE 367

GGGACCGCTATAAGGCCAGTCGGACTGCGACATAGCCCATCCCCTCGACCGCTCGCGTCGCATTGGCCGCCTCC
CTACCGCTCCAAGCCCAGCCCTCAGCCATGGCATGCCCCCTGGATCAGGCCATTGGCCTCCTCGTGGCCATCTTC
CACAAGTACTCCGGCAGGGAGGGTGACAAGCACACCCTGAGCAAGAAGGAGCTGAAGGAGCTGATCCAGAAGGAG
CTCACCATTGGCTCGAAGCTGCAGGATGCTGAAATTGCAAGGCTGATGGAAGACTTGGACCGGAACAAGGACCAG
GAGGTGAACTTCCAGGAGTATGTCACCTTCCTGGGGGCCTTGGCTTTGATCTACAATGAAGCCCTCAAGGGCTGA

AAATAAATAGGGAAGATGGAGACACCTCTGGGGGTCTCTCTGAGTCAAATCCAGTGGTGGGTAATTGTACAATA
AATTTTTTTTGGTCAAATTT

398/6881
FIGURE 368

MACPLDQAIGLLVAIFHKYSGREGDKHTLSKKELKELIQKELTIGSKLQDAETIARLMEDLDRNKDQEVNFQEYVT
FLGALALIYNEALKG

399/6881
FIGURE 369

ATTCTTCCCCTCTCTACAACCCTCTCTCCTCAGCGCTTCTTCTTTCTTGGTTTGATCCTGACTGCTGTCTCATGGCG
TGCCCTCTGGAGAAGGCCCTGGATGTGATGGTGTCCACCTTCCACAAGTACTCGGGCAAAGAGGGTGACAAGTTC
AAGCTCAACAAGTCAGAACTAAAGGAGCTGCTGACCCGGGAGCTGCCCAGCTTCTTGGGGAAAAGGACAGATGAA
GCTGCTTTCCAGAAGCTGATGAGCAACTTGGACAGCAACAGGGACAACGAGGTGGACTTCCAAGAGTACTGTGTC
TTCCTGTCTGTCATCGCCATGATGTGTAACGAATTCTTTGAAGGCTTCCCAGATAAGCAGCCCAGGAAGAAATGA

AAACTCCTCTGATGTGGTTGGGGGGTCTGCCAGCTGGGGCCCTCCCTGTGCGCCAGTGGGCACTTTTTTTTTTTCCA
CCCTGGCTCCTTCAGACACGTGCTTGATGCTGAGCAAGTTCAATAAAGATTCTTGGAAGTTT

400/6881
FIGURE 370

MACPLEKALDVMVSTFHKYSGKEGDKFKLNKSELKELLTRELP SFLGKRTDEAA FQKLMSNLDSNRDNEVDFQEY
CVFLSCIAMMCNEFFEGFPDKQPRKK

401/6881

FIGURE 371

GGTGCTTCTGAGATGTGGGCTTGACACGCTGTTGCTATAGTACGTGTGATCCTGACTGCTGTC**ATG**GCGTGCCC
TCTGGAGAAGGCCCTGGATGTGATGGTGTCCACCTTCCACAAGTACTCGGGCAAAGAGGGTGACAAGTTCAAGCT
CAACAAGTCAGAACTAAAGGAGCTGCTGACCCGGGAGCTGCCCAGCTTCTTGGGGAAAAGGACAGATGAAGCTGC
TTTCCAGAAGCTGATGAGCAACTTGGACAGCAACAGGGACAACGAGGTGGACTTCCAAGAGTACTGTGTCTTCCT
GTCCTGCATCGCCATGATGTGTAACGAATTCTTTGAAGGCTTCCCAGATAAGCAGCCCAGGAAGAAA**TG**AAAACT
CCTCTGATGTGGTTGGGGGGTCTGCCAGCTGGGGCCCTCCCTGTCGCCAGTGGGCACTTTTTTTTTTCCACCCTG
GCTCCTTCAGACACGTGCTTGATGCTGAGCAAGTTCAATAAAGATTCTTGGAAGTTT

402/6881
FIGURE 372

MACPLEKALDVMVSTFHKYSGKEGDKFKLNKSELKELLTRELP SFLGKRTDEAA FQKLMSNLDSNRDNEVDFQEY
CVFLSCIAMMCNEFFEGFPDKQPRKK

403/6881
FIGURE 373

ACACATTCCCCACCCTCTGGGAGCTCCTAGTCTGAGAGAGGAAACACTCCTGCCCAAGGGAGCTTCCAGTTAGAT
GGCAGAGAGAGATGCCTCTGGCTTCAGGAGTCCCGAGTCTAAGGAGGGAAACGACTCCTTCAGGGAGCTTCCTGC
TCCTAGGCTGTAGCCATGGCTCCTGCCAGACTGCACAGGAGCCCCCATCTGCCAGCCGGTGCATGTGGCCCTGCT
CCCCAGAGCCTGCGCAGATGCCATCAAAATGGGACTCTGGTCAACCTGTCATTTCCCTTCTGGCAGACACTAAAA
TGGGGAGCCCTGCCCTCAGGGGGGTGTCCCAAGTGCCATCAGAGGAGGCTTGGTGA CTCCCAGACACAAGGGAAG
CTTTAGCGTCTGCCCTCAGGGTGAGATGGAGGTATCGCCTCCGGCCTCAGGGAACACAGTCTGAGGGGGAGATG
CAGCCCCTGCCTTCCCATTCAGAGAGGGGTTTTGTGAGGTGGCTTGGGGGCATAGGGCAGAAGTGGATCCTACAG
GCTGAGCTAAGGCCCAAGAGCCTCAGCAGTGTACCCATCACCTGGCACCTCTGCAGCCACAGATCCATGATGTG
CAGTTCTCTGGAGCAGGCGCTGGCTGTGCTGGTCACTACCTTCCACAAGTACTCCTGCCAAGAGGGCGACAAGTT
CAAGCTGAGTAAGGGGGAAATGAAGGAACTTCTGCACAAGGAGCTGCCCAGCTTTGTGGGGGAGAAAAGTGGATGA
GGAGGGGCTGAAGAAGCTGATGGGCAGCCTGGATGAGAACAGTGACCAGCAGGTGGACTTCCAGGAGTATGCTGT
TTTCCTGGCACTCATCACTGTGATGTGCAATGACTTCTTCCAGGGCTGCCCAGACCGACCCTGAAGCAGAACTCT
TGACTTCCTGCCATGGATCTCTTGGGCCCAGGACTGTTGATGCCTTTGAGTTTTGTATTCAATAAACTTTTTTTG
TCTGTTGATAATATTTTAATTGCTCAGTGATGTTCCATAACCCGGCTGGCTCAGCTGGAGTGCTGGGAGATGAGG
GCCTCCTGGATCCTGCTCCCTTCTGGGCTCTGACTCTCCTGGAAATCTCTCCAAGGCCAGAGCTATGCTTTAGGT
CTCAATTTTGGAATTTCAAACACCAGCAAAAAATTGGAAATCGAGATAGGTTGCTGACTTTTATTTTGTCAAATA
AAGATATTAAAAAAGGC

404/6881
FIGURE 374

GGACTGTTGAAGACAGGTCTCCACACACAGCTCCAGCAGCCACATTTGCAACCTTGGCCATCTGTCCAGAACCTG
CTCCCACCTCAGGCCCAGGCCAACCGTGCACTGCTGCAATGGGCTCTGAGCTGGAGACGGCGATGGAGACCCTCA
TCAACGTGTTCCACGCCCCTCGGGCAAAGAGGGGGACAAGTACAAGCTGAGCAAGAAGGAGCTGAAAGAGCTGC
TGCAGACGGAGCTCTCTGGCTTCCTGGATGCCCAGAAGGATGTGGATGCTGTGGACAAGGTGATGAAGGAGCTAG
ACGAGAATGGAGACGGGGAGGTGGACTTCCAGGAGTATGTGGTGCTTGTGGCTGCTCTCACAGTGGCCTGTAACA
ATTTCTTCTGGGAGAACAGTTGAGCAGACAGCCACATTGGGCAGCGCCCTTCCTCTCCACCCTCCCAGACCTGCC
TCTTCCCCCTGCTTCCACCTCACCCCACTTATCCCTCTCCATAACCCACCCCTTGCCCACCCCACCCCCACCCCC
ACCAAGGGCGCAAGAGTAGCGGTCCAAGCCTGCAACTCATCTTTCATTAAAGGCTTCTCTCTCACCAGCAAAAAA
AAAAAAA

405/6881
FIGURE 375

MGSELETAMETLINVFHAHSGKEGDKYKLSKKELKELLQTELSGFLDAQKDVAVDKVMKELDENG DGEVDFQEY
VVLVAALTVACNNFFWENS

406/6881
FIGURE 376

TCAGACAAGCACTGGACGTGGCGGCCATTTTGT TTTTGGACACCGAGCAGGAGCTGGCGGCCGCTGCAGACGAAAG
GCAGGAAAGGGCAGGCCGGGTGAGCAGACGGATCGGCCGACTAGACAGCCAACCAGCAACAACGAACTGAGCTCG
CATACTACCGCTTACGCATCTAACCAACCGCCCATCTAGCTAACCCGAGCCCCCTCCACCGTCAACTCAGGTTCCG
CCGGTCCCCGGCCCGCCTGCCGGAGCCGTGGTGGCAGCCCCGGGAGGAGCACTGGCGTCTGTTTCCCTTCGATTCT
CGGGATTCTGAAGATGGCTGCACAGTCAGCGCCGAAAGTTGTGCTAAAAAGCACCACCAAGATGTCTCTAAATGAG
CGCTTTACTAATATGCTGAAGAACAAACAGCCGACGCCAGTGAATATTTCGGGCTTCGATGCAGCAACAACAGCAG
CTAGCCAGTGCCAGAAACAGAAGACTGGCCCAGCAGATGGAGAATAGACCCTCTGTCCAGGCAGCATTAAACTT
AAGCAGAGCTTAAAGCAGCGCCTGGGTAAGAGTAACATCCAGGCACGGTTAGGCCGACCCATAGGGGCCCTGGCC
AGGGGAGCAATCGGAGGACGAGGCCTACCCATAATCCAGAGAGGCTTGCCAGAGGAGGACTACGTGGGGGACGT
GCCACCAGAACCCTACTTAGGGGCGGGATGTCACTCCGAGGTCAAAACCTGCTCCGAGGTGGACGAGCCGTAGCT
CCCCGAATGGGCTTAAGAAGAGGTGGTGTTCGAGGTTCGTGGAGGTCCTGGGAGAGGGGGCCTAGGGCGTGGAGCT
ATGGGTTCGTGGCGGAATCGGTGGTAGAGGTGGGGTATGATAGGTGGGGAAGAGGGGGCTTTGGAGGCCGAGGC
CGAGGCCGTGGACGAGGGAGAGGTGCCCTTGCTCGCCCTGTATTGACCAAGGAGCAGCTGGACAACCAATTGGAT
GCATATATGTCGAAAACAAAAGGACACCTGGATGCTGAGTTGGATGCCTACATGGCGCAGACAGATCCCGAAACC
AATGATTGAAGCCTGCCCATCCTCCCATGAGAGACTCTTGTTAGTCAACACATCTGTAAATAACCTTGAGATAAC
AGATGAGAAGAAATCTGATTGATGCTGGATGGACCTATCACAATAGGCTGTGGACTTACTTGCCACCAGCTTGTG
CATTTAGTGTGTTCCCTTTTACTTTTTGATACTGTGTTGTATGAAACCCTTTTGTCTTTGATTTGGTTTTTTGTT
TTTGTTTTTTTTAGGGGGGAGGGGGGGTTTTCCCTCCTTTGCCCAGACTTCTCTTTGAACACAAATGCATTAGCCT
TGTGGCTAGAACACCCTCTTCCTACCTCTGTCTCCCTCACTTGTCAATGCTCTGACATGCTAACATTTCTTTT
GTTTCATCCCTGTTGCCCCCACAGAAACATCCAGAAAAACCGGTCAGTGTTCCTTCCTCCCTGATCCTTAGGTTT
CTGAAATAGGGTTCTGTTACATCCTCTTCGATAGCCTGTTTAAATGTTTAGAAGGTCTGGAGCTCAAAAATGCG
TTCTTCC

407/6881
FIGURE 377

AGGGGTGACAGAGGCCGTGGTCGTGGTGGGCGCTTTGGTTCCAGAGGAGGCCAGGAGGAGGGTTTCAGGCCCTTT
GTACCACATATCCCATTGACTTCTATTTGTTGTTTACTTCTGGTTTAGTGTGAAATGGCCTTTCCCCGGGTCAA
GCCAGCACCTGATGAAACTTCCTTCAGTGAGGCCTTGCTGAAGAGGAATCAGGACCTGGCTCCCAATTCTGCTGA
ACAGGCATCTATCCTTTCTCTGGTGACAAAAATAACAATGTGATTGATAATCTGATTGTGGCTCCAGGGACATT
TGAAGTGCAAATTGAAGAAGTTCGACAGGTGGGATCCTATAAAAAGGGGACAATGACTACAGGACACAATGTGGC
TGACCTGGTGGTGATACTCAAGATTCTGCCAACGTTGGAAGCTGTTGCTGCCCTGGGGAACAAAGTCGTGGAAAG
CCTAAGAGCACAGGATCCTTCTGAAGTTTTAACCATGCTGACCAACGAAACTGGCTTTGAAATCAGTTCTTCTGA
TGCTACAGTGAAGATTCTCATTACAACAGTGCCACCCAATCTTCGAAAACCTGGATCCAGAACTCCATTTGGATAT
CAAAGTATTGCAGAGTGCCTTAGCAGCCATCCGACATGCCCCGCTGGTTCGAGGAAAATGCTTCTCAGTCCACAGT
TAAAGTTCTCATCAGACTACTGAAGGACTTGAGGATTCGTTTTCTGGCTTTGAGCCCCCTCACACCCTGGATCCT
TGACCTACTAGGCCATTATGCTGTGATGAACAACCCCAACAGACAGCCTTTGGCCCTAAACGTTGCATACAGGCG
CTGCTTGCAGATTCTGGCTGCAGGACTGTTCTGCCAGGTTTCACTGAGGTATCACTGACCCCTGTGAGAGTGGCAA
CTTTAGAGTACACACAGTCATGACCCTAGAACAGCAGGACATGGTCTGCTATACAGCTCAGACTCTCGTCCGAAT
CCTCTCACATGGTGGCTTTAGGAAGATCCTTGGCCAGGAGGGTGATGCCAGCTATCTTGCTTCTGAAATATCTAC
CTGGGATGGAGTGATAGTAACACCTTCAGAAAAGGCTTATGAGAAGCCACCAGAGAAGAAGGAAGGAGAGGAAGA
AGAGGAGAATACAGAAGAACCACCTCAAGGAGAGGAAGAAGAAAGCATGGAAACTCAGGAGTGACATTCCCTTCA
CTCCTTTTCTACCCAAGGGGGAAGACTGGAGCCTAAGCTGCCTGCTACTGGGCTTTACATGGTGACAGACATTT
CCGTGGGATAGGGAAGATAGCAGGAAGAAAAGTAACTCCATAGAAGTGTCATTCCACTGGGTTTTGATATTGGC
TTAGCTGCCAGTCTCCCATTTGTGACCTATGCCATCCATCTATAATGGAGGATACCAACATTTCTTCTTAATATT
CTATAATCTCCAACCTCCTGAAAACCCCTCTCTCAACTAATACTTTGCTGTTGAAATGTTGTGAAATGTTAAGTGT
CTGGAAATTTTTTTTTTCTAAGAAAAACTATTAAAGTACTT

408/6881

FIGURE 378

MRGDRGRGRGGFRFGSRGGPGGGFRPFVPHIPFD FYLCEMAFPRVKPAPDETSFSEALLKRNQDLAPNSAEQASIL
SLVTKINNVIDNLIVAPGTFEVQIEEVQRQVGSYKKGTMTTGHNVADLVVILKILPTLEAVAALGNKVVESLRAQD
PSEVLTMLTNETGFEISSDATVKILITTVPFNLRLKLDPELHLDIKVLQSALAAIRHARWFEENASQSTVKVLIR
LLKDLRIRFPGFEP LTPWILDLLGHYAVMNNPTRQPLALNVAYRRCLQILAAGLFLPGSVGITDPCESGNFRVHT
VMTLEQQDMVCYTAQTLVRILSHGGFRKILGQEGDASYLASEISTWDGVIVTPSEKAYEKPPEKKEGEEEEENTE
EPPQGEEEEESMETQE

409/6881
FIGURE 379

CACACCCGCACTCCTCCCGGGTTTCTGCTCTCCGCCCGTGTGGAGTGGTGGGGGCCTGGGTGGGAATGGGCGTGT
GCCAGCGCACGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTTCGGAAGGGAGGAT
CAGGGATGTTTGCGAGCGGCTGGAACCAGACGGTGCCGATAGAGGAAGCGGGCTCCATGGCTGCCCTCCTGCTGC
TGCCCCTGCTGCTGTTGCTACCGCTGCTGCTGCTGAAGCTACACCTCTGGCCGCAGTTGCGCTGGCTTCCGGCGG
ACTTGGCCTTTGCGGTGCGAGCTCTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGCGGCTGCCGCCG
ACCCGGAAGGTCCCGAGGGGGGCTGCAGCCTGGCCTGGCGCCTCGCGGAAGTGGCCAGCAGCGCGCCGCGCACA
CCTTTCTCATTACGGCTCGCGGCGCTTTAGCTACTCAGAGGCGGAGCGCGAGAGTAACAGGGCTGCACGCGCCT
TCCTACGTGCGCTAGGCTGGGACTGGGGACCCGACGGCGGCGACAGCGGCGAGGGGAGCGCTGGAGAAGGCGAGC
GGGCAGCGCCGGGAGCCGGAGATGCAGCGGCCGGAAGCGGCGCGGAGTTTGCCGGAGGGGACGGTGCCGCCAGAG
GTGGAGGAGCCGCCGCCCTCTGTACCTGGAGCAACTGTGGCGCTGCTCCTCCCCGCTGGCCAGAGTTTCTGT
GGCTCTGGTTGCGGCTGGCCAAGGCCGGCCTGCGCACTGCCTTTGTGCCACCGCCCTGCGCGGGGGCCCCCTGC
TGCACTGCCTCCGCACTGCGGCGCGCGCGCTGGTGCTGGCGCCAGAGTTTCTGGAGTCCCTGGAGCCGGACC
TGCCCGCCCTGAGAGCCATGGGGCTCCACCTGTGGGCTGCAGGCCCAGGAACCCACCCTGCTGGAATTAGCGATT
TGCTGGCTGAAAGTGTCGCTGAAGTGGATGGGCCAGTGCCAGGATACCTCTCTTCCCCCAGAGCATAACAGACA
CGTGCTGTACATCTTCACCTCTGGCACCACGGGCCTCCCCAAGGCTGCTCGGATCAGTCATCTGAAGATCCTGC
AATGCCAGGGCTTCTATCAGCTGTGTGGTGTCCACCAGGAAGATGTGATCTACCTCGCCCTCCCACTCTACCACA
TGTCGGGTTCCCTGCTGGGCATCGTGGGCTGCATGGGCATTGGGGCCACAGTGGTGCTGAAATCCAAGTTCTCGG
CTGGTCAGTTCTGGGAAGATTGCCAGCAGCACAGGGTGACGGTGTTCAGTACATTGGGGAGCTGTGCCGATACC
TTGTCAACCAGCCCCGAGCAAGGCAGAACGTGGCCATAAGGTCCGGCTGGCAGTGGGCAGCGGGCTGCGCCCAG
ATACCTGGGAGCGTTTTGTGCGGCGCTTCGGGCCCCCTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACG
TGGCCACCATCAACTACACAGGACAGCGGGGCGCTGTGGGGCGTGCTTCCTGGCTTTACAAGCATATCTTCCCCT
TCTCCTTGATTGCTATGATGTACCACAGGAGAGCCAATTCGGGACCCCAGGGGCACTGTATGGCCACATCTC
CAGGTGAGCCAGGGCTGCTGGTGGCCCCGTAAGCCAGCAGTCCCATTCTGGGCTATGCTGGCGGGCCAGAGC
TGGCCAGGGGAAGTTGCTAAAGGATGTCTTCGGCCTGGGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCT
GCGATGACCAAGGTTTTCTCCGCTTCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTGGCCA
CAACCGAGGTGGCAGAGGTCTTCGAGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATGGAGTCACTGTGCCAG
GGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCCCCACGCTTTGGACCTTATGCAGCTCTACA
CCCACGTGTCTGAGAACTTGCCACCTTATGCCCGGCCCGATTCTCAGGCTCCAGGAGTCTTTGGCCACCACAG
AGACCTTCAAACAGCAGAAAGTTCCGATGGCAAATGAGGGCTTCGACCCAGCACCTGTCTGACCCACTGTACG
TTCTGGACCAGGCTGTAGGTGCCTACCTGCCCCCTCACAAGTCCCGGTACAGCGCCCTCCTGGCAGGAAACCTTC
GAATCTGAGAACTTCCACACCTGAGGCACCTGAGAGAGGAACCTCTGTGGGGTGGGGGCCGTTGCAGGTGTACTGG
GCTGTGAGGGATCTTTTCTATACCAGAACTGCGGTCACTATTTTGTAAATAAATGTGGCTGGAGCTGATCCAGCTG
TCTCTGACCTACAAAAAAAAAAAAAAAAAAAA

410/6881
FIGURE 380

MGVCQRTRAPWKEKSQLERAALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLLPLLLLLPLLLLLKLHLWPQLRW
LPADLAFAVRALCCKRALRARALAAAAADPEGPEGGCSLAWRLAELAQQRAAHTFLIHGSRRFSSYSEAERESNR
ARAFRLALGWDWGPDGGDSGEGSAGEGERAAPGAGDAAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGP
EFLWLWFGGLAKAGLRRTAFVPTALRRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAG
ISDLLAEVSAEVDGFPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKIQCQGFYQLCGVHQEDVIYLLALP
LYHMSGSLLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPPSKAERGHKVRLAVGSG
LRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRASWLYKHIFPFSLIRYDVTTGEPIRDPOGHCM
ATSPGEPGLLVAPVSQQSPFLGYAGGPPELAQ GKLLKDVF RPDVFFNTGDLLVCDDQGFLRFHDRTGDTFRWKGE
NVATTEVAEVFEALDFLQEVNVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPYARPRFLRLQESL
ATTETFKQQKVRMANEGFDPSTLSDPYVLDQAVGAYLPLTTARYSALLAGNLRI

411/6881
FIGURE 381

GGCACGAGGGGGCTTCAGGACAATTCGTGATGGCGGGGGCTGGTTCCGCCGCTGTATCGGGGGCAGGGACCCCGG
TGGCGGGGCCCACAGGCCGCGACCTTTTCGCCGAAGGGCTGCTGGAGTTCCTGCGACCCGCTGTGCAGCAGCTCG
ACTCTCACGTACACGCCGTCAGAGAGAGCCAGGTAGAGCTCCGGGAACAAATTGACAACCTAGCCACAGAACTGT
GCCGCATAAATGAGGATCAGAAGGTGGCCCTGGATCTTGACCCCTATGTTAAGAAGCTACTTAATGCCCGGCGAC
GCGTTGTCTTGGTTAACAACATTCTACAGAATGCTCAGGAACGACTGAGACGGCTAAACCACAGTGTTGCCAAGG
AAACAGCCCGCAGGAGAGCAATGCTGGATTGCGGAATTTACCCCCCTGGCTCCCCAGGCAAATAACAGATGAGCC
TATGGACTCAGTAGCACAAGTACTGTTCCCCAGCTGCCTTGTTTCAACAGACATGCAAAGATCCTAGGAGACAGT
CCCCATAGACCTTCAGACATTAAAAAGGGAGCCGTACAGTTTGTTTGAAGCACTTCGTCTTACCCATTTATGTAG
GGGCCCCAGGAAACCTACACACAGCCAGAATGAGGTTCCCAAAGGACTTACATTAATTATGGCTCTTGCTTCCTT
TCACAAATGAGCTGAGGCCTCTACTTTTTTTTTTTTAAAGCTGCATACTTGAGGCTTACCTTCTTCAGGACTAGTT
AACCAGAGGGGGCTTCCTTTGTATGTTACATGCCTGGTTACATGGGCCTGGACAGCATGTCCCTACCTGTGACTT
CTCATTTTCCCTGTTTACACTGGGGATTTGGAGGGGGCAGGCAAAGTCAAAGTGAATGACCTCTGTCCACCCACTT
TTTTATTGCACTGGCTTGAATACAGTAGCAGTGTTGATAGAATCATTTTATTCAATAAATACTTAAATGAAAA
AAAAAAAAAAAAAAAAAAAAA

412/6881
FIGURE 382

MAGAGSAAVSGAGTPVAGPTGRDLFAEGLLEFLRPAVQQLD SHVHAVRESQVELREQIDNLATELCRINEDQKVA
LDLDPYVKKLLNARRRVVLVNNILQNAQERLRRLNHSVAKETARRRAMLDSGIYPPGSPGK

413/6881
FIGURE 383

CTATGATAAGCTAATTATTTATGTTTGCATAATATTTATGTTTGCATGTTAGTGACATATATTTTAAAATGTGAT
ACACTCCTGTAATTTATGAGAGTATGTTTCATTGCTGTGAGCTTTGAAGGTGCTCTAATCCTTCCTCATATTTGGC
CTTAGAATGCACCTCGGATCCCCCAAGGTTTAGGCTTTCTTCATTTGTCTTTGAAACTATATCTTCTGTCTCTTG
TCATATCTGCTTATTGCGTGTTTTTCATACCTTCCACCTCTCTAAAAGCCGTTACCTGAGCCCTCGTTATCACTT
TTGGTTGAATGTGCTGCACTTAGCTGCATTTCTAAGTTTCTGATTCTTGCAAGTTTGTGGAAACAGAGGAGTCTT
TAACCCACATCAGCCTTGATCTAAGTGTACCACCTTACTTAAAAGTTCTGTTGGGATCTGGAGCTCCTGGTCTAGCA
AGCCATGAAAATGCCAATAAATGTTTGTAAATAAGCTTTTATTTAAACATCCATTTTGTTCGACCTTGAAGCTTT
ACTAATATGCTGAAGAACAACAGCCGACGCCAGTGAATATTCGGGCTTCGATGCAGCAACAACAGCAGCTAGCC
AGTGCCAGAAACAGAAGACTGGCCCAGCAGATGGAGAATAGACCCTCTGTCCAGGCAGCATTAAAACCTAAGCAG
AGCTTAAAGCAGCGCCTGGGTAAGAGTAACATCCAGGCACGGTTAGGCCGACCCATAGGGGGCCCTGGCCAGGGGA
GCAATCGGAGGACGAGGCCTACCCATAATCCAGAGAGGCTTGCCCAGAGGAGGACTACGTGGGGGACGTGCCACC
AGAACCCTACTTAGGGGCGGGATGTCACTCCGAGGTCAAACCTGCTCCGAGGTGGACGAGCCGTAGCTCCCCGA
ATGGGCTTAAGAAGAGGTGGTGTTCGAGGTGCTGGAGGTCTGGGAGAGGGGGCCTTAGGGCGTGGAGCTATGGGT
CGTGGCGGAATCGGTGGTAGAGGTGGGGTATGATAGGTGGGGGAAGAGGGGGCCTTGGAGGCCGAGGCCGAGGC
CGTGGACGAGGGAGAGGTGCCCTTGCTCGCCCTGTATTGACCAAGGAGCAGCTGGACAACCAATTGGATGCATAT
ATGTGCGAAAACAAAAGGACACCTGGATGCTGAGTTGGATGCCTACATGGCGCAGACAGATCCCGAAACCAATGAT
TGAAGCCTGCCCATCCTCCCATGAGAGACTCTTGTTAGTCAACACATCTGTAAATAACCTTGAGATAACAGATGA
GAAGAAATCTGATTGATGCTGGATGGACCTATCACAATAGGCTGTGGACTTACTTGCCACCAGCTTGTGCATTTA
GTGTGTTCTTTTTACTTTTTTGATACTGTGTTGTATGAAACCCTTTTGTCTTTGATTGTTTTTTGTTTTTGT
TTTTTAGGGGGGAGGGGGGTTTTCCCTCCTTTGCCCAGACTTCTCTTTGAACACAAATGCATTAGCCTTGTGGC
TAGAACACCCTCTTCCTACCTCTGTCTCCCTCACTTGTCATATGCTCTGACATGCTAACATTTCTTTGTTCAT
CCCTGTTGCCCCACAGAAACATCCCAGAAAAACCGGTCAGTGTTCCTTCCTCCCTGATCCTTAGGTTTCTGAAA
TAGGGTTCTGTTACATCCTCTTCGATAGCCTGTTTAAAATGTTTAGAAGGTCTGGAGCTCAAAAATGCGTTCTTC
C

414/6881
FIGURE 384

CCACAGATCCATGATGTGCAGTTCTCTGGAGCAGGCGCTGGCTGTGCTGGTCACTACCTTCCACAAGTACTCCTG
CCAAGAGGGCGACAAGTTCAAGCTGAGTAAGGGGGAAATGAAGGAAGTTCTGCACAAGGAGCTGCCCAGCTTTGT
GGGGGAGAAAGTGGATGAGGAGGGGCTGAAGAAGCTGATGGGCAGCCTGGATGAGAACAGTGACCAGCAGGTGGA
CTTCCAGGAGTATGCTGTTTTCTGGCACTCATCACTGTCATGTGCAATGACTTCTTCCAGGGCTGCCCAGACCG
ACCCTGAAGCAGAACTCTTGAAGTTCCCTGCCATGGATCTCTTGGGCCCAGGACTGTTGATGCCTTTGAGTTTGT
TTCAATAAACTTTTTTGTCTGTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

415/6881
FIGURE 385

MMCSSLEQALAVLVTTTFHKYSCQEGDKFKLSKGEMKELLHKELPSFVGEKVDEEGLKKLMGSLDENSQQVDFQE
YAVFLALITVMCNDFQGCPRP

416/6881
FIGURE 386

GCGCCCAGACTTGCTGCCGGGCTGGACGGTCCGCACGGTGCTGGGCAGCAGCGAAAACGCGCTGGGCGTGTGCTC
CGACACCGCAGCGCCCCCTGGCCGCGGTGGACCTCAAGTGGGAGCACAACCCCGCTGTGTTCTGGGCCCCGGCTG
CGTGTACGCCGCCGCCAGTGGGGCGCTTCACCGCGCACTGGCGGGTCCCGCTGCTGACCGCCGGCGCCCCGGC
GCTGGGCTTCGGTGTCAAGGACGAGTATGCGCTGACCACCCGCGCGGGGCCAGCTACGCCAAGCTGGGGGACTT
CGTGGCGGCGCTGCACCGACGGCTGGGCTGGGAGCGCCAAGCGCTCATGCTCTACGCCTACCGGCCGGGTGACGA
AGAGCACTGCTTCTTCTCGTGGAGGGGCTGTTTCATGCGGGTCCGCGACCGCTCAATATTACGGTGGACCACCT
GGAGTTGCGCGAGGACGACCTCAGCCACTACACCAGGCTGCTGCGGACCATGCGCGCAAAGGCCGAGTTATCTA
CATCTGCAGCTCCCCTGATGCCTTCAGAACCTCATGCTCCTGGCCCTGGAAGCTGGCTTGTGTGGGGAGGACTA
CGTTTTCTTCCACCTGGATATCTTTGGGCAAAGCCTGCAAGGTGGACAGGGCCCTGCTCCCCGAGGCCCTGGGA
GAGAGGGGATGGGCAGGATGTCAAGTGGCCGCCAGGCCTTTCAGGCTGCCAAAATCATTACATATAAAGACCCAGA
TAATCCCCGAGTACTTGGAATTCCTGAAGCAGTTAAAACACCTGGCCTATGAGCAGTTCAACTTCACCATGGAGGA
TGGCCTGGTGAACACCATCCCAGCATCCTTCCACGACGGGCTCCTGCTCTATATCCAGGCAGTGACGGGAGACTCT
GGCACATGGGGGAACGTGTTACTGATGGGGAGAACATCACTCAGCGGATGTGGAACCGAAGCTTTCAAGGTGTGAC
AGGATACCTGAAAATTGATAGCAGTGGCGATCGGGAAACAGACTTCTCCCTCTGGGATATGGATCCCCGAGAATGG
TGCCCTTCAGGGTTGTACTGAAGTACAATGGGACTTCCCAAGAGCTGGTGGCTGTGTGCGGGCGCAAAGTGAAGT
GCCCCGAGGGTACCTCCTCCTGACATCCCCAAATGTGGCTTTGACAACGAAGACCCAGCATGCAACCAAGATCA
CCTTTCACCCCTGGAGGTGCTGGCTTTGGTGGGCGAGCCTCTCCTTGCTCGGCATTCTGATTGTCTCCTTCTTCAT
ATACAGGAAGATGCAGCTGGAGAAGGAAGTGGCCTCGGAGCTGTGGCGGGTGCCTGAGGAGGACGTTGAGCCAG
TAGCCTTGAGAGGCACCTGCGGAGTGCAGGCAGCCGGCTGACCCTGAGCGGGAGAGGCTCCAATTACGGCTCCCT
GCTAACACAGAGGGCCAGTTCCAAGTCTTTGCCAAGACAGCATATTATAAGGGCAACCTCGTGGCTGTGAAACG
TGTGAACCGTAAACGCATTGAGCTGACACGAAAAGTCTGTTGAACTGAAGCATATGCGGGATGTGCAGAATGA
ACACCTGACCAGGTTTGTGGGAGCCTGCACCGACCCCCCAATATCTGCATCCTCACAGAGTACTGTCCCCGTGG
GAGCCTGCAGGACATTCTGGAGAATGAGAGCATACCCCTGGACTGGATGTTCCGGTACTCACTACCAATGACAT
CGTCAAGGGCATGCTGTTTCTACACAATGGGGCTATCTGTTCCCATGGGAACCTCAAGTCATCCAAGTGCCTGGT
AGATGGGCGCTTTGTGCTCAAGATCACCGACTATGGGCTGGAGAGCTTCAGGGACCTGGACCCAGAGCAAGGACA
CACCGTTTATGCCAAAAGCTGTGGACGGCCCTGAGCTCCTGCGAATGGCTTCACCCCTGTGCGGGGCTCCCA
GGCTGGTGACGTATACAGCTTTGGGATCATCCTTCAGGAGATTGCCCTGAGGAGTGGGGTCTTCCACGTGGAAGG
TTTGGACCTGAGCCCCAAAGAGATCATCGAGCGGGTGAAGTGGGGTGGAGCAGCCCCCTTCCGGCCCTCCCTGGC
CCTGCAGAGTCACCTGGAGGAGTTGGGGCTGCTCATGCAGCGGTGCTGGGCTGAGGACCCACAGGAGAGGCCACC
ATTCCAGCAGATCCGCTGACGTTGCGCAAATTTAAGAGGGAGAAGCAGCAGCAACATCCTGGACAACCTGCTGTC
CCGCATGGAGCAGTACGCGAACAATCTGGAGGAAGTGGTGGAGGAGCGGACCCAGGCATACCTGGAGGAGAAGCG
CAAGGCTGAGGCCCTGCTCTACAGATCCTGCCTCACTCAGTGGCTGAGCAGCTGAAGCGTGGGGAGACGGTGCA
GGCCGAAGCCTTTGACAGTGTACCATCTACTTCAGTGACATTGTGGGTTTACAGCGCTGTGCGGCGGAGAGCAC
ACCCATGCAGGTGGTGACCCTGCTCAATGACCTGTACACTTGCTTTGATGCTGTGCATAGACAACCTTTGATGTGTA
CAAGGTGGAGACAATTGGCGATGCCTACATGGTGGTGTGAGGCTCCCTGTGCGGAACGGGCGGCTACACGCCTG
CGAGGTAGCCCGCATGGCCCTGGCACTGCTGGATGCTGTGCGCTCCTTCCGAATCCGCCACCGGCCCCAGGAGCA
GCTGCGCTTGCGCATGGCATCCACACAGGACCTGTGTGTGCTGGAGTGGTGGGACTGAAGATGCCCCGTACTG
TCTCTTTGGGGATACAGTCAACACAGCCTCAAGAATGGAGTCTAATGGGGAAGCCCTGAAGATCCACTTGTCTTC
TGAGACCAAGGCTGTCTTGAGGAGTTTGGTGGTTTCGAGCTGGAGCTTCGAGGGGATGTAGAAATGAAGGGCAA
AGGCAAGGTTTCGGACCTACTGGCTCCTTGGGGAGAGGGGGAGTAGCACCCGAGGCTGACCTGCCTCCTCTCCTAT
CCCTCCACACCTCCCTACCCTGTGCCAGAAGCAACAGAGGTGCCAGGCCTCAGCCTCACCCACAGCAGCCCCATC
GCCAAAGGATGGAAGTAATTTGAATAGCTCAGGTGTGCTGACCCAGTGAAGACACCAGATAGGACCTCTGAGAG
GGGACTGGCATGGGGGGATCTCAGAGCTTACAGGCTGAGCCAAGCCACGGCCATGCACAGGGACACTCACACAG
GCACACGCACCTGCTCTCCACCTGGACTCAGGCCGGGCTGGGCTGTGGATTCTGATCCCTCCCTCCCATGC
TCTCTCCCTCAGCCTTGCTACCCTGTGACTTACTGGGAGGAGAAAAGTACCTGAAGGGGAACATGAAAAGAG
ACTAGGTGAAGAGAGGGGAGGGGAGCCACATCTGGGGCTGGCCCAATACCTGCTCCCCGACCCCTCCACC
CAGCAGTAGACACAGTGCACAGGGGAGAAGAGGGGTGGCGCAGAAGGGTTGGGGGCTGTATGCCTTGCTTCTAC
CATGAGCAGAGACAATTAATCTTTATTCCAGTG

417/6881
FIGURE 387

MPGPRRPAGSRLRLLLLLLLLLPLLLLLLRGSHAGNLTAVVVLPLANTSYPWSWARVGPAVELALAQVKARPDLLPG
WTVRTLGLSSENALGVCSDTAAPLAAVDLKWEHNPAVFLGPGCVYAAAPVGRFTAHWRVPLLTAGAPALGFGVKD
EYALTTRAGPSYAKLGDFVAALHRRRLGWERQALMLYAYRPGDEEHCFLLVEGLFMRVRDRLNITVDHLEFAEDDL
SHYTRLLRTMPRKGRVIYICSSPDAFRTLMLLALAEAGLCGEDYVFFHLDIFGQSLQGGQGPAPRRPWERGDGQDV
SARQAFQAAKIITYKDPDNPEYLEFLKQLKHLAYEQFNFTMEDGLVNTIPASFHDGLLLYIQAVTETLAHGGTIVT
DGENITQRMWNRSFQGVGTGYLKIDSSGDRETDFSLWMDPENGAFRVVLNYNGTSQELVAVSGRKLNWPLGYPPP
DIPKCGFDNEDPACNQDHLSTLEVLALVGSLSLGILIVSFFIYRKMQLKELASELWRVRWEDVEPSSLERHLR
SAGSRLTLSGRGSNYGSLTTEGQFQVFAKTAYYKGNLVAVKRVNRKRIELTRKVL FELKHM RDVQNEHLTRFVG
ACTDPPNICILTEYCPRGS LQDILENESITLDWMFRYSLTNDIVKGMLFLHNGAICSHGNLKSSNCVVDGRFVLK
ITDYGLESFRDLDP EQGHTVYAKKLWTAPELLRMASPPVRGSQAGDVYSFGIILQEIALRSGVFHVEGLDLSPE
I IERVTRGEQPPFRPSLALQSHLEELGLLMQRCWAEDPQERPPFQQIRLTLRKFNRENS SNILDNLLSRMEQYAN
NLEELVEERTQAYLEEKRKAEALLYQILPHSVAEQLKRGETVQAEAFDSVTIYFSDIVGFTALSAESTPMQVVTL
LNDLYTCFDAVIDNFDVYKVETIGDAYMVVSGLPVRNGRLHACEVARMALALLDAVRSFRIRHRPQEQLRLRIGI
HTGPVCAGVVGLKMPRYCLFGDTVNTASRMESNGEALKIHLSETKAVLEEFGGFELELRGDVEMKGKGKVRTYW
LLGERGSSTRG

418/6881
FIGURE 388

CTGGGTGGCGGTTATGGTGGGGCCAGCGGCATGGGAGGCATCACCGCAGTCATGGTCAACCAGAACCTGCTGAGC
CCCCTTGTCTTGAGGTGGACCCCAACATCCAGGCCGTGTGCACCCAGGAGAAGGAGCCGATCAAGACCCTCAAC
AACAAGTTTGCCTCCTTCATAGACAAGGTACGGTTCCTGGAGCAGCAGAACAAGATGCCGGAGACCAAGTGGAGC
CTCCTGCAGCAGCAGAAGACGGCTCGGAGCAACATGGACAAGTTCGAGAGCTACATCAACAACCTTAGGCAGCAG
CTGGAGATTCTGGGCCAGGAGAAGCTGAAGCTGGAGGCGGAGCTTGGCAACATGCAGGGGCTGGTGGAGGACTTC
AAGAACAAGTATGAGGATGAGATCAATAAGCGTACAGAGATGGAGAATGAATTTGTGCTCACCAAGAAGGATGTG
GATGAAGCTTACATGAACAAGGTAGAGCTGGAGTCTCGCCTGGAAGGGCTTACTGAAGAGATCAGCTTCCTCAGG
CAGCTGTATGAAGAGGAGATCCGGGAGCTGCAGTCCCAGATCTCAGACACATCATTGCTGAGGTCAAGGCACAGT
ACGAGGACCGCCAGCCGCAGCCAGGCTGAGGCTGAGAGCATGTACCAGATCAAGAATGAGGAGCTGCAAGAGCCT
GGCTGGGAAGCACGGGGATGA

419/6881
FIGURE 389

TTGCCCCGGGACTAGGAGCTTAAGTGAAGAGGTACGCCTTGTTTCGGTGGAAATCAGCCGTAGCCATGAGTTTCTGC
CGGGGCTAGCCCTAGAGTACGGAGCAGGCGGACTTTTCGGTTCCCCGCCCCGCCAGGTGGCGGGGCCTACTAGGC
CTCCGGGCATCCCCGGTCTCAAGTAGGCCTCATCTGCCGGCAAGGGCGCCCCGAAACGCGGGAGGCGCCATGTCGC
TGGTTGCTTACGCCAGCAGCGATGAGAGCGAGCCGGATGAGGCTGAGCCCGAGCCGGAGGAAGAGGAGGCGGTGG
CTCCTACATCTGGGCCCCGCTTTAGGGGGCTTGTTTCGCTTCTCTCCCTGCGCCCAAGGGTCCGGCCTTGCTGCCTC
CGCCCCCTCAGATGCTGGCGCCAGCCTTTCCCCCGCCGCTGTTGCTTCCCCACCCACCGGAGACCCAGGCTTC
AGCCTCCTCCCCCCTTGCCCTTCGGCCTGGGAGGCTTCCCCCACCTCCAGGCGTGAGCCCGGCTGAAGCGGCGG
GAGTTGGGGAGGGACTGGGATTGGGGTTGCCCTCGCCCCGAGGCCCTGGCCTCAATCTGCCCCCTCCAATTGGCG
GTGCCGGTCCCCCGCTGGGGCTTCCCAAGCCAAAGAAGAGGAAAGAGCCCGTGAAGATCGCGGCGCCGGAGTTGC
ATAAGGGAGATTCAAGATTCTGAGGAAGATGAACCCACAAAGAAGAAAACCTATCCTTCAGGGATCCAGTGAGGGGA
CTGGTTTGTCTGCCTTGCTTCCCCAACCTAAAAACCTGACTGTGAAAGAGACTAACAGGTTGCTCCTGCCCATG
CCTTCTCCCGCAAACCTCGGATGGCTCCCCTGATACTAAGCCCTCCAGACTGGCTTCTAAGACCAAGACTTCCT
CTCTTGCCCCCTGTTGTGGGCACCACAACCACCACTCCGTCGCCCTCTGCTATCAAGGCTGCTGCCAAGAGTGCTG
CCCTGCAGGTGACAAAGCAGATCACGCAGGAAGAAGACGACAGTGATGAGGAAGTAGCCCCCGAAAACCTTTTTCT
CCCTCCCTGAAAAGGCTGAGCCACCTGGAGTTGAGCCATACCCTTACCCCATCCCCACTGTCCCTGAAGAGCTGC
CTCCAGGCACGGAACCAGAGCCGGCTTTCCAGGACGATGCAGCCAATGCCCCCCTTGAATTCAAGATGGCAGCAG
GTTCAAGTGGGGCCCCCTTGATGCCTAAGCCTGGGGACGACTACAGCTACAATCAGTTTTCCACATATGGCGATG
CCAATGCCGCTGGTGCTTATTATCAGGATTATTACAGTGTTGGCTACTATCCTGCACAGGACCCGGCCCTGGTCC
CCACCCAGGAAATTGCCCCAGATGCCTCCTTCATCGATGACGAAGCATTTAAGCGGCTGCAGGGCAAGAGGAACC
GAGGGAGAGAAGAAATCAACTTTGTGGAGATCAAAGGTGATGACCAGCTCAGTGGGGCCCAGCAATGGATGACTA
AGTCATTGACAGAAGAGAAAACCATGAAGTCATTACGCAAAAAGAAAGGTGAGCAGCCAACAGGCCAGCAGCGGC
GGAAACACCAGATCACATATCTTATTATCAGGCCAAGGAGCGGGAGCTGGAAGTGAAGAACACCTGGTCAGAGA
ACAAGCTCAGCCGCCGTCAGACCCAAGCCAAATATGGATTCTAGGGCTCTGGAAGTGAATTGCTCCCAGGATCTCC
TGCCAGCCCAGCTGGCCTGGCCCCAGCTTCACCTCTGGGACCCAGCTGCTCTAAGCCCAGGATCTCTTTCCCC
AAGGACCCAGCCCTCGCCTCTGCGAGAATGAACATATTTGATAGATTTTTCTTAACAAGTTAGAAAATTCAGCTC
CTTTCTGTCTGGAGCTAGCAAAGACTTGTTGTGATGCCTCCGAAGGGGCTCTGAGTTCTGGGGTGGGAGTTTTGC
TCTCTGTCAGGTGTGATAAAATGTTGAACCTCCCCACCACCACTTTTTTTTTTTTTTAAACCAGGGATGTCGTGT
GAAATAAAACATTTCAGTCTGACAAAAA

420/6881
FIGURE 390

MSLVAYASSDESEPDEAEPEPEEEEEAVAPTSGPALGGLFASLPAPKGPALLPPPPQMLAPAFPPPLLLPPPTGDP
RLQPPPPPLPFGLGGFPPPPGVSPAEEAGVGEGLGLGLPSPRGPGLNLPPPIGGAGPPLGLPKPKKRKEPVKIAAP
ELHKGDSSEDEPTKKKTIHQSSSEGTGLSALLPQPKNLTVKETNRLLPHAFSRKPSDGSPDTKPSRLASKTK
TSSLAPVVGTTTTTPSPSAIKAAAKSAALQVTKQITQEEDDSDEEVAPENFFSLPEKAEPPGVEPYPIPTVPE
ELPPGTEPEPAFQDDAANAPLEFKMAAGSSGAPWMPKPGDDYSYNQFSTYGDANAAGAYYQDYSSGGYYPAQDPA
LVPTQEIAPDASFIDDEAFKRLQGKRNRGREGINFVEIKGDDQLSGAQQWMTKSLTEEKTMKSFSSKKKGEOPTGQ
QRRKHQITYLIHQAKERELELKNTWSENKLSRRQTQAKYGF

421/6881
FIGURE 391

GAGGAGGAGTGGGGACCGGGCGGGGGGTGGAGGAAGAGGCCTCGCGCAGAGGAGGGAGCAATTGAATTTCAAACA
CAAACAACCTGCACGAGCGCGCACCCACCGCGCCGGAGCCTTGCCCCGATCCGCGCCCGCCCCGTCCGTGCGGGCGC
GCGGGCGGAGACGCCGTGGCCGCGCCGGAGCTCGGGCCGGGGGCCACCATCGAGGCGGGGGCCGCGCGAGGGCCG
GAGCGGAGCGGGCGCCGCCACCGCCGCACGCGCAAACCTTGGGCTCGCGCTTCCCGGCCCGGCGCGGAGCCCGGGGC
GCCCCGAGCCCCGCCATGTCGCGATCCAACCGGCAGAAGGAGTACAAATGCGGGGACCTGGTGTTCGCCAAGATG
AAGGGCTACCCACACTGGCCGGCCCGGATTGACGAGATGCCTGAGGCTGCCGTGAAATCAACAGCCAACAAATAC
CAAGTCTTTTTTTTCGGGACCCACGAGACGGCATTCTTGGGCCCCAAAGACCTCTTCCCTTACGAGGAATCCAAG
GAGAAGTTTGGCAAGCCCAACAAGAGGAAAGGGTTTACGCGAGGGGCTGTGGGAGATCGAGAACAACCTTACTGTC
AAGGCTTCCGGCTATCAGTCTCTCCAGAAAAAGAGCTGTGTGGAAGAGCCTGAACCAGAGCCCCGAAGCTGCAGAG
GGTGACGGTGATAAGAAGGGGAATGCAGAGGGCAGCAGCGACGAGGAAGGGAAGCTGGTCATTGATGAGCCAGCC
AAGGAGAAGAACGAGAAAGGAGCGTTGAAGAGGAGAGCAGGGGACTTGCTGGAGGACTCTCCTAAACGTCCCAAG
GAGGCAGAAAACCTGAAGGAGAGGAGAAGGAGGCAGCCACCTTGGAGGTTGAGAGGCCCCCTTCTATGGAGGTG
GAAAAGAATAGCACCCCTCTGAGCCCGGCTCTGGCCGGGGGGCCTCCCCAAGAGGAAGAAGAGGAGGAGGATGAA
GAGGAAGAGGCTACCAAGGAAGATGCTGAGGCCCCAGGCATCAGAGATCATGAGAGCCTGTAGCCACCAATGTTT
CAAGAGGAGCCCCCACCTGTTCCTGCTGCTGTCTGGGTGCTACTGGGGAACTGGCCATGGCCTGCAAACTGGG
AACCCTTTTCCACCCCAACCTGCTCTCCTCTTCTACTCACTTTCCCACTCCAAGCCCAGCCCATGGAGATTGA
CCTGGATGGGGCAGGCCACCTGGCTCTCACCTCTAGGTCCCCATACTCCTATGATCTGAGTCAGAGCCATGTCTT
CTCCCTGGAATGAGTTGAGGCCACTGTGTTCTTCCGCTTGGGAGGGGCAATCCTCAAATGCGGGGTGGGGGCAG
CACAGGAGGGCGGCCTCCTTCTGAGCTCCTGTCCCCTGCTACACCTATTATCCCAGCTGCCTAGATTCAGGGAAA
GTGGGACAGCTTGTAGGGGAGGGGCTCCTTTCCATAAATCCTTGATGATTGACAACACCCATTTTTCTTTTGCC
GACCCCAAGAGTTTTGGGAGTTGTAGTTAATCATCAAGAGAATTTGGGGCTTCCAAGTTGTTTCGGGCCAAGGACC
TGAGACCTGAAGGGTTGACTTTACCCATTTGGGTGGGAGTGTGAGCATCTGTCCCCCTTTAGATCTCTGAAGCC
ACAAATAGGATGCTTGGGAAGACTCCTAGCTGTCCTTTTTCTCTCCACACAGTGCTCAAGGCCAGCTTATAGTC
ATATATATCACCCAGACATAAAGGAAAAGACACATTTTTTAGGAAATGTTTTTAATAAAAAGAAAATTACAAAAA
AAATTTTAAAGACCCCTAACCCTTTGTGTGCTCTCCATTCTGCTCCTTCCCCATCGTTGCCCCCATTTCTGAGGT
GCACTGGGAGGCTCCCCCTTCTATTTGGGGCTTGATGACTTTCTTTTTGTAGCTGGGGCTTTGATGTTCTCTCCAG
TGTCATTTCTCATCCACATACCCTGACCTGGCCCCCTCAGTGTTGTCACCAGATCTGATTTGTAACCCACTGAGA
GGACAGAGAGAAAATAAGTGCCCTCTCCACCCCTCTTCCCTACTGGTCTCTCTATGCCTCTCTACAGTCTCGTCTCT
TTTACCCTGGCCCCCTCTCCCTTGGGCTCTGATGAAAAATTGCTGACTGTAGCTTTGGAAGTTTAGCTCTGAGAAC
CGTAGATGATTTCAAGTTCTAGGAAAATAAAACCCGTTGATTACT

422/6881
FIGURE 392

AGCTTTGGGGTTGTCCCTGGACTTGTCTTGGTTCCAGAACCTGACGACCCGGCGACGGCGACGTCTCTTTTGA
AAAAGACAGTGTCCAGTGCTCCAGCCTAGGAGTCTACGGGGACCGCCTCCCGCGCCGCCACCATGCCCAACTTCT
CTGGCAACTGGAAAAATCATCCGATCGGAAAACTTCGAGGAATTGCTCAAAGTGCTGGGGGTGAATGTGATGCTGA
GGAAGATTGCTGTGGCTGCAGCGTCCAAGCCAGCAGTGGAGATCAAACAGGAGGGAGACACTTTCTACATCAAAA
CCTCCACCACCGTGCGCACCACAGAGATTAACTTCAAGTTGGGGAGGAGTTTGAGGAGCAGACTGTGGATGGGA
GGCCCTGTAAGAGCCTGGTGAATGGGAGAGTGAGAAATAAAATGGTCTGTGAGCAGAAGCTCCTGAAGGGAGAGG
GCCCCAAGACCTCGTGGACCAGAGAACTGACCAACGATGGGGAACTGATCCTGACCATGACGGCGGATGACGTTG
TGTGCACCAGGGTCTACGTCCGAGAGTTGAGTGGCCACAGGTAGAACC GCGGCCGAAGCCCCACCACTGGCCATGCT
CACCGCCCTGCTTCACTGCCCCCTCCGTCCCAACCCCTCCTTCTAGGATAGCGCTCCCCCTTACCCCAGTCACTTC
TGGGGGTCACTGGGATGCCTCTTGCAAGGTCTTGCTTTCTTTGACCTCTTCTCTCCTCCCCCTACACCAACAAAGA
GGAATGGCTGCAAGAGCCCAGATCACCCATTCCGGGTTCCTCCCGCCTCCCAAGTCAGCAGTCTTAGCCCCA
AACCAGCCCAGAGCAGGTCTCTCTAAAGGGGACTTGAGGGCCTGAGCAGGAAAGACTGGCCCTCTAGCTTCTAC
CCTTTGTCCCTGTAGCCTATACAGTTTAGAATATTTATTTGTTAATTTTATTAAAATGCTTTAAAAAAA

423/6881
FIGURE 393

MPNFSGNWKIIRSENFEELLKVLGVNVMLRKIAVAAASKPAVEIKQEGDTFYIKTSTTVRTTEINFKVGEEFEEQ
TVDGRPCKSLVKWESENKMVCEQKLLKGEGPKTSWTRELTNDGELILTMTADDVVCTRVYVRE

424/6881
FIGURE 394

GCAGTCTCCGCCGCAGTCTCAGCTGCAGCTGCAGGACTGAGCCGTGCACCCGGAGGAGACCCCCGGAGGAGGCGA
CAAACCTTCGCAGTGCCGCGACCCAACCCAGCCCTGGGTAGCCTGCAGCATGGCCCAGCTGTTCTGCCCCCTGCT
GGCAGCCCTGGTCTTGGCCCAGGCTCCTGCAGCTTTAGCAGATGTTCTGGAAGGAGACAGCTCAGAGGACCGCGC
TTTTCGCGTGCATCGCGGGCGACGCGCCACTGCAGGGCGTGCTCGGCGGCGCCCTCACCATCCCTTGCCACGT
CCACTACCTGCGGCCACCGCCGAGCCGCGGGCTGTGCTGGGCTCTCCGCGGGTCAAGTGGACTTTCCTGTCCCG
GGGCCGGGAGGCAGAGGTGCTGGTGGCGCGGGGAGTGCGCGTCAAGGTGAACGAGGCCTACCGGTTCCGCGTGCG
ACTGCCTGCGTACCCAGCGTCGCTCACCGACGTCTCCCTGGCGCTGAGCGAGCTGCGCCCCAACGACTCGGGTAT
CTATCGCTGTGAGGTCCAGCACGGCATCGATGACAGCAGCGACGCTGTGGAGGTCAAGGTCAAAGGGGTGCTCTT
TCTCTACCGAGAGGGCTCTGCCCCGCTATGCTTTCTCCTTTTCTGGGGCCAGGAGGCCTGTGCCCGCATTGGAGC
CCACATCGCCACCCCGGAGCAGCTCTATGCCGCTACCTTGGGGGCTATGAGCAATGTGATGCTGGCTGGCTGTC
GGATCAGACCGTGAGGTATCCCATCCAGACCCACGAGAGGCCTGTTACGGAGACATGGATGGCTTCCCCGGGGT
CCGGAACATATGGTGTGGTGGACCCGGATGACCTCTATGATGTGTACTGTTATGCTGAAGACCTAAATGGAGAACT
GTTCTGGGTGACCTCCAGAGAAGCTGACATTGGAGGAAGCACGGGCGTACTGCCAGGAGCGGGGTGCAGAGAT
TGCCACCACGGGCCAACTGTATGCAGCCTGGGATGGTGGCCTGGACCACTGCAGCCCAGGGTGGCTAGCTGATGG
CAGTGTGCGCTACCCCATCGTCACACCCAGCCAGCGCTGTGGTGGGGGCTTGCCTGGTGTCAAGACTCTCTTCCT
CTTCCCCAACCCAGACTGGCTTCCCCAATAAGCACAGCCGCTTCAACGTCTACTGCTTCCGAGACTCGGCCCAGCC
TTCTGCCATCCCTGAGGCCTCCAACCCAGCCTCCAACCCAGCCTCTGATGGACTAGAGGCTATCGTCACAGTGAC
AGAGACCCCTGGAGGAACCTGCAGCTGCCTCAGGAAGCCACAGAGAGTGAATCCCGTGGGGCCATCTACTCCATCCC
CATCATGGAGGACGGAGGAGGTGGAAGCTCCACTCCAGAAGACCCAGCAGAGGCCCCCTAGGACGCTCCTAGAATT
TGAACACAATCCATGGTACCGCCACGGGGTTCTCAGAAGAGGAAGGTAAGGCATTGGAGGAAGAAGAGAAATA
TGAAGATGAAGAAGAGAAAGAGGAGGAAGAAGAAGAGGAGGAGGTGGAGGATGAGGCTCTGTGGGCATGGCCCAG
CGAGCTCAGCAGCCCGGGCCCTGAGGCCTCTCTCCCCACTGAGCCAGCAGCCAGGAGAAGTCACTCTCCAGGC
GCCAGCAAGGGCAGTCTTGCAGCCTGGTGCATCACTTCTCTGATGGAGAGTCAGAAGCTTCCAGGCCTCCAAG
GGTCCATGGACCACCTACTGAGACTCTGCCCCTCCAGGGAGAGGAACCTAGCATCCCCATCACCTTCCACTCT
GGTTGAGGCAAGAGAGGTGGGGGAGGCAACTGGTGGTCTGAGCTATCTGGGGTCCCTCGAGGAGAGAGCGAGGA
GACAGGAAGCTCCGAGGGTGGCCCTTCCCTGCTTCCAGCCACACGGGGCCCTGAGGGTACCAGGGAGCTGGAGGC
CCCCTCTGAAGATAATTCTGGAAGAACTGCCCCAGCAGGGACCTCAGTGCAGGCCCAGCCAGTGCTGCCACTGA
CAGCGCCAGCCGAGGTGGAGTGGCGTGGTCCCCGCATCAGGTGACTGTGTCCCCAGCCCTGCCACAATGGTGG
GACATGCTTGGAGGAGGAGGAAGGGGTCCGCTGCCTATGTCTGCCTGGCTATGGGGGGGACCTGTGCGATGTTGG
CCTCCGCTTCTGCAACCCCGGCTGGGACGCCTTCCAGGGCGCCTGCTACAAGCACTTTTCCACACGAAGGAGCTG
GGAGGAGGCAGAGACCCAGTGCCGGATGTACGGCGCGCATCTGGCCAGCATCAGCACACCCGAGGAACAGGACTT
CATCAACAACCGGTACCGGGAGTACCAGTGATCGGACTCAACGACAGGACCATCGAAGGCGACTTCTTGTGGTC
GGATGGCGTCCCCCTGCTCTATGAGAACTGGAACCTGGGCAGCCTGACAGCTACTTCTGTCTGGAGAGAACTG
CGTGGTCAATGGTGTGGCATGATCAGGGACAATGGAGTGACGTGCCCTGCAACTACCACCTGTCTTACACCTGCAA
GATGGGGCTGGTGTCTGTGGGCGGCCACCGGAGCTGCCCTGGCTCAAGTGTTTCGGCCGCCCACGGCTGCGCTA
TGAGGTGGACACTGTGCTTCCGTACCGGTGCCGGGAAGGACTGGCCAGCGCAATCTGCCGCTGATCCGATGCCA
AGAGAACGGTTCGTTGGGAGGCCCCCAGATCTCCTGTGTGCCAGAAAGACCTGCCCGAGCTCTGCACCCAGAGGA
GGACCCAGAAGGACGTACGGGGAGGCTACTGGGACGCTGGAAGGCGCTGTTGATCCCCCTTCCAGCCCCATGCC
AGGTCCCTAGGGGGCAAGGCCTTGAACACTGCCGCCCACAGCACTGCCCTGTACCCAAATTTTCCCTCACACCC
TGCGCTCCCCGCCACCACAGGAAGTGACAACATGACGAGGGGTGGTGTGGAGTCCAGGTGACAGTTCTTGAAGGG
GCTTCTGGGAAATACCTAGGAGGCTCCAGCCCAGCCCAGGCCCTCTCCCCCTACCCTGGGCACCAGATCTTCCAT
CAGGGCCGGAGTAAATCCCTAAGTGCCTCAACTGCCCTCTCCCTGGCAGCCATCTTGTCCCCTCTATTCTCTAG
GGAGCACTGTGCCCACTCTTTCTGGGTTTTCCAAGGGAATGGGCTTGCAAGGATGGAGTGTCTGTAAATCAACAG
GAAATAAACTGTGTATGAGCCCAGGCCAAAAA

425/6881
FIGURE 395

MAQLFLPLLAALVLAQAPAAADVLEGDSSDRAFRVRIAGDAPLQGVLGALTIPCHVHYLRPPPSRRRAVLGSP
RVKWTFLSRGREAEVLVARGVRVKVNEAYRFRVALPAYPASLTDVSLALSELRPNDSGIYRCEVQHGIDDSSDAV
EVKVKGVVFLYREGSARYAFSFGAQEACARIGAHIAITPEQLYAAYLGGYEQCDAGWLSAQTVRYP IQTPREACY
GDMDGFPGVRNYGVVDPDDLVDVYCYAEDLNGELFLGDPPEKLTLEEARAYCQERGAEIATTGQLYAAWDGGLDH
CSPGWLADGSVRYPIVTPSQRCGGGLPGVKTLFLFPNQTGFPPNKHSRFRNVYCFRDSAQPSAIPASNPASNPASD
GLEAIVTVTETLEELQLPQEATESESARGAIYSIPIMEDGGGGSSTPEDPAEAPRTLLEFETQSMVPPTGFSEEEG
KALEEEEEKYEDDEEEKEEEEEEEVEDEALWAWPSELSSPGPEASLPTEPAAQEKSLSQAPARAVLQPGASPLPDG
ESEASRPPRVHGPPTETLPTPRERNLASPSPSTLVEAREVGEATGGPELSGVPRGESEETGSSEGAAPSLLPATRA
PEGTRELEAPSEDNSGRTPAGTSVQAQPVLP TDSASRGGVAVVPASGDCVPSPCHNGGTCLEEEEGVRCCLCLPG
YGGDLCDVGLRFCNPGWDAFQGACYKHFSTRRSWEEAETQCRMYGAHLASISTPEEQDFINNRYREYQWIGLNDR
TIEGDFLWSDGVPLLYENWNPGQPD SYFLSGENCVVMVWHDQGGQWSDVPCNYHLSYTCMKGLVSCGPPPELPLAQ
VFGRPRLRYEVDTVLRYRCREGLAQRLPLIRCQENGRWEAPQISCVPRRPARALHPEEDPEGRQGRLLGRWKAL
LIPPSSPMPGP

426/6881
FIGURE 396

CTCCTCACAGAAGCCTGGAGCTGGGCATCCAAGAAGAAGCAGCCTCATTGTGTTTTCTGGTGTCATCGTAGGTGGC
CACCTATGGCTTTTGGGAATGTAAAAAGGGCAGCTCTCTGGCATGTTCCTGACTGAGGATCTCATAACATTTAAC
TTGAGGAACCTCCTCCTTTTCCAGCTTTGGGAGTCAAGCTTCTCACCTGGGGCGGGTGGGTTCTGCACCACCCTC
CCACCCTCCTTCCCTCCGTGTGGACGATAGAGCCACATCCAGCACCACGGACAGCTCCCGGGCGCCTTCATCTCCT
CGTCCTCCAGGCAGCACAAGCCATTGTGGAATCTCCACCAGGTGTACAGAACGGTGCCTCTGCGTCCTGCCACTC
AGGACCTCTCAAGTCCCCGATGTGATGGCTCCTCAGCATGATCAGGAGAAATTCCATGATCTTGCTTATTCCTGT
CTTGGGAAGTCCTTCTCCATGTCTAACCAAGATCTATATGGCTATAGCACCAGCTCTTTGGCTCTTGGCTTGGCA
TGGCTAAGTTGGGAGACCAAAAAGAAGAATGTACTTCATCTGGTTGGGCTGGATTCCCTCTTGATAAGCCTTCCCA
GTTGACTGAAAGATGAGGCTAGGCTCTAGCAAGTTGAAGTCAAACCAGCTCCTTCAAGAAGCTTTGAGCAGAATG
AAGTGGGGAGGACCCAGCTTCCAGCCCAGGAAGCCCAGTGTACCTGGAGCCATCTGGGATAAGACTTTGACCCAT
GACTCCCATATCCACAGCCTGTCCATCCTAGCCCATCCCAGTTTATCCTGTATCATTGAGCTGGGATTCCCACA
TCCTCTGAGTTGGAAGTCCCATCTCAAGTCTTCAATAAAGACTCTTGAATATTG

427/6881
FIGURE 397

MFLTEDLITFNLRNFFLLFQLWESSFSPGAGGFCTTLPPSFLRVDDRATSSTDSSRAPSSPRPPGSTSHCGISTR
CTERCLCVLPLRTSQVPDVMAPQHDQEKFDLAYSCLGKSFMSNQDLYGYSTSSLALGLAWLSWETKKKNVLHL
VGLDSL

428/6881
FIGURE 398

TTGCGTAGGGGGCGGGACTAAGGCTGTCAATTGGTCTGTTTTTGTGCCGATCAATGAGATGGGTGCGGTGATTGG
CGACTACCTTGAGAGTAGCGGGTTGAGGTGTAAGCCCTGAGGAGGCAGCGTTTTCTGGGCTTCTGTCTGGTTCTC
TCTCTCCAGAAGGTTCTGCCGGTTCCCCAGCTCTGGGTACCCGGCTCTGCATCGCGTCGCCATGATGGGCCATC
GTCCAGTGCTCGTGCTCAGCCAGAACACAAAGCGTGAATCCGGAAGAAAAGTTCAATCTGGAAACATCAATGCTG
CCAAGACTATTGCAGATATCATCCGAACATGTTTGGGACCCAAGTCCATGATGAAGATGCTTTTGGACCCAATGG
GAGGCATTGTGATGACCAATGATGGCAATGCCATTCTTCGAGAGATTCAAGTCCAGCATCCAGCGGCCAAGTCCA
TGATCGAAAATTAGCCGGACCCAGGATGAAGAGGTTGGAGATGGGACCACATCAGTAATTATTCTTGCAGGGGAAA
TGCTGTCTGTAGCTGAGCACTTCTCGGAGCAGCAGATGCACCCAACAGTGGTGATCAGTGCTTACCGCAAGGCAT
TGGATGATATGATCAGCACCCCTAAAGAAAATAAGTATCCCAGTCGACATCAGTGACAGTGATATGATGCTGAACA
TCATCAACAGCTCTATTACTACCAAAGCCATCAGTCGGTGGTCACTTTTGGCTTGCAACATTGCCCTGGATGCTG
TCAAGATGGTACAGTTTTGAGGAGAATGGTCGGAAAGAGATTGACATAAAAAAATATGCAAGAGTGGAAGATAAC
CTGGAGGCATCATTTGAAGACTCCTGTGTCTTGGCGTGGAGTCATGATTAACAAGGATGTGACCCATCCACGTATGC
GGCGCTATATCAAGAACCCTCGCATTGTGTCTGCTGGATTCTTCTCTGGAATACAAGAAAGGAGAAAAGCCAGACTG
ACATTGAGATTACACGAGAGGAGGACTTCACCCGAATTCTCCAGATGGAGGAAGAGTACATCCAGCAGCTCTGTG
AGGACATTATCCAAGTGAAGCCGATGTGGTCATCACTGAAAAGGGCATCTCAGATTTAGCTCAGCACTACCTTA
TGCGGGCCAATATCACAGCCATCCGCAGAGTCCGGAAGACAGACAATAATCGCATTGCTAGAGCCTGTGGGGCCC
GGATAGTCAGCCGACCAGAGGAAGTGAAGAGATGATGTTGGAACAGGAGCAGGCCTGTTGGAAATCAAGAAAA
TTGGAGATGAATACTTTACTTTTCACTGACTGCAAAGACCCCAAGGCCTGCACCATTCTCCTCCGGGGGGGCTA
GCAAAGAGATTCTCTCGGAAGTAGAACGCAACCTCCAGGATGCCATGCAAGTGTGTGCAATGTTCTCCTGGACC
CTCAGCTGGTGCCAGGGGGTGGGGCTCCGAGATGGCTGTGGCCCATGCCTTGACAGAAAAATCCAAGGCCATGA
CTGGTGTGGAACAATGGCCATACAGGGCTGTTGCCCAGGCCCTAGAGGTCATTCTCGTACCCTGATCCAGAACT
GTGGGGCCAGCACCATCCGTCTACTTACCTCCCTTCGGGCCAAGCACACCCAGGAGAACTGTGAGACCTGGGGTG
TAAATGGTGAGACGGGTACTTTGGTGGACATGAAGGAAGTGGGCATATGGGAGCCATTGGCTGTGAAGCTGCAGA
CTTATAAGACAGCAGTGGAGACGGCAGTTCTGCTACTGCGAATTGATGACATCGTTTCAGGCCACAAAAAGAAAG
GCGATGACCAGAGCCGGCAAGGCGGGGCTCCTGATGCTGGCCAGGAGTGAGTGCTAGGCAAGGCTACTTCAATGC
ACAGAACCAGCAGAGTCTCCCTTTTCTGAGCCAGAGTGCCAGGAACACTGTGGACGTCTTTGTTTCAGAAGGGA
TCAGGTGGGGGGCAGCCCCAGTCCCTTTCTGTCCAGCTCAGTTTTCCAAAAGACACTGACATGTAATTCTTC
TCTATTGTAAGGTTTCCATTTAGTTTGCTTCCGATGATTAAATCTAAGTCATTTG

429/6881
FIGURE 399

MGHRPVLVLSQNTKRESGRKVQSGNINAAKTIADIIRTCLGPKSMMKMLLDPMGGIVMTNDGNAILREIQVQHPA
AKSMIEISRTQDEEVGDGTTSVIILAGEMLSVAEHFLEQQMHPTVVISAYRKALDDMISTLKKISIPVDISDSM
MLNIINSSITTKAISRWSSLACNIALDAVKMVQFEENGRKEIDIKKYARVEKIPGGIIEDSCVLRGVMINKDVTH
PRMRRYIKNPRIVLLDSSLEYKKGESQTDIEITREEDFTRILQMEEYIQQLCEDIIQLKPDVVITEKGISDLAQ
HYLMRANITAIRRVKTDNNRIARACGARIVSRPEELREDDVGTGAGLLEIKKIGDEYFTFITDCKDPKACTILL
RGASKEILSEVERNLODAMQVCRNVLLDPQLVPGGGASEMAVAHALTEKSKAMTGVEQWPYRAVAQALEVIPRTL
IQNCGASTIRLLTSLRAKHTQENCETWGVNGETGTILVDMKELGIWEPLAVKLQTYKTAVETAVLLLRIDDIVSGH
KKKGDDQSRQGGAPDAGQE

430/6881
FIGURE 400

GAATTGCGGCCGTATGCGCGGCTCTGTGGAGTGCACCTGGGGTTGGGGGCACTGTGCCCCAGCCCCCTGCTCCT
TTGGACTCTACTTCTGTTTGAGCCCCATTTGGCCTGCTGGGGGAGAAGACCCGCCAGGTGTCTCTGGAGGTCAT
CCCTAACTGGCTGGGCCCCCTGCAGAACCTGCTTCATATACGGGCAGTGGGCACCAATTCCACACTGCACTATGT
GTGGAGCAGCCTGGGGCCTCTGGCAGTGGTAATGGTGGCCACCAACACCCCCACAGCACCTGAGCGTCAACTG
GAGCCTCCTGCTATCCCCTGAGCCCGATGGGGGCTGATGGTGTCCCTAAGGACAGCATTTCAGTTTTCTTCTGC
CCTTGTTTTTACCAGGCTGCTTGAGTTTGACAGCACCAACGTGTCCGATACGGCAGCAAAGCCTTTGGGAAGACC
ATATCCTCCATACTCCTTGGCCGATTTCTCTTGGAACAACATCACTGATTTCATTGGATCCTGCCACCCTGAGTGC
CACATTTCAAGGCCACCCCATGAACGACCCTACCAGGACTTTTGCCAATGGCAGCCTGGCCTTCAGGGTCCAGGC
CTTTTCCAGGTCCAGCCGACCAGCCCAACCCCCCTCGCCTCCTGCACACAGCAGACACCTGTCAGCTAGAGGTGGC
CCTGATTGGAGCCTCTCCCCGGGGAACCGTTCCCTGTTTGGGCTGGAGGTAGCCACATTGGGCCAGGGCCCTGA
CTGCCCCCTCAATGCAGGAGCAGCACTCCATCGACGATGAATATGCACCGGCCGTCTTCCAGTTGGACCAGCTACT
GTGGGGCTCCCTCCCATCAGGCTTTGCACAGTGGCGACCAGTGGCTTACTCCCAGAAGCCGGGGGGCCGAGAATC
AGCCCTGCCCTGCCAAGCTTCCCTCTTCATCCTGCCTTAGCATACTCTCTTCCCCAGTCACCCATTGTCCGAGC
CTTCTTTGGGTCCCAGAATAACTTCTGTGCCTTCAATCTGACGTTCCGGGGCTTCCACAGGCCCTGGCTATTGGGA
CCAACACTACCTCAGCTGGTCGATGCTCCTGGGTGTGGGCTTCCCTCCAGTGGACGGCTTGTCCCCACTAGTCTT
GGGCATCATGGCAGTGGCCCTGGGTGCCCCAGGGCTCATGCTGCTAGGGGGCGGCTTGGTTCTGCTGCTGCACCA
CAAGAAGTACTCAGAGTACCAGTCCATAAATTAAGGCCCGCTCTCTGGAGGGAAGGACATTACTGAACCTGTCTT
GCTGTGCCTCGAAACTCTGGAGGTTGGAGCATCAAGTTCAGCCGGCCCCCTTCACTCCCCCATCTTGCTTTTCTG
TGGAACCTCAGAGGCCAGCCTCGACTTCCTGGAGACCCCCAGGTGGGGCTTCCTTCATACTTGTGGGGGACTT
TGGAGGCGGGCAGGGGACAGGGCTATTGATAAGGTCCCCTTGGTGTTCCTTGCATCTCCACACATTTCCCT
TGGATGGGACTTGCAGGCCTAAATGAGAGGCATTCTGACTGGTTGGCTGCCCTGGAAGGCAAGAAAATAGATTTA
TTTTTTTTTC

431/6881
FIGURE 401

M R G S V E C T W G W G H C A P S P L L L W T L L L F A A P F G L L G E K T R Q V S L E V I P N W L G P L Q N L L H I R A V G T N S T L H Y V W S S L
G P L A V V M V A T N T P H S T L S V N W S L L L S P E P D G G L M V L P K D S I Q F S S A L V F T R L L E F D S T N V S D T A A K P L G R P Y P P Y
S L A D F S W N N I T D S L D P A T L S A T F Q G H P M N D P T R T F A N G S L A F R V Q A F S R S S R P A Q P P R L L H T A D T C Q L E V A L I G A
S P R G N R S L F G L E V A T L G Q G P D C P S M Q E Q H S I D D E Y A P A V F Q L D Q L L W G S L P S G F A Q W R P V A Y S Q K P G G R E S A L P C
Q A S P L H P A L A Y S L P Q S P I V R A F F G S Q N N F C A F N L T F G A S T G P G Y W D Q H Y L S W S M L L G V G F P P V D G L S P L V L G I M A
V A L G A P G L M L L G G G L V L L L H H K K Y S E Y Q S I N

[illegible]

433/6881
FIGURE 403

MTEQETLALLEVKRSDSPEKSSPQALVPNGRQPEGEGGAESPGAESLRVGSSAGSPTAIEGAEDGLDSTVSEAAT
LPWGTGPQPSAPFPDPPGWRDIEPEPPESEPLTKLEELPEDDANLLPEKAARAFVPIDLQCIERQPQEDLIVRCE
AGEGECRTFMPPRVTHPDPTERKWAEAVVRPPGCSCGGCGSCGDREWLRAVASVGAALILFPCLLYGAYAFLPFD
VPRLPMTSSRLIYTLRCGVFATFPIVLGILVYGLSLLCF SALRPFGEPRREVEIHRRYVAQSVQLFIFYFFNLAV
LSTYLPQDTLKLPLLTGLFAVSRLIYWLTFVGRSFRGFGYGLTFLPLLSMLMWNLYYMFVVEPERMLTATESR
LDYPDHARSASDYRPRPWG

434/6881
FIGURE 404

ACTCAGTGTTTCGCGGGAGCCGCACCTACACCAGCCAACCCAGATCCCGAGGTCCGACAGCGCCCGGCCAGATCC
CCACGCCTGCCAGGAGCAAGCCGAGAGCCAGCCGGCCGGCGCACTCCGACTCCGAGCAGTCTCTGTCTTCGACC
CGAGCCCCCGCGCCCTTTCCGGGACCCCTGCCCCGCGGGCAGCGCTGCCAACCTGCCGGGCCATGGAGACCCCGTCC
CAGCGGGCGGCCACCCGCAGCGGGGCGCAGGCCAGCTCCACTCCGCTGTCGCCCACCCGCATCACCCGGCTGCAG
GAGAAGGAGGACCTGCAGGAGCTCAATGATCGCTTGGCGGTCTACATCGACCGTGTGCGCTCGCTGGAAACGGAG
AACGCAGGGCTGCGCCTTCGCATCACCGAGTCTGAAGAGGTGGTCAGCCGCGAGGTGTCCGGCATCAAGGCCGCC
TACGAGGCCGAGCTCGGGGATGCCCCGAAGACCCCTTGACTCAGTAGCCAAGGAGCGCGCCCGCCTGCAGCTGGAG
CTGAGCAAAGTGCGTGAGGAGTTTAAGGAGCTGAAAGCGCGCAATACCAAGAAGGAGGGTGACCTGATAGCTGCT
CAGGCTCGGCTGAAGGACCTGGAGGCTCTGCTGAACTCCAAGGAGGCCGCACTGAGCACTGCTCTCAGTGAGAAG
CGCACGCTGGAGGGCGAGCTGCATGATCTGCGGGGCCAGGTGGCCAAGCTTGAGGCAGCCCTAGGTGAGGCCAAG
AAGCAACTTCAGGATGAGATGCTGCGGCGGGTGGATGCTGAGAACAGGCTGCAGACCATGAAGGAGGAACTGGAC
TTCCAGAAGAACATCTACAGTGAGGAGCTGCGTGAGACCAAGCGCCGTCATGAGACCCGACTGGTGGAGATTGAC
AATGGGAAGCAGCGTGAGTTTGAGAGCCGGCTGGCGGATGCGCTGCAGGAAGTGCGGGCCCCAGCATGAGGACCAG
GTGGAGCAGTATAAGAAGGAGCTGGAGAAGACTTATTCTGCCAAGCTGGACAATGCCAGGCAGTCTGCTGAGAGG
AACAGCAACCTGGTGGGGGCTGCCCACGAGGAGCTGCAGCAGTCGCGCATCCGCATCGACAGCCTCTCTGCCAG
CTCAGCCAGCTCCAGAAGCAGCTGGCAGCCAAGGAGGCCAAGCTTCGAGACCTGGAGGACTCACTGGCCCGTGAG
CGGGACACCAGCCGGCGGCTGCTGGCGGAAAAGGAGCGGGAGATGGCCGAGATGCGGGCAAGGATGCAGCAGCAG
CTGGACGAGTACCAGGAGCTTCTGGACATCAAGCTGGCCCTGGACATGGAGATCCACGCCTACCGCAAGCTCTTG
GAGGGCGAGGAGGAGAGGCTACGCCTGTCCCCCAGCCCTACCTCGCAGCGCAGCCGTGGCCGTGCTTCCTCTCAC
TCATCCCAGACACAGGGTGGGGGCAGCGTCACCAAAAAGCGCAAAGTGGAGTCCACTGAGAGCCGCAGCAGCTTC
TCACAGCACGCACGCACTAGCGGGCGCGTGGCCGTGGAGGAGGTGGATGAGGAGGGCAAGTTTGTCCGGCTGCGC
AACAAGTCCAATGAGGACCAGTCCATGGGCAATTGGCAGATCAAGCGCCAGAATGGAGATGATCCCTTGCTGACT
TACCGGTTCCCACCAAAGTTACCCCTGAAGGCTGGGCAGGTGGTGACGATCTGGGCTGCAGGAGCTGGGGCCACC
CACAGCCCCCTACCGACCTGGTGTGGAAGGCACAGAACACCTGGGGCTGCGGGAACAGCCTGCGTACGGCTCTC
ATCAACTCCACTGGGGAAGAAGTGCCATGCGCAAGCTGGTGCGCTCAGTGACTGTGGTTGAGGACGACGAGGAT
GAGGATGGAGATGACCTGCTCCATCACCAACATGTGAGTGGTAGCCGCCGCTTGAGGGCCGAGCCTGCACTGGGGCC
ACCCAGCCAGGCCTGGGGGCAGCCTCTCCCCAGCCTCCCCGTGCCAAAATCTTTTCATTAAAGAATGTTTGAA
CTTT

435/6881
FIGURE 405

METPSQRRATRSGAQASSTPLSPTRITRLQEKEDLQELNDRLAVYIDRVRSLETENAGLRLRITESEEVVSREVS
GIKAA YEAE LGDARKTLD SVAKERARLQELSKVREEFKELKARNTKKEGDLIAAQARLKDLEALLNSKEAALST
ALSEKRTLEGELHDLRGQVAKLEAALGEAKKQLQDEMLRRVDAENRLQTMKEELDFQKNYSEELRETKRRHETR
LVEIDNGKQREFESRLADALQELRAQHEDQVEQYKKELEKTYSAKLDNARQSAERNNSNLVGAAHEELQQSRIRID
SLSAQLSQLQKQLAAKEAKLRDLED SLARERDTSRLLAEKEREMAEMRARMQQQLDEYQELLDIKLALDMEIHA
YRKLLEGE EERLRLSPSPTSQRSRGRASSHSSQTQGGGSVTKKRKLESTESRSSFSQHARTSGRVAVEEVDEEGK
FVRLRNKS NEDQSMGNWQIKRQNGDDPLLTYRFPPKFTLKAGQVVTIWAAGAGATHSPPTDLVWKAQNTWGCNS
LRTALINSTGEEVAMRKLVRSVTVVEDDEDEDGDDLLHHHHVSGSRR

[illegible]

437/6881
FIGURE 407

LRLKGSSNTTECVPVPTSEHVAEIVGRQGCKIKALRAKTNTYIKTPVRGEEPVFMVTGRREDVATARREIISAAE
HF5MIRASRNKSGAAGVAPALPGQVTIRVRVPYRVVGLVVGPKGATIKRIQQQTNTYIITPSRDRDPVFEITGA
PGNVERAREEIEITHIAVRTGKILEYNNENDFLAGSPDAAIDSRYSDAWRVHQPCKPLSTFRQNSLGCIGECGVD
SGFEAPRLGEQGGDFGYGGYLFPGYGVGKQDVYYGVAETSPPLWAGQENATFTSVLFSSASSSSSSSAKARAGPP
GAHRSPATSAGPELAGLPRRPPG

438/6881
FIGURE 408

GGAGGAGCCGGGCGGGCTGGCGGGCGGCCGGGTGGCGGCGGCGGCATGGCGGAGCCGAGCGGGGCGGAGACGAGG
CCCCCATTCGGGTCAACGTC AAGACCCCAAGGACAAGGAGGAAATTGTGATCTGCGATCGAGCCTCGGTCAAG
GAGTTCAAAGAGGAAATCTCCCGGAGGTTTAAGGCTCAGCAGGATCAGCTGGTCCTGATCTTCGACGGCAAGATC
CTCAAGGATGGGGACACACTGAACCAGCACGGAATCAAGGACGGGCTCACTGTCCATCTGGTCATCAAGACCCCT
CAGAAGGCTCAAGATCCAGCTGCTGCCACTGCTTCTTCCCCCTCCACACCTGACCCTGCCTCAGCACCCCTCCACC
ACGCCTGCTTCACCCGCCACCCCTGCCAGCCCTCCACCTCTGGCAGTGCCCTCTTCAGATGCTGGCAGTGGAAGC
CGGAGGAGCAGTGGTGGGGGGCCCTCTCCGGGGGCTGGGGAGGGATCCCCCAGTGCTACTGCGTCCATACTCTCT
GGCTTTGGGGGCATCCTGGGGCTGGGCAGCCTAGGCCTGGGCTCTGCCAACTTCATGGAGCTGCAGCAGCAGATG
CAGCGGCAGCTGATGTCCAATCCTGAGATGCTGTACAGATCATGGAGAACCCCTGGTCCAGGATATGATGTCT
AACCCTGATCTGATGCGTCACATGATTATGGCCAACCCCAAGATGCAGCAGTTGATGGAGCGGAACCCCTGAGATC
AGCCACATGCTCAATAACCCTGAACCTCATGAGGCAGACAATGGAGCTTGCTCGGAATCCAGCCATGATGCAAGAG
ATGATGCGGAACCAGGACCGGGCCCTGAGCAACCTTGAGAGCATCCCTGGAGGGTATAATGCCCTCCGCCGCATG
TACACGGACATCCAGGAGCCCATGTTCACTGCTGCCCGGGAACAGTTTGGCAACAATCCCTTCTCTTCCCTGGCC
GGGAACCTCCGACAGCTCATCCTCCAGCCTCTGCGGACTGAGAATCGAGAGCCCTCCCTAACCCTTGAGCCCC
TCGCCCCCACCCTCCAGGCCCCCGGGTCCGGTGGGGAGGGCACCAGGATCGGGGACCAGCCAGGTGCACCCG
ACAGTCTCGAACCCCTTTGGGATCAATGCGGCTAGCCTGGGGTCAGGGATGTTCAATAGCCCAGAAATGCAAGCC
CTCCTCCAGCAGATCTCTGAGAACCCCAAGCTGATGCAGAATGTGATCTCAGCACCCCTACATGCGCAGCATGATG
CAGACGCTTGCCCAGAACCCGACTTTGCTGCTCAGATGATGGTGAATGTGCCGCTCTTCGCGGGGAACCCCCAA
CTGCAGGAGCAGCTCCGCCTGCAGCTCCAGTCTTCTGCAGCAGATGCAGAACCAGAGTCACTCTCCATCCTT
ACCAATCCCCGAGCCATGCAGGCATTGCTGCAGATCCAGCAGGGACTACAGACCTTGAGACCGAGGCCCTGGG
CTGGTACCCAGCCTTGCTCCTTTGGGATATCCCGGACCCAGCACCCCTCAGCAGGCAGCAACGCAGGGTCTACG
CCCAGGCCCCCACTTCTCACCAGCCACGCCAGCCACATCTTCTCCAACAGGGGCTTCAGCGCCCAGCAGCAA
CTCATGCAGCAGATGATCCAGCTTTTGGCTGGAAGTGGAACCTCACAGGTGCAGACGCCAGAAGTGAGATTTAG
CAGCAGCTGGAGCAGCTCAACTCCATGGGCTTCATCAATCGTGAGGCTAACCTGCAGGCCCTGATTGCCACAGGA
GGGGACATCAACGCAGCTATCGAGAGACTGCTGGGCTCCAGCTCTCCTAATCCCTCGGCCCATGCCTCCTGCCT
CTCCCCCTCCCTCGATGTCAGCATTCGGTTCTTCTGTCAATCCTTACCCTCTGCAGCTTGCTCCTCCCTCCGTCTT
CTCCCTCATCCTTTCCAAACAGCAGGGTGACTTTAGAGGCATGGGCTCCAACCCCTTAGCTCTGTCTGAGAATTA
TGGTTTTACTGCTACGTCTCTAACAGACTCTTCTCTCCTGGTCTCCTTGAGCAGTGCTACTTAAACAGTTTTTAC
AGTTTCATTGATTGACTCTACCTCCTTGCCCCACACCCTTTTGCAATCTTTAAACTTTAGTGGCTGTGCAGAG
TCGAGGGAGGAACCAGCTCTCTGGTTTACTGGAACATAGTCTTCCATCTATACCACTAGGGTTTTGTCTTATGTT
TACTTTTTGGTAACTCTCTTCTCTTTTTCTCCCTACCCCCCAACCCCTAGCCCAACCAATGCTAGAATTTCTTG
CTCTGAAGGAGGAGCAGGTGAAACAGGTGGTAATTTTCTTCTCGGCCCTATTCTGGTTTATTTCAGCACTTTTT
GGTGGGAACCTGTTGGAAATTCCAGGGTAAGGAGGAAGATGCCTGTTCTCCCTGTCTGAAGAGGGAGATGAGACAG
CTCTCTGGACAGGAATTAACAAACGCTGGAGCAGCCAGAGGAAATTCGTGTGAAAGAGGAGGGAATGAGATTAT
TCGGAGGAAGGGAATGGGGGAGACAGCCTGAGTAAAAGGCTTGGAAGTTGGAATTAACAGTGGGGAGCAGAAGCA
CTCATAGCTCTTTTAGGCAGAAGAATCCAGGCCCGAGCTGGCAGAAGAGACTTAGAGATGCTAATGGAATTTAAA
CTGAAAAAAGGAGCCCAATGAAGCTAAGCGCCACGCCCCACAAGGGGTCATATTGGCTTTAGTTCCCTCAAGCATA
TGTGCTTATATGCACACACACACATTTCCATGGACCCAGGTCTTGCTTGTGTCCCAGGCACCAAGTAGTTTGA
GCCCCCTCAAAAGACATGAAGGGGGTTGGGGTCTGTGTGAGTAGTGGGGAGGTGCATGTGTATCCACATGTGTG
CATACACTCTTAAGTTGGGTGGGAAGTGGATTCTTGTGGTTTCTGGTTTCTGAGTGTCTCTCCACCACCAGAGA
CAAGTGGGTAAAAAGGTCAGTCCATTGCAGGAATATATATCCGGGAGAGCTAGGTCCCTTGGGGCTCTGGATGCT
GGGTAACCCAGAGGTAATGTGGGTACCCCTTCTGAAGCTGTCAGGGCTGTGACTAGCACCCCTTATACCCCTCAC
TGCCTTGTGGGAATAGTAGAGGGTTTTTCTCCTCCAGAGCCCCCTGGCCTTTCAGTTCTTAACTATTTCCCTCCAG
GCCAGAAAGTTTTCTTTGAGGAAGGAGAGGAGAGGGTGGCAATGATGCCTTTGATCTGGAATTGGACATTTCTCT
GTCAGAGCACAGAGGAGGCTCATATCACCTCTTCCCTCTCCTACTTGGCCCAGCTGCTTGGAGGACCGACCCCAT
GGCTGAGAATATGACGGCAAGAGGAACAGAGTTTGCTCCAAGTGGGAAAGGGTCCCAAGCAGTCCAGAGAAGATG
TCTGTGTGGCTTTCCCTCCCTGCCTCCCCAGCTCCACACTGGCCTTTGTAAATAAATGGCGTGGTCTTTGTTG
TG

439/6881
FIGURE 409

GGCTCTCTTCCTGTCTTTGTGGCTCCGGAAAGGCGTTTGGGATGCCAACGATGAGGCTGCTGTCATTTGTGGTGT
TGGCTCTATTTGCTGTCACTCAAGCAGAGGAAGGAGCCAGGCTTTTGGCTTCCAAATCACTGCTGAACAGATACG
CCGTGGAGGGACGAGACCTGACCTTGCAGTACAACATCTACAATGTTGGCTCAAGTGCTGCATTAGACGTGGAAC
TATCTGATGATTCTTCCCTCCAGAAGACTTTGGCATTGTGTCTGGAATGCTCAATGTCAAATGGGACCGGATTG
CCCCTGCTAGCAATGTCTCCCACTGTGGTCCTGCGCCCTCTCAAGGCTGGTTATTTCAACTTCACCTCGGCAA
CAATTACTTACCTGGCCCAGGAGGATGGGCCCCTGTGATTGGCTCTACCAGTGCACCTGGACAGGGAGGAATCC
TGGCTCAGCGGGAGTTTGACAGGCGATTCTCCCCTCATTTTCTGGACTGGGCAGCCTTTGGGGTCATGACCCTTC
CCTCCATCGGCATCCCCCTGCTATTGTGGTACTCCAGCAAGAGGAAATATGACACTCCCCAAACGAAGAAGAACTT
GATTGGGGCTTCCACAGCCCTCCTCTCCCAAGAAATCCAGGCTCCTCTCCCAAGAAATCCAGGTGCTTTCCAGAC
TCCAAAGGGTATCTTAAATGCAATCTCTTCTCTTAGCCCTTGGCCACTTTCTCCTGGATCCTGCCCTGCTCTC
AGCCATAGTGAAGGACCAGCCCTAGGAGTCTGCGAGAGCCTCCTTGGTTCCATCGTGAAGCCATAAACAGGAATG
CCTTTGGCAATAGCCTTGAGCCTAGAGGGCCCTCTGATGCCCCACTGAGGTGCTGTTGGTTTATTGCTGGCAACG
TGAATTCTCTCAGGGGTCTAGGAGGGGCATTTTGGAGACTGCCTGACACCACCCCTATCCCCTGCCTCCCCCTCT
CAGAAGAGGGTGGAAGATGAAATGAAAGCTATGGGACTCTTGGAGGATACCCAGTGTCTATTCTGGGTTAGAGAA
GTGCTTACTAAGGGGTTTTCTAATAAAAACAAATGCCAATTGC

440/6881
FIGURE 410

MRLLSFVVLALFAVTQAEEGARLLASKSLLNRYAVEGRDLTLQYNIYNVGSSAALDVELSDDSFPPEDFGIVSGM
LNVKWDRIAPASNVSHTVVLRPLKAGYFNFTSATITYLAQEDGPVVGSTSAPGQGGILAQREFDRRFSPHFLDW
AAFGVMTLP SIGIPLLLWYSSKRKYDTPKTKKN

441/6881
FIGURE 411A

GAGACCAACGCGTGCGGGCCGAACCCCTCCCCCGCCTTCCCCCAACAATACAGGACGCCGGGGTCCGCGCCGCG
TCCTCCCTGGTCCCCCGTCCGATTATGTCTCGGATCGAATCCCTCACGCGGGCGCGGATCGACCGGAGCAGAGA
GCTGGCGAGCAAGACCCGGGAAAAGGAGAAAATGAAGAAAGCCAAGGATGCCCGCTATACAAATGGGCACCTCTT
CACCACCATTTCAGTTTCAGGCATGACCATGTGCTATGCCTGTAACAAGAGCATCACAGCCAAGGAAGCCCTCAT
CTGCCCCAACCTGCAATGTGACTATCCACAACCGCTGTAAAGACACCCTCGCCAACTGTACCAAGGTCAAGCAGAA
GCAACAGAAAGCGGGCCCTGCTGAAGAACAACACCGCCTTGACAGTCCGTTTCTCTTCGAAGTAAGACAACCATCCG
GGAGCGGCCAAGCTCGGCCATCTACCCCTCCGACAGCTTCCGGCAGTCCCTCCTGGGCTCCCGCCGTGGCCGCTC
CTCCTTGCTCTTTAGCCAAGAGTGTTTCTACCACCAACATTGCTGGACATTTCAATGATGAGTCTCCCTGGGGCT
GCGCCGGATCCTCTCACAGTCCACAGACTCCCTCAACATGCGGAACCGAACCCTATCCGTGGAATCCCTCATTGA
CGAAGAGGTAATCTACAGTGAGCTGATGAGTGACTTTGAGATGGATGAGAAGGACTTTGCAGCTGACTCTTGAG
TCTTGCTGTGGACAGCAGCTTCCTGCAGCAGCATAAAAAGGAGGTGATGAAGCAGCAAGATGTCATCTATGAGCT
AATCCAGACAGAGCTGCACCATGTGAGGACACTGAAGATCATGACCCGCCTCTCCGCACGGGGATGCTGGAAGA
GCTACACTTGAGGCCAGGAGTGGTCCAGGGCCTGTTCCCCTGCGTGGACGAGCTCAGTGACATCCATACACGCTT
CCTCAGCCAGCTATTAGAACGCCGACGCCAGGCCCTGTGCCCTGGCAGCACCCGGAACCTTTGTCATCCATCGCTT
GGGTGATCTGCTCATCAGCCAGTCTCAGGTCCTAGTGCGGAGCAGATGTGTAAGACCTACTCGGAGTTCTGCAG
CCGCCACAGCAAGGCCTTAAAGCTCTATAAGGAGCTGTACGCCCGAGACAAACGCTTCCAGCAATTCATCCGGAA
AGTGACCCGCCCGCCGTGCTCAAGCGGCACGGGTACAGGAGTGCATCCTGCTGGTGACTCAGCGCATCACCAA
GTACCCGTTACTCATCAGCCGCATCCTGCAGCATTCACACGGGATCGAGGAGGAGCGCCAGGACCTGACCACAGC
ACTGGGGCTAGTGAAGGAGCTGCTGTCCAATGTGGACGAGGGTATTTATCAGCTGGAGAAAGGGGCCCGTCTGCA
GGAGATCTACAACCGCATGGACCTCGGGCCCAACCCCACTGCTGGCAAGGGCCCCCTTTGGCCGAGAGGAACT
TCTGAGGCGCAAACCTCATCCACGATGGCTGCCTGCTCTGGAAGACAGCGACGGGGCGCTTCAAAGATGTGCTAGT
GCTGCTGATGACAGATGTACTGGTGTCTTCTCCAGGAAAAGGACCAGAAAGTACATCTTTCCTACCCTGGACAAGCC
TTCAGTGGTATCGCTGCAGAATCTAATCGTACGAGACATTGCCAACCAAGGAGAAAGGGATGTTTCTGATCAGCGC
AGCCCCACCTGAGATGTACGAGGTGCACACAGCATCCCGGGATGACCGGAGCACCTGGATCCGGGTCAATCAGCA
GAGCGTGCGCACATGCCCATCCAGGGAGGACTTCCCCCTGATTGAGACAGAGGATGAGGCTTACCTGCGGCGAAT
TAAGATGGAGTTGCAGCAGAAGGACCGGGCACTGGTGGAGCTGCTGCGAGAGAAGGTCGGGCTGTTTGCTGAGAT
GACCCATTTCCAGGCCGAAGAGGATGGTGGCAGTGGGATGGCCCTGCCACCCCTGCCAGGGGCTTTTCCGCTC
TGAGTCCCTTGAGTCCCTCGTGCGGAGCGGCTGCTGCAGGATGCCATCCGTGAGGTGGAGGGTCTGAAAGACCT
GCTGGTGGGGCCAGGAGTGGAACCTGCTCTTGACACCCCGAGAGCCAGCCCTGCCCTTGGAACCAGACAGCGGTGG
TAACACGAGTCTGGGGTCACTGCCAATGGTGGAGGCCAGAACCTTCAATGGCTCCATTGAACTCTGCAGAGCTGA
CTCAGACTCTAGCCAGAGGGATCGAAATGGAAATCAGCTGAGATCACCGCAAGAGGAGGCGTTACAGCGATTGGT
CAATCTCTATGGACTTCTACATGGCTACAGGCAGCTGTGGCCAGCAGGACACTCTGATGGAAGCCCGGTTCCC
TGAGGGCCCTGAGCGGCGGGAGAAGCTGTGCCGAGCCAACCTCTCGGGATGGGAGGCTGGCAGGGCTGGGGCTGC
CCCTGTGGCCCTGAAAAGCAGGCCACGGAACCTGGCATTACTGCAGCGGCAACATGCGCTGCTGCAGGAGGAGCT
ACGGCGCTGCCGGCGGCTAGGTGAAGAACGGGCAACCGAAGCTGGCAGCCTGGAGGCCCGGCTCCGGGAGAGTGA
GCAGGCCCGGGCACTGCTGGAGCGTGAGGCCGAAGAGGCTCGAAGGCAGCTGGCCGCCCTGGGCCAGACCGAGCC
ACTCCAGCTGAGGCCCCCTGGGCCCGCAGACCTGTGGATCCTCGGCGGCGCAGCCTCCCCGCAGGCGATGCCCT
GTACTTGAGTTTCAACCCCCACAGCCAGCCGAGGCACTGACCGCCTGGATCTACCTGTCTACTACTCGCTCTGT
CCATCGAACTTTGAGGACCGAGAGAGGCAAGGACTGGGGAGCCCCGAAGAGCGGCTGCAAGACAGCAGTGACCC
TGACACTGGCAGCGAGGAGGAAGGTAGCAGCCGTCTGTCTCCGCCCCACAGTCCACGAGACTTTACCAGAATGCA
GGACATCCCGGAGGAGACGGAGAGCCGCGACGGGGAGGCTGTAGCCTCCGAGAGCTAAGGGGGCCCCCTCCCCCT
GCCCCGTGCCCCACTGAAGAACATTACTGAGGGGGCTAACCTTGGGGACTCCAATTTGCCAATGATGAGGGAACA
TTTGAAAGAACTGCAAATTGTCTTGCCAGCTCTTGGGATCCTTGGATACCTGGGGCCATTTAAGAAGCTAGGGG
AATTAGGCCACAACACCCCTGGGACATCCGAAAGCTACACCACAGATGCCAGTGGTTCATGCCTTCTTCCCGCA
ACTTTAGGAAAATTTATTTATTTATTGTTTATTAGTTATGGGGGAGAGGGGAGATTTAAAGGACCAGGGACATG
GGAACCAAGCCATAGGGATCAGAGGGCCTTGTCCTTGAACACTACTGGGGTATATTCAGGCTCATCCACGCAGCT
GCTGGGTTCTTGCCCTAACGGCCCTCCCCTGCAACATCCGTCTTGGAGGAGAGGCTGCAGCCACAGCACCCCTACT
GCCCTTTAAATAAAGGAGGGCTGTGGGCAGGGCCATGTCCCTTCTCCTCTCCCTCAACCTCTTACTGCTGTTT

442/6881

FIGURE 411B

TCCCTTTCTCCGTCCTTCATGGAAGCCCTGGGAGATAACCTGGCTTCCTGGAGTTGATGGAATAAAGGTTGGGGT
GGCCATAATGGTTTGTTGGGGGTGAGGGAAAAACCCACAGGGACCAGAATGTTTTGTTGTTCTTTTGTTCCTT
TTTTGTACCAAAGTCAACTGCACGTGTTTTATATTTTAAGAGATCGTAGGCAATTAGAGATCGAAGCCTCCTAT
CTCCACATCTCTGAAGAAGTTGAGGGGTGGGGGAGAGAATGACTTCTGCCTTCATCTGCAGTAACGGGGGGACCT
ATACTGACCTCTTCCCCAGCCATTTAGAAACAAGTTCTAGGGTGGGTTGGAAAATCTCCAAGAGCCCTGACCTCA
TCTTCCACCTCAGCAACCATGACCTGAAACCTCAGCGTGAATTTGGGGGATTTTTCAGTGGAACCCCTTGCCCCA
AATGTCGACCAGCCCCAAATGTCGAAGAATTTCTTCTTGCCAATTTTGTTGTTTAAAAAAAAAATTCAGGGAA
AATTAAAAACCTGGAACCTCA

443/6881
FIGURE 412

ATGCAGCAGCACGTTTCAGCTCTTGACCCAAATCCACCTTCTTGCCACCTGCAACCCCAACCTCAATCCGGAGGCC
ACTACCACCAGGATATTTCTTAAAGAGCTGGGAACCTTTGCTCAAAGCTCCATCGCCCTTACCATCAGTACAAC
CCCAAGTTTCAGACCCTGTTCCAACCCTGTAACTTGATGGGAGCTATGCAGCTGATTGAAGACTTCAGCACACAT
GTCAGCATTGACTGCAGCCCTCATAAACTGTCAAGAAGACTGCGAATGAATTTCCCTGTTTGCCAAAGCAAGTG
GCTTGGAATTCTGGCCACAAGCAAGGTTTTTCATGTATCCAGAGTTACTTCCAGTGTGTTCCCTGAAGGCAAAGAAT
CCCCAGGATAAGATCGTCTTCACCAAGGCTGAGGACAATTTGTTAGCTTTAGGACTGAAGCATTTTGAAGGAACT
GAGTTTCCTAATCCTCTAATCAGCAAGTACCTTCTAACCTGCAAACTGCCCACCAACTGACAGTGAGAATCAAG
AACCTCAACATGAACAGAGCTCCTGACAACATCATTAAATTTTATAAGAAGACCAAAACAGCTGCCAGTCCTAGGA
AAATGCTGTGAAGAGATCCAGCCACATCAGTGGAAGCCACCTATAGAGAGAGAAGAACACCGGCTCCCATTCTGG
TTAAAGGCCAGTCTGCCATCCATCCAGGAAGAAGCTGCGGCACATGGCTGATGGTGCTAGAGAGGTAGGAAATATG
ACTGGAACCACTGAGATCAACTCAGATCGAAGCCTAGAAAAAGACAATTTGGAGTTGGGGAGTGAATCTCGGTAC
CCACTGCTATTGCCTAAGGGTGTAGTCTGAACTGAAGCCAGTTGCCACCCGTTTCCCCAGGAAGGCTTGGAGA
CAGAAGCGTTTCATCAGTCTGAAGCCCTCCTTATCCAACCCAGCCCTCTCTCCAGCCCAGCTTCAACCCTGGG
AAAACACCAGCCCGATCAACTCATTGAGAAGCCCTCCGAGCAAAATGGTGCTCCGGATTCTCACCCTAACATACAG
CCAGCCACTGTTTTACAGACAGTTCAGGTGTCCCTCCACTGGGGGTGAGTGGAGGTGAGAGTTTTGAGTCTCCT
GCAGCACTGCCTGCTGTGCCCCCTGAGGCCAGGACAAGCTTCCCTCTGTCTGAGTCCCAGACTTTGCTCTCTTCT
GCCCCTGTGCCCAAGGTAATGCTGCCCTCCCTTGCCCCTTCTAAGTTTCGAAAGCCATATGTGAGACGGAGACCC
TCAAAGAGAAGAGGAGTCAAGGCCTCTCCCTGTATGAAACCTGCCCCTGTTATCCACCACCCTGCATCTGTTATC
TTCAGTGTTCCTGCTACCACTGTGAAGATTGTGAGCCTTGCGGTGGCTGTAACATGATCCAGCCTGTCAATGCG
GCTGTGGCCCAGAGTCCCCAGACTATTTCCCATCACTACCCTCTTGGTTAACCTACTTCTTCCCCTGTCCATTG
AACCAGTCCCTTGTGGCCTCCTCTGTCTCACCCTTAATTGTTTCTGGCAATTCTGTGAATCTTCTTATACCATCC
ACCCCTGAAGATAAGGCCACGTGAATGTGGACATTGCTTGTGCTGTGGCTGATGGGGAAAATGCCTTTTCAGGGC
CTAGAACCCAAATTAGAGCCCCAGGAAGTATCTCCTCTCTCTGCTACTGTTTTCCCGAAAGTGGAACATAGCCCA
GGGCCTCCACTAGCAGATGCAGAGTGCCAAGAAGGATTGTCAGAGAATAGTGCTGTGCTGGACCGTTGTGAAA
ACAGAGGAGGGGAGGCAAGCTCTGGAGCCGCTCCCTCAGGGCATCCAGGAGTCTCTAAACAACCCTACCCCTGGG
GATTTAGAGGAAATTGTCAAGATGGAACCTGAAGAAGCTAGAGAGGAAATCAGTGGATCCCCTGAGCGTGATATT
TGTGATGACATCAAAGTGGAACATGCTGTGGAATTGGACACTGGTGCCCCAAGCGAGGAGTTGAGCAGTGCTGGA
GAAGTAACGAAACAGACAGTCTTACAGAAGGAAGAGGAGAGGAGTCAAGCAACTAAAACCCCTTCATCTTCTCAA
GAGCCCCCTGATGAAGGAACCTCAGGGACAGATGTGAACAAAGGATCATCAAAGAATGCTTTGTCTCAATGGAT
CCTGAAGTGAGGCTTAGTAGCCCCCAGGGAAGCCAGAAGATTTCATCCAGTGTGATGGTCAGTCAGTGGGGACT
CCAGTTGGGCCAGAACTGGAGGAGAGAAGAATGGGCCAGAAGAAGAGGAAGAAGAGGACTTTGATGACCTCACC
CAAGATGAGGAAGATGAAATGTCATCAGCTTCTGAGGAATCTGTGCTTTCTGTCCCAGAACTCCAGGTGAGAGCT
GGAGAATATTCTCAAGTATTTCTGTGACTCAGTAATATGTATCACTTATTGATATGCCACCTGCTTGCTTGCTGC
ACTATGGATAGTCCTAAAATCATTGTATTTGA

444/6881

FIGURE 413

MQQHVQLLTQIHLLATCNPNLNPEATTTTRIFLKELGTFQAQSSIALHHQYNPKFQTLFQPCNLMGAMQLIEDFSTH
VSIDCSPHKTVKKTANEFPCLPKQVAVILATSKVEMYPELLPVCSLKAKNPQDKIVFTKAEDNLLALGLKHFEFT
EFPNPLISKYLLTCKTAHQTLVRIKLNLMNRAPDNI IKFYKKTQQLPVLGKCCEETQPHQWKPP IEREHRLPFW
LKASLPSIQEELRHMDAGAREVGNMTGTTEINSDRSLEKDNLELGSESRYP LLLPKGVVLKLPVATRFPRKAWR
QKRSSVLKPLLIQSPSLQPSFNPGKTPARSTHSEAPPSKMVLRIHPHIQPATVLTQTVPGVPPPLGVSGGESFESP
AALPAVPPEARTSFPLSESQTLSSAPVPKVMLPSLAPSKFRKPYVRRRPSKRRGVKASPCMKPAPVIHHPASVI
FTVPATTVKIVSLGGGCNMIQPVNAAVAQSPQTIPITTLVNPTSFPCPLNQSLVASSVSPLIVSGNSVNLP IPS
TPEDKAHVNVDIACAVADGENAFQGLEPKLEPQELSPLSATVFPKVEHSPGPPLADAECQEGLSSENSACRWTVVK
TEEGRQALEPLPQGIQESLNNPTPGDLEEIVKMEPEEEAREEISGSPERDICDDIKVEHAVELDTGAPSEELSSAG
EVTKQTVLQKEEERSQPTKTPSSSQEPPEDEGTSGTDVNKGSSKNALSSMDPEVRLSSPPGKPEDSSSVDGQSVGT
PVGPETGGEKNGPEEEEEEDFDDLTQDEEDEMSSASEESVLSVPELQVRAGEYSQVFRGLSNMYHLLICHLLACC
TMDSPKIICI

445/6881
FIGURE 414

GCCTTTTTTGCAGTCTCAGGACGGGCGCTTTGGAGCCGGCCCCAGGCAGCGTGTGTGCGGTCGCCTAGTCTGGAGA
ACTAGTCCTCGACTCACGTGCAAGGATGATGCTGAAAGGAATAACAAGGCTTATCTCTAGGATCCATAAGTTGGA
CCCTGGGCGTTTTTTACACATGGGGACCCAGGCTCGCCAAAGCATTGCTGCTCACCTAGATAACCAGGTTCCAGT
TGAGAGTCCGAGAGCTATTTCCCGCACCAATGAGAATGACCCGGCCAAGCATGGGGATCAGCACGAGGGTCAGCA
CTACAACATCTCCCCCAGGATTTGGAGACTGTATTTCCCATGGCCTTCCTCCTCGCTTTGTGATGCAGGTGAA
GACATTCAAGTGAAGCTTGCCTGATGGTAAGGAAACCAGCCCTAGAACTTCTGCATTACCTGAAAAACACCAGTTT
TGCTTATCCAGCTATACGATATCTTCTGTATGGAGAGAAGGGAAACAGGAAAAACCCTAAGTCTTTGCCATGTTAT
TCATTTCTGTGCAAAACAGGACTGGCTGATACTACATATTCCAGATGCTCATCTTTGGGTGAAAAATTGTCGGGA
TCTTCTGCAGTCCAGCTACAACAAACAGCGCTTTGATCAACCTTTAGAGGCTTCAACCTGGCTGAAGAATTTCAA
AACTACAAATGAGCGCTTCCTGAACCAGATAAAAGTTCAAGAGAAAGTATGTCTGGAATAAGAGAGAAAAGCACTGA
GAAAGGGAGTCCTCTGGGAGAAGTGGTTGAACAGGGCATAACACGGGTGAGGAACGCCACAGATGCAGTTGGAAT
TGTGCTGAAAGAGCTAAAGAGGCAAAGTTCTTTGGGTATGTTTTACCTCCTAGTGGCCGTGGATGGAATCAATGC
TCTTTGGGGAAGAACCCTCTGAAAAGAGAAGATAAAAGCCCGATTGCCCCCGAGGAATTAGCACTTGTTTCA
CTTGAGGAAAATGATGAAAAATGATTGGCATGGAGGCGCCATTGTGTGCGGCTTTGAGCCAGACTGGGTCTCTCTT
TAAGCCCCGGAAAGCCTATCTGCCCCAGGAGTTGCTGGGAAAGGAAGGATTTGATGCCCTGGATCCCTTTATTC
CATCCTGGTTTTCCAATAACCCAAAGGAATTTGAAAGTTGTATTCAAGTATTATTTGGAAAACAATTGGCTTCA
ACATGAGAAAGCTCCTACAGAAGAAGGGAAAAAAGAGCTGCTGTTCTAAGTAACGCGAACCCCTCGCTGCTGGA
GCGGCACTGTGCCTACCTCTAAGCCAAGATCACAGCATGTGAGGAAGACAGTGGACATCTGCTTTATGCTGGACC
CAGTAAGATGAGGAAGTCGGGCAGTACACAGGAAGAGGAGCCAGGCCCTTGTACCTATGGGATTGGACAGGACTG
CAGTTGGCTCTGGACCTGCATTAAAATGGGTTTTCACTGTGAATGCGTGACAATAAGATATTCCCTTGTTTCTAAA
ACTTTATATCAGTTTATTGGATGTGGTTTTTTCACATTTAAGATAATTATGGCTCTTTTCTAAAAAATAAAATAT
CTTTCTAAAAA

446/6881
FIGURE 415

MMLKGITRLISRIHKLDPGRFLHMGTOARQSIAAHLDNQVPVESPRAISRNTNENDPAKHGDQHEGQHYNISPQDL
ETVFPHGLPPRFVMQVKTSEACLMVRKPALELLHYLKNTSFAYPAIRYLLYGEKGTGKTLCHVIHFCAKQDW
LILHIPDAHLWVKNCRDLLQSSYNKQRFDOPLEASTWLKNFKTTNERFLNQIKVQEKYVWNKRESTEKGSPLGEV
VEQGITRVNATDAVGIVLKELKRQSSLGMFHLLVAVDGINALWGRITTLKREDKSPIAPEELALVHNLKMMKND
WHGGAIVSALSQTGSLFKPRKAYLPQELLGKEGFDALDPFIPILVSNYNPKEFESCIQYYLENNWLQHEKAPTEE
GKKELLFLSNANPSLLERHCAYL

447/6881
FIGURE 416

TCTTCACCACTGCTCTCCCAGAGGTCCAGGTCCGGGAGATGACAGTGGCTCCCAGAAAGCCCAGGATTCAATCGC
TGAGAGAGTGCCTTAGGCCCCGAATGCCGGCCCCAAATCGTTCTACTCACC GTGTCGGAGGCCGAGAGCGATGAGAGT
ACAGGGGAAGTGAGGAAGAGGGGGTGGCCGCCAGGCTCCTCCGCTTCCCTGGGTCCACCGCGGATCCCTCCCGCTT
GTCAGGAGGCGGCCAGCGGGTAAGCCGACTGGCGGAAATGCGAGAGAGGAGAAGGGAAAGGTGGAGGGCTAAAGG
GGCAAAC TGAGAGGAGGCGGATCCCGCAACCGACACTGGGATCGTTTCCCTCGCAAAGCGAACC CAAAATGGCG
GCGGCAGCGGCGGCAGCAGAGTGGCCGCGGCAGCTCCTCCAGAGGGAGGAGCTAAGGGCGCCTAGCGACACCCC
CAACCTCCC ACTCCTCCCTCCTCGCGTTCTTCCCCACGGTCCCCCGCTTCGCCCCGACTCCGGCCATGTAGCGCGC
ACGTCAGCCCGCACGCGTACGAGTGTCTACGGGCTCGTTCGCTGGCTGCTCCACCAACCACCACTTCGGCCGTC
CTGCGAGCCAGCCATCCCGTACGCGCTCACCACGCGGAACCTCCTCGCCAGTTCTCCACTCCCCCTCAGACCCT
GTCAAGCCGGCTCCAGCGCAGGCCCTCACGCGTACCTCAGCGGCGCGAGCCCAAGCCTTCTCCACCTCCTCTTC
TCTCCTCCCCCTCCCTCCCCGCGCGCACGGCCACCAACCGCCGCCAAAGCAGCCGCCGCCAGCACCCCCACCCTA
CACTCCTCGCGCGTGC GCCTCCACAGTCCCCACCGCGGGACTGTTCCATTCTTGCGGGCTGCAGGGGCAGGAGA
GGAAGGGACCGGCAAAGCGAGTCTGGCTTGCCGTTTGACTGGAATTGCCAGGGTGGCCGGCCGAGTCCCATGACA
ACCTACCTCCCTGGGTTCTGTCGCGCGCGCGCTGCGGCTCGCCTCCTCCTCCATGGGACCGCGGCGAGGGGATCGA
GGGCGGCCTAGCGCCCCCTCTGCGCGCCGGTGGTTGGAGGCCGCGGCGGCTGCGCGTTGAGTCGTTTCTGCGGGA
TGACCCGACCCTTTTTTGCAGTCTCAGGACGGGCGCTTTGGAGCCGGCCCCAGGCAGCGTGTGTCGGTCGCCTAG
TCTGGAGAACTAGTCTCGACTCACGGTGAGGGAATGGACCGACACGGGTATTGTACCGCTGAGGGAAAGGAGCG
GGACTCCGGACCTCCAGGAGGTAGGGAGTGAGGCCGGTAGACCGGCGCGCCTCCGGGGGGGATTCTCCCGGGCG
TTGAGTTGCCAACCTGGGACCCGAGGAAGTTCGGCGTGGTGGTGTGCTTTTTGTTGTTGTTAACCCTCCTCGGAT
TTCTCGAATTTACACC ACTGTCCATATGCGATGATGTTTGTGTTGCCCTTGACGCACTTACTCATGGATGGTACT
TCAGCCTCGTTAGACAGCCTGGTGATGGAGGATGAAGAAACCATGTGCTTCTCATT CAGTTCTGGACTCAGTTTC
CCTTGTCTTCAGCAAGTTATTTTTGTTAGTTCCTTATCAAAAAGTGTACATAAAAATTAGGCAACTCCAAACATG
CCTCCAGGGTTGGTGTGTGAAATAATAAGATAGGGCTGGGCGCGGTGGCTCAGCCTGTAATCC CAGCACTTTGG
GAGGCCGAGGCAGGTGGATGACAAGGTGAAGAGATCGAGACAATCCTGGCCAACATGGTGAAACCCCGTCTCTAC
TAAAAATACAAATATTAGCCGGCCGTGGTGGCGGGCGCCTGTAGCCCCAGCTACTCGGGAGGCTGAGGCAGGAGA
ATTGCTTGAAACCCGGGCGGCGGAAGTTGCAGTGAGCCGAGATCGCGCCACTGCACTCCAGCCTGGCGACAAAGCG
AGACTCCGTCACACACACACACACACACGAAATAATAATATATGTAAAGTGGAATTAGCTCCAAGTCGTTAAT
AAAACAAAGCAGGCCGGGCGTCTTGTTAAATAGTTGTATCAATGACTTGATTTAGATTAAATGAGGATATATTTTT
CAAATTTATGCCTTTTACAAAATTTTTAAAGAGTAGGTAATGTCGGTGATAGATATAAAGAAAGGAAAAGATCTC
CAGATGTGGAATCTTCTACTGGATCCTGTAACAGAAAGAAGACATTAGGCTGGGCGCAGTGGCTCACACCTGTAA
TCTCAGCACTTTGGGAGGCGGAGGAGGGCGCATTGCTTGAGCCTAGGAGTTCGAGACCAGCTTAGGCAACACGGT
GAAACCCCATCTCTACAAAAGACACAAAATTAGACAGGTGTGGCACACGCTTGTAAGTCTGAGCTACTTGGGAG
GCTGAAGCAGGAGGATTGAGGAAGAGGTTGCAAAGTTAGCCGAGATCACGCCATCACACTGCAGCCTAGGTGACA
GAGCGAGACCCTGTCTCAAAAAAAGAAAGAAGACATTAGCAGAAAAGCTGAGGAAATGCAAATAAAGTCTGCAAT
TTTTAAAT

448/6881
FIGURE 417

MTRPFFAVSGRALWSRPQAACVGRLVWRITSPRLTVREWTDTGIVPLRERSGTPDLQEVGSEAGRPARLRGGFLPG
VELPTWDPKFGVVCFLLLLTLLGFLEFHTTVHMR

[illegible]

450/6881
FIGURE 419

MGFSNMEDDGPEEEERVAEPQANFNTPQALRFEELLANLLNEQHQIAKELFEQLKMKKPSAKQQKEVEKVKPQCK
EVHQTLILDPAQRKRLQQQMQQHVQLLTQIHLLATCNPNLNPEASSTRICLKELGTFAQSSIALHHQYNPKFQTL
FQPCNLMGAMQLIEDFSTHVSIDCSPHKTVKKTANEFPCLPKQVAVILATSKVFMYPELLPVCSLKAKNPQDKIL
FTKAEDNLLALGLKHFEGTEFLNPLISKYLLTCKTARQLTVRIKNLNMNRAPDNI IKFYKKTQQLPVLGKCCEEI
QPHQWKPPIEREEHRLPFWLKASLPSIQEELRHMADGAREVGNMTGTTEINSDQGLEKDNSELGSETRYPLLLPK
GVVLKLPVADRFPKKAWRQKRSSVLKPLLIQPSPSLQPSFNPGKTPAQSTHSEAPPSKMVLRIPHPIQPATVLQ
TVPGVPPLGVSGGESFESPAALPAMPPEARTSFPLSESQTLLSSAPVPKVMMPSPASSMFRKPYVRRRPSKRRGA
RAFRCIKPAPVIHPASVIFTVPATTVKIVSLGGGCNMIQPVNAAVAQSPQTIPATLLVNPTSFPCLNQPLVAS
SVSPLIVSGNSVNLPIPSTPEDKAHMNVDIACAVADGENAFQGLEPKLEPQELSPLSATVFPKVEHSPGPPPVDK
QCQEGLSSENSAYRWTIVKTEEGRQALEPLPQGIQESLNNSSPGDLEEVVKMEPEDATEEISGFL

451/6881
FIGURE 420

AGCGCAGT**ATG**CGGGCGGGGCCCCGGGAGGTGCTCACACTGCAGTTGGGACATTTTGCCGGTTTCGTGGGCGCGC
ACTGGTGGAACCAGCAGGATGCTGCGCTGGGCCGAGCGACCGATTCCAAGGAGCCCCGGGAGAGCTGTGCCCCG
ACGTCCTGTATCGTACGGGCCGGACGCTGCACGGCCAGGAGACCTACACGCCGCGACTCATCCTCATGGATCTGA
AGGGTAGTTTTGAGCTCCCTAAAAGAGGAAGGTGGACTCTACAGGGACAAACAGTTGGATGCTGCAATAGCATGGC
AGGGGAAGCTCACACACACAAAGAGGAAGTCTATCCCAAGAACCCTTATCTCCAAGACTTTCTGAGTGCAGAGG
GAGTGCTGAGTAGTGATGGTGTCTGGAGGGTCAAATCCATTCCAATGGCAAAGGTTCCCTCACCCTCCCCACCG
CTACAACCTCCAAAACCACTTATCCCTACAGAGGCCAGCATCAGGGTCTGGTCAGACTTCCTCAGAGTCCATCTCC
ATCCCCGGAGCATCTGTATGATTGAGTACAACACGATGGGGAAGCAGGTCGGCTGGAGGCTTTTGGCCAAG
GGGAAAGTGTCTTAAAGGAACCCAAGTACCAGGAAGAGCTGGAGGACAGGCTGCATTTCTACGTGGAGGAATGTG
ACTACTTGCAGGGCTTCCAGATCCTGTGTGACCTGCACGATGGCTTCTCTGGGGTAGGCGCGAAGGCGGCAGAGC
TGCTACAAGATGAATATTGAGGGCGGGGAATAATAACCTGGGGCCTGCTACCTGGTCCCTACCATCGTGGGGAGG
CCCAGAGAAACATCTATCGTCTATTAAACACAGCTTTTGGTCTCGTGACCTGACTGCTCACAGCTCTCTTGTCT
GCCCCTTGTCTTGGGTGGGAGCCTGGGCCTGCGACCCGAGCCACCTGTGAGCTTCCCTTACCTGCATTATGATG
CCTCTGCCCCTTCCACTGCAGTGCCATCCTGGCTACAGCCCTGGACACAGTCACGTGTTCCCTTATCGCCTGTGTT
CCTCTCCAGTTTCCATGGTTTCTGCTGAGCTTCTGTGGGAAAAAGGTGGTGACAGCAGGAGCAA
TCATCCCTTTCCCTTGGCTCCAGGCCAGTCCCTTCCCTGATTCCCTGGTGCAGTTTGGAGGAGCCACCCCATGGA
CCCCACTGTCTGCATGTGGGGAGCCTTCTGGAACACGTTGCTTTGCCAGTCAGTGGTGTGAGGGGTATAGACA
GAGCATGCCACACAAGCCAGCTCACCCAGGGACACCTCCACCCTCTGCCCTTCATGCATGTACCACTGGGGAAG
AAATCTTGGCTCAGTATTTACAACAGCAGCAGCCTGGAGTCATGAGTTCTTCCCATCTGCTGCTGACTCCCTGCA
GGGTGGCTCCTCCTTACCCCCACCTCTTCTCAAGCTGCAGTCCACCGGGTATGGTTCTGGATGGTTCCCCAAGG
GAGCAGCAGTGGAGAGCATCCCAGTGTTTGGGGCACTGTGTTCCCTCTTCGTCCCTGCACCAGACCCTGGAAGCCT
TGGCCAGAGACCTCACAAACTCGACTTGCGGCGCTGGGCCAGCTTCATGGATGCTGGAGTGGAGCACGATGACG
TAGCAGAGCTGCTGCAGGAGCTACAAAGCCTGGCCAGTGTACCAGGGTGGTGACAGCCTCGTGGAC**TAA**AGTT
CCCAGTGTGGGAGAAAGGAGCTAGTTTGCAATAAAAAACAGCTGGATGCAGGAGCCCAGTGTCTTCATGCAGAGGA
GCTCAATGTCGCGGGACTAGCTACACCAACATATGCACTTTTTACATTTAGAAACACTGTGATTAGACCACAGAA
CAATAAATATGTGCCATCAGACC

452/6881
FIGURE 421

MAGGAREVLTTLQLGHFAGFVGAAHWNQQDAALGRATDSKEPPGELCPDVLYRTGRTLHGQETYPRLILMDLKGS
LSSLKEEGGLYRDKQLDAAIAWQGKLTTHKEELYPKNPYLQDFLSAEGVLSSDGVWRVKSIPNGKGSSPLPTATT
PKPLIPTEASIRVWSDFLRVHLHPRSICMIQKYNHDGEAGRLEAFGQGESVLKEPKYQEELEDRLHFYVEECDYL
QGFQILCDLHDGFSGVGAKAAELLQDEYSGRGIITWGLLPGPYHRGEAQRNIIYRLNNTAFGLVHLTAHSSLVCPL
SLGGSLLGRPEPPVSFPYLHYDATLPFHCSAILATALDVTVPYRLCSSPVSMVHLADMLSFCGKKVVTAGAIIP
FPLAPGQSLPDSLVSQFGGATPWTPLSACGEPSGTRCFAQSVVLRGIDRACHTSQLTGTPPPSALHACTTGEEIL
AQYLQQQQPGVMSSSHLLTPCRVAPPYPHLFSSCSPPGMVLDGSPKGAAVESIPVFGALCSSSSSLHQTLEALAR
DLTKLDLRRWASFMDAGVEHDDVAELLQELQSLAQCYQGGDSLVD

453/6881
FIGURE 422

AGGTGAGAGAGGATGTGTGCTGGGCCTTGGAGGAAGGGGGCCGAGACCGGGCCTTACTTCTGTAAACGATACTGTG
AGGCATCGGAAGGCCAGCCTGTTGTGTCCGTTTTGAAGGATGCCCCCTGTCCCGCTGGTTGAGATCTGTGGGGGTC
TTCTTGCTGCCAGCCCCCTACTGGGCACCCCGGGAGAGGTGGCTGGGTTCCCTACGGCGGCCCTCCCTGGTGAC
GGGTACCCAGTCCTGGCCTGGCACAGTGCCCGCTGCTGGTGCCAAGCGTGGACAGAGGAACCTCGAGCCCTTTGC
TCCTCCCTCAGAATGAACGGAGACCAGAATTCAGATGTTTATGCCCAAGAAAAGCAGGATTCGTTTCAGCACTTC
TCCCAGATCGTTAGGGTGCTGACTGAGGATGAGATGGGGCACCCAGAGATAGGAGATGCTATTGCCCGGCTCAAG
GAGGTCCTGGAGTACAATGCCATTGGAGGCAAGTATAACCGGGGTTTGACGGTGGTAGTAGCATTCCGGGAGCTG
GTGGAGCCAAGGAAACAGGATGCTGATAGTCTCCAGCGGGCCTGGACTGTGGGCTGGTGTGTGGAACCTGCTGCAA
GCTTTCTTCCTGGTGGCAGATGACATCATGGATTCATCCCTTACCCGCCGGGGACAGATCTGCTGGTATCAGAAG
CCGGGCGTGGGTTTGGATGCCATCAATGATGCTAACCTCCTGGAAGCATGTATCTACCGCCTGCTGAAGCTCTAT
TGCCGGGAGCAGCCCTATTACCTGAACCTGATCGAGCTCTTCCTGCAGAGTTCCTATCAGACTGAGATTGGGCAG
ACCCTGGACCTCCTCACAGCCCCCAGGGCAATGTGGATCTTGTTCAGATTCACTGAAAAGAGGTACAAATCTATT
GTCAAGTACAAGACAGCTTTCTACTCCTTCTACCTTCCTATAGCTGCAGCCATGTACATGGCAGGAATTGATGGC
GAGAAGGAGCACGCCAATGCCAAGAAGATCCTGCTGGAGATGGGGGAGTTCTTTCAGATTTCAGGATGATTACCTT
GACCTCTTTGGGGACCCAGTGTGACCGGCAAAATTGGCACTGACATCCAGGACAACAAATGCAGCTGGCTGGTG
GTTTCAGTGTCTGCAACGGGCCACTCCAGAACAGTACCAGATCCTGAAGGAAAATTACGGGCAGAAGGAGGCTGAG
AAAGTGGCCCGGTGAAGGCGCTATATGAGGAGCTGGATCTGCCAGCAGTGTTCTTGCAATATGAGGAAGACAGT
TACAGCCACATTATGGCTCTCATTGAACAGTACGCAGCACCCCTGCCCCAGCCGTCTTCTGGGGCTTGCGCGC
AAAATCTACAAGCGGAGAAAGTGAACCTAGAGATTGCAAGGGCGGGGAGAGGAGGCTCTCAATAAATAATCGTGTA
ACCTT.

454/6881
FIGURE 423

MPLSRWLRSVGVFLLPAPYWAPRERWLGSILRRPSLVHGYPVLAHWSARCWCQAWTEEPRALCSSLRMNGDQNSDV
YAQEKQDFVQHFSQIVRVLTEDEMGHPEIGDAIARLKEVLEYNAIGGKYNRGLTVVVAFRELVEPRKQDADSLQR
AWTVGWCVELLQAFFLVADDIMDSSLTRRGQICWYQKPGVGLDAINDANLLEACIYRLKLYCREQPYYLNLIEL
FLOSSYQTEIGQTLDLLTAPQGNVDLVRFTEKRYKSIVKYKTAFYSFYLP IAAAMYMAGIDGEKEHANAKKILLE
MGEFFQIQDDYLDLFGDPSVTGKIGTDIQDNKCSWLVVQCLQRATPEQYQILKENYGQKEAEKVARVKALYEELD
LPAVFLQYEEDSYSHIMALIEQYAAPLPPAVFLGLARKIYKRRK

455/6881
FIGURE 424

GGTAGTTGGTTGTGGGCACTGGGTTAGAGGTATCACGTGGGGGCACTTTCGTCTTAGCTTTTGGACAAGACGCAG
GCGCAACCCACGGCTGCTGCGGGGATCCTTGTGGCCCTTCCGGTCGGTGGAACCAATCCGTGCACAGAGAAGCGG
GGCGAACTGAGGCGAGTGAAGTGGACTCTGAGGGCTACCGCTACCGCCACTGCTGCGGCAGGGGCGTGGAGGGCA
GAGGGCCGCGGAGGCCGCGAGTTGCAAACATGGCTCAGAGCAGAGACGGCGGAAACCCGTTTCGCCGAGCCCAGCGA
GCTTGACAACCCCTTTTCAGGACCCAGCTGTGATCCAGCACCGACCCAGCCGGCAGTATGCCACGCTTGACGTCTA
CAACCCCTTTTGAGACCCGGGAGCCACCACCAGCCTATGAGCCTCCAGCCCCTGCCCCATTGCCTCCACCCTCAGC
TCCCTCCTTGCAGCCCTCGAGAAAGCTCAGCCCCACAGAACCTAAGAACTATGGCTCATAACAGCACTCAGGCCTC
AGCTGCAGCAGCCACAGCTGAGCTGCTGAAGAAACAGGAGGAGCTCAACCGGAAGGCAGAGGAGTTGGACCGAAG
GGAGCGAGAGCTGCAGCATGCTGCCCTGGGGGGCACAGCTACTCGACAGAACAATTGGCCCCCTCTACCTTCTTT
TTGTCCAGTTTCAGCCCTGCTTTTTTCCAGGACATCTCCATGGAGATCCCCAAGAATTTCAGAAGACTGTATCCAC
CATGTACTACCTCTGGATGTGCAGCACGCTGGCTCTTCTCCTGAACTTCCTCGCCTGCCTGGCCAGCTTCTGTGT
GGAAACCAACAATGGCGCAGGCTTTGGGCTTTCTATCCTCTGGGTCTCCTTTTCACTCCCTGCTCCTTTGTCTG
CTGGTACCGCCCCATGTATAAGGCTTTCCGGAGTGACAGTTCAATTCATTTCTTCGTTTTCTTCTTCATTTTCTT
CGTCCAGGATGTGCTCTTTGTCTCCAGGCCATTGGTATCCCAGGTTGGGGATTCACTGGCTGGATCTCTGCTCT
GGTGGTGCCGAAGGGCAACACAGCAGTATCCGTGCTCATGCTGCTGGTCGCCCTGCTCTTCACTGGCATTGCTGT
GCTAGGAATTGTCATGCTGAAACGGATCCACTCCTTATACCGCCGCACAGGTGCCAGCTTTCAGAAGGCCAGCA
AGAATTTGCTGCTGGTGTCTTCTCCAACCCCTGCGGTGCGAACCGCAGCTGCCAATGCAGCCGCTGGGGCTGCTGA
AAATGCCTTCCGGGGCCCCGTGACCCCCTGACTGGGATGCCCTGGCCCTGCTACTTGAGGGAGCTGACTTAGCTCCC
GTCCCTAAGGTCTCTGGGACTTGAGAGACATCACTAACTGATGGCTCCTCCGTAGTGCTCCCAATCCTATGGCC
ATGACTGCTGAACCTGACAGGCGTGTGGGGAGTTCACTGTGACCTAGTCCCCCATCAGGCCACACTGCTGCCAC
CTCTCACACGCCCCAACCCAGCTTCCCTCTGCTGTGCCACGGCTGTTGCTTCGGTTATTTAAATAAAAAGAAAGT
GGAAGTGGAACTGACAAAAAAAAAAAAAAAAAAAAAAAAA

456/6881
FIGURE 425

MAQSRDGGNPFAEPSELDNPFQDPAVIOHRPSRQYATLDVYNPFETREPPPAYEPPAPAPLPPPSAPSLQPSRKL
SPTEPKNYGSYSTQASAAAATAELLKKQEELNRKAEELDRRERELQHAALGGTATRQNNWPPLPSF'CPVQPCFFQ
DISMEIPQEFQKTVSTMYYLWMCSTLALLLNFLACLASFVETNNGAGFGLSILWVLLFTPCSFVCWYRPMYKAF
RSDSSFNFFVFFFIFFVQDVLFLVLAIGIPGWGFSGWISALVVPKGNTAVSVLMLLVALLFTGIAVLGIVMLKRI
HSLYRRTGASFQKAQQEFAAGVFSNPAVRTAAANAAAGAAENAFRAP

457/6881
FIGURE 426

GGTAGTTGGTTGTGGGCACTGGGTTAGAGGTATCACGTGGGGGCACTTTCGTCTTAGCTTTTGGACAAGACGCAG
GCGCAACCCACGGCTGCTGCGGGGATCCTTGTGGCCCTTCCGGTCGGTGGAACCAATCCGTGCACAGAGAAGCGG
GGCGAACTGAGGCGAGTGAAGTGGACTCTGAGGGCTACCGCTACCGCCACTGCTGCGGCAGGGGCGTGGAGGGCA
GAGGGCCGCGGAGGCCGCGAGTTGCAAACATGGCTCAGAGCAGAGACGGCGGAAACCCGTTTCGCCGAGCCCAGCGA
GCTTGACAACCCCTTTTCAGCCACCACCAGCCTATGAGCCTCCAGCCCCTGCCCATTTGCCTCCACCCTCAGCTCC
CTCCTTGACGCCCTCGAGAAAGCTCAGCCCCACAGAACCTAAGAACTATGGCTCATAACAGCACTCAGGCCTCAGC
TGCAGCAGCCACAGCTGAGCTGCTGAAGAAACAGGAGGAGCTCAACCGGAAGGCAGAGGAGTTGGACCGAAGGGA
GCGAGAGCTGCAGCATGCTGCCCTGGGGGGCACAGCTACTCGACAGAACAATTGGCCCCCTCTACCTTCTTTTG
TCCAGTTCAGCCCTGCTTTTTTCCAGGACATCTCCATGGAGATCCCCAAGAATTTCAGAAGACTGTATCCACCAT
GTACTACCTCTGGATGTGCAGCACGCTGGCTCTTCTCCTGAACTTCCTCGCCTGCCTGGCCAGCTTCTGTGTGGA
AACCAACAATGGCGCAGGCTTTGGGCTTTTCTATCCTCTGGGTCTCCTTTTCACTCCCTGCTCCTTTGTCTGCTG
GTACCGCCCCATGTATAAGGCTTTCCGGAGTGACAGTTCATTCAATTTCTTCGTTTTCTTCTTCATTTTCTTCGT
CCAGGATGTGCTCTTTGTCTCCAGGCCATTGGTATCCAGGTTGGGGATTTCAGTGGCTGGATCTCTGCTCTGGT
GGTGCCGAAGGGCAACACAGCAGTATCCGTGCTCATGCTGCTGGTTCGCCCTGCTCTTCACTGGCATTGCTGTGCT
AGGAATTGTCATGCTGAAACGGATCCACTCCTTATACCGCCGCACAGGTGCCAGCTTTCAGAAGGCCAGCAAGA
ATTTGCTGCTGGTGTCTTCTCCAACCCTGCGGTGCGAACC GCAGCTGCCAATGCAGCCGCTGGGGCTGCTGAAAA
TGCCTTCGGGGCCCCGTGACCCCCTGACTGGGATGCCCTGGCCCTGCTACTTGAGGGAGCTGACTTAGCTCCCGTC
CCTAAGGTCTCTGGGACTTGAGAGACATCACTAACTGATGGCTCCTCCGTAGTGCTCCCAATCCTATGGCCATG
ACTGCTGAACCTGACAGGCGTGTGGGGAGTTCACTGTGACCTAGTCCCCCATCAGGCCACACTGCTGCCACCTC
TCACACGCCCCAACCAGCTTCCCTCTGCTGTGCCACGGCTGTTGCTTCGGTTATTTAAATAAAAAAGAAAGTGGA
ACTGGAAGTGAATAAAAAAAAAAAAAA

458/6881
FIGURE 427

MAQSRDGGNPF AEPS ELDNPFQPPPAYEPPAPAPLP PPSAPSLQPSRKLSPT EPKNYGSYSTQASAAAATAELLK
KQEELNRKAEELDRRERELQHAALGGTATRQNNWPPLPSFCPVQPCFFQDISMEIPQEFQKTVSTMYYLWMCSTL
ALLLNFLACLASF CVETNNGAGFGLSILWVLLFTPCSFVCWYRPMYKAFRSDSSFNFFVFFFIFFVQDVLFLVLA
IGIPGWGFSGWISALVVPKGNTAVSVLMLLVALLFTGIAVLGIVMLKRIHSLYRRTGASFQKAQQEFAAGVFSNP
AVRTAAANAAAGAAENAFRAP

459/6881
FIGURE 428

CCTGCGGCAGCCGGAGCTCGGGGAGCGGAGCGTGCTGGGGAGGGGAGCGGGACAGGGGACACAGGAGACAGCGGC
GCCGCGGCCTCTCCCCACCAGGCGGCCCCGGATCCTACTGGACGCCCTGAGGGCACACCGACCGCGCCTCTAGAG
TCACCCACAGCCGACCCCTCCCCTCTTCTCTAGACTTATTTCCATCCTTCCCGCTTTTACCCTCCCCACCCGTCC
CTGGGCTCCAGGCGCGCGCCCCCTCCTCACTCCTGGACCGGCCCTTCTCGGTGCCCCCTCTTCCCTAGGGAGATGC
GATGAGCCGGTGCCCCCGCGTCTCATCGTCGCCCCGGGCACGGTGCCCCGTCCAGTGCCCGTGGTGGGGAGGGAG
CACTCCGCGGTCCCTCCGTGACGCCCCCTCGCTTGGCCCCCCCCACAGCTGGCGTCCCTCGGCCATGCCCCAGGGG
ACCCAGCCAGGGGGTGGGCTCTAGAGCGAGTGGGGTGGAGAGGAGAAAGGACGGGGCCTTGGGGGCTCTGAGAT
GCTCCCAAGTGCCAGGGAGGGCCGAGCGAGGCGCAGGCAACCGGGCAGCAGGCATGATGCCCTCGCCTAGTGACT
CCAGCCGCTCGCTGACCAGCCGGCCCCAGCACAGGGGCCCTTACCCACCTCCGCCTCCACCGACCTGGCTGCAGG
CCCTGCTTACGCTGGGGCTGGTCCAAGTGCTCCTGGGCATCCTGGTGGTCACTTTCAGCATGGTGGCCTCTTCCG
TCACCACCACCGAGAGCATCAAGAGGTCCGTGCGCTCTTGGGCTGGGTCTCGCTGGCGTTCTCCGGGGTGGTTG
GCATTGTGTCTGGAAGCGGCCATTCACTCTAGTGATCTCCTTCTTCTCCTTGCTTTCGGTGCTCTGTGTATGC
TTAGCATGGCTGGCTCTGTTCTCTCCTGTAAGAATGCTCAACTGGCCCGAGACTTCCAACAGTGCTCTCTGGAAG
GAAAGGTCTGTGTGTGTGTGTCTCCCTCTGTTCCCTCCTCCGGCCCTGTCCAGAGTCGGGGCAGGAAGTGAAGTTG
CCCCTAACTCCACCTGTGATGAAGCCCGAGGGGCCCTCAAGAACCTGCTCTTCAGCGTCTGTGGGCTCACCATT
GTGCCGTATAATCTGTACACTCTCTGCTATTGTCTGCTGCATCAAATCTTCTCCCTGGACCTCGTGCATACGC
AGCTGGCCCTGAGCGGTCACTCTCAGGCCACTGGGACCTCTGGGCTGCACGTCCCCGCCCCAGCCCTCTCC
TACACACCATGCTGGACCTGGAGGAATTTGTCCCGCTGTGCCCCACCGCCCTACTATCCCCAGAGTATACCT
GCAGCTCAGAAACAGATGCACAGAGCATCACGTACAATGGCTCCATGGACAGCCCAGTGCCCTTGTACCCTACCG
ATTGCCCCCTTCTTATGAGGCAGTCATGGGACTACGAGGAGACAGCCAGGCCACTCTCTTTGACCCTCAGCTTC
ACGATGGCTCGTGCATCTGTGAACGAGTGGCCTCCATTGTAGACGTGTCCATGGACAGCGGTCTCTGGTGTGT
CAGCCATTGGTGACCTCCCTGGGGGCTCTAGCCCGTCGGAGGACTCGTGCTGCTGGAGCTGCAGGGCTCCGTGC
GCTCCGTGGACTACGTTCTCTTTCGCTCCATCCAGCGCAGCCGTGCCGGCTACTGCCTCAGCCTGGACTGTGGCC
TGCGGGGCCCTTCGAGGAAAGCCCCCTGCCACGGCGCCCCCACGGGCTGCCCGCTCCTATTCTGCTCTGCC
CTGAAGCTCCACCCCACTGGGTGCCCCACAGCTGCCCGCAGCTGCCACCGGTTGGAGGGCTGGCCGCCCTGGG
TGGGACCCTGCTTCCCCGAGCTGAGGCGGCGGGTCCCCCGGGGAGGGGCGCCAGCCGAGCCCCGCCACCC
GAGCCCCGACTCGTCGCTTACGCGATAGCTCAGGTTCCCTACCCACCGGGGCACCGGCCTCCTCATCCGGCAT
CCCCACCACCGCTGCTGCTGCCACGTTCCACAGCGACCCAGGCATCACGACCTCCAGTGACACTGCTGACTTCA
GGGACCTTTATACCAAAGTGCTTGAGGAAGAAGCTGCTTCTGTTTCTCTGCAGATACAGGGCTCTGCTCTGAAG
CCTGCCTCTTCCGCCTAGCCCGCTGCCCTTCCCCCAAGTTGCTACGTGCCCGGTGAGCCGAGAAACGGCGCCCTG
TGCCACCTTCCAAAAGTTCCCTGCCCTCGGGCCCTGCACCTGCCCACTCCCTGGGGGACCTAAAGGGCAGCT
GGCCAGGTGCGGGCCTGGTCACTCGTTTCCCTCCAGATATCCAGGAAAGCCCCAGACCCAGTGGGACTGGAGCTC
ATGGACATAAGCAGGTGCCCCGAGCCTGTGGGGCCGGCCTGGCCGAGAGAGCCTCCACCTTCGCAGCTGCGGAG
ATCTGAGCTCTAGCTCTTCCCTGCGGCGTCTCCTGTCTGGCCGAGGCTGGAGCGTGGTACCCGCCCCACAGCC
TCAGCCTCAACGGGGGAGCCGGGAGACTGGGCTCTGACCTAGGCTTCTTGTACACTGAACACATCCAGCCACA
GGCACCAGCTGGTTGGGACCAGCAGCCCCAGCATCCTTTCAGCTGGCTGGCACAAAAGAAACCTGCTGTATA
CCCCCAAAGTGCTCCCTTCCCTCCTACCTCTGGGGTCTCTTGCTGCTTGCCTCTGCTGCTCTGGTCTGGGAGAG
CTTCTGTCTGTGCTGCATGGGTATTTAGACTGTGGGGGAGATGCCCCCTTCTTATAGCACTGGAGGAGGAAAACA
AATTCTTGTCCCCCTCAGAATGAGAGTGGCTCTTCTGATTTGCAAGGGCACTATGGTCAGGGCAAAGGCATGGC
CCAGGTGTTTAAGTACAGGGTGACGTGTGCCTATGCAATGGGGTGGTAAGGCAGGCACGAAGAGTCCAAAAATC
TAGGTGGCCTCTCAGCTCTGCCACCTCTAGCTGCATGACCTTGGGCAAGCTATGTAACCCCAATTGCCTGCTCCA
TTAAAGACTGTGAAGGTAGAATGTTTGTAAAGCTCTTAACAGTATGTAAGCCTTCAATAAATTTAGTTTTCCCC
TT

460/6881
FIGURE 429

MMPSPSDSSRSLTSRPSTRGLTHLRLHRPWLQALLTLGLVQVLLGILVVTFSMVASSVTTTESIKRSCPSWAGFS
LAFSGVVGIVSWKRPFLLVISFFSLLSVLCVMLSMAGSVLSCKNAQLARDFQQCSLEGKVCVCCPSVPLLRCPE
SGQELKVAPNSTCDEARGALKNLLFSVCGLTICAAICTLSAIVCCIQIFSLDLVHTQLAPERSVSGPLGLGCT
SPPPAPLLHTMLDLEEFVPPVPPPPYYPPEYTCSETDAQSITYNGSMDSPVPLYPTDCPPSYEAVMGLRGDSQA
TLFDPQLHDGSCICERVASIVDVSMDSGSLVLSAIGDLPGGSSPSEDSCLLELQGSVRSVDYVLFVRSIQRSRAGY
CLSLDCGLRGPFEEESPLPRRPPRAARSYSCSAPEAPPPLGAPTAARSCHRLEGWPPWVGPCFPFLRRRVPRGGGR
PAAAPPTRAPTRRFSDSSGSLTPPGHRPPHPASPPPLLLPRSHSDPGITTSSDTADFRDLYTKVLEEEAASVSSA
DTGLCSEACLFRLARCPSPKLLRARSAEKRRPVPTFQKVPLPSGPAPAHSLGDLKGSWPGRGLVTRFLQISRKAP
DPSGTGAHGKQVPRSLWGRPGRESLHLRSCGDLSSSSSLRRLLSGRRLERGRPHSLSLNGGSRETGL

461/6881
FIGURE 430

CAGTGCCCCACAGCTCTTCAGGCCCTTCCTGTGCCTGGCTGCCCTCCCACCCTACCCTTTTGTACCTCTGAGAAG
GCTCTGGCCCCACGCACAGCCCCACTGTACCAGGGCCAGTATCTGTCTCAGGGACCTCCTATCCAGAGCCTGAG
CCAGCCCCAGCCCCAGCCCCAGCTCCAGCTGCTCCATCTGAACCTGTATCTTCTTCCAAGCCACCCATTACCCTC
TTGGAGTCAGACTCACGCATCTCCAAAGAAGAACTTTTGAGAGCCCAGGCGCTGAGAGAGCAGGGTCAGACACTC
CCGAGCCTCTCGGTACAGCTGTAGGGGCGACACAGGTAGGCTTGCAGCTGCGGGAACAGTGCCACCTCCGCACCT
AAGCACTCCCATTTCTGGCCAGCATCCTTGGGGCTCATCTCATACAATAGCCCCCGGTCTCAGAGCTACCTCCTT
CTCCAGCTCTTCCTCGTCCCTCAGGCCTGTGCTCCCCAGTCAGCAGCTGTAGCCGTTCCATGTACTGCCGCTGCAT
GCGGCCAGGCAGGAAGAAGTTGAGGGGAAAGGGCATAGCCTCTGCATACCACTTCCGGGTCACTTCTACGTAGTT
CTTGGTGTCTATCCAAAAGTATGTACCTGGATTGGGTGGGCAGGAAGAAACAGGCAGGTCTGAGCCAGTGCACC
TGTCTGATTCAAGGTGGGCTTCTGACCTCCATGCTCTCCTGAGTCTCTGTGTGGGTCTGTGTGTTCCCGTCCCCT
CCCCGGCTGGCCATGGATGCTGGGAGGTCTGGGCACACTCACCAGCACCGGGATCAAACTTCTCCTCCAGGAGAGA
CATGAAGGCCAGGGTGTCTGCCCCCTTGTCTGAGCTGACAGATCATAAATCAGCATTGTACTTCTGTGGAGGAAATAT
CCATGGCGTGGACGCTGGGGAGCTGCAAGGGCACTTCACCAGGGAGGAAGGAGTCTGTCTGGTACCCCCCTCAC
TGGCCTCTGAGTGCAGTGGAGGTACAGCAAGGAACCTTTTCTGCCAAGGCCCCCTTGCCCTGGGCCCAGCCAGTAG
CCTGTTGCTGTTGGCAAAAAGCCTGGGCCTTGGAGCCCGCTGGCCGTCAAGGTCTGGGCCCCATTGAGAAGAAGG
AAGAAAGGTTGGGCCGCAAACTAGGAGCAGCTCCCAGAATTTCCATGGAAAGCTGGAACAATGCCTGCTAGCAGC
AACTTTCTAACAGTAACTTTCCCGACCCAGACACCACAAAGCTAGCACAAACGGAGCTCAGATGCAGGCTAGGACT
CGGTCCATGCCTCAGGAACCAGGGAAAGCCATCCTCACACTCCCTGGATCCAGGGAACCCACGCCCAGGGCCCCC
CAGCTTGTTCCCTCAGTGCCCACTCTTGGCTATTTCTTTCACTTCATTCCATCGCCAGACACCATTACCACAT
ACACATTCCATCCATACCCCCAGGTCTCAGCCTGCCCTACCTTCCCAGGCTCCAGTCCCTGTTCCCTCAGCATCCC
CCACCACATCCTGAGTAAGCTTTGTCCCCAGATAACCTCTTCAGCATGATCCTTAAATCTCCCTAAGCCTCAGTT
TCTCCCCTGTGGAATGGGGGTAAAGAACTCTTTCTCTGAATGCCCTGTGTTAGGAAATAATTTAGAATACTTCG
GAAACAAAAAGCTCTGTTACACCTAAGCAATCAGGGCAGTGGCCCTGGCCTTGCCAGGAACTTAGGCTTTTATC
TGGATCCTCTTTCCAGGCCTCTCAATTAATCCCCAGGTCCTTAACCTTTGGGAAATTAGAAATTAGGAAGAGTG
TCCCCTTCTGACACTGTGTTCCCTCTTGGAACTGACCGTCAATGCTAGAAGAACCCTTGGAACATGCTGGC
CCAGCCCTCTAGTTTTTACAAATAAGGGAGTGCACAGCCCTGAGAGGTTACATGGCCTGCCCCAAGATCACGCAGTC
AATGGCAGAGTAAAGAGCATAGCCTAGGCCTCCCCACTCCTCTAGTAATGCTCTTTTCATCTTCTCCAACCTGGCT
CTAAGCCTTGTTCCATCCTGAGCCCCATATCTAGCCCAACCTAGTCCCTGAAAACAAGAAGTGGCCCTTAGAAATC
TCTCTCCAGTCCCCTATCAGAGGCCAACTGCTGTCTTCCAGTCTCCTTCAGCCTGTGCTCCTCTCCCTCCCTGA
CTGACAGGCAGAAGGTACCGTGCCCTCTGGATATCCCCACAGTGCCTGAGCTGCATCTCTTGCCGACTGCTTTAA
TACATCACAGTGACATTGTGTGTGCTCTGCCACCAGACTATTGCTCCTTGATGCTCTGGGTACCTGCATCTAG
CATGGCATATATCTAGTGCTCAATAAATGTGTATTGTACGG

462/6881
FIGURE 431

MAWTLGSCCKGTSPGRKESCLVPPSLASECSGGTARNFSCQGFLAWAQPVACCCWQKAWALEPAGRQGPPIEKKE
ERLGRKLGAAAPRISMESWNNAC

463/6881
FIGURE 432

AAGCCCCAGCCCGGCCTCCGCTCCGGCCGCCGCCACCGCCCCTGTTTTGTTTCCATGGCGACAGGCGGCGCAGGG
CCCGCTCCAAACATAACGCGCTGTGGAAAACATGCTGCTCGGGGGACCCCCCGCAGTCCCCGCTCGGGGACGAG
CCCCAAGGGGCCCTGGAGCAGTACAGGCCACGTGCAGTTTGGCAAGAGCCCCCAGACCTGGCCCAGGCGCACAA
ACCCCGCTCTCCAGAGCCTGCCGCGCCTTCAAGGGTTCGGGGCTCCACTTGGACGAGGCGCCGTGACTCTCCGAG
GCGCGCCGGGCCGACAGCGCTGTCCGCTACGTGGGCCACCTCTGGATGGGCCGGCGGCCGCCCTCCCCGAGGC
CCGCGGCCCAGTCCCCCGCAGTTCAGCTGCCAGTCGGGGCCAGAAGAAGCCTCGCCTCCCCGGGGATCTCCCCAGG
CCCCCTGACCGCAACGATCGGAGGGGCGGTGGCGGGGGCGGGGCCAGGCAGGGGAGGGCAGAAGCACACAAGGA
AGTGTTTTCCGGGACAGAGGGTGGGCAAGATGGCGGCGCCCATGGAGCTGTTCTGCTGGTCAGGGGGCTGGGGCT
GCCGTCAGTGGACCTGGACAGCCTGGCCGTGCTGACCTATGCCAGATTTACTGGTGCTCCACTGAAGGTACACAA
GATCAGCAACCCCTGGCAGAGCCCTTCAGGAACCTCTGCCTGCCCTTCGGACCAGTCATGGAGAGGTCATCTCAGT
TCCACACAAGATCATCACCCACCTTCGAAAAGAGGTACATACTTTTTGGATAGACACCAAGAACTACGTGGAAGT
GACCCGGAAGTGGTATGCAGAGGCTATGCCCTTTCCCTCAACTTCTTCCTGCCTGGCCGCATGCAGCGGCAGTA
CATGGAACGGCTACAGCTGCTGACTGGGGAGCACAGGCCTGAGGACGAGGAAGAGCTGGAGAAGGAGCTGTACCG
AGAGGCTCGGGAGTGTCTGACCCTGCTCTCTCAGCGCCTGGGCTCTCAAAAGTTCTTCTTTGGAGATGCCCCTGC
CTCCTTGGACGCCTTCGTCTTCAGCTACTTGGCCCTGCTGCTGCAGGCAAAGCTGCCCAGTGGGAAGCTGCAGGT
CCACCTGCGTGGGCTGCACAACCTCTGTGCCTATTGTACCCACATTCTCAGTCTCTACTTCCCCCTGGGATGGAGC
TGAGGTACCACCGCAACGCCAGACACCAGCAGGCCCAGAGACTGAGTGAGTGAGCCATACCGGCGCCGGAACCAG
ATCCTATCTGTGCTGGCAGTGAAGTGGCAGCCATGGTGGGCTACGCCTTGCTCAGCGGCATTGTCTCCATCCAGCG
GGCAACGCCTGCTCGTGGCCCCAGGCACCCGGACCTGGGCATGGCTGAGGAGGATGAAGAGGAATGATTTGTCC
TCACGCTCCCAAGACTGGTTTTTCTACTCTCATGCATTCCAGAGGCCCCCGTGCCTCCTCGTTGTTGGTACAGCC
GGACACGGGGTGTGCCACCCAGAATAAAGCCACTCACACTG

464/6881
FIGURE 433

GCCGGAAGCGCGCGGAGACCATGTAGTGAGACCCTCGCGAGGTCTGAGAGTCACTGGAGCTACCAGAAGCATCAT
GGGGCCCTGGGGAGAGCCAGAGCTCCTGGTGTGGCGCCCCGAGGCGGTAGCTTCAGAGCCTCCAGTGCCTGTGGG
GCTGGAGGTGAAGTTGGGGGCCCTGGTGCTGCTGCTGGTGCTCACCTCCTCTGCAGCCTGGTGCCCATCTGTGT
GCTGCGCCGCGCCAGGAGCTAACCATGAAGGCTCAGCTTCCCGCCAGAAAGCCCTGAGCCTAGTAAGCTGTTTCGC
GGGGGGCGTCTTTTTGGCCACTTGTCTCCTGGACCTGCTGCCTGACTACCTGGCTGCCATAGATGAGGCCCTGGC
AGCCTTGACGTGACGCTCCAGTTCCCACTGCAAGAGTTCATCCTGGCCATGGGCTTCTTCTGGTCTGTGGTGAT
GGAGCAGATCACACTGGCTTACAAGGAGCAGTCAGGGCCGTCACCTCTGGAGGAAACAAGGGCTCTGCTGGGAAC
AGTGAATGGTGGGCGCAGCATTGGCATGATGGGCCAGGGGTCCCACAGGCGAGTGGAGCCCCAGCAACCCCCCTC
AGCCTTGCGTGCCTGTGTACTGGTGTTCICCTGGCCCTCCACTCCGTGTTTCGAGGGGGCTGGCGGTAGGGCTGCA
GCGAGACCGGGCTCGGGCCATGGAGCTGTGCCTGGCTTTGCTGCTCCACAAGGGCATCCTGGCTGTGAGCCTGTG
CCTGCGGCTGTTGACAGAGCCACCTTAGGGCACAGGTGGTGGCTGGCTGTGGGATCCTCTTCTCATGCATGACACC
TCTAGGCATCGGGCTGGGTGCAGCTCTGGCAGAGTCGGCAGGACCTCTGCACCAGCTGGCCCAGTCTGTGCTAGA
GGGCATGGCAGCTGGCACCTTTCTCTATATCACCTTTCTGGAAATCCTGCCCCAGGAGCTGGCCAGTTCTGAGCA
AAGGATCCTCAAGGTCAATTCTGCTCCTAGCAGGCTTTGCCCTGCTCACTGGCCTGCTCTTCATCCAAATCTAGGG
GGCTTCAAGAGAGGGGCAGGGGAGATTGATGATCAGGTGCCCCCTGTTCTCCCTTCCCTCCCCAGTTGTGGGGAA
TAGGAAGGAAAGGGGAAGGGAAATACTGAGGACCAAAAAGTTCTCTGGGAGCTAAAGATAGAGCCTTTGGGGCTA
TCTGACTAATGAGAGGGAAGTGGGCAGACAAGAGGCTGGCCCCAGTCCCAAGGAACAAGAGATGGTCAAGTCGCT
AGAGACATATCAGGGGACATTAGGATTGGGGAAGACACTTGACTGCTAGAATCAGAGGTTGGACACTATACATAA
GGACAGGCTCACATGGGAGGCTGGAGGTGGGTACCCAGCTGCTGTGGAACGGGTATGGACAGGTCATAAACCTAG
AGTCAGTGTCTGTTGGTCCCTAGCCCCATTTACAGCACCTGCCACTTGGAGTGGACCCCTCCTACTCTTCTTAGCG
CCTACCCCTCATACCTATCTCCCTCCTCCCATCTCCTAGGGGACTGGCGCCAAATGGTCTCTCCCTGCCAATTTTG
GTATCTTCTCTGGCCTCTCCAGTCCTGCTTACTCCTCTATTTTTAAAGTGCCAAACAAATCCCCTTCTCTTTCT
CAAAGCACAGTAATGTGGCACTGAGCCCTACCCAGCACCTCAGTGAAGGGGGCCTGCTTGCTCTTTATTTTGGTC
CCGGATCCTGGGGTGGGGCAGAAATATTTCTGGGCTGGGGTAGGAGGAAGGTTGTTGCAGCCATCTACTGCTGC
TGTACCCTAGGAATATGGGGACATGGACATGGTGTCCCATGCCAGATGATAAACACTGAGCTGCCAAAACATTT
TTTTAAATACACCCGAGGAGCCCAAGGGGGAAGGGCAATGCCTACCCCCAGCGTTATTTTTGGGGAGGGAGGGCT
GTGCATAGGGACATATTCTTTAGAATCTATTTTATTAAGTACCTGTTTTGGGACCTGTTACCCAAATAAAAGAT
GTTTCTAG

465/6881
FIGURE 434

AGAAAGAAAAGGTGTAGTGTGTTTGGGGAGGTCAACGGGCTATGCTGGCTTGACAGGGCTGGGCTCTTCAGAACAGA
AGCATGGGATCTCGGAATCCCTGACCTGCTGGACGCGTGGCTGGAGCCCCAGAGGATATCTTCTCGACAGGATCC
GTCTGGAGCTGGGACTCCACTGCCCCCTCCAGAGGTTCCGGTAACTAGGCTACAGGAACAGGGACTGCAAGGC
TGGAAGTCCGGTGGGGACCGTGGCTGTGGCCTTCAAGAGAGTGAGCCTGAAGATTCTTGAAGCTTTTCATTGAT
CCCAATGAGGTGTACTGCTCAGAAGCATCTCCTGGCAGTGACAGTGGCATCTCTGAGGACCCCTGCCATCCAGAC
AGTCCCCCTGCCCCAGGGCAACCAGTTCTCCTATGCTCTATGAGGTTGTCTATGAGGCAGGGGCCCTGGAGAGG
ATGCAGGGGGAACTGGGCCAAATGTAGGCCTTATCTCCATCCAGCTAGATCAGTGGAGCCCAGCATTTATGGTG
CCTGATTCTGTCATGGTCAGTGAGCTGCCCTTTGATGCTCATGCCCACATCCTGCCCAGAGCAGGCACCGTAGCC
CCAGTGCCCTGTACAAACCCTGCTGCCCTGTCAAACCCTGTTCTGACCGATGAGGAGAAGCGTCTGCTGGGGCAG
GAAGGGGTTTTCCCTGCCCTCTCACCTGCCCTCACCAAGGCAGAGGAGAGGGTCCCTCAAGAAGGTCAGGAGGAAA
ATCCGTAAACAAGCAGTCAGCTCAGGACAGTCGGCGGCGGAAGAAGGAGTACATTGATGGGCTGGAGAGCAGGGTG
GCAGCCTGTTCTGCACAGAACCAAGAATTACAGAAAAAAGTCCAGGAGCTGGAGAGGCACAACATCTCCTTGGT
GCTCAGCTCCGCCAGCTGCAGACGCTAATTGCTCAAACCTTCCAACAAAGCTGCCCAGACCAGCACTTGTGTTTTG
ATTCTTCTTTTTTCCCTGGCTCTCATCATCCTGCCAGCTTCAGTCCATTCCAGAGTCGACCAGAAGCTGGGTCT
GAGGATTACCAGCCTCACGGAGTGACTTCCAGAAATATCCTGACCCACAAGGACGTAACAGAAAATCTGGAGACC
CAAGTGGTAGAGTCCAGACTGAGGGAGCCACCTGGAGCCAAGGATGCAAATGGCTCAACAAGGACACTGCTTGAG
AAGATGGGAGGGAAGCCAAGACCCAGTGGGCGCATCCGGTCCGTGCTGCATGCAGATGAGATGTGAGCTGGAACA
GACCTTCCTGGCCCACTTCCTGATCACAAGGAATCCTGGGCTTCCTTATGGCTTTGCTTCCCACTGGGATTCTTA
CTTAGGTGTCTGCCCTCAGGGGTCCAAATCACTTCAGGACACCCCCAAGAGATGTCCTTTAGTCTCTGCCTGAGGC
CTAGTCTGCATTTGTTTGATATATGAGAGGGTACCTCAAATACTTCTGTTATGTATCTGTGATTTTATTTCTTC
TTTGGGTATAGGGTTGAGGGGAAATAAGTTTTGAGTGAGAAATAAACGTTTTAGCTGAAATTGT

466/6881

FIGURE 435

MDLGIPDLLDAWLEPPEDIFSTGSVLELGLHCPPPEVPVTRLQEQGLQGWKSGGDRGCGLQESEPEDFLKLFIDP
NEVYCSEASPGSDSGISEDPCHPDSPPAPRATSSPMLYEVVYEAGALERMQGETGPNVGLISIQLDQWSPAFMVP
DSCMVSELPFDAHAILPRAGTVAPVPCTTLLPCQTLFLTDEEKRLLGQEGVSLPSHLPLTKAEERVLLKKVRRKI
RNKQSAQDSRRRKKEYIDGLESRVAACSAQNQELQKKVQELERHNISLVAQLRQLQTLIAQTSNKAQTSTCVLI
LLFSLALIILPSFSPFQSRPEAGSEDYQPHGVTSRNILTHKDV TENLETQVVESRLREPPGAKDANGSTRITLLEK
MGGKPRPSSGRIRSVLHADEM

467/6881
FIGURE 436

GCGAGGCGCCACCGACGCGGAAGACTATAAGCCCCAGCGGGCGACGACCGAACGCCCCCGGGAACACCGGGCCCC
GAGCTCGGTCCCCGCGCCCGAGGATCCTCCACGGGGCTAGATGGCTGCGTCGGGGGCGGGAGCGGAGGTGAGCGGG
CGCTAGGGCCGCGAGCCCCCGCGGCCCTTCCTCCAGCGCCCTGCGGACCCCGCAGAAGGCGCTCGCCTCCCTAG
CCCGCAAAACATATCGATTTTTCTCGCTGTGGCAACGGGGACGTCCTGATAGATCCTCTGCTCCAATAGGCAAC
TCCGGCCTTCCCTGCCCTGACCTGGAACCTCTGGGAGGGCTGCAGAGTAAGTGCCGCCTCTGCGCTCCGACGGAG
GCACGAGGCCTGTGGAGTAGGTCCCTCTGTTCCGACAGGTGCGACACTTGGCGCTCCATGCTTGCGGGTGCCGGG
AGGCCTGGCCTCCCCCAGGGCCGCCACCTCTGCTGGTTGCTCTGTGCTTTCACCTTAAAGCTCTGCCAAGCAGAG
GCTCCCGTGCAGGAAGAGAAGCTGTCAGCAAGCACCTCAAATTTGCCATGCTGGCTGGTGGAAGAGTTTGTGGTA
GCAGAAGAGTGCTCTCCATGCTCTAATTTCCGGGCTAAAACTACCCCTGAGTGTGGTCCCACAGGATATGTAGAG
AAAATCACATGCAGCTCATCTAAGAGAAATGAGTTCAAAAGCTGCCGCTCAGCTTTGATGGAACAACGCTTATTT
TGGAAGTTCGAAGGGGCTGTCTGTGTGTGGCCCTGATCTTCGCTTGCTTGTTCATCATTCGTCAGCGACAATTG
GACAGAAAGGCTCTGGAAGAGGTCCGGAAGCAAATCGAGTCCATATAGCTACATTCCACCCTTGTATCCTGGGTC
TTAGAGACCCTATCTCAGACAGTGAAAGTGAAATGGACTGATTTGCACTCTTGGTTCTTTGGAGCCTTGTGGTGG
AATCCCCTTTTCCCCTCTTCTTCTTTCAGATCATTAATGAGCAGAATAAAAAGAGTAAAATGGT

468/6881
FIGURE 437

MLAGAGRPGLPQGRHLCWLLCAFTLKLCQAEAPVQEEKLSASTSNLPCWLVEEFVVAEECSPCS NFRAKTTPECG
PTGYVEKITCSSSKRNEFKSCRSALMEQRLFWKFE GAVVCVALIFACLVIIRQRQLDRKALEKVRKQIESI

469/6881
FIGURE 438

GAATTCGAGGATCCGGGTACCATGGGAGGAAACTTCTTCTGGCCTGGGGCTCCGTGCCGCTCTGTTTGCCAACC
GTCCAGTCCCGCCTACCAGTGCCGGGCGCTCCCCACCCCTCCCCGGCTCCCCCGGTGTCCGCC**ATGG**CCAAAGC
CTACGACCACCTCTTCAAGTTGCTGCTGATCGGGGACTCGGGGGTGGGCAAGACTTGTCTGATCATTGCTTTGC
AGAGGACAACCTTCAACAACACTTACATCTCCACCATCGGAATTGATTTCAAGATCCGCACTGTGGATATAGAGGG
GAAGAAGATCAAAC TACAAGTCTGGGACACGGCTGGCCAAGAGCGGTTCAAGACAATAACTACTGCCTACTACCG
TGGAGCCATGGGCATTATCCTAGTATACGACATCACGGATGAGAAATCTTTCGAGAATATTCAGAACTGGATGAA
AAGCATCAAGGAGAATGCCTCGGCTGGGGTGGAGCGCCTCTTGCTGGGGAACAAATGTGACATGGAGGCCAAGAG
GAAGGTGCAGAAGGAGCAGGCCGATAAGTTGGCTCGAGAGCATGGAATCCGATTTTTTCGAAACTAGTGCTAAATC
CAGTATGAATGTGGATGAGGCTTTTAGTTCCCTGGCCCGGGACATCTTGCTCAAGTCAGGAGGCCGGAGATCAGG
AAACGGCAACAAGCCTCCCACTACTGACCTGAAAACCTTGTGACAAGAAGAACCAACAAGTGCTCCCTGGGC**TG**
AGGACCCTTTCTTGCTCCCCACCCCGGAAGCTGAACCTGAGGGAGACAACGGCAGAGGGAGTGAGCAGGGGAGA
AATAGCAGAGGGGCTTGGAGGGTCACATAGGTAGATGGTAAAGAGAATGAGGAGAAAAAGGAGAAAAGGGAAAAG
CAGAAAGGAAAAAAAGGAAGAGAGAGGAAGGGAGAAGGGAGAGGAATGAATTGAGGAAGTGAAAGAAGGCAAGGA
GGTAGGAAGAGAGGGAGGAGGAAAGGAAGGAGAGAGATGCCTCAGGCTTCAGACCTTACCTGGGTTTTTCAGGGCA
AACATAAATGTAAATACACTGATTTATTCTGTTACTAGATCAGGTTTTAGGGTCCTGCAAAAGGCTAGCTCGGCA
CTACACTAGGGAATTTGCTCCTGTTCTGTCACTTGTGCATGGTCTTTCTTGGTATTAAAGGCCACCATTTGCACAA
AAAAAAAAAAAAAACCATGGTACCCGATCCTCGAATTC

470/6881
FIGURE 439

MAKAYDHLFKLLLLIGDSGVGKTCLIIIRFAEDNFNNTYISTIGIDFKIRTVDIEGKKIKLQVWDTAGQERFKTITT
AyyRGAMGIILVYDITDEKSFENIQNWMKSIKENASAGVERLLLGNKCDMEAKRKVQKEQADKLAREHGIRFFET
SAKSSMNVDFAFSSLARDILLKSGGRRSGNGNKPPSTD LKTCDDKNTNKCSLG

471/6881
FIGURE 440

CCTTTCCGGCGGTGACGACCTACGCACACGAGAACATGCCTCTCGCAAAGGATCTCCTTCATCCCTCTCCAGAAG
AGGAGAAGAGGAAACACAAGAAGAAACGCCTGGTGCAGAGCCCCAATTCCTACTTCATGGATGTGAAATGCCCAG
GATGCTATAAAATCACCACGGTCTTTAGCCATGCACAAACGGTAGTTTTGTGTGTTGGCTGCTCCACTGTCCTCT
GCCAGCCTACAGGAGGAAAAGCAAGGCTTACAGAAGGATGTTCCCTTCAGGAGGAAGCAGCACTTAAAAGCACTCTG
AGTCAAGATGAGTGGGAAACCATCTCAATAAACACATTTTGGAT

472/6881
FIGURE 441

MPLAKDLLHPSPEEEKRKHKKKRLVQSPNSYFMDVKCPGCIKITTTFSHAQTVVLCVGCSTVLCQPTGGKARLTE
GCSFRRKQH

473/6881
FIGURE 442

ACTCAGGCAGCAGCCCCCTTCTTTCTTGCCCCAGTCTCCAGTTCTCCAGTGTTTCACAGGTGAGCCTACCAACAGCC
ACTGCTCATGATGGAGGCCATCAAGAAAAAGATGCAGATGCTGAAGTTAGACAAGGAGAATGCTCTGGATCGGGC
AGAGCAAGCTGAAGCTGAGCAGAAGCAGGCAGAAGAAAGAAGTAAACAGCTGGAGGATGAGCTGGCAGCCATGCA
GAAGAAGCTGAAAGGGACAGAGGATGAGCTGGACAAGTATTCTGAAGCTTTGAAGGATGCCCAGGAGAAGCTGGA
ACTGGCAGAGAAGAAGGCTGCTGATGCTGAGGCTGAGGTGGCCTCCTTGAACCGTAGGATCCAGCTGGTTGAAGA
AGAGCTGGACCGTGCTCAGGAGCGCCTGGCCACTGCCCTGCAAAAGCTGGAAGAAGCTGAAAAAGCTGCTGATGA
GAGTGAGAGAGGTATGAAGGTTATTGAAAACCGGGCCTTAAAAGATGAAGAAAAGATGGAATCCAGGAAATCCA
ACTCAAAGAAGCTAAGCACATTGCAGAAGAGGCAGATAGGAAGTATGAAGAGGTGGCTCGTAAGTTGGTGATCAT
TGAAGGAGACTTGGAACGCACAGAGGAACGAGCTGAGCTGGCAGAGTCTAAGTGTTCTGAGCTGGAGGAGGAGCT
GAAGAATGTCACCAACAACCTCAAGTCTCTTGAGGCTCAGGCGGAGAAGTACTCTCAAAAAGAAGATAAATATGA
GGAAGAAATCAAGATTCTTACTGATAAACTCAAGGAGGCAGAGACCCGTGCTGAGTTTGCTGAGAGATCGGTAGC
CAAGCTGGAAAAAGACAATTGATGACCTGGAAGATGAGCTCTATGCCAGAACTGAAGTACAAGGCCATTAGCGA
GGAGCTGGACCACGCCCTCAATGACATGACCTCTATATTAAATTATCACCGTTTCTGCTCTGTTCTGGATCTGCCCC
CTTTACTCCTCGGGGAACCCAAGGCCCACTCTCGCTCTGGATTCCATTGGGTGAGCCTGGCTGGTCCCCAAGG
CATTAGGATGGGGGAGCAAAAAGCAACTTATGTATTTTCTTCCACCCCCACCCCAAATTAATAATGTTAAGCTGCT
GGA

474/6881
FIGURE 443

MMEAIIKKKMQLKLDKENALDRAEQAEAEQKQAEERSKQLEDELAAMQKKLKGTEDELDKYSEALKDAQEKELELA
EKKAADAEAEVASLNRRIQLVEEELDRAQERLATALQKLEEAEKAADESERGMKVIENTRALKDEEKMELQEIQLK
EAKHIAEEADRKYEEVARKLVIIIEGDLERTEERAELAESKCSLEEEELKNVTNNLKSLEAQAEKYSQKEDKYEEE
IKILTDLKLEAETRAEFAERSVAKLEKTIDDLLEDELYAQKLKYKAISEELDHALNDMTSI

475/6881
FIGURE 444

GTCAGCGGGGAAGCTGGAAGGCGTCGTTCTCCTTTCCCAGCTCTCCTGCCTGTCCGCCATGTTTTCAGGCCGGGT
CTGGCTTGGTCTTCCCCCGTAAGGAAATGGCCGGGGAGCTCCAGGGGACCCAGGCGCCGTCGCTTCGGCGGAGCT
GGGCTGACCAGCCAGGACAGCGGGGTAAACCCGAACAATTCTGCGCGAGGTAGGGAGGCCATGGCGTCCGGCAGT
AACTGGCTCTCCGGGGTGAATGTCGTGCTGGTGATGGCCTACGGGAGCCTGGACTTGAAAGAGGAGATTGATATT
CGACTCTCCAGGGTTCAGGATATCAAGTATGAGCCCCAGCTCCTTGAGATGATGATGCTAGACTACTACAAGT
GAAACCCAGGGAAATCAAAGTTGCTACAAGTATCTGTATAGGATGAAAGCTCTGGATGCCATTTCGTACCTCTGAG
ATCCCATTTTCAATTCTGAAGGCCGGCATCCCCGTTCTTAATGGGCAAGAATTTCCGCTCCTACCTGCTGGATCTG
CGAAACACTAGTACGCCCTTCAAGGGTGTACGCAAAGCACTCATTGATACCCTTTTGATGGCTATGAAACAGCC
CGCTATGGGACAGGGGTCTTTGGCCAGAATGAGTACCTACGCTATCAGGAGGCCCTGAGTGAGCTGGCCACTGCG
GTTAAAGCACGAATTGGGAGCTCTCAGCGACATCACCAGTCAGCAGCCAAAGACCTAACTCAGTCCCCTGAGGTC
TCCCCAACAAACCATCCAGGTGACATACCTCCCCTCCAGTCAGAAGAGTAAACGTGCCAAGCACTTCCTTGAATTG
AAGAGCTTTAAGGATAACTATAACACATTGGAGAGTACTCTGTGACGGAGCTGAAGGACTCTTGCCGTAGATTAA
GCCAGTCAGTTGCAATGTGCAAGACAGGCTGCTTGCCGGGGCCGCCCTCGGAACATCTGGCCCAGCAGGCCAGAC
TGTATCCATCCAAGTTCCCGTTGTATCCAGAGTTCTTAGAGCTTGTGTCTAAAGGGTAATTTCCCCAACCCCTTCCT
TATGAGCATTTTTTAGAACATTGGCTAAGACTATTTTTCCCCAGTAGCGCTTTTTTCTGGATTTGCATTCGGGTGT
TATTCTTAATGTTTCTGTCAAAGCTTCTTAAAAATCTTCACTTGGTTTCAGCCATAGTTACCTTCCCTGTTCCA
GGTTTATTTAATTCCAAAGGTGAGAGTTGGAGTGAGATGTCTTCCATATCTATACCTTTGTGCACAGTTGAATGG
GAAGTGTGGGTTTAGGGCATCTTAGAGTTGATTGATGGAAAAAGCAGACAGGAAGTGGTGGGAGGTCAAGTGG
GGAAGTTGGTGAATGTGAATAACTTACCTTTGTGCTCCACTTAAACCAGATGTGTTGCAGCTTTCTGACATGC
AAGGATCTACTTTAATTCCACACTCTCATTATAAATGAATAAAAGGGAATGTTTTGGCACCTGATATAATCTG
CCAGGCTATGTGACAGTAGGAAGGAATGGTTTCCCCTAACAAAGCCCAATGCACTGGTCTGACTTTATAAATTATT
TAATAAAATGAAGTATTATCAAATAAAACGTATGAATCAGTAAAAAAAAAAAAAAAAAAAAA

476/6881
FIGURE 445

MASGSNWLSGVNVVLVMAYGSLDLKEEIDIRLSRVQDIKYEPQLLADDDARLLQLLETQGNQSCYNYLYRMKALDA
IRTSEIPFHSEGRHPRSLMGKNFRSYLLDLRNTSTPFKGVRKALIDTLDDGYETARYGTGVFGQNEYLRQEALS
ELATAVKARIGSSQRHHQSAAKDLTQSPEVSPTTIQVTYLPSSQSKRAKHFLELKSFKDNyntLESTL

477/6881
FIGURE 446

CCCGACTAAGTGACTTAAACTCCCACCTACTCCTGGAATAAGGAGTCAAAGCCCGGATAGGCGCAGTATTCTACC
TTGTAAATACTGTTATTTGTATATACTGTAAATGATGACATCGGTGGGCACTAACCGAGCCCGGGGAAACTGGGA
ACAACCTCAAAACCAAAACCAGACACAGCACAAGCAGCGGCCACAGGCCACTGCAGAACAAATTAGACTTGCACA
GATGATTTTCGGACCATAATGATGCTGACTTTGAGGAGAAGGTGAAACAATTGATTGATATTACAGGCAAGAACCA
GGATGAATGTGTGATTGCTTTGCATGACTGCAATGGAGATGTCAACAGAGCTATCAATGTTCTTCTGGAAGGAAA
CCCAGACACGCATTCTGCGGAGATGGTCGGGAAGAAGAAGGGAGTCTCAGGCCAGAAGGATGGTGGCCAGACGGA
ATCCAATGAGGAAGGCAAAGAAAATCGAGACCGGGACAGAGACTATAGTCGGCGACGTGGTGGGCCACCAAGACG
GGGGAGAGGTGCCAGCCGTGGACGAGAGTTTCGAGGTTCAGGAAAATGGATTGGATGGCACCAAGAGTGGAGGGCC
TTCTGGAAGAGGAACAGAAAGAGGCAGAAAGGGGCCGTGGCCGAGGCAGAGGTGGCTCTGGTAGGCGAGGAGGAAG
GTTTTCTGCTCAAGGAATGGGAACCTTTAACCAGCTGATTATGCAGAGCCAGCCAATACTGATGATAACTATGG
CAATAGCAGCGGCAATACGTGGAACAACACTGGCCACTTTGAACCAGATGATGGGACGAGTGCATGGAGGACTGC
AACAGAGGAGTGGGGGACTGAAGATTGGAATGAAGATCTTTCTGAGACCAAGATCTTCACTGCCTCTAATGTGTC
TTCAGTGCTCTGCCTGCGGAGAATGTGACAATCACTGCTGGTCAGAGAATTGACCTTGCTGTTCTGCTGGGGAA
GACACCATCTACAATGGAGAATGATTCATCTAATCTGGATCCGTCTCAGGCTCCTTCTCTGGCCCAGCCTCTGGT
GTTCAAGTAATTCGAAGCAGACTGCCATATCACAGCCTGCTTCAGGGAACACATTTTCTCATCACAGTATGGTGAG
CATGTTAGGGAAAGGATTTGGTGATGTCGGTGAAGCTAAAGGCGGCAGTACTACAGGCTCCCACTTCTTGGAGCA
ATTCAAGACTGCCCAAGCCCTGGCTCAGTTGGCAGCTCAGCATTCTCAGTCTGGAAGCACCACCACCTCCTCTTG
GGACATGGGCTCGACGACACAATCCCCATCACTGGTGCAGTATGATTTGAAGAACCCAAGTGATTACAGCAGTGCA
CAGCCCCCTTACAAAGCGCCAGGCTTTTACCCCATCTTCAACCATGATGGAGGTGTTCTTCAGGAGAAGTCACC
TGCAGTGGCTACCTCCACAGCTGCACCTCCACCTCCGTCTTCTCCTCTGCCAAGCAAATCCACATCGGCTCCACA
GATGTCGCCTGGATCTTCAGACAACCAGTCTCTAGCCCTCAGCCGGCTCAGCAGAACTGAAACAGCAGAAGAA
AAAAGCCTCCTTGACTTCTAAGATTCTGCTCTGGCTGTGGAGATGCCTGGCTCAGCAGATATCTCAGGGCTAAA
CCTGCAGTTTGGGGCATTGCAGTTTGGGTGAGAGCCTGTCTTTCTGATTATGAGTCCACCCCCACCACGAGCGC
CTCTTCAAGCCAGGCTCCAAGTAGCCTGTATACCAGCACGGCCAGTGAATCATCTCTACAATTTTCATCTAACCA
GAGTCAGGAGTCTGGTTATCAGAGCGGCCCAATTAGTCGACAACCTATACCTCCCAAATAATGCTCAGGGCCC
TCTTTATGAACAGAGATCCACACAGACTCGGCGGTACCCAGCTCCATCTCTTCATCACCCCCAAAAGGACCTGAC
TCAGGCAAAGAATGGCTTCAGTTCTGTGCAAGCCACGCAGTTACAGACCACACAATCTGTTGAAGGTGCTACAGG
CTCTGCAGTGAATCTGATTCACCTTCCACTTCTAGCATCCCCCTCTCAATGAAACGGTATCTGCAGCTTCTCTT
ACTGACGACAACCAATCAGCATTTCATCTCTCTGGGTGGCTTGAGCCACAGTGAGGAGATTCCAAATACTACCAC
CACACAACACAGCAGCACGTTATCTACGCAGCAGAATACCCTTTTCATCATCAACATCTTCTGGGCGCACTTCGAC
ATCCACTCTTTTGCACACAAGTGTGGAGAGTGAGGCGAATCTCCATTCTTCTCCAGCACTTTTTCCACCACATC
CAGCACAGTCTCTGCACCTCCCCCAGTGGTCACTGTCTCTCTCCAGTCTCAATAGTGGCAGTAGCCTGGGCCTCAG
CCTAGGCAGCAACTCCACTGTACAGCCTCGACTCGAAGCTCAGTTGCTACGACTTCAGGAAAAGCTCCTCCCAA
CCTCCCTCCTGGGGTCCCGCCGTGTTGCCTAATCCGTATATTATGGCTCCAGGGCTGTTACATGCCTACCCGCC
ACAAGTATATGGTTATGATGACTTGACAGATGCTTCAGACAAGATTTCCATTGGATTACTACAGCATCCCATTTCC
CACACCCACTACTCCGCTGACTGGGAGGGATGGTAGCCTGGCCAGCAACCCCTATTCTGGTGACCTCACAAAGTT
CGGCCGTGGGGATGCCTCCTCCCCAGCCCCGCCACAACCTTGGCCCAACCCCAACAGAACCAGACGCAGACTCA
CCATACCACGCAGCAGACATTCCTGAACCCGGCGCTGCCTCCTGGCTACAGTTACACCAGCCTGCCATACTATAC
AGGGGTCCCGGGCTCCCCAGCACCTTCCAGTATGGGCCTGCTGTGTTCCCTGTGGCTCCTACCTCTTCCAAGCA
GCATGGTGTGAATGTGAGTGTGAATGCATCGGCCACCCCTTTCCAACAGCCGAGTGGATATGGGTCTCATGGATA
CAACACTGGAAGAAAATATCCACCCCTTACAAGCATTTCTGGACGGCTGAGAGCTAAATTTGGCCCAAGGCTGGG
GGCTGTGTTTTGTGTGTGTGTATAAATTTGCACTGAAGTCTTGTTCAGAAACCAGACCACTGAGGAGAGCCTGC
TGAGCTGAGGCCATGGCCTGCGTGGCTTGGGGAAATGAGTTGGTGGATACCTTCTGGGCTTTTGAACCTTGCCCT
CCCCCATTTCCCTCTCCCCATGTGCTGACCCTGTCTTACCCATTTCAAGTTCAAGCGGTGCAGCACCTTCGAA
GCATCAATGCACACACCTGCTGTTGCTTTTGATTCTGGAAGGCATGTAGTTTCAACTTGTAAACAAAATATTTG
TAGTCTTCAATAAACTGTGGTATTTCTTTAGCTAAC

478/6881
FIGURE 447

MMTSVGTNRARGNWEQPQNQNQTQHKQRPQATAEQIRLAQMISDHNDADFEKVKQLIDITGKNQDECVIALHDC
NGDVNRRAINVLLEGNPDTHSWEMVGKKKGVSGQKDGGQTESNEEGKENRDRDRDYSRRRGPPRRGRGASRGREF
RGQENGLDGTKSGGPSGRGTERGRRGRGRGRGGSGRRGGRFSAQGMGTFPADYAEPANTDDNYGNSSGNTWNNT
GHFEPDDGTSAWRTATEEWGTEDWNEDLSETKIFTASNVSSVPLPAENVTTITAGQRIDLAVLLGKTPSTMENDSS
NLDPSQAPSLAQPLVFSNSKQT AISQPASGNTFSHHSMVSM LGKGFGDVGEAKGGSTTGSQFLEQFKTAQALAQL
AAQHSQSGSTTTSSWDMGSTTQSPSLVQYDLKNP SDSAVHSPFTKRQAFTPSSTMMEVFLQEKSPAVATSTAAPP
PPSSPLPSKST SAPQMSPGSSDNQSSSPQPAQQKLKQKKKASLT SKIPALAVEMPGSADISGLNLQFGALQFGS
EPVLSDYESTPTTSASSSQAPSSLYTSTASESSSTISSNQSQESGYQSGPIQSTTYTSQNNAQGPLYEQRSTQTR
RYPSSISSSPQKDLTQAKNGFSSVQATQLQTTQSVEGATGSAVKSDSPSTSSIPPLNETVSAASLLTTTNQHSSS
LGGLSHSEEIPNTTTTQHSSTLSTQQNTLSSSTSSGRTSTSTLLHTSVESEANLHSSSSSTFSTTSSTVSAPPPVV
SVSSSLNSGSSLGLSLGSNSTVTASTRSSVATTSGKAPPNLPFGVPELLPNPYIMAPGLLHAYPPQVYGYDDLQM
LQTRFPLDYYSIPFPTPTTPLTGRDGSLASNYPYSGDLTKFGRGDASSPAPATTLAQPQQNQTQTHHTTQQTFLNP
ALPPGYSYTSLPYYTGVPGLPSTFQYGPVFPVAPTSSKQHGVNVSVNASATPFQQPSGYGSHGYNTGRKYPPPY
KHFWTAES

479/6881
FIGURE 448

CCTACAGAGGGGTCCATACCGTGTGTTCTGGATTCCCGTTGTAACCTAAAGGGAAATTTTCACAATGTCCAGAG
CCCTTGATGTCCTGCAAATGAAGGAGGAGGATGTCCTTAAGTTCCTTGCAGCAGGAACCCACTTAGGTGGCACTA
ATCTTGACTTCCAGATGGAACAGTACATCTATAAAAGGAAAAGTGATGGCATCTACATCATAAATCTGAAGAGGA
CCTGGGAGAAGCTTCTGCTGGCAGCTCGTGCCATTGTTGCCATTGAAAACCCTGCTGATGTCAGTGTTATATCCT
CCAGGAATACTGGCCAGAGGGCCATGCTGAAGTTTGCTGCTGCCACTGGAGCCACTCCAATTGCTGGCCACTTCA
CTCCTGGAACCTTCACTAACCGGATCCAGGCAGCCTCCGGGAGCCACAGCTTCCTGTGGTTACTGACCCAGGG
CTGACCACCAGCCTCTCACGGAGGTATCTTATGTTAACTTACCTACCATTGCGCTGTGTAACACAGATTCTCCTC
TGCGCTATGTGGACATTGCCATCCCATGCAACAATAAGGGAGCTCACTCAGTGGGTTGGATGTGGTGGATGCTGG
CTCAGGAAGTTCTGCGCATGCGTGGCACCATTTCCTGTAACACCCATGGGAGGTCATGCCTGATCTCTGCTTCT
ACAGAGATCCTGAAGAGATTGAAAAAGAAGAGCAGGCTGCTGCTGAAGAGGCAGTGACCAAGGAGGAATTTCAGG
GTGAATGGACTGCTCCAGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAGACTGGTCTGAAGGTCTGCAGG
TGCCCTCTGTGTCTATTAGTAGTTCCCTACTGAAGACTGGAGCGCTCAGCCTGCCACGGAAGACTGGTCTGCAG
CTCCCACTGCTCAGGCCACTGAATGGGTAGGAGCAACCACTGAATGGTCTTAAGCTGTTCTTGCATGGGCTCTTA
AGCAACATGGAAAAATGGTTGATGGAAAATAAATAAACATCAGTTTCT

480/6881
FIGURE 449

MSRALDVLQMKEEDVLKFLAAGTHLGGTNLDFQMEQYIYKRKSDGIYIINLKRTWEKLLLAARAIVAIENPADVS
VISSRNTGQRAMLKFAAATGATPIAGHFTP GTFTNRIQAAFREPQLPVVTDPRADHQPLTEVS YVNLPTIALCNT
DSPLRYVDIAIPCNNKGAHSGVMMWMLAQEVLRMRTISREHPWEVMPDLCFYRDPEEIEKEEQAAAEAEVTK
EFQGEWTAPAPEFTATQPEVADWSEGLQVPSVSIQSSLLKTGALS LPRKTGLQLPLLRPLNGVGATTEWS

481/6881
FIGURE 450A

CGAAATTGAACCGGAGCCATCTTGGGCCCGGCGCGCAGACCCGCGGAGTTTCCCGTGCCGACGCCCCGGGGCCAC
TTCCAGTGCGGAGTAGCGGAGGCGTGGGGGCCTCGAGGGGCTGGCGCGGCCACGGTCGGGGCCAGGGTCTGTGCC
GCCGGCGGGTTCGGGCCGGGCAATGCCTCGCGGGCGCAATGAATCCGCGGCAGGGGTATTCCCTCAGCGGATACTA
CACCCATCCATTTCAAGGCTATGAGCACAGACAGCTCAGGTACCAGCAGCCTGGGCCAGGATCTTCCCCCAGTAG
TTTCCTGCTTAAGCAAATAGAATTTCTCAAGGGGCAGCTCCCAGAAAGCACCGGTGATTGGAAAGCAGACACCGTC
ACTGCCACCTTCCCTCCCAGGACTCCGGCCAAGGTTTCCAGTACTACTTGCCCTCCAGTACCAGAGGCAGGCAAGT
GGACATCAGGGGTGTCCCCAGGGGCGTGCATCTCAGAAAGTCAGGGGCTCCAGAGAGGGTTCCAGCATCCTTCACC
ACGTGGCAGGAGTCTGCCACAGAGAGGTGTTGATTGCCTTTCCCTCACATTTCCAGGAAGTGTATCTACCAAGA
TCAGGAACAAAGGATCTTAAAGTTCCTGGAAGAGCTTGGGGAAGGGAAGGCCACCACAGCACATGATCTGTCTGG
GAAACTTGGGACTCCGAAGAAAGAAATCAATCGAGTTTATACTCCCTGGCAAAGAAGGGCAAGCTACAGAAAGA
GGCAGGAACACCCCCCTTTGTGGAAAATCGCGGTCTCCACTCAGGCTTGGAACCAGCACAGCGGAGTGGTAAGACC
AGACGGTCATAGCCAAGGAGCCCCAAACTCAGACCCGAGTTTGGAACCGGAAGACAGAAACTCCACATCTGTCTC
AGAAGATCTTCTTGAGCCTTTTATTGTCAGTCTCAGCTCAGGCTTGGAACCAGCACAGCGGAGTGGTAAGACCAGA
CAGTCATAGCCAAGGATCCCCAAACTCAGACCCAGGTTTGGAACCTGAAGACAGCAACTCCACATCTGCCTTGGA
AGATCCTCTTGAGTTTTTAGACATGGCCGAGATCAAGGAGAAAATCTGCGACTATCTCTTCAATGTGTCTGACTC
CTCTGCCCTGAATTTGGCTAAAAATATTGGCCTTACCAAGGCCGAGATATAAATGCTGTGTCTAATTGACATGGA
AAGGCAGGGGGATGTCTATAGACAAGGGACAACCCCTCCCATATGGCATTGACAGACAAGAAGCGAGAGAGGAT
GCAAATCAAGAGAAATACGAACAGTGTTCCTGAAACCGCTCCAGCTGCAATCCCTGAGACCAAAGAAACGCAGA
GTTCTCTACCTGTAATATACCCACATCAAATGCCTCAAATAACATGGTAACCACAGAAAAAGTGGAGAATGGGCA
GGAACCTGTCTATAAAGTTAGAAAACAGGCAAGAGGCCAGACCAGAACCAGCAAGACTGAAACCACCTGTTTCTTA
CAATGGCCCCCTCAAAGCAGGGTATGTTGACTTTGAAAATGGCCAGTGGGCCACAGATGACATCCCAGATGACTT
GAATAGTATCCGCGCAGCACCAGGTGAGTTTCGAGCCATCATGGAGATGCCCTCCTTCTACAGTCATGGCTTGCC
ACGGTGTTCACCCCTACAAGAACTGACAGAGTGCCAGCTGAAGAACCCCATCAGCGGGCTGTTAGAATATGCCCA
GTTTCGCTAGTCAAACCTGTGAGTTCAACATGATAGAGCAGAGTGGACCACCCCATGAACCTCGATTTAAATTC
GGTTGTCTCAATGGCCGAGAGTTTCCCCCAGCTGAAGCTGGAAGCAAGAAAGTGGCCAAGCAGGATGCAGCTAT
GAAAGCCATGACAATTCTGTCTAGAGGAAGCCAAAGCCAAGGACAGTGGAAAATCAGAAGAATCATCCCACTATTC
CACAGAGAAAGAATCAGAGAAGACTGCAGAGTCCCAGACCCCCACCCCTTCAGCCACATCCTTCTTTTCTGGGAA
GAGCCCCGTACCCACACTGCTTGAGTGTATGCACAAATTGGGGAACTCCTGCGAATTCCGTCTCCTGTCCAAAGA
AGGCCCTGCCCATGAACCCAAGTTCCAATACTGTGTTGCAGTGGGAGCCCCAAACTTTCCCCAGTGTGAGTGCTCC
CAGCAAGAAAGTGGCAAAGCAGATGGCCGAGAGGAAGCCATGAAGGCCCTGCATGGGGAGGCGACCAACTCCAT
GGCTTCTGATAACCAGCCTGAAGGTATGATCTCAGAGTCACTTGATAACTTGGAATCCATGATGCCCAACAAGGT
CAGGAAGATTGGCGAGCTCGTGAGATACCTGAACACCAACCCCTGTGGGTGGCCTTTTGGAGTACGCCCCGTCCCA
TGGCTTTGCTGTCTGAATTCAAGTTGGTTCGACCAGTCCGGACCTCCTCAGAGCCCAAGTTCTGTTTACCAAGCAAA
AGTTGGGGGTCTGCTGGTTCCAGCCGTCTGCGCACACAGCAAGAAGCAAGGCAAGCAGGAAGCAGCAGATGCGGC
TCTCCGTGTCTTGATTGGGGAGAACGAGAAGGCAGAACGCATGGGTTTCACAGAGGTAACCCAGTGACAGGGGC
CAGTCTCAGAAGAACTATGCTCCTCCTCTCAAGGTCCCCAGAACACAGCCAAAGACACTCCCTCTCACTGGCAG
CACCTTCCATGACCAGATAGCCATGCTGAGCCACCGGTGCTTCAACACTCTGACTAACAGCTTCCAGCCCTCCTT
GCTCGGCCGCAAGATTCTGGCCGCCATCATTATGAAAAAAGACTCTGAGGACATGGGTGTCTGTCGTCTGAGCTTGGG
AACAGGGAATCGCTGTGTGAAAGGAGATTCTCTCAGCCTAAAAGGAGAACTGTCAATGACTGCCATGCAGAAAT
AATCTCCCGGAGAGGCTTCATCAGGTTTCTCTACAGTGAGTTAATGAAATACAACCTCCAGACTGCGAAGGATAG
TATATTTGAACCTGCTAAGGGAGGAGAAAAGCTCCAAATAAAAAAGACTGTGTCAATCCATCTGTATATCAGCAC
TGCTCCGTGTGGAGATGGCGCCCTCTTTGACAAGTCCTGCAGCGACCGTGCTATGGAAAGCACAGAATCCCGCCA
CTACCCTGTCTTCGAGAATCCCAAACAAGGAAAGCTCCGCACCAAGGTGGAGAACGGAGAAGGCACAATCCCTGT
GGAATCCAGTGACATTGTGCCTACGTGGGATGGCATTTCGGCTCGGGGAGAGACTCCGTACCATGTCTGTAGTGA
CAAAATCCTACGCTGGAACGTGCTGGGCCTGCAAGGGGCACTGTTGACCCACTTCTGCAGCCCATTATCTCAA
ATCTGTCTACATTGGGTTACCTTTTTCAGCCAAGGGCATCTGACCCGTGCTATTTGCTGTCTGTGACAAGAGATGG
GAGTGCATTTGAGGATGGACTACGACATCCCTTTATTGTCAACCACCCCAAGGTTGGCAGAGTCAGCATATATGA
TTCCAAAAGGCAATCCGGGAAGACTAAGGAGACAAGCGTCAACTGGTGTCTGGCTGATGGCTATGACCTGGAGAT

482/6881
FIGURE 450B

CCTGGACGGTACCAGAGGCACTGTGGATGGGCCACGGAATGAATTGTCCCGGGTCTCCAAAAAGAACATTTTTCT
TCTATTTAAGAAGCTCTGCTCCTTCCGTTACCGCAGGGATCTACTGAGACTCTCCTATGGTGAGGCCAAGAAAGC
TGCCCGTGACTACGAGACGGCCAAGAATACTTTCAAAAAAGGCCTGAAGGATATGGGCTATGGGAACTGGATTAG
CAAACCCCAGGAGGAAAAAGAACTTTTATCTCTGCCCAGTATAGTATGCTCCAGTGACAGATGGATTAGGGTGTGT
CATACTAGGGTGTGAGAGAGGTAGGTCGTAGCATTCTCATCATGGTCAGGGGATTTTTTTTTTCTCCTTTTTT
TTTCTTTTTAAGCCATAATTGGTGATACTGAAAACCTTTGGGTTCCCATTTATCCTGCTTTCTTTGGGATTGCTAG
GCAAGGTCTGGCCAGGCCCCCTTTTTTCCCCCAAGTGAAGAGGCAGAAACCTAAGAAGTTATCTTTTCTTTCTA
CCCAAAGCATACATAGTCACTGAGCACCTGCGGTCCATTTCTCTTAAAAAGTTTTGTTTTGATTTGTTTCCATTT
CCTTTCCCTTTGTGTTTGCTACACTGACCTCTTGCGGTCTTGATTAGGTTTCAGTCAACTCTGGATCATGTCAGG
GACTGATAATTTCAATTTGTGGATTACGCAGACCCCTCTACTTTCCCTCTTTCCCTTCTGAGATTCTTTCTTTGTG
ATCTGAATGTCTCCTTTTTCCCCCTCAGAGGGCAAAGAGGTGAACATAAAGGATTTGGTGAAACATTTGTAAGGGT
AGGAGTTGAAAACCTGCAGTTCCCAAGTGCCACGGAAGTGTGATTGGAGCCTGCAGATAATGCCAGCCATCCTCCC
ATCCTGCACTTTAGCCAGCTGCAGGGCGGGCAAGGCAAGGAAAGCTGCTTCCCTGGAAGTGTATCACTTTCTCCG
GCAGCTGGGAAGTCTAGAACCAGCCAGACTGGGTAAAGGGAGCTGCTCAAGCAATAGCAGAGGTTTACCCGGCA
GGATGACACAGACCACTTCCAGGGAGCACGGGCATGCCTTGGAATATTGCCAAGCTTCCAGCTGCCTCTTCTCC
TAAAGCATTCTAGGAATATTTTCCCCGCCAATGCTGGGCGTACACCCTAGCCAACGGGACAAATCCTAGAGGGT
ATAAAATCATCTCTGCTCAGATAATCATGACTTAGCAAGAATAAGGGCAAAAAATCCTGTTGGCTTAACGTCCT
GTTCCACCCGGTGTAAATATCTCTCATGACAGTGACACCAAGGGAAGTTGACTAAGTCACATGTAAATTAGGAGTG
TTTTAAAGAATGCCATAGATGTTGATTCTTAACTGCTACAGATAACCTGTAATTGAGCAGATTTAAATTCAGGC
ATACTTTTCCATTTATCCAAGTGCTTTCAATTTTCCAGATGGCTTCAGAAGTAGGCTCGTGGGCAGGGCGCAGAC
CTGATCTTTATAGGGTTGACATAGAAAGCAGTAGTTGTGGGTGAAAGGGCAGGTTGTCTTCAAACTCTGTGAGGT
AGAATCCTTTGTCTATACCTCCATGAACATTGACTCGTGTGTTTCAGAGCCTTTGGCCTCTCTGTGGAGTCTGGCT
CTCTGGCTCCTGTGCATTCTTTGAATAGTCACTCGTAAAACTGTGAGTCTTGAAGTGTCTTCTTTACTCATG
TTGAAGGGACTTTGTTGGCTTTTAGAGTGTGGTTCATGACTCCAAGAGCAGAGCAGGGAAGAGCCCAAGCATAGA
CTTGGTGCCGTGGTGATGGCTGCAGTCCAGTTTTGTGATGCTGCTTTTACGTGTCCCTCGATAACAGTCAGCTAG
ACACACTCAGGAGGACTACTGAGGCTCTGCGACCTTCAGGAGCTGAGCCTGCCTCTCTCCTTTAGATGACAGACC
TTCATCTGGGAACGTGCTGAGCCAGCACCCCTCAGATGATTTCCCTCCAACTGCTGACTAGGTCATCCTCTGTCT
GGTAGAGACATTCACATCTTTGCTTTTATTCTATGCTCTCTGTACTTTTGACCAAAAATTGACCAAGTAAGAAA
ATGCAAGTTCTAAAAATAGACTAAGGATGCCTTTGCAGAACACCAAGCATCCCAAGGAACCTGGTAGGGAAGTGG
CGCCTGTCTCCTGGAGTGGAAGAGGCCTGCTCCCTGGCTCTGGGTCTGCTGGGGGCACAGTAAATCAGTCTTGGC
ACCCACATCCAGGGCAGAGAGGTCTGTGGTTCTCAGCATCAGAAGGCAGCGCAGCCCCCTCTCCTCTCAGGCTAC
AGGGTTGTACCTGCTGAGTCTCAGGTTGTTTGGCCTCTCTGGTCCATCTTGGGCATTAGGTTCTCCAGCAGAG
CTCTGGCCAGCTGCCTCTTCTTTAACTGGGAACACAGGCTCTCACAAGATCAGAACCCCCACTCACCCCAAGAT
CTTATCTAGCAAGCCTGTAGTATTCTAGTTTCTGTTGTAGGAAGAGAGCGAGGCATCCCTGAATTCACGCATCTG
CTGGAAACGAGCCGTGTCAGATCGCACATCCCTGCGCCCCCATGCCCTCTGAGTCACACAGGACAGAGGAGGCA
GAGCTTCTGCCCAGTGTATCTTCACTTTCTTTGTCCAGTCTTTTGTTTTAAATAAGCAGTGACCCTCCCTACTC
TTCTTTTAAATGATTTTTGTAGTTGATTTGTCTGAAGTGTGGCTACTGTGCATTCTTGAATAATCACTTGTA
AATTGTGAGTGTGAGCTGTTTCTTTACTCACATTGAAGGGACTTCGTTGGTTTTTGGAGTCTTGGTTGTG
ACTCCAAGAGCAGAGTGAGGAAGACCCCAAGCATAGACTCGGGTACTGTGATGATGGCTGCAGTCCAGTTTTAT
GATTCTGCTTTTATGTGTCCCTTGATAACAGTGACTTAACAATATACATTCTCATAAATAAAAAAAAAACAAGA
ATCTGAATTCTT

483/6881
FIGURE 451

GAGCCAGCGAGGAGTGAAGCTGAGCCTGGCCTCACACGCTCCTAGAGGACCACCTCCTGAGAGAGTTCTTTACCC
CCCTCTTCTTTCTCCAAGCTCCCCCTCCTGCTCTCCCTCCCTGCCCAATACAATGCATTCTTGAGTGGCAGCGTCT
GGACTCCAGGCAGCCCCAGAGAACCGAAGCAAGCCAAAGAGAGGACTGGAGCCAAGATACTGGTGGGGGAGATTG
GATGCCTGGCTTTCTTTGAGGACATCTTTGGAGCGAGGGTGGCTTTGGGGTGGGGGCTTGTGCTGCAGGGAATAC
AGCCAGGCCCCAAGATGGACACTTCTGGGCACTTCCATGACTCGGGGGTGGGGGACTTGGATGAAGACCCCAAGT
GCCCCGTGTCATCCTCTGGGGATGAGCAGCAGCAGCAGCAGCAGCAACAGCAGCAGCAGCCACCACCGCCAG
CGCACCAGCAGCCCCCAGCAGCCCCCTGGGACCCTCGCTGCAGCCTCAGCCTCCGCAGCTTCAGCAGCAGCAGC
AGCAGCAGCAGCAGCAGCAGCAGCAGCAGCCACCGCATCCCCGTGTCTCAGCTCGCCCAACTCCAGAGCCAGCCCG
TCCACCCTGGCCTGCTGCACTCCTCTCCACCGCTTTCAGGGCCCCCCTTCGTCCAACCTCCACCGCCATCCTCC
ACCCTTCCCTCCAGGCAAGGCAGCCAGCTCAATCTCAATGACCACCTTGCTTGGCCACTCTCCAAGTTCACAGCTA
CAAGTGGGCCTGGCGGAGGCAGCCGGCACCGACAGGCCAGCCCCCTGGTGCACCGGCGGGACAGCAACCCCTTCA
CGGAGATCGCCATGAGCTCCTGCAAGTATAGCGGTGGGGTCAAGAGCCCTCAGCCGCCTCAGCGCTCCCGGA
GGAACCTCATCGAGGCCGAGACTGAGGGCCAAACCCCTCAGCTTTTCAGCCCTAGCAACCCCCGGAGATCGTCA
TCTCCTCCCGGGAGGACAACCATGCCCCACCAGACCTGCTCCATCACCTAATGCCACCCACAACCACCAGCATG
CCGGCACCAACCGCCAGCAGCACCACCTTCCCCAAAGCCAACAAGCGGAAAAACCAAAACATTGGCTATAAGCTGG
GACACAGGAGGGCCCTGTTTGAAAAGAGAAAGCGACTGAGTGACTATGCTCTGATTTTTGGGATGTTTGGAATTG
TTGTTATGGTGATAGAGACCGAGCTCTCTTGGGGTTTGTACTCAAAGGACTCCATGTTTTCGTTGGCCCTGAAAT
GCCTTATCAGTCTGTCCACCATCATCCTTTTGGGCTTGATCATCGCCTACCACACACGTGAAGTCCAGCTCTTCG
TGATCGACAATGGCGCGGATGACTGGCGGATAGCCATGACCTACGAGCGCATCCTGTACATCAGCCTGGAGATGC
TGGTGTGCGCCATCCACCCATTCTGGCGAGTACAAGTTCTTCTGGACGGCACGCCTGGCCTTCTCCTACACAC
CCTCCCGGGCGGAGGCCGATGTGGACATCATCCTGTCTATCCCCATGTTCTGCGCCTGTACCTGATCGCCCCGAG
TCATGCTGCTGCACAGCAAGCTCTTCACCGATGCCTCGTCCCGCAGCATCGGGGCCCTCAACAAGATCAACTTCA
ACACCCGCTTTGTGATGAAGACGCTCATGACCATCTGCCCTGGCACTGTGCTGCTCGTGTTCAGCATCTCTCTGT
GGATCATTTGCTGCTGGACCGTCCGTGTCTGTGAAAGGTACCATGACCAGCAGGACGTAAGTAACTTTCTGG
GTGCCATGTGGCTCATCTCCATCACATTCTTTCCATTGGTTATGGGGACATGGTGGCCACACATACTGTGGGA
AAGGTGTCTGTCTCCTCACTGGCATCATGGGTGCAGGCTGCACTGCCCTTGTGGTGGCCGTGGTGGCCCGAAAGC
TGGAACCTACCAAAGCGGAGAAGCACGTTTCACTAATTTTCAATGATGGACACTCAGCTCACCAAGCGGATCAAGAATG
CTGCAGCCAATGTCCTTCGGGAAACATGGTTAATCTATAAACACACAAAGCTGCTAAAGAAGATTGACCATGCCA
AAGTGAGGAAACACCAGAGGAAGTTCTTCCAAGCTATCCACCAGTTGAGGAGCGTCAAGATGGAACAGAGGAAGC
TGAGTGACCAAGCCAACACTCTGGTGGACCTTTCCAAGATGCAGAATGTCATGTATGACTTAATCACAGAACTCA
ATGACCGGAGCGAAGACCTGGAGAAGCAGATTGGCAGCCTGGAGTGAAGCTGGAGCATCTCACCGCCAGCTTCA
ACTCCCTGCCGCTGCTCATCGCCGACACCCTGCGCCAGCAGCAGCAGCAGCTCCTGTCTGCCATCATCGAGGCC
GGGGTGTGAGCGTGGCAGTGGGCACCAACCCACACCCCAATCTCCGATAGCCCCATTGGGGTCACTCCACCTCCT
TCCCGACCCCGTACACAAGTTCAAGCAGTTGCTAAATAAATCTCCCCACTCCAGAAGCATTACCCATAGGTCTTA
AGATGCAAATCAACTCTCTCCTGGTCGCTTTGCCATCAAGAAACATTGAGACCAGGGAACGGAAGAAGAGAGAC
CGAGCTAATTAATAACTCATGTTTCAATTCAGCGTGCTTGGTCCGACATGCCTTGAAACCAGAAATCTAATCTCTG
TTTAGGTGCCCTCTACTTGGGAGCGGGAAGAGGAGATGACAGGAAGCGACGCCTCTGGCAGGGCCCTTGCTGCAGA
GTTGGTGGAGAACAGAAATCCACGCTCAATCTCAGGTCTTACGCGGGGGGTGGGGGTGAGATGCACTGAAGTAG
CCAACAGCGAAGCCAGTCCAGAAGAGGGGTCCGCTGGGAGGGAGGGTTGTGTGAGGCTTGGGGGATGGGCTCTTC
GCCATGGGGGTCTTTGAACACACCTCTCTCCTTTCTTTGTCTACGGAAGCCTCTGGGTGACAAAAGTAAAAGA
GAGCTGCCCACAACCTTGCCAAAACAGATATACTCGAATCAGACTGAAAAA

484/6881
FIGURE 452

GAAGGTTCTGGGCGGGGCTGGACTGTTCTAAGTGAGTTTCGGGTGGGGGAGCTTCACGAGGGGAGGCTGCTCTGTG
AAGGAACCGCCTTTCTCTCCGCGTGTCTCACCCTTTTCTCCCCATATCTGTTTGGACATGAGCTGAGGGCACGGT
CGCGGGCGGTTCAGCCCTGTTTCGCAGCTACGGCGAGGAGGGGCGGATTGTTCCCTTGTTGCCGCTCCGCTTAGTGG
CCGCGTCCATTCCGCGCGGTGTCCCGATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGGCGTGGC
GGCCCC**ATG**GGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAATCCGGGAAGGAC
TTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCCCTCCGGCTCTCTGGTCCACTCAAG
GAACAGTATGCTCAGGAGCATGGCTTGAACCTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTTCGG
AAGGACATGATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGC
ATCTCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGCTGTGACATCCAGTGGTTCGGGAGGCCTATGGG
GCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGAGCCGACAGCAGCGGGGCTGGGTGTTACAGCCAGGG
GTGGACGATGCTGAGTCAGAAATGTGGCCTGGACAACCTTCGGGGACTTTGACTGGGTTCATCGAGAACCATGGAGTT
GAACAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTT**TAGT**CACTAGGTTCTAGG
AGTGAGCTGGGGCCTGCTGAGGTGGGGGTGGGGCTGACTCTGCAAAATGGGGGTGTCCCCGATCCTGGCCGAGG
TGAGGAACAGACAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGGATATTGGGCAAGGCAGGAAACCTCTGGAGAC
CTCATTTTCTCCATGGGGAAGACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCAAAGGAGGGTGTCTTGGCTG
TGCTTGAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCCCCTCAGCCTGTGGTGGCCTTGCATCCTGACTGGA
TGTCTCAGCCCCTTGTCTGGGCAAGAACCAGAGCTCCCAGTGTGGATACTAATAAACCTCTTGGAGCACAC
TCTCAAAACAACCTCGGG

485/6881
FIGURE 453

MAPLGGA~~PRLVLL~~FSGKRKSGKDFVTEALQSRLGADVCAVLRLSGPLKEQY~~AE~~EHGLNFQRL~~LD~~STYKEAFRKD
MIRWGEEKRQADPGFFCRKIVEGISQPIWLVS~~DTRRVSDI~~QWFREAYGAVTQTVRVV~~AEQSRQQ~~RGWVFTPGVD
DAESECGLDNFGDFDWVIENHGVEQRLEE~~QLENLIE~~FIRSL

486/6881
FIGURE 454

ATGGGGCCTGAAACTGTCTGGGTCTGAGCTGGGGAGCGGAAGCCACTTGTCCCTCTCCCTCCCCAGGACTTCTGT
GACTCCTGGGCCACAGAGGTCCAACCAGGCTAAGGGCCTGGGGATACCCCTGCCTGGCCCCCTTGCCCAAACCTG
GCAGGGGGGCCAGGCTGGGCAGCAGCCCCTCTTTACCTCAACTATGGATCTCCTGCCCCCAAGCCCAAGTACA
ATCCACTCCGGAATGAGTCTCTGTCTATCGCTGGAGGAAGGGGCTTCTGGGTCCACCCCCCGGAGGAGCTGCCTT
CCCCATCAGCTTCATCCCTGGGGCCCATCCTGCCTCCTCTGCCTGGGGACGATAGTCCCACTACCCTGTGCTCCT
TCTTCCCCCGGATGAGCAACCTGAGGCTGGCCAACCCGGCTGGGGGGCGCCAGGGTCTAAGGGGGAGCCAGGAA
GGGCAGCTGATGATGGGGAGGGGATCGTAGGGGCAGCCATGCCAGACTCAGGCCCCCTACCCCTCCTCCAGGACA
TGAACAAGCTGAGTGGAGGCGGCGGGCGCAGGACTCGGGTGGAAAGGGGGCCAGCTTGGGGGCGAGGAGTGGACCC
GCCACGGGAGCTTTGTCAATAAGCCCACGCGGGGCTGGCTGCATCCCAACGACAAAGTCATGGGACCCGGGGTTT
CCTACTTGGTTTCGGTACATGGGTTGTGTGGAGGTCTCCAGTCAATGCGTGCCCTGGACTTCAACACCCGGACTC
AGGTCAACCAGGGAGGCCATCAGTCTGGTGTGTGAGGCTGTGCCGGGTGCTAAGGGGGCGACAAGGAGGAGAAAGC
CCTGTAGCCGCCCCGCTCAGCTCTATCCTGGGGAGGAGTAACCTGAAATTTGCTGGAATGCCAATCACTCTCACCG
TCTCCACCAGCAGCCTCAACCTCATGGCCGAGACTGCAAAACAGATCATCGCCAACCACCACATGCAATCTATCT
CATTTCATCCGGCGGGGATCCGGACACAGCCGAGTATGTCGCCATGTTGCCAAAGACCCTGTGAATCAGAGAG
CCTGCCACATTCTGGAGTGTCCCGAAGGGCTTGCCCAGGATGTCATCAGCACCATTTGGCCAGGCCTTCGAGTTGC
GCTTCAAACAATACCTCAGGAACCCACCCAAACTGGTCACCCCTCATGACAGGATGGCTGGCTTTGATGGCTCAG
CATGGGATGAGGAGGAGGAAGAGCCACCTGACCATCAGTACTATAATGACTTCCCGGGGAAGGAACCCCCCTTGG
GGGGGGTGGTAGACATGAGGCTTCGGGAAGGAGCCGCTCCAGGGGCTGCTCGACCCACTGCACCCAATGCCCAGA
CCCCCAGCCACTTGGGAGCTACATTGCCTGTAGGACAGCCTGTTGGGGGAGATCCAGAAGTCCGCAAACAGATGC
CACCTCCACCACCCTGTCCAGGCAGAGAGCTTTTTGATGATCCCTCCTATGTCAACGTCCAGAACCTAGACAAGG
CCCGGCAAGCAGTGGGTGGTGTGCTGGGCCCCCAATCCTGCTATCAATGGCAGTGCACCCGGGACCTGTTTGACA
TGAAGCCCTTCGAAGATGCTCTTCGCTGCTCCACCTCCCAGTCGGTGTCCATGGCTGAGCAGCTCCGAGGGG
AGCCCTGGTTCCATGGGAAGCTGAGCCGGCGGGAGGCTGAGGCACTGCTGCAGCTCAATGGGGACTTCCTGGTAC
GGGAGAGCACGACCACACCTGGCCAGTATGTGCTCACTGGCTTGCAAGTGGGCAGCCTAAGCATTGTCTACTGG
TGGACCCTGAGGGTGTGGTTCGGACTAAGGATCACCGCTTTGAAAGTGTGAGTCACTTATCAGCTACCACATGG
ACAATCACTTGCCCATCATCTCTGCGGGCAGCGAACTGTGCTACAGCAACCTGTGGAGCGGAACTGTGATCTG
CCCTAGCGCTCTCTTCCAGAAGATGCCCTCCAATCCTTTCCACCCTATTCCCTAACTCTCGGGACCTCGTTTGGG
AGTGTCTGTGGGCTTGGCCTTGTGTGAGAGCTGGGAGTAGCATGGACTCTGGGTTTCATATCCAGCTGAGTGAG
AGGGTTTGAGTCAAAAGCCTGGGTGAGAATCCTGCCTCTCCCCAAACATTAATCACCAAAGTATTAATGTACAGA
GTGGCCCCCTCACCTGGGCCTTTCTGTGCCAACCTGATGCCCCCTCCCCAAGAAGGTGAGTGTCTGTCATGGAAA
ATGTCCTGTGGTGACAGGCCAGTGAACAGTCAACCTTCTGGGCAAGGGGGAACAAATCACACCTCTGGGCTTC
AGGGTATCCCAGACCCCTCTCAACACCCGCCCCCCCCCATGTTTAACTTTGTGCCTTTGACCATCTCTTAGGTCT
AATGATATTTTATGCAAACAGTTCTTGGACCCCTGAATTCAATGACAGGGATGCCAACACCTTCTTGGCTTCTGG
GACCTGTGTTCTTGCTGAGCACCTCTCCGGTTTGGGTTGGGATAACAGAGGCAGGAGTGGCAGCTGTCCCCTCT
CCCTGGGGATATGCAACCCTTAGAGATTGCCCCAGAGCCCCACTCCCGGCCAGGCGGGAGATGGACCCCTCCCTT
GCTCAGTGCCCTCCTGGCCGGGGCCCCCTCACCCCAAGGGGTCTGTATATACATTTTCATAAGGCCTGCCCTCCCATG
TTGCATGCCTATGTACTCTACGCCAAAGTGACGCCCTTCTCCTGAAGCCTCTGCCCTGCCCTCCCTTTCTGGGAG
GGCGGGGTGGGGGTGACTGAATTTGGGCCTCTGTGACAGTTAACTCTCCAGGTGGATTTTGTGGAGGTGAGAAA
AGGGGCATTGAGACTATAAAGCAGTAGACAATCCCCACATACCCTCTGTAGAGTTGGAAGTGCATTCTTTTAAAG
TTTTATATGCATATATTTTAGGGCTGTAGACTTACTTTCTATTTTCTTTTCCATTGCTTATTCTTGAGCACAAA
ATGATAATCAATTATTACATTTATACATCACCTTTTGTACTTTTCCAAGCCCTTTTACAGCTCTTGGCATTTTCC
TCGCCTAGGCCTGTGAGGTAACCTGGGATCGCACCTTTTATACCAGAGACCTGAGGCAGATGAAATTTATTTCCAT
CTAGGACTAGAAAACTTGGGTCTCTTACC GCGAGACTGAGAGGCAGAAGTCAGCCCGAATGCCTGTGAGTTTCA
TGGAGGGGAAACGCAAAACCTGCAGTTCTGTAGTACCTTCTACAGGCCGGCCAGCCTAGGCCCGGGGTGGCCA
CACCACAGCAAGCCGGCCCCCCCCCTCTTTTGGCCTTGTGGATAAGGGAGAGTTGACCGTTTTCATCCTGGCCTCCT
TTTGCTGTTTGGATGTTTCCACGGGTCTCACTTATACCAAAGGGAAAACCTTTCATTAAAGTCCGTATTTCTTCT

487/6881
FIGURE 455

GAAAGAGCCGGTGAAGGGGCAGAACAGGCAGGTTCCCTCGACCCAGGACCCCCTGTTCCCAGGCTATGGCCCCCA
GTGCCCTGTAGACCTGGCAGGCCCCCGTGCTTGCGACCCCTATTTGGGGGTCTGGGTGGCTACTGGAGGGCCTT
GCAGAGGGGCAGAGAAGGCAGGACCATGACATCTAGGGCCTCTGAACTTTCTCCGGGGCGCAGCGTGACGGCTGG
CATCATCATTGTTGGAGATGAGATCCTTAAGTTGGAAACAACAAATGGCTTTTGAGTCCAAGAGTGATGCAATCA
CAGTGACGCATTAAAACGGTTACTCCGGAGACATCAGAGCACTGTGGCTGGAGGCTGGGAGCCTGGCCAGGAAGC
TGTCGCCATTGTCCAGGTGAAAGGTGCTAAGGACCTGCTTGGTGGCAGTGGGGACAGAAAGAAGAAAGCAGGCCA
GGCGTGGTGGCTCACACCTATAATTCCAGCACTTTGGGAGGCTGAGGCAGGAGGATCACTTGAGACCAGGAATTC
AACACCAGCCTGGGCAACATGGCAAGACCCCATTCTACAAAAAAATTTAAAATGAGCTGAATGTGGTGGCAGC
CGCCTGTAGTCCCAGCTACTCGGAAGGCTGGGGTGGCCCTTGAAAGCCAGGAGGTTGAGGCTGCAGTGAAGTGTGA
CTGAGCCACTATACTCCAGCCTGGGTGACAGAGACCCAGCTTTAAACCACAAATGGATTTTCCCACTCTTGT
GTCCAGTCCAGGCCCCCTCAGCAGCCTGAGGTGGTGTCTTCAAAGAGCAGAGCACTGCATCATCAGGTGGATCCA
GCCATCATCTTCAACCCCTCCCCTTCATCCCTACAGTACTGATGGCCTCATCTTCCCTTCAACCCCCAGGGACA
CACTCAGGACACCAACACCTTCTTCTGTGCCGGACACTGCGCTCCCTAGGGGTCCAGGTTTGCCGAGTCTCAGT
TGTACCTGATGAGGTAGCCACCATTGCAGCTGAGGTCACTTCTTTCTCCAACCGCTTCACCCATGTCTCACAGC
AGGGGGCATCGGCCCCACTCATGATGATGTGACCTTTGAGGCAGTGGCACAGGCCTTTGGAGATGAGCTGAAGCC
ACACCCCAAGTTGGAAGCAGCCACCAAAGCCCTAGGAGGGGAAGGCTGGGAGAAGCTATCATTGGTGGCCCTCTC
TGCCCGCCTGCATTATGGCACAGATCCTTGCACTGGTCAACCTTTAGATTCCCTCTGGTCTCCGTCCGAAACGT
CTACCTCTTCCCAGGCATTCCAGAGCTGCTGCGGCGGGTGTGGAGGGGATGAAGGGACTATTCCAAAACCCAGC
TGTTTCAAGTTCCACTCAAAGGAGCTATATGTGGCTGCTGATGAAGCCTCCATCGCCCCATTCTGGCTGAGGCCCA
GGCCCACTTTGGACGTAGGCTTGGCCTGGGTTTCTACCCTGACTGGGGCAGCAACTACTATCAGGTGAAGCTGAC
TCTAGACTCAGAGGAAGAAGGACCCCTGGAGGAATGCTTGGCCTACCTGACTGCCCGTTTGCCCCAGGGATCGCT
GGTCCCCTACATGCCCAACGCTGTGGAGCAGGCCAGTGAGGCTGTATACAACTCGCTGAATCAGGTAGGGACCT
TATGGAGGAGGGGCATTATGCCCAAAGCCATTGGTGGCACCCAGATCTCAGTAATGCAGGGGCTGTTGGGTGCT
TCCTGCAAATCCCTGAGAGGGCAGAAGATAGCTTCTGTTAATTCATTATTCTTCCAATAAATGTTGATTGAGTAC
CTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

488/6881
FIGURE 456

MQPSSSTPPLHPYSTDGLIFPFNPQGHTQDTNTFFLCRTLRLSLGVQVCRVSVVPDEVATIAAEVTSFSNRFTHL
TAGGIGPTHDDVTFEAVAQAFGDELKPHPKLEAATKALGGEGWEKLSLVPSSARLHYGTDPCGTGQPFREFPLVSVR
NVYLFPGIPELLRRVLEGMKGLFQNPVQFHSKELYVAADEASIAPILAEQAHFGRRLGLGSYPDWGSNYYQVK
LTLDSEEEGPLEECLAYLTARLPQGSLVPYMPNAVEQASEAVYKLAESGRDLMEEGHYAQSHWWHPRSQ

489/6881
FIGURE 457

CGCTGCCATGCGGCTGGCGCTGCTCTGGGCCCTGGGGCTCCTGGGCGCGGGCAGCCCTCTGCCTTCCTGGCCGCT
CCCAAATATAGGTGGCACTGAGGAGCAGCAGGCAGAGTCAGAGAAGGCCCGAGGGAGCCCTTGAGCCCCAGGT
CCTTCAGGACGATCTCCCAATTAGCCTCAAAAAGGTGCTTCAGACCAGTCTGCCTGAGCCCCCTGAGGATCAAGTT
GGAGCTGGACGGTGACAGTCATATCCTGGAGCTGCTACAGAATAGGGAGTTGGTCCCAGGCCGCCAACCCTGGT
GTGGTACCAGCCCCGATGGCACTCGGGTGGTCAGTGAGGGACACACTTTGGAGAACTGCTGCTACCAGGGAAGAGT
GCGGGGATATGCAGGCTCCTGGGTGTCCATCTGCACCTGCTCTGGGCTCAGAGGCTTGGTGGTCTGACCCCA
GAGAAGCTATACCCTGGAGCAGGGGCTGGGGACCTTCAGGGTCTCCATTATTTGCGGAATCCAAGATCTCCA
CCTGCCAGGCCACACCTGTGCCCTGAGCTGGCGGGAATCTGTACACACTCAGACGCCACCAGAGCACCCCTGGG
ACAGCGCCACATTGCGCGGAGGCGGGATGTGGTAACAGAGACCAAGACTGTGGAGTTGGTGATTGTGGCTGATCA
CTCGGAGGCCCAGAAATACCGGGACTTCCAGCACCTGCTAAACCGCACACTGGAAGTGGCCCTCTTGCTGGACAC
ATTCTTCCGGCCCCCTGAATGTACGAGTGGCACTAGTGGGCCCTGGAGGCCCTGGACCCAGCGTGACCTGGTGGAGAT
CAGCCCCAAACCAGCTGTACCCCTCGAAAACCTTCCTCCACTGGCGCAGGGCACATTTGCTGCCTCGATTGCCCCA
TGACAGTGCCAGCTGGTGACTGGTACTTCACTTCTCTGGGCCTACGGTGGGCATGGCCATTGAGAACTCCATCTG
TTCTCCTGACTTCTCAGGAGGTGTGAACATGGACCACTCCACCAGCATCCTGGGAGTCGCCCTCCTCCATAGCCCA
TGAGTTGGGCCACAGCCTGGGCCTGGACCATGATTTGCCTGGGAATAGCTGCCCCCTGTCCAGGTCCAGCCCCAGC
CAAGACCTGCATCATGGAGGCCTCCACAGACTTCCTACCAGGCCTGAACTTCAGCAACTGCAGCCGACGGGCCCT
GGAGAAAGCCCTCCTGGATGGAATGGGCAGCTGCCTCTTCGAACGGCTGCCTAGCCTACCCCTATGGCTGCTTT
CTGCGGAAATATGTTTGTGGAGCCGGGCGAGCAGTGTGACTGTGGCTTCCTGGATGACTGCGTCGATCCCTGCTG
TGATTCTTTGACCTGCCAGCTGAGGCCAGGTGCACAGTGTGCATCTGACGGACCCTGTTGTCAAATTGCCAGCT
GCGCCCGTCTGGCTGGCAGTGTCTGCTTACCAGAGGGGATTGTGACTTGCCTGAATTCTGCCCAGGAGACAGCTC
CCAGTGTCCCCCTGATGTACGCTAGGGGATGGCGAGCCCTGCGCTGGCGGGCAAGCTGTGTGCATGCACGGGCG
TTGTGCCTCCTATGCCCAGCAGTGCCAGTCACTTTGGGGACCTGGAGCCCAGCCCGCTGCGCCACTTTGCCTCCA
GACAGCTAATACTCGGGGAAATGCTTTTGGGAGCTGTGGGCGCAACCCCAAGTGGCAGTTATGTGTCTTGCACCCC
TAGAGATGCCATTTGTGGGCAGCTCCAGTGCCAGACAGGTAGGACCCAGCCTCTGCTGGGCTCCATCCGGGATCT
ACTCTGGGAGACAATAGATGTGAATGGGACTGAGCTGAACTGCAGCTGGGTGCACCTGGACCTGGGCAGTGATGT
GGCCCAGCCCCCTCTGACTCTGCCTGGCACAGCCTGTGGCCCTGGCCTGGTGTGTATAGACCATCGATGCCAGCG
TGTGGATCTCCTGGGGGCACAGGAATGTGGAAGCAAATGCCATGGACATGGGGTCTGTGACAGCAACAGGCACTG
CTACTGTGAGGAGGGCTGGGCACCCCTGACTGCACCACTCAGCTCAAAGCAACCAGCTCCCTGACCACAGGGCT
GCTCCTCAGCCTCCTGGTCTTATTGGTCTGGTGATGCTTGGTGCCGGCTACTGGTACCGTGCCCGCCTGCACCA
GCGACTCTGCCAGCTCAAGGGACCCACCTGCCAGTACAGGGCAGCCCAATCTGGTCCCTCTGAACGGCCAGGACC
TCCGCAGAGGGCCCTGCTGGCACGAGGCACTAAGTCTCAGGGGCCAGCCAAGCCCCCAGCCCCAAGGAAGCCACT
GCCTGCCGACCCCCAGGGCCGGTGCCCATCGGGTGACCTGCCCGGCCAGGGGCTGGAATCCCGCCCCCTAGTGGT
ACCCTCCAGACCAGCGCCACCGCCTCCGACAGTGTCTCGCTCTACCTCTGAACCTCTCCGGAGGTTCCGCTGCCT
CCAAGCCGGACTTAGGGCTTCAAGAGGCGGGCGTGCCCTCTGGAGTCCCCTACCATGACTGAAGGCGCCAGAGAC
TGGCGGTGTCTTAAGACTCCGGGCACCGCCACGCGTGTCAAGCAACACTCTGCGGACCTGCCGGCGTAGTTGCA
GCGGGGGCTTGGGGAGGGGCTGGGGGTGGACGGGATTGAGGAAGGTCCGCACAGCCTGTCTCTGCTCAGTTGCA
ATAAACGTGACATCTTGGGAGCGTTAAAAAAAAAAAAAAAAA

490/6881
FIGURE 458

MRLALLWALGLLGAGSPLPSWPLPNIGGTEEQQAESEKAPREPLEPQVLQDDLPI SLKKVLQTS LPEPLRIKIEL
DGD SHILELLQNRELVPGRPTLVWYQPDGTRVVSEGHTLENCCYQGRVRGYAGSWVSICTCSGLRGLVVLTPERS
YTLEQGP GDLQGPP IISRIQDLHLP GHTCALSWRESVHTQTPPEHPLGQRHIRRRRDVVTETKTVELVIVADHSE
AQKYRDFQHLLNRTLEVALLLDTFFRPLNVRVALVGLEAWTQRDLVEISPNPAVTLENFLHWRRRAHLLPRLPHDS
AQLVTGTSFSGPTVGMAIQNSICSPDFSGGVNMDHSTSILGVASSIAHELGHSLGLDHDLPGNSCPCPGPAPAKT
CIMEASTDFLPGLNFSNCSRRRALEKALLDGMGSCLFERLP SLPPMAAFCGNMFVEPGEQCDCGFLDDCVDPCDS
LTCQLRPGAQCASDGPCCQNCQLRPSGWQCRPTRGDCDLPEFCPGDSSQC PPDVSLGDGEPCAGGQAVCMHGRCA
SYAQQCQSLWGPGAQPAAPLCLQTANTRGNAFGSCGRNPSGSYVSCTPRDAICGQLQCQTGRTQPLLSIRDLLW
ETIDVNGTELNCSWVHLDLGSDVAQPLLTLPGTACGPGLVCIDHRCQRVDLLGAQECSRKCHGHGVCD SNRHCYC
EEGWAPPDCTTQLKATSSLTTGLLLSLLVLLVLVMLGAGYWYRARLHQRLCQLKGPTCQYRAAQSGP SERPGPPQ
RALLARGTKSQGPAKPPPPRKPLPADPQGRCPSGDLPGPGAGIPPLVPSRPAPPPPTVSSLYL

491/6881
FIGURE 459

CGACTTTCCCGATCGCCAGGCAGGAGTTTCTCTCGGTGACTACTATCGCTGTCATGTCTGGTCGTGGCAAGCAAG
GAGGCAAGGCCCGCGCCAAGGCCAAGTCGCGCTCGTCCCGCGCTGGCCTTCAGTTCCCGGTAGGGCGAGTGCATC
GCTTGCTGCGCAAAGGCAACTACGCGGAGCGAGTGGGGGCCGGCGCGCCGCTCTACATGGCTGCGGTCCTCGAGT
ATCTGACCGCCGAGATCCTGGAGCTGGCGGGCAACGCGGCTCGGGACAACAAGAAGACGCGCATCATCCCTCGTC
ACCTCCAGCTGGCCATCCGCAACGACGAGGAACTGAACAAGCTGCTGGGCAAAGTCACCATCGCCCAGGGCGGCG
TCTTGCCTAACATCCAGGCCGTACTGCTCCCTAAGAAGACGGAGAGTCACCACAAGGCAAAGGGCAAGTGAGGGCT
GACGTCCGGCCCAAGTGGGCCCAGCCCGGCCCGCGTCTCGAAGGGGCACCTGTGAACTCAAAAGGCTCTTTTCAG
AGCCACCCA

492/6881
FIGURE 460

MSGRGKQGGKARAKAKSRSSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNK
KTRIIPRHLQLAIRNDEELNKLLGKVTIAQGGVLPNIQAVLLPKKTESHHKAKGK

493/6881
FIGURE 461

CTTTCGCCATGGCTGCCGGGCCGATCTCCGAGCGGAATCAGGATGCCACTGTGTACGTGGGGGGCCTGGATGAGA
AGGTTAGTGAACCGCTGCTGTGGGAAC TGTTTCTCCAGGCTGGACCAGTAGTCAACACCCACATGCCAAAGGATA
GAGTCACTGGCCAGCACCAAGGCTATGGCTTTGTGGAATTCTTGAGTGAGGAAGATGCTGACTATGCCATTAAGA
TCATGAACATGATCAAACCTCTATGGGAAGCCAATACGGGTGAACAAAGCATCAGCTCACAACAAAAACCTGGATG
TAGGGGCCAACATTTTCATTGGGAACCTGGACCCTGAGATTGATGAGAAGTTGCTTTATGATACTTTTCAGCGCCT
TTGGGGTCATCTTACAAACCCCCAAAATTATGCGGGACCCCTGACACAGGCAACTCCAAAGGTTATGCCTTTATTA
ATTTTGCTTCATTTGATGCTTCGGATGCAGCAATTGAAGCCATGAATGGGCAGTACCTCTGTAAACCGTCCTATCA
CCGTATCTTATGCCTTCAAGAAGGACTCCAAGGGTGAGCGCCATGGCTCAGCAGCCGAACGACTTCTGGCAGCTC
AGAACCCGCTCTCCCAGGCTGATCGCCCTCATCAGCTGTTTGCAGATGCACCTCCTCCACCCTCTGCTCCCAATC
CTGTGGTATCATCATTGGGGTCTGGGCTTCCTCCACCAGGCATGCCTCCTCCTGGCTCCTTCCCACCCCCAGTGC
CACCTCCTGGAGCCCTCCCACCTGGGATACCCCCAGCCATGCCCCCACCACCTATGCCTCCTGGGGCTGCAGGAC
ATGGCCCCCATCGGCAGGAACCCCAGGGGCAGGACATCCTGGTCATGGACACTCACATCCTCACCCATTCCCAC
CGGGTGGGATGCCCCATCCAGGGATGTCTCAGATGCAGCTTGACACCATGGCCCTCATGGCTTAGGACATCCCC
ACGCTGGACCCCCAGGCTCTGGGGGCCAGCCACCGCCCCGACCACCACCTGGAATGCCTCATCCTGGACCTCCTC
CAATGGGCATGCCCCCCGAGGGCCTCCATTTCGGATCTCCCATGGGTCACCCAGGTCTATGCCTCCGCATGGTA
TGCGTGGACCTCCTTCCACTGATGCCCCCATGGATACACTGGCCCTCCACGACCCCCACCCTATGGCTACCAGC
GGGGGCCTCTCCCTCCACCCAGACCCACTCCCCGGCCACCAGTTCCCCCTCGAGGCCCACTTCGAGGCCCTCTCC
CTCAGTAAATTACATTTTCCTTCCTCCTGTTACATTTTCCCAATATCTTTTCTATTCTTGGACCAATCAGAGA
TGCTGTAGCTCCTTGGGGCAAAGGTACTAATCCCTTTCAGCACCCCCACTCCATTCCCCTTTTAAATGTAACTTT
TTCCACAGGAGGTATTTCTTTTTTATGTTGGTCCTGAGTATTTTGCAAATGCACAGAGAAAATAAACTAAACTC
CTTGTTAAAAAAAAAAAAAAAAAAAAA

494/6881

FIGURE 462

MAAGPISERNQDATVYVGGLDEKVSEPLLWELFLQAGPVVNTHMPKDRVTGQHQQGYGFVEFLSEEDADYAIKIMN
MIKLYGKPIRVNKASAHNKNLDVGANIFIGNLDPEIDEKLLYDTFSAFGVILQTPKIMRDPDTGNSKGYAFINFA
SFDASDAAIEAMNGQYLCNRPITVSYAFKKDSKGERHGSAAERLLAAQNPLSQADRPHQLFADAPPPPSAPNPVV
SSLGSGLPPPGMPPPGSFPPPVPPPGALPPGIPFAMPPPPMPPGAAGHGPPSAGTPGAGHPGHGHSHPHPFPFPGG
MHPHPGMSQMLAHHGPHGLGHPHAGPPGSGGQPPFRPPPGMHPGPPPMGMPPRGPPFGSPMGHPGMPPHGMRG
PPPLMPFHGYTGPPRPPPYGYQRGPLPPPRPTPRPPVPPRGPLRGPLPQ

495/6881
FIGURE 463A

GCCGGGAGCAGTCGCCGCTGCCGCCTCCGCCCGCGCCGGGACCCCCGTCTCGCCCCGGGACTCCTTACCCGGGG
AACCTAGACCAGGTCTCCAGAGGCTTGTGGAAGAGAAGCAGGCGACCCCTTCCTGAGTTATCCTGGCTTAGCCTCC
CAATCTGGCTCCCCTTCCCCTTCCCATTCCTTCCCTGCTCCCCCTGTCCCTTCCCCATCCACCCAAGTGAAGTGGGTA
TAGGTCAAAGCTCCTCTCCTTCCCTTTCCCTTCCCTAGGCACTCATTGGCTAGGACCTGTTTGCTCTTTTTTTTGTG
CCCAGAGATACTGGAACACGCTTCATCTAAGTAACTGTGGGGAGGGGTCTTTTTGACTCTACAAGTCCTTGAGCA
AAAAGCTGAAAAAGAAGCAGGAGGTGGAGAAAGACCCAGTGAAGTGCCCCAAGCCCCATCCATGGAAGAGGGCTTCC
GAGACCGGGCAGCTTTCATCCGTGGGGCCAAAGACATTGCTAAGGAAGTCAAAAAGCATGCGGCCAAGAAGGTGG
TGAAGGGCCTGGACAGAGTCCAGGACGAATATTCCTCGAAGATCGTACTCCCGCTTTGAGGAGGAGGATGATGATG
ATGACTTCCCTGCTCCAGTGATGGTTATTACCGAGGAGAAGGGACCCAGGATGAGGAGGAAGGTGGTGCATCCA
GTGATGCTACTGAGGGCCATGACGAGGATGATGAGATCTATGAAGGGGAATATCAGGGCATTCCCCGGGCAGAGT
CTGGGGGCAAAGGCGAGCGGATGGCAGATGGGGCGCCCTGGCTGGAGTAAGGGGGGGCTTGAGTGATGGGGAGG
GTCCCCCTGGGGGCCGGGGGGAGGCAACAACGACGGAAGAAGCAGAGAAGAACTGGCCCCAACAGTATGAAGCCATCC
TACGGGAGTGTGGCCACGGCCGCTTCCAGTGGACACTGTATTTTGTGCTTGGTCTGGCGCTGATGGCTGACGGTG
TGGAGGTCTTTGTGGTGGGCTTCGTGCTGCCAGCGCTGAGAAAGACATGTGCCTGTCCGACTCCAACAAAGGCA
TGCTAGGCCTCATCGTCTACCTGGGCATGATGGTGGGAGCCTTCTCTGGGGAGGTCTGGCTGACCGGCTGGGTC
GGAGGCAGTGTCTGCTCATCTCGCTCTCAGTCAACAGCGTCTTCGCCTTCTTCTCATCTTTTGTCCAGGGTTACG
GCACTTTCTCTTCTGCCGCCTACTTTCTGGGGTTGGGATTGGAGGGTCCATCCCCATTGTCTTCTCCTATTTCT
CCGAGTTTCTGGCCCAGGAGAAACGAGGGGAGCATTGTAGCTGGCTCTGCATGTTTGGATGATTGGTGGCGTGT
ACGCAGCTGCTATGGCCTGGGCCATCATCCCCACTATGGGTGGAGTTTTAGATGGGTCTGCCTACCAGTTCC
ACAGCTGGAGGGTCTTCGTCTCGTCTGCGCCTTCTCTTCTGTGTTTGCCATTGGGGCTCTGACCACGCAGCCTG
AGAGCCCCCGTTTCTTCTAGAGAATGGAAAGCATGATGAGGCCTGGATGGTGCTGAAGCAGGTCCATGATACCA
ACATGCGAGCCAAAGGACATCCTGAGCGAGTGTTCTCAGTAACCCACATTAAGACGATTTCATCAGGAGGATGAAT
TGATTGAGATCCAGTCGGACACAGGGACCTGGTACCAGCGCTGGGGGGTCCGGGCCTTGAGCCTAGGGGGGCAGG
TTTGGGGGAATTTTCTCTCCTGTTTTGGTCCCGAATATCGGCGCATCACTCTGATGATGATGGGTGTGTGGTTCA
CCATGTCAATTCAGCTACTATGGCCTGACCGTCTGGTTTCTGACATGATCCGCCATCTCCAGGCAGTGGACTACG
CATCCCGCACCAAGTGTTCCCCGGGGAGCGCGTAGAGCATGTAACCTTTAACTTCACGTTGGAGAATCAGATCC
ACCGAGGCGGGCAGTACTTCAATGACAAAGTTCATTGGGCTGCGGCTCAAGTCAGTGTCCTTTGAGGATTCCCTGT
TTGAAGAGTGTTATTTTGGAGATGTCACATCCAGCAACACGTTTTTCCGCAACTGCACATTTCATCAACACTGTGT
TCTATAACACTGACCTGTTTCGAGTACAAGTTTGTGAACAGCCGTCTGATAAACAGTACATTCTGCACAACAAGG
AGGGCTGCCCGCTAGACGTGACAGGGACGGGCGAAGGTGCCTACATGGTATACTTTGTGAGCTTCTGGGGACAC
TGGCAGTGCTTCCCTGGGAATATCGTGCTGCTGCTCATGGACAAGATCGGCAGGCTCAGAATGCTTGCTGGCT
CCAGCGTGATGTCTGTGTCTCCTGCTTCTTCTGCTTTTTGGGAACAGTGAGTCGGCCATGATCGCTCTGCTCT
GCCTTTTTGGCGGGGTGAGCATTGCATCCTGGAATGCGCTGGACGTGTTGACTGTTGAACTCTACCCCTCAGACA
AGAGGACCACAGCTTTTGGCTTCCCTGAATGCCCTGTGTAAGCTGGCAGCTGTGCTGGGGATCAGCATCTTCACAT
CCTTCGTGGGAATCACCAGGCTGCACCCATCCTCTTTGCCTCAGCTGCCCTTGCCCTTGGCAGCTCTCTGGCCC
TGAAGCTGCCTGAGACCCGGGGCAGGTGCTGCAGTGAAGGGGTCTCTAGGGCTTTGGGATTGGCAGGCACACTG
TGAGACCAACAACCTCCTTCCCTTCCCTGCCCTGCCATCCTGACCTCCAGAGCCCTCACTCCCCACTCCCCG
TGTTTGGTGTCTTAGCTGTGTGTGCGTGTGCGTGTGCATGTGTGTAAACCCCGTGGGCAGGGACTACAGGGAAGG
CTCCTTCATCCAGTTTTGAGATGAAGCTGTACTCCCCATTTCCCACTGCCCTTGACTTTGCACAAGAGAAGGCT
GAGCCCCATCCTTCTCCCCCTGTTAGAGAGGGGCCCTTGCTTCCCTGTTCCAGGGGTTCAGAATAGGCTTCCCTG
CCTTCCCCATCATTCCCTCTGCCTAGGCCCTGGTGAAACCACAGGTATGCAATTATGCTAGGGGCTGGGGCTCTG
GTGTAGACCATGGACCAAAAGAACTTCTTAGAGTCTGAAGAGTGGGCCTCGGGTGCCCTCTCACATCTCCTGTTG
GATGCTGGGGGAGAAGCAATAAACCTCAGCCCTCTGGCCTCCACTTTCCTCTCAATTTGGGCTGCAATATGAAG
CCTGAATTTTATGAAATTAGCTTTCTGATTCTTATTTATTAATAGATTAAGTTCTGAGGCAGCTCCGCAGGACTG
TGTGTGAATGTGTATGTATACTTACATATGTGTGTGCATGTGCCATGGGGCGGGGGGTATCACTATACTGTCTC
AAATATAAGCCAAGGGTAATTTTCAGCGGATGCACACACAACCCTGCCTCCACAGTTCCTCCCCTAATCTGGTTT
CTGTGTTGAGCCTGGGATGGAGGAGCCCTAGGCCAGCCTGGGATAAGAGTCCACAGTCTAGGGAGATCTGAGGG
CATCCGACAAGGCCCATCTCCTTCCCTCCTCAAGAAGCAGAGGCCTCCTCTGGAGTGAGAGGCTCCACCCACTAC

496/6881

FIGURE 463B

AGCACAGGCGGGAATAGCACAGCTGCCCTCCCATGCTCCCTACCTGTCCCCTCACAGGGAGGGGAGCAGGGGAGG
GAAAGAAACCAGGCATCTGGTCAAACCAGCAGATCAAAAAGCACAAAGAGCTGGGGCAGAGGCAGGAAGCAGGGG
CCCTCCTGGCAGCTCCTCTGAGTGGGGAGAGGTTGGGCAGTGAGTGAGGGACCCCTAATGCAGGGACTAGAAGCC
TCAGTTTCCCCATTTTACCCTTCCACACAATAGCCTCTGTAGGTTAGGCTGCCCCATCCCACCCTACTCTGTGTG
GCTGCTTTCTTTGGTGCCCTCCCCTCACCCCACTGTAGCTGTGACGTGTTGTAGTTTTTTAGATGTTTGTAAAATG
TTTAAAAAATGTTAAAAGGAAAAAAGTGAAAATAACAAAAAAGAAAATCAAATTCACCTTCGTGCTGCTGCGT
CCAGTGCCCCAACCCCTGTGGTCACTCTCCCCATTTTGTAACACTGTACCAGGTGGTGACTGTTTAACTCTTTGGT
GTCTGTGCTCAAAAGACTGCCTTCTCCAGTGCCCACTGTATGAGTGTTGCCCCTGTGCCCTTGCTCCCTCACTCCC
CACATGCTGGACGTAGCCCTCTTCCTCGCACCCCTGGGAGGGACCCATCCATCTCCCTTGCTCTCCTGGGGAACC
CTAAACCCAACTCTGTTGATGTGAAAAATGCAGTGAAAAATATTGACGAAAAATAAAACGGAAACAAATCCTCAA
AAT

497/6881
FIGURE 464

MEEGFRDRAAFIRGAKDIAKEVKKHAAKKVVKGLDRVQDEYSRRSYSRFEEDDDDDDFPAPSDGYRGEQTQDEE
EGGASSDATEGHDEDEIYEGEYQGIPRAESGGKGERMADGAPLAGVRGGLSDGEGPPGGRGEAQRRKEREELAQ
QYEAAILRECGHGRFQWTLYFVLGLALMADGVEVFVVGFLVPSAEKDMCLSDSNKGMLGLIVYLGMMVGAFWLWGGL
ADRLGRRQCLLISLSVNSVFAFFSSFVQGYGTFLFCRLLSGVGIGGSIPFIVFSYFSEFLAQEKRGEHLSWLCMFW
MIGGVYAAAMAWAIIPHYGWSFQMGSAYQFHSWRVFVLVCAFPVFAIGALTTPESPRFFLENGKHDEAWMVLK
QVHDTNMRAKGHPERFVSVTHIKTIHQEDELIEIQSDTGTWYQRWGVRLSLGGQVWGNFLSCFGPEYRRITLMM
MGVWFTMSFSYYGLTVWFPDMIRHLQAVDYASRTKVFPGERVEHVTNFNTLENQIHRGGQYFNDKFIGLRLKSVS
FEDSLFEECYFEDVTSSNTFFRNCTFINTVFYNTDLFEYKFVNSRLINSTFLHNKEGCPLDVTGTGEGAYMVYFV
SFLGTLAVLPGNIVSALLMDKIGRLRMLAGSSVMSCVSCFFLSFGNSESAMIALLCFLGGVSIASWNALDVLTV
LYPSDKRTTAFGFLNALCKLAAVLGISIFTSFVGITKAAPILFASAALALGSSLALKLPETRGQVLQ

498/6881
FIGURE 465

GGCAGGAAAAGCGGAAGAGGGAGCGAAAACCAACGTGTTTCGGTGACAGACCCAGCGCCGACTGAGCCTCTAAAG
CGACTTCAGCTCTGCCCCACCAACACCACCGCGCGCCCGGGAACAGCCGCTCCGGGAAGAAACCTGAGGGGACTG
CGGGGGGCACGAGGGACAGCTGAGGGAAGGGAGGACGCGAGAGAAAACAGCGCGAGCACGCTGAGGGCCGGGGGTT
GCCAGGAGAGGGGCCCCGCGGACCCGCGAGAGCGGAGGAAGGTCCGGGAGAAAAGGGGCGGGACGGAGGAGAATCCG
GGATCGCCTGGCAGAAAAAGAGAAGGGAGTTTCTGAATCCTGGGAAGAGGAGGCGTGGGTAGGGACGCTTAGCCC
GAGATCCGACAGCAGGGAACCGGAGCGCTCCGGGGGAGGGGCTTAATGCTGGGGAAGGGATGTCTTAAAGAGGA
GAAGCTTTAAATTAGACGATCGGAGAAGGCTGAGGGAATTGCTATGAAGGGGCGGGAGCTGAAGTGTAGAGGACT
CCTTTAGACAGCAGAAAAGGGAAGCCGTTGAGAAGTTCCTTCAAACCTCCACCTGCCTCCTCTCCAATTCAAACCT
CCACTCCCTTCTCCAAAAGTTAAAGGAAAGCCAAGTTTACCACGCTCCCTGTTTCTACTCAATAAATACTTCT
TCTACTCCGCCACCGGGAACAGAAAAAAACTAATTTCCCTTCCCAATATTAGGACTTAGAAAAGCTCTAGGT
CCCGCAATTTGAATTTTAGCCTAGGGGAATCAAATAGTAGGAGCATTACTCTTGTTTCTTTTTCAAATCCCA
CACCTCATCTTCTGCGACGCCATGTCCACCAACATTTGTAGTTTCAAGGACAGGTGCGTGTCCATCCTGTGTT
GCAAATTTCTGTAAACAAGTGCTCAGCTCTAGGGGAATGAAGGCTGTTTTGCTGGCTGATACTGAAATAGACCTTT
TCTCTACAGACATCCCTCCTACCAACGCAGTGGACTTCACTGGAAGATGCTATTTACCAAATCTGCAAATGTA
AACTGAAGGACATCGCATGTTTAAAATGTGGGAACATTGTAGGTTATCATGTGATTGTTCCATGTAGTTCCCTGTC
TTCTTTCTGCAACAACAGACACTTCTGGATGTTTTCACAGCCAGGCAGTTTATGATATTAACAGACTAGACTCCA
CAGGTGTAAACGTCCTACTTCCGGGGCAACTTGCCAGAGATAGAAGAGAGTACAGATGAAGATGTGTTAAATATCT
CAGCAGAGGAGTGTATTAGATAAATGGAATTATGATATATATGATATACAACTTTTTTCTATTTAAAAATATAT
TAATGGATCAACTTTAAAATTGTTAGTTGCCAGTGATCTTTTTTGGAACAAAAATGGGGCATTTGTTGATTTA
TTTATTTTCTGTCTCTAATTAGTTACCTCAGTTTGATTGAAGCCAGTGGAGTTGTGCTTTTCTCTACTTCTACT
TCCTCTCCCCACCTTTTTCTGCCCAGTGTAGGTGTATTCTTAAATTCAGACGGGAAGATTCTTTCACATATCAC
TCAGTTACCTCCCAATCTGGGGGAGTTTTTCTTACAACCTTGATACCAGATACCATTAATTTTACATTCTGAATA
AAGGCCTAGTACCCACGCATATTTCAACCATGCATATATCAAGTTCAACCGAGTTTTAATAGGGGATTAAAAAA
CAAGCTGTTAGGTTTCCATGGGCACTGGTTCTCATAGTTCTATTGGTGATAACTGCTTTAACATGGAGCAAGAG
TTTGTAATCAGGAAATAGAATAAATTTAAATTTAAATATATAGAGGAATCCTCTTGATTGCTCAGCATGATGT
TAGATAAATGAGTTTGTGAGAAAATATCAGTATACGCTGTTTACCAATGTTATTTATTTACATTCTTCTAAAGCC
ATTATGGATATTGTATTATGAGAGCTAAACCTAAATAAGTTATCCTGTTCCCTAGGACCTTCTCTGTAAATAGTG
AATTTTAGACGAGTGGTCTGTCTAAATCTTAAATAGAAAAAAACTAAAGCGATTGCTTAAGCCATTGTACA
TTATAAAGAGCTGTTTTGTTTTGCTTTGCTTTGCTTTGTTTTGTTTTTTAAAGCTGCATTACAGAGCTACAAAGG
AATAGGAAAGTAGGGTAGTGTTGGATTCTGGTTTTATGTAACTCTAAATAAATGTATCTCTTTAATATCTCAGT
TGTAGGGATTTTGTCAATACCAAAGCAGACTGAGTTGTGGTTTTGTAAATAAAGTTTTTTCTAAAAATGACCATT
CTTCCTTTAATTTTTTGTATGCCCACATATTGTATGTAAAAATATAAATAAATAGTACTTAAAGTAT

499/6881
FIGURE 466

CAGCAGTGCTGTTTACTCATTGGAGGAACAGTACCTTGGCTTGGCTCTTGACGTGGACAGAATTAAAAAGGACCA
AGAAGAGGAAGAAGACCAAGGCCACCATGCCCCAGGCTCAGCAGGGAGCTGCTGGAGGTAGTAGAGCCTGAAGT
CTTGACAGGACTCACTGGATAGATGTTATTCAACTCCTTCCAGTTGTCTTGAACAGCCTGACTCCTGCCAGCCCTA
TGGAAGTTCCCTTTTATGCATTGGAGGAAAAGCATGTTGGCTTTTCTCTTGACGTGGGAGAAATTGAAAAGAAGGG
GAAGGGGAAGAAAAGAAGGGGAAGAAGATCAAAGAAGGAAAAGAAGGGGAAGAAAAGAAGGGGAAGAAGATCA
AAACCCACCATGCCCCAGGCTCAGCAGGGAGCTGCTGGATGAGAAAGGGCCTGAAGTCTTGCAGGACTCACTGGA
TAGATGTTATTCAACTCCTTCAGGTTGTCTTGAAGTACTGACTCATGCCAGCCCTACAGAAGTGCCTTTTACAT
ATTGGAGCAACAGCGTGTTGGCTTGGCTGTTGACATGGATGAAATTGAAAAGTACCAAGAAGTGGAAGAAGACCA
AGACCCATCATGCCCCAGGCTCAGCAGGGAGCTGTTGGATGAGAAAGAGCCTGAAGTCTTGCAGGAGTCACTGGA
TAGATGCTATTCAACTCCTTCAGGTTGTCTTGAAGTACTGACTCATGCCAGCCCTACAGAAGTGCCTTTTACAT
ATTGGAGCAACAGCGTGTTGGCTTGGCTGTTGACATGGATGAAATTGAAAAGTACCAAGAAGTGGAAGAAGACCA
AGACCCATCATGCCCCAGGCTCAGCAGGGAGCTGCTGGATGAGAAAGAGCCTGAAGTCTTGCAGGACTCACTGGG
TAGATGTTATTTCGACTCCTTCAGGTTATCTTGAAGTGCCTGACTTAGGCCAGCCCTACAGCAGTGCTGTTTACTC
ATTGGAGGAACAGTACCTTGGCTTGGCTCTTGACGTGGACAGAATTAAAAAGGACCAAGAAGAGGAAGAAGACCA
AGGCCACCATGCCCCAGGCTCAGCAGGGAGCTGCTGGAGGTAGTAGAGCCTGAAGTCTTGCAGGACTCACTGGA
TAGATGTTATTCAACTCCTTCCAGTTGTCTTGAACAGCCTGACTCCTGCCAGCCCTATGGAAGTTCCCTTTTATGC
ATTGGAGGAAAAACATGTTGGCTTTTCTCTTGACGTGGGAGAAATTGAAAAGAAGGGGAAGGGGAAGAAAAGAAG
GGGAAGAAGATCAAAGAAGGAAAGAAGAAGGGGAAGAAAAGAAGGGGAAGAAGATCAAACCCACCATGCCCCAG
GCTCAACAGCATGCTGATGGAAGTGGAAGAGCCTGAAGTCTTGCAGGACTCACTGGATATATGTTATTTCGACTCC
GTCAATGTACTTTGAACTACCTGACTCATTCCAGCACTACAGAAGTGTGTTTTACTCATTTGAGGAAGAGCATAT
CAGCTTCGCCCTTTACGTGGACAATAGGTTTTTTACTTTGACGGTGACAAGTCTCCACCTGGTGTTCCAGATGGG
AGTCATATTCCCACAATAAGCAGCCCTTACTAAGCCGAGAGGTGTCATTCTGCAGGCAGGACCTATAGGCACGT
GAAGATTTGAATGAAAGTACAGTTCCATTTGGAAGCCAGACATAGGATGGGTCAGTGGGCATGGCTCTATTCCCT
ATTCTCAAACCATGCCAGTGGCAACCTGTGCTCAGTCTGAAGACAATGGACCCACGTTAGGTGTGACACGTTTAC
ATAACTGTGCAGCACATGCCGGGAGTGATCAGTCAGACATTTTAATTTGAACCACGTATCTCTGGGTAGCTACAA
AATTCCTCAGGGATGTCATTTTGCAGGCATGTCTCTGAGCTTCTATACCTGCTCAAGGTCATTGTATCTTTGTG
TTTAGCTCATCCAAAGGTGTTACCCTGGTTTCAATGAACCTAACCTCATTCTTTGTGTCTTCAGTGTTGGCTTGT
TTTAGCTGATCCATCTGTAAACACAGGAGGGATCCTTGGCTGAGGATTGTATTTTCAAGAACCAACTGCTCTTGA
CAATTGTTAACCCGCTAGGCTCCTTTGGTTAGAGAAGCCACAGTCCTTCAGCCTCCAATTGGTGTCAGTACTTAG
GAAGACCACAGCTAGATGGACAAACAGCATTGGGAGGCCTTAGCCCTGCTCCTCTCAATTCCATCTGTAGAGAA
CAGGAGTCAGGAGCCGCTGGCAGGAGACAGCATGTACCCAGGACTCTGCCGGTGCAGAATATGAGCAATGCCAT
GTTCTTGCAGAAAACGCTTAACCTGAGTTTCATAGGAGGTAATCACCAGACAACCTGCAGAATGTAGAACACTGAG
CAGGACAACCTGACCTGTCTCCTTCACATAGTCCATATCACCACAAATCACACAACAAAAGGAGAAGAGATATTT
TCGGTTGAAAAAAGTAAAAAGATA

500/6881
FIGURE 467

MDEIEKYQEVEEDQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEEQYLGLALD
VDRIKKDQEEEEEDQGPPCPRLSRELLEVAEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLD
VGEIEKKGKGKKRRGRRSKKERRRRGRKEGEEDQNPPCPRLNGVLMEVEEPEVLQSLDICYSTPSMYFELPDSFQ
HYRSVFYSFEEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFTQ

501/6881
FIGURE 468

ATGACGCGAGACCCCGCCCCCGCAGCGCCCGCTTCCAAGATGGCGGCAGCGATGCCTGCCCGGCTGTTGGGGTGG
CGGTGACGACAGGCAGCAAAAGACCAGCTGGTCCCAGATTGCTGCTGGAGTGCTGGATGGAGCCTTTCTCTGCC
CTCTGTGACATTTCCAATTTTAGATAATGCCTCACATCTCTGTCCCCCGGGACCCCTGGAGCCCCCATGATCC
CTAAGAAGACAGCTTGAACCTAGATCTCACCCCCAGGATGTTGCGGAGGCTGCTGGAGCGGCCTTGACGCTGGC
CCTGCTTGTGGGCTCCCAGCTGGCTGTCATGATGTACCTGTCACTGGGGGGCTTCCGAAGTCTCAGTGCCCTATT
TGGCCGAGATCAGGGACCGACATTTGACTATTCTCACCTCGTGATGTCTACAGTAACCTCAGTCACCTGCCTGG
GGCCCCAGGGGGTCTCCAGCTCCTCAAGGTCTGCCCTACTGTCCAGAACGATCTCCTCTCTTAGTGGGTCTGT
GTCGGTGTCTTTAGCCCAGTGCCATCACTGGCAGAGATTGTGGAGCGGAATCCCCGGGTAGAACCAGGGGGCCG
GTACCGCCCTGCAGGTGTGTAGCCCCGCTCCCGAACAGCCATCATTGTGCCTCATCGTGCCCGGGAGCACCACT
GCGCCTGCTGCTCTACCACCTGCACCCCTTCTTGACGCGCCAGCAGCTTGCTTATGGCATCTATGTATCCACCA
GGCTGGAATGGAACATTTAACAGGGCAAACTGTTGAACGTTGGGGTGCGAGAGGCCCTGCGTGATGAAGAGTG
GGACTGCCTGTTCTTGACGATGTGGACCTCTTGCCAGAAAATGACCACAATCTGTATGTGTGTGACCCCCGGG
ACCCCGCCATGTTGCCGTTGCTATGAACAAGTTTGATACAGCCTCCCGTACCCCACTACTTCGGAGGAGTCTC
AGCACTTACTCCTGACCAGTACCTGAAGATGAATGGCTTCCCCAATGAATACTGGGGCTGGGGTGGTGAGGATGA
CGACATTGCTACCAGGGTGCGCCTGGCTGGGATGAAGATCTCTCGGGCCCCACATCTGTAGGACACTATAAGAT
GGTGAAGCACCGAGGAGATAAGGGCAATGAGGAAAATCCCCACAGATTTGACCTCCTGGTCCGTACCCAGAATTC
CTGGAUCGAAGATGGGATGAACTCACTGACATACCAGTTGCTGGCTCGAGAGCTGGGGCCTCTTTATACCAACAT
CACAGCAGACATTGGGACTGACCTCGGGGTCTCGGGCTCCTTCTGGGCCACGTTACCCACCTGGTTCTCCCA
AGCCTTCCGTCAAGAGATGCTGCAACGCCGGCCCCAGCCAGGCCTGGGCCTCTATCTACTGCCAACACACAGC
CCTCCGAGGTTTACACTGACTCCTCTCCTGTCTACCTTAATCATGAAACCGAATTCATGGGGTTGTATTCTCC
CCACCCTCAGCTCCTCACTGTTCTCAGAGGGATGTGAGGGAAGTGAACCTCTGGTGCCGTGCTAGGGGGTAGGGGC
CTCTCCCTCACTGCTGGACTGGAGCTGGGCTCCTGTAGACCTGAGGGGTCCCTCTCTCTAGGGTCTCCTGTAGGG
CTTATGACTGTGAATCCTTGATGTATGATTTTATGTGACGATTCTAGGAGTCCCTGCCCCTAGAGTAGGAGCA
GGGCTGGACCCCAAGCCCCCTCCCTCTTCCATGGAGAGAAGAGTGATCTGGCTTCTCCTCGGACCTCTGTGAATAT
TTATTCTAATTTATGTTCCCGGAAGTTGTTTGGTGAAGGAAGCCCTCCCTGGGCATTTTCTGCCTATGCTGGA
ATAGCTCCCTCTTCTGGTCTGGCTCAGGGGGCTGGGATTTTGATATATTTTCTAATAAAGGACTTTGTCTCGC

502/6881
FIGURE 469

MLRRLLERPCTLALLVGSQ LAVMMYLSLGGFRSL S ALFGRDQGPTFDYSHPRDVYSNL SHLP GAPGGPPAPQGLP
YCPERSPLLVG PVSVSFSPVPSLAE IVERNPRVEPGGRYRPAGCEPRSR TAIIVPHRAREHHLRLLLYHLHPFLQ
RQQLAYGIYVIHQAGNGTFNRAKLLNVGVREALRDEEWDCLFLHDVDLLPENDINGNLVCDPRGPRHVAVAMNKFG
YSLPYPQYFGGVSALTPDQY LKMNGFPNEYWGWGGEDDDIATRVRLAGMKISR PPTSVGHYKMVKHRGDKGNEEN
PHRFDLLVRTQNSWTQDGMNSLT YQLLARELGPLYTNITADIGTDPRGPRAPSGPRYPPGSSQAFRQEMLQRRPP
ARPGPLSTANHTALRGSH

503/6881
FIGURE 470

GGCACGAGGGCCCCAGGAGAGGCAGAGAGTGAGGGAAAGGGCCTGGCCGGCATGCACAGATAGGATCACGGTCCT
GGGAGAATTCCCTGCTCTTATAGTCTAACCTACCATGGCTTCTCTTTTCTCAAGGCTCCCTCATGCTGCCCTTTGG
CCCTAGTGGCTGGTTTCCAGGGCTGAGGGGACTGAGTGAGCTGCCTGAGAAAAGAGGGTAGGGAACAGAAAAGCC
AGCCAGGAGCTGTGGGAGGAAACGCCCTCAGTAAAGATGACCGCGGTCACTGTTATCTAAACGCAAGTGAAGCCG
AGTCACAGGACCCGGATGTTGTGTCAGTTTCGACGGTAAACGACCCTGCCAGCTTCCAAGAGGGCGGCTTCACTGTGC
GAATAGGTGAGAAGCCAAGAAGGAGGCGCGCTGGAGTTACTTCCGCGCGGTTCTCCTTCCCGCAGTCTGCAGCCG
GAGTAAGATGCGCGCGCTGAGGGCTTTGTGCGGCTTCCGGGGCGTCGCGGCCAGGTGCTGCGGCCCTGGGGCTGG
AGTCCGATTGCCGATTCAGCCCAGCAGAGGTGTTCCGGCAGTGGCAGCCAGATGTGGAATGGGCACAGCAGTTTGG
GGGAGCTGTTATGTACCCAAGCAAAAGAAACAGCCCCTGGAAGCCTCCACCTTGGAATGATGTGGACCCTCCAAA
GGACACAATTGTGAAGAACATTACCCTGAACTTTGGGCCCCAACACCCAGCAGCGCATGGTGTCTGCGACTAGT
GATGGAATTGAGTGGGGAGATGGTGCAGGAGTGTGATCCTCACATCGGGCTCCTGCACCCAGGCACTGAGAAGCT
CATTGAATACAAGACCTATCTTCAGGCCCTTCCATACTTTGACCGGCTAGACTATGTGTCCATGATGTGTAACGA
ACAGGCCTATTCTCTAGCTGTGGAGAAGTGTGTAACATCCGGCCTCCTCCTCGGGCACAGTGGATCCGAGTGCT
GTTTGGAGAAATCACACGTTTGTGTAACCACATCATGGCTGTGACCACACATGCCCTGGACCTTGGGGCCATGAC
CCCTTTCTTCTGGCTGTTTGAAGAAAGGAGAGATGTTTGAAGTTCTACGAGCGAGTGTCTGGAGCCCGAATGCA
TGCTGCTTATATCCGGCCAGGAGGAGTGCACCAGGACCTACCCCTTGGGCTTATGGATGACATTTATCAGTTTTTC
TAAGAACTTCTCTCTTCGGCTTGATGAGTTGGAGGAGTGTCTGACCAACAATAGGATCTGGCGAAATCGGACAAT
TGACATTGGGGTTGTAACAGCAGAAGAAGCACTTAAGTATGGTTTTAGTGGAGTGATGCTTCGGGGCTCAGGCAT
CCAGTGGGACCTGCGGAAGACCCAGCCCTATGATGTTTACGACCAGGTTGAGTTTGATGTTTCTGTTGGTTCTCG
AGGGGACTGCTATGATAGGTACCTGTGCCGGGTGGAGGAGATGCGCCAGTCCCTGAGAATTATCGCACAGTGTCT
AAACAAGATGCCTCCTGGGGAGATCAAGGTTGATGATGCCAAAGTGTCTCCACCTAAGCGAGCAGAGATGAAGAC
TTCCATGGAGTCACTGATTCACTTTAAGTTGTATACTGAGGGCTACCAAGTTCCTCCAGGAGCCACATATAC
TGCCATTGAGGCTCCCAAGGGAGAGTTTGGGGTGTACCTGGTGTCTGATGGCAGCAGCCGCCCTTATCGATGCAA
GATCAAGGCTCCTGGTTTTGCCCATCTGGCTGGTTTGGACAAGATGTCTAAGGGACACATGTTGGCAGATGTCTGT
TGCCATCATAGGTACCCAAGATATTGTATTTGGAGAAGTAGATCGGTGAGCAGGGGAGCAGCGTTTGATCCCCC
TGCCATCAGCTTCTTCTGTGGAGCCTGTTTCTCACTGGAAATTGGCCTCTGTGTGTGTGTGTGTGTGTGTGTGT
GTGTGTGTATGTTCTGTGTACACTTGGCTGTCAGGCTTTCTGTGCATGTACTAAAAAAGGAGAAATTATAATAAAT
TAGCCGTCTTGCGGCCCTAGGCCTAAAAA

504/6881
FIGURE 471

MAALRALCGFRGVAAQVLRPGAGVRLPIQPSRGVRQWQPDVEWAQQFGGAVMYP SKETAHWKPPPWNVDVDPKDT
IVKNITLNF GPQHAAHGVLRLVMELSGEMVRKCDPHIGLLHRGTEK LIEYKTYLQALPYFDRLDYVSMMCNEQA
YSLAVEKLLNIRPPPRAQWIRVLFGEITRLLNHIMAVTTHALDLGAMTPFFWLFEEREKMF EYERVS GARMHAA
YIRPGGVHQDLPLGLMDDIYQFSKNFSLRLDELEELLTNNRIWRNRTIDIGVVTAEEALNYGFSGVMLRGSGIQW
DLRKTQPYDVYDQVEFDVPVGSRGDCYDRYLCRVEEMRQSLRIIAQCLNKMPPGEIKVDDAKVSPPKRAEMKTS M
ESLIHHFKLYTEGYQVPPGATYTAIEAPKGEFGVYLVSDGSSRPYRCKIKAPGFAHLAGLDKMSKGHMLADVVAI
IGTQDIVFGEVDR

505/6881
FIGURE 472

CCGGAACCCAAGATGGCTGCGCTGTTGCTGAGACACGTTGGTCGTCATTGCCTCCGAGCCCACCTTTAGCCCTCAG
CTCTGTATCAGAAATTGGTCTCTTCCCATGGCGATGTCCATCTGCCACCGTGGCACTGGTATTGCTTTGAGTGCA
GGGGTCTCTCTTTTTGGCATGTCGGCCCTGTTACTCCCTGGGAACCTTTGAGTCTTATTTGGAACCTTGGAAGTCC
CTGTGTCTGGGGCCAGCACTGATCCACACAGCTAAGTTTGCACCTTGCTTCCCTCTCATGTATCATACCTGGAAT
GGGATCCGACACTTGATGTGGGACCTAGGAAAAGGCCTGAAGATTCCCCAGCTATACCAGTCTGGAGTGGTTGTC
CTGGTTCTTACTGTGTTGTCCTCTATGGGGCTGGCAGCCATGTGAAGAAAGGAGGCTCCCAGCATCATCTTCCTA
CACATTATTACATTCACCCATCTTTCTGTTTGTCACTTATCTCCAGCCTGGGAAAAGTTCTCCTTATTTGTTT
AGATCCTTTTGTATTTTCAGATCTCCTTGGAGCAGTAGAGTACCTGGTAGACCATAATAGTGGAAGGGTCTAG
TTTTCCCCTTGTTTCTAAAGATGAGGTGGCTGCATCTCTCTCCATATTGGGCTTT

506/6881
FIGURE 473

AATCATAGTGAAAGATTCGTTTTTCATTGCAGAGTGGTATGATCCAAATGCTTCACTTCTTCGACGTTATGAGCTT
TTATTTTACCCAGGGGATGGATCTGTTGAAATGCATGATGTAAAGAATCATCGCACCTTTTTTAAAGCGGACCAAA
TATGATAACCTGCACCTTGGAAGATTTATTTATAGGCAACAAAGTGAATGTCCTTTTCTCGACAACCTGGTATTAATT
GACTATGGGGATCAATATACAGCTCGCCAGCTGGGCAGTAGGAAAGAAAAACGCTAGCCCTAATTAAACCAGAT
GCAATATCAAAGGCTGGAGAAATAATTGAAATAATAAACAAAGCTGGATTTACTATAACCAAACCTCAAAATGATG
ATGCTTTCAAGGAAAGAAGCATTGGATTTTCATGTAGATCACCAGTCAAGACCCTTTTTTCAATGAGCTGATCCAG
TTTATTACAACCTGGTCCTATTATTGCCATGGAGATTTTAAAGAGATGATGCTATATGTGAATGGAAAAGACTGCTG
GGACCTGCAAACTCTGGAGTGGCACGCACAGATGCTTCTGAAAAGCATTAGAGCCCTCTTTGGAACAGATGGCATA
AGAAATGCAGCGCATGGCCCTGATTCTTTTGCTTCTGCGGCCAGAGAAATGGAGTTGTTTTTTCCTTCAAGTGGA
GGTTGTGGGCCCGGCAAACTGCTAAATTTACTAATTGTACCTGTTGCATTGTTAAACCCCATGCTGTCAGTGAA
GGACTGTTGGGAAAAGATCCTGATGGCTATCCGAGATGCAGGTTTTGAAATCTCAGCTATGCAGATGTTCAATATG
GATCGGGTTAATGTTGAGGAATTCATGAAGTTTATAAAGGAGTAGTGACCGAATATCATAGGACATGGTGACAG
AAATGTATTCTGGCCCTTGTGTAGCAATGGAGATTCAACAGAATAATGCTACAAAGACATTTGAGAATTTTGTG
GACCTGCTGATCCTG

507/6881
FIGURE 474

GCCCTTGCCCTTGAGTCAGTGCGCTGCTCTCCAGCCCGCTTGAACGCTCCCCGCAGCCACCGCCACCCATTGGAAT
GGCCAACAGGGGACCTGCATATGGCCTGAGCCGGGAGGTGCAGCAGAAGATTGAGAAACAATATGATGCAGATCT
GGAGCAGATCCTGATCCAGTGGATCACCACCCAGTGCCGAAAGGATGTGGGCCGGCCCCAGCCTGGACGCGAGAA
CTTCCAGAACTGGCTCAAGGATGGCACGGTGCTATGTGAGCTCATTAATGCACTGTACCCCGAGGGGCAGGCCCC
AGTAAAGAAGATCCAGGCCTCCACCATGGCCTTCAAGCAGATGGAGCAGATCTCTCAGTTCTTGCAAGCAGCTGA
GCGCTATGGCATTAAACACCACTGACATCTTCCAAACTGTGGACCTCTGGGAAGGAAAGAACATGGCCTGTGTGCA
GCGGACGCTGATGAATCTGGGTGGGCTGGCAGTAGCCCGAGATGATGGGCTCTTCTCTGGGGATCCCAACTGGTT
CCCTAAGAAATCCAAGGAGAATCCTCGGAACTTCTCAGATAACCAGCTGCAAGAGGGCAAGAACGTGATCGGGTT
ACAGATGGGCACCAACCGCGGGGCGTCTCAGGCAGGCATGACTGGCTACGGGATGCCACGCCAGATCCTCTTGATC
CCACCCAGGCCTTGCCCCCTGCCCTCCACGAATGGTTAATATATATGTTAGATATATATTTTAGCAGTGACATTC
CCAGAGAGCCCCAGAGCTCTCAAGCTCCTTTCTGTGAGGGTGGGGGGTTCAGCCTGTCCTGTACCTCTGAGGTG
CCTGCTGGCATCCTCTCCCCCATGCTTACTAATACATTCCCTTCCCCATAGCCATCAAAACTGGACCAACTGGCC
TCTTCCCTTTCCCTGGGACCAAAATTTAGGGGCCTCAGTCCCTCACCGCCATGCCCTGGCCTATTCTGTCTCTCC
TTCTTCCCCCTGGCCTGTTCTGTCTCTGAGCTCTGTGTCTCCGTTTCATTCCATGGCTGGGAGTCACTGATGCTG
CCTCTGCCTTCTGATGCTGGACTGGCCTTGCTTCTACAAGTATGCTTCTCCCACAGCTGTGGCTGCAGGAACCTTA
ATTTATAGGGAGGAGCCTGTGGCAGCTGCTGCCCCAGCCACAGCTGCACTGACTGTGCTCACACACATCTGGGG
CAGCCTTCCCTGGCAGGGGCCCTCGTGGCTTCTCATTTTCCATTCCCTTCACTGTGGCTAAGGGGTGGGGTGAGG
GGATGGAGAGGGAGGGCTGCCTACCATGGTCTGGGGCTTGAGGAAGATGAGTTTGTTGATTTAAATAAAGAATTT
GTCATTTTTG

508/6881
FIGURE 475

MANRGPAYGLSREVQQKIEKQYDADLEQILIQWITTQCRKDVGRPQPGRENFQNLKDGTVLCELINALYP EGQA
PVKKIQASTMAFKQMEQISQFLQAAERYGINTTDIFQTVDLWEGKNMACVQRTLMNLLGGLAVARDDGLFSGDPNW
FPKKSKENPRNFSDNQLQEGKNVIGLQMGITNRGASQAGMTGYGMPRQIL

509/6881
FIGURE 476A

GTGGAGCCGAGCGGTGCGGAGCAGATCTGGTGGTTCTCCGGAGAGCAGCTTCCTCGGGTGTTACATGAGCCAAGC
CCTCACTGTACAGAAGAGTGAGAGCTGAAACCTGTTCCCTGAGCTGATCAGAAGGACATCCCTTGGCCCCCTCCAT
CTGGGCTCCTGTGGATAGGAGGGGCTGGGTGAGCAGGCCAGCTGGGCTATGGTGTGGTGCCTCGGCCTGGCCGTC
CTCAGCCTGGTCACTAGCCAGGGGGCTGACGGTCGAGGGAAGCCTGAGGTGGTATCGGTGGTGGGCCGGGCTGGG
GAGAGTGTGGTGCTGGGCTGTGACCTGCTGCCCCGGCCGGCCGGCCCCCCTGCATGTCATCGAGTGGCTGCGC
TTTGGATTCTGTCTCCCATCTTCATCCAGTTCGGCCTCTACTCTCCCGAATTGACCCTGATTACGTGGGACGA
GTCCGGCTGCAGAAGGGGGCCTCTCTCCAGATTGAGGGTCTCCGGGTGGAAGACCAGGGCTGGTACGAGTGCCGC
GTGTTCTTCTGGACCAGCACATCCCTGAAGACGATTTTGCTAACGGCTCCTGGGTGCATCTGACAGTCAATTCA
CCCCCTCAATTCCAGGAGACACCTCCTGCTGTGTTGGAAGTGCAGGAAGTGGAGCCTGTGACCCTGCGTTGTGTG
GCCCCGTGGCAGCCCCCTGCCTCATGTGACGTGGAAGCTCCGAGGAAAGGACCTTGGCCAGGGCCAGGGCCAGGTG
CAAGTGCAGAACGGGACGCTGCGGATCCGCCGGGTAGAGCGAGGCAGCTCTGGGGTCTACACCTGCCAAGCCTCC
AGCACTGAGGGCAGCGCCACCCACGCCACCCAGCTGCTAGTGTAGGACCCCCAGTCATCGTGGTGGCCCCCAAG
AACAGCACAGTCAATGCCTCCCAGGATGTTTCATTGGCCTGCCATGCTGAGGCATACCCCTGCTAACCTCACCTAC
AGCTGGTTCAGGACAACATCAATGTCTTCCACATTAGCCGCTGCAGCCCCGGGTGCGGATCCTGGTGGACGGG
AGCCTGCGGCTGCTGGCCACCCAGCCTGATGATGCCGGCTGCTACACCTGTGTGCCAGCAATGGCCTCCTGCAT
CCACCCTCAGCCTCTGCCTACCTCACTGTGCTCTACCCAGCCCAGGTGACAGCTATGCCTCCTGAGACACCCCTG
CCCATAGGCATGCCGGGGGTGATCCGCTGCCCGTTCTGTCCAACCCCCACTGCTCTTTGTGAGCTGGACCAAG
GATGGAAGGGCCTGCAGCTGGACAAGTTCCTGGCTGGTCCCAGGGCACAGAAGGCTCACTGATCATCGCCCTG
GGGAACGAGGATGCCCTGGGAGAATACTCCTGCACCCCTACAACAGTCTTGGTACCGCCGGGCCCTCTCCTGTG
ACCCGCGTGCTGCTCAAGGCTCCCCAGCTTTTATAGAGCGGCCCAAGGAAGAATATTTCCAAGAAGTAGGGCGG
GAGCTGCTCATCCCCTGCTCCGCCCAAGGGGACCCTCCTCCTGTTGTCTCTTGGACCAAGGTGGGCCGGGGGCTG
CAAGGCCAGGGCCAGGTGGACAGCAACAGCAGCCTCATCCTGCGACCATTGACCAAGGAGGGCCACGGGCACTGG
GAATGCAGTGCCAGCAATGCTGTGGCCCGAGTGGCCACCTCCACGAACGTCTACGTGCTGGGCACTAGCCCTCAT
GTTGTCACCAATGTGTCCGTGGTGGCTTTGCCCAAGGGTGCCAATGTCTCCTGGGAGCCTGGCTTTGATGGTGGT
TATCTGCAGAGATTCAAGTGTCTGGTACACCCCACTGGCCAAGCGTCTGACCGAATGCACCATGACTGGGTGTCC
TTGGCAGTGCCTGTGGGGGCTGCTCACCTCCTAGTGCCAGGGCTGCAGCCCCACCCAGTACCAGTTCAGCGTG
CTAGCTCAGAACAAGCTGGGGAGTGGTCCCTTCAGCGAAATCGTCTTGTCTGCTCCGGAAGGGCTTCCTACCACG
CCAGCTGCACCCGGGCTTCCCCCAACAGAGATACCGCCTCCCTGTCCCCTCCGCGGGGTCTGGTGGCAGTGAGG
ACACCCCGGGGGTACTCCTGCATTGGGATCCCCCAGAGCTGGTCCCTAAGAGACTGGATGGCTACGTCTTGAA
GGCCGGCAAGGCTCCCAGGGCTGGGAGGTGCTGGACCCGGCTGTGGCAGGCACAGAAACAGAGCTGCTGGTGCCA
GGCCTCATCAAGGTATGTTCTCTACGAGTTCGCCTCGTGGCCTTCGCGGGCAGCTTCGTGACGACCCCAAGCAA
CACGGCCAACGTCTCCACTTCCGGTCTGGAGGTCTACCCTTCGCGCACGCAGCTGCCGGGCCTCCTGCCTCAGCC
CGTGCTGGCCGGCGTGGTGGGCGGAGTCTGCTTTCTGGGAGTGGCCGTCTTGTGAGCATCCTGGCCGGCTGCCT
CCTGAACCGGCGCAGGGCTGCCCGCCGCCGCCGAAGCGCCTCCGCCAAGATCCACCTCTTATCTTCTCTCCGAC
CGGGAAGTCAGCTGCACCCCTCTGCTCTGGGCTCAGGCAGTCTGACAGCGTGGCGAAGCTGAAGCTCCAGGGATC
CCCAGTCCCCAGCCTGCGCCAGAGTCTGCTCTGGGGGATCCTGCCGGAAGTCCCAGCCCCCAGCCGATCCTCC
ATCTAGCCGGGGACCTTACCTCTGGAGCCCATTTGCCGGGGCCAGACGGGCGCTTTGTGATGGGGCCCACTGT
GGCGGCCCCCAGGAAAGGTGAGGCCGGGAGCAGGCAGAACCTCGGACTCCAGCCCAGCGTCTGGCCCGGTCTCTT
TGACTGTAGCAGCAGCAGCCCCAGTGGGGCAGCCAGCCCTCTGCATTGAAGACATCAGCCCTGTGGCACCCCC
TCCAGCAGCCCCACCCAGTCCCTTGCCAGGTCTTGACCCCTGCTCCAGTACCTGAGCCTGCCCTTCTTCCGAGA
GATGAATGTGGATGGGGACTGGCCCCGCTTGAGGAGCCAGCCCTGCTGCACCCCAAGATTACATGGATAACCCG
GCGCTGTCCACCTCATCTTCTCCTTCGTTCTCCAGAAACCCCTCCTGTATCCCCAGGGAATCACTTCTGGGGC
TGTGGTAGGGGCTGGGGCCACTGCAGAGCCCCCTTACACAGCCCTGGCTGACTGGACACTGAGGGAGCGGCTGCT
GCCAGGCCTTCTCCCTGCTGCCCCCTGAGGCAGCCTCACCAGCCAGAGCAGTGGGCGAGGCAGCGCTTCGTTCCT
GCGGCCCCCTCCACAGCCCCCTCTGCAGGAGGCAGCTACCTCAGCCCTGCTCCAGGAGACACCAGCAGCTGGGC
CAGTGGCCCTGAGAGATGGCCCCGAAGGGAGCATGTGGTGACAGTCAGCAAGAGGAGGAACACATCTGTGGACGA
GAACTATGAGTGGGACTCAGAATTCCCTGGGGACATGGAATTGCTGGAGACTTTGCACCTGGGCTTGGCCAGCTC
CCGGCTCAGACCTGAAGCTGAGCCAGAGCTAGGTGTGAAGACTCCAGAGGAGGGCTGCCTCCTGAACACTGCCCA

511/6881
FIGURE 477

TTTCCGTGCTACCTACAGAGGGGTCCATATGGCGTTGTTCTGGATTCCCGTCGTAACTCAAAGGGAACTTTCA
CAATGTCCGGAGCCCTTGATGTCCTGCAAATGAAGGAGGAGGATGTCCTTAAGTTCCTTGACGAGGAACCCACT
TAGGTGGCACCAATCTTGACTTACAGATGGAACAGTATATCTATAAAAGGAAAAGTGATGGCATCTACATCATAA
ATCTGAAGGGAACCTGGGAGAAGCTTCTGCTGGCAGCTCGTGCTATTGTTGCCATTGAAAACCCTGCTGATGTCA
GTGTTATATCCTCCAGGAATACTGGCCAGAGGGCTGTGCTGAAGTTTGCTGCTGCCACTGGAGCCACTCCAATTG
CTGGCCACTTCACTCCTGGAACCTTCACTAACCAGATCCAGGCAGCCTTCTGGGAGCCATGGCTTCTTATGGTTA
CTGACCCCAGGGGCTTGACCATCAGCCTCTCACAGAGGCATCTTATGTTAATCTACCTACCATCGCTCTGTGTAA
ACAGATTCTCCTCTGCGCTATGTGGACATTGCCATCCCGTGCAACAACAAGGGAGCTCACTGAGTGGGTTTGATG
TGGTGGATGCTGGCTCGGGAAGTACTGTGCATGCGTGGCACCATTTCCCGTGAACACCCATGGGAGGTCATGCCT
GATCTCTGCTTCTACAGAGATCCTGAAGAGATTGAAAAAGAAGAGCAGGCTGCTGCTGAAAAGGCAGTGACCAAG
GAGGAATTTGAGGGTGAATGGTCTGCTCCAGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAGACTGGTTT
GAAGGTATACAGGTGCCCTCTGTGCCTATTGAGCAGTTCTACTGAACAATGGAGCACTCAGCCTGCCACGGAAT
ACTGGTCTGCAGCTCCCACTGCTCAGGCCACTGAATGGGTAGGAGCAACCACTGAATGGTCTTAAGCTGTTCTTG
CATGGGCTCTTAAGCAACATGGAAAAATGGTTGATGGAAAATAACATCAGTTTCT

512/6881
FIGURE 478

MSGALDVLQMKEEDVLKFLAAGTHLGGTNLDLQMEQYIYKRKSDGIYIINLKGTWEKLLLAARAIVAIENPADVS
VISSRNTGQRAVLKFAAATGATPIAGHFTPGTFTNQIQAAFWEPPWLLMVTDPGR

513/6881
FIGURE 479

AAAGGGAAACTTTTCAATGTCCGGAGCCCTTGATGTCCTGCAAATGAAGGAGGAGGATGTCCTTAAGTTCCTTG
CAGCAGGAACCCACTTAGGTGGCACCAATCTTGA CTTACAGATGGAACAGTATATCTATAAAAGGAAAAGTGATG
GCATCTACATCATAAATCTGAAGGGAACCTGGGAGAAGCTTCTGCTGGCAGCTCGTGCTATTGTTGCCATTGAAA
ACCCTGCTGATGTCAGTGTTATATCCTCCAGGAATACTGGCCAGAGGGCTGTGCTGAAGTTTGCTGCTGCCACTG
GAGCCACTCCAATTGCTGGCCACTTCACTCCTGGAACCTTCACTAACCAGATCCAGGCATCTTATGTTAATCTAC
CTACCATCGCTCTGTGTAACACAGATTCTCCTCTGCGCTATGTGGACATTGCCATCCCGTGCAACAACAAGGGAG
CTCACTGAGTGGGTTTGATGTGGTGGATGCTGGCTCGGGAAGTACTGTGCATGCGTGGCACCATTTCCTCGTGAAC
ACCCATGGGAGGTCATGCCTGATCTCTGCTTCTACAGAGATCCTGAAGAGATTGAAAAAGAAGAGCAGGCTGCTG
CTGA

514/6881
FIGURE 480

MSGALDVLQMKEEDVLKFLTAGTHLGGTNLDFQMEQYIYKRRSDGIYIINLKRTWEKLLLAARAIVAIENPAVVS
VISSRNTGQRAVLKFAAVTGATPIAGRFTPGNFTNQIQEASYVNLPTIALCNTDSPLHFVDIAIPCNNKGAH

515/6881
FIGURE 481A

AGGTAGCAAGATGCCCGCTGAGGAAGGCTGTAGTGTGCGGGCCGAAGCGGACAGGGAATTGGAGGAGCTTCT
GGAAAGTGCTCTTGATGATTTGATAAAGCCAAACCCTCCCCAGCACCCCCTTCTACCACCACGGCCCCCTGATGC
TTCGGGGCCCCAGAAGAGATCGCCAGGAGACACTGCCAAAGATGCCCTCTTCGCTTCCCAAGAGAAGTTTTTCCA
GGAACATATTCGACAGTGAACCTGGCTTCCCAAGCCACTGCGGAGTTTCGAGAAGGCAATGAAGGAGTTGGCTGAGGA
AGAACCCACCTGGTGGAGCAGTTCCAAAAGCTCTCAGAGGCTGCAGGGAGAGTGGGCAGTGATATGACCTCCCA
ACAAGAATTCACCTTCTTGCTAAAGGAAACACTAAGTGGATTAGCCAAAAATGCCACTGACCTTCAGAACTCCAG
CATGTCGGAAGAAGAGCTGACCAAGGCCATGGAGGGGCTAGGCATGGACGAAGGGGATGGGGAAGGGAACATCCT
CCCCATCATGCAGAGTATTATGCAGAACCTACTCTCCAAGGATGTGCTGTACCCATCACTGAAGGAGATCACAGA
AAAGTATCCAGAATGGTTGCAGAGTCATCGGGAATCTCTACCTCCAGAGCAGTTTGAAAAATATCAGGAGCAGCA
CAGCGTCATGTGCAAAATATGTGAGCAGTTTGAGGCAGAGACCCCCACAGACAGTGAAACCACTCAAAGGCTCG
TTTTGAGATGGTGTGATCTTATGCAGCAGCTACAAGATTTAGGCCATCCTCCAAAAGAGCTGGCTGGAGAGAT
GCCTCCTGGCCTCAACTTTGACCTGGATGCCCTCAATCTTTTCGGGGCCACCAGGTGCCAGTGGTGAACAGTGTCT
GATCATGTGAACACAACACGTTTTCTCTCTGAGTCCCAGCTATGGGGAACATCTGGAGTCAGCAGAACCATTG
GGACCTGAGGCAGGAGTGTACCTGCGGGAGAAGTCTGCCCGCTGCCCTCTGTCTATCCCATTCAGATTGTGCCA
TACCAGCTGAGGTTTTTCTCTGTCTCTCTAGGAATAGGGTCTGTTTTACAGGCCATTTCTGTGAACCCTACTCC
ATTGTGGTTTTCTGCCACTATCAAAGTTCAGCTACCTGCAAGGTGAAGGAAGGCATCCCTTTTGGGGCATGCACT
TTCTTTCTTTCTCAAATAATGTTATATGTGGCCACACTGATGTTACCTTTACGTCCAGGGTCTTTGTGCCTT
GTCTCTACTCCCTCTCTTGATCTGGGAGGAGGGGCAGAGACCTGGGACTCTGTATTTCTATAGTTCTCCTGGC
AGAGCCTTTGAGAATGGGGAGAAACAGCCTGGGCTGGGGCTACAGGTCTGTCACTATGCTCTCTTGCCCTTCAGAC
AGACCATTCTGAATTCTCTAAAGGGAAAGGGCTTTTGATCTAATCACAATAGAGTTGAAAGAGAGGCCTTAGGA
TTCTCCTCTCTCTAGGTGCTGAGCCCTCACCTCCCTGTTCCAGGCTGAGAACTCAAATGGTTACCCTGCTTCTTC
CTACAATGCTGTGTGATATGGGTGAACCCAGCCCTGACCTTCTCTATCCCTGCCATCCTCCCTTTTACCTC
CTCTCTTTTTTAAACACCTGTTTATCCCAACCTTTTTGAGCTCAAGCTGTGATAAAGAAGGGCCCATCCTATTTT
CCCTCATCTAGTCCATTTACGATTCTCACTGACTCCCGTCTTCTGTCAGACACAAATAAACCCAGTGTCAAGT
CTAGGAAATTAATGGCTATTCTTCCCAGATACATTCTGGCTTATTTGAGATACATGATTCTCTTAGAATCCTGT
CCCTTGGTTTCAGGAAAGTAGCTTGGAAGAGGAGTAGGGGTATAGCTTGGGTCCCTTTTCTGCAAGGCCCCATGG
GGCAGAATATAATAAATATTCTGAGTGAGGAGTGTGGTCTTTTTCTGATCTTCTCAGCTTCCGTAAGTTGCAGA
GTGAGGTATATTAGGAGACTAGTTCTACACAATATTGTAATGCTGGGTCCATCAACACCCACCTTCCACAACCTC
AGTCTGCACCTCAGTTGGCAAAGGAGACTGGATGGCCATCTTCTCATGTTCCCTTGAGTATTTCAATGTAGAA
AGCCCTTCAAGTGGTATTATATTTTAACTTTTACATTATTGTTATTAATGTTAGTAATATATTGTTATGTTTTT
TAAATTATTTTTCTTTAAGCTGACGTGGCTTTTTTCTGTGGCTCCCAGTGGGTCTACGGACCTTGGCTGACATA
TGTTGGTAGGTACTCTGGTCAGCTCAGCTGGCTGTCTGGTTCACTCAGAAGATAAGTCTCTCAAAGCAAATTC
ACATGCATTATGAGTCGCTTTGAGCTTCTGACATGTCACTTGCCCCGAGGTTAAACTTTTACCCCTTGAAGAC
CTTACATGTTTTATGGTATTGGTGAGGAAGGAAATGTTCTCAAGGTCTCAGGCTATTTGGGAAATTCCAACCTCT
ATACCTTACCAGAGCATGGAAGAGCCCAGATCTGAATGTAAACGTCCTGTTCTGCCAGAGATGGAAAAAATAC
AGGTATACTTGTGATATAGTCATGGGGCTTCAGTGTCACTATTTTCTCCTTAAAGCTCCAGCCAAAAACTGGACA
AGGATAGAGAGGAGGAGGAAGAACAAGAGCCCTTCTCTATGAACCTTGTGCCTTCTGTCTACCAGTTTTCT
TTTACAGATTCTCACTTCTGCTAGCCTAGCCAGGGCTTACTCCAGGAATCTAAATAGATGCCCTAGTCCACTTTA
TCTTTGTTCCCAAGGCACTCATTTTTATTTGATTTTGATTGAATGTGAGCAGGTTGACCTCAGGTCACACTTTG
TTCCAAAACTTTTGAATTATTCAGGACTTGTGGTGGAGTTATGGTACTCTAGGGCAGTCTTTCTCAAACCTAT
GTATGGTAAAGGACCAGGTTTTTGTGTTTCCAGTCTTCACTTATCAATATGCATTCTTATTGCCGATGACAGGT
ATGGAGTTCACACTGTGTGCTGCCGACCCGGCAAGTTTGACAGCACCCAACTGGCCAGACTGTTCTGTAGGTTA
AGTCCATTGATCATGTACTTGATATCACAGCAACATTGAAATGCTAAAAAGTTTTTAAACACTCTCAATTTCTA
ATTACCATGTACAGACTGGTGAAAAAAGGTGTTCACTGACCAGCACAAAGTCTGCAGATCATCTTG
AGTAGCACTGTTTTGGGGCCCTCGGTCTCTCTGAAGACCCTAGCAGAACTGATACCTACCTGTATCTCTGTTCT
CTCCTATTTGAGTTTCACTTCCAGAGAACTTGTTCTTCAGCAAGAATGTGTCACTAGTAAGGACATCTCTAGCAT
TTCTCTAGCCTTCTTTTCTGTCTGCTCAAAAATAATCGTTACAAAGCTTAGGTTTAAAGCTGTATATGAAATATTT
ATGCGACTCTCAAACCTTTAAAGGAGTTGCTCCTTTGTTCCAAAATTAATGTGTTAGATAAATTTGTGATTGTAT

516/6881
FIGURE 481B

GGGTGGCTTCATGAATTAAGAATTGAATTAATACAGACTTTTGGATAATAAAAAAAAAAAAAA

517/6881
FIGURE 482

MAAAEEGCSVGAEADRELEELLESALDDFDKAKPSAPPSTTTAPDASGPQKRSPGDTAKDALFASQEKFFQELF
DSELASQATAEFKAMKELAEELPHLVEQFQKLSEAAGRVSMTSQQEFTSCLKETLSGLAKNATDLQNSSMSE
EELTKAMEGLGMDEGDGEGNILPIMQSIMQNLLSKDVLYPSLKEITEKYPEWLQSHRESLPPEQFEKYQEHSVM
CKICEQFEAETPTDSETTQKARFEMVLDLMQQLQDLGHPPKELAGEMPGLNFDLDAIINLSGPPGASGEQCLIM

518/6881
FIGURE 483A

GAGAAGGGACCTTCAGGTCCAGGCAAAGGGGGAAGTCTCTGTCGTGGGAACGAAAAAGAAAGAGGATTTACAGGGT
GGGGGGACAGAGGGGCAGCAGGAACCAGAAGGGGAGACAGTGGCGGTTCGCGCGGGGCGGATCCGAGAGTTCCCTT
TAGAGAACGGAGCTCACGGGCGGGGAGGCCCTCACCTGCTAGTAGGACGCAGAAAGACAGAAGGCGAAGGAGACCC
CGACTTCCCGGGTCAGCCCCAGAGCCACCCCTGCCGTAGCCATCTTGCCCTCTCTGCTGAGCGGAAGCCCCCGTT
CGGCTCCTGTCTGTTAGCGGCCTCTCTAGGCTACCACTGACACCGTCTCTGTGGCCCGGAGCCTAAGAGACCGGA
AGTTCGTGTTTTCCAGGCGCTTCCGGAAACCGCGGGAGAGGGTTCGCTGACGTGGAGGCGTCCGAAGGGCAGCAGGG
TGTGTCGGGGCTCGGATTAAGACATCGGAGTCGGAGACCTGAGAGATGTTAACCAAATTCGAGACCAAGAGCGCG
CGGGTCAAAGGGCTCAGCTTTCACCCCAAAAGACCTTGGATCCTGACTAGTTTACATAATGGGGTCATCCAGTTA
TGGGACTATCGGATGTGCACTCTCATTGACAAAGTTTGATGAACATGATGGTCCAGTGCGAGGCATTGACTTCCAT
AAGCAGCAGCCACTGTTTCGTCTCTGGAGGAGATGACTATAAGATTAAGGTTTGGAATTACAAGCTTCGGCGCTGT
CTTTTCACATTGCTTGGGCACCTTAGATTATATTCGCACCACGTTTTTTCATCATGAATATCCCTGGATTCTGAGT
GCCCTCCGATGATCAGACCATCCGAGTGTGGAAGTGGCAATCTAGAACCTGTGTTTGTGTGTTAACAGGGCACAAC
CATTATGTGATGTGTGCTCAGTTCCACCCACAGAAGACTTGGTAGTATCAGCCAGCCTGGACCAGACTGTGCGC
GTTTGGGATATTTCTGGTCTGAGGAAAAAAACCTGTCCCTGGTGCGGTGGAATCGGATGTGAGAGGAATAACT
GGGGTTGATCTATTTGGAAGTACAGATGCAGTGGTGAAGCATGTACTAGAGGGTCACGATCGTGGAGTAACTGG
GCTGCCTTCCACCCCACTATGCCCCCTATTGTATCTGGGGCAGATGATCGTCAAGTGAAGATCTGGCGCATGAAT
GAATCAAAGGCATGGGAGGTTGATACCTGCCGGGGCCATTACAACAATGTATCTTGTGCCGTCTTCCACCCTCGC
CAAGAGTTGATCCTCAGCAATTCTGAGGACAAGAGTATTCGAGTCTGGGATATGTCTAAGCGGACTGGGGTTCAG
ACTTTCGCAGAGACCATGATCGTTTCTGGGTCTAGCTGCTCACCTAACCTTAACCTCTTGCAGCAGGCCAT
GATGGTGGTATGATTGTGTTTAAGCTGGAACGGGAACGGCCAGCCTATGCTGTTTCATGGCAATATGCTACACTAT
GTCAAGGACCGATTCTTACGACAGCTGGATTTCACAGCTCCAAAGATGTAGCTGTGATGCAGTTGCGGAGTGGT
TCCAAGTTTCCAGTATTCAATATGTCATACAATCCAGCAGAAAATGCAGTCTGCTTTGTACAAGAGCTAGCAAT
CTAGAGAATAGTACCTATGACCTGTACACCATCCCTAAAGATGCTGACTCCAGAAATCCTGATGCGCCTGAAGGG
AAACGATCCTCAGGCCTGACAGCCGTTTGGGTGCTCGAAATCGGTTTGCTGTCCTAGATCGGATGCATTGCGCTT
CTGATCAAGAATCTGAAGAATGAGATCACCAAAAAGGTACAGGTGCCCAACTGTGATGAGATCTTCTATGCTGGC
ACAGGCAATCTCCTGCTTCGAGATGCGGACTCTATCACACTCTTTGACGTACAGCAGAAAGCGGACTCTGGCATCT
GTGAAGATTTCTAAAGTGAAATACGTTATCTGGTTCAGCAGACATGTACATGTAGCACTACTAGCCAAACACGCC
ATTGTGATCTGTAACCGCAAAGTGGATGCTTTATGTAACATTTCATGAGAACATTTCGTGTCAAGAGTGGGGCTTG
GATGAGAGTGGGGTATTTATCTATACCACAAGCAACCACATCAAATATGCTGTCACCACTGGGGACCACGGGATC
ATTGAACTCTGGATTTACCCATCTATGTACACAGGGTGAAGGGCAACAATGTATACTGCCAGACAGGGAGTGT
CGTCCCCGGGTACTACCATTGATCCCACTGAGTTCAAATTCAGCTGGCCCTGATCAACAGAAAATATGATGAG
GTACTGCACATGGTGAGGAATGCCAAACTAGTTGGCCAGTCTATTATTGCTTATCTCCAGAAGAAGGGCTATCCT
GAAGTGGCACTGCATTTTGTCAAGGATGAGAAACTCGCTTTAGTCTGGCACTGGAGTGTGGAACATTGAGATT
GCTCTGGAAGCAGCCAAAGCACTGGATGACAAGAAGTCTGGGAAAAGCTGGGAGAAAGTGGCCCTGCTGCAGGGG
AACCACCAGATTGTGGAATGTGCTATCAGCGTACCAAAAACCTTTGACAAAACCTTCTCTCTGTATCTTATCACT
GGCAACTTAGAAAACTTCGCAAGATGATGAAGATTGCTGAGATCAGAAAGGACATGAGTGGCCACTATCAGAAT
GCCCTATACCTGGGTGATGTGTCAGAGCGTGTGCGGATCCTGAAGAAGTGTGGACAGAAGTCCCTGGCCTATCTC
ACAGCTGCTACCCATGGCTTAGATGAAGAAGCTGAGAGCCTAAAGGAGACATTTGACCCAGAGAAGGAGACAATC
CCAGACATTGACCCTAATGCCAAGCTGCTCCAGCCACCTGCACCTATCATGCCATTGGATACCAATTGGCCTTTA
TTGACTGTATCCAAAGGATTTTTTGAAGGCACCATTGCCAGCAAAGGGAAGGGAGGAGCACTGGCTGCTGACATT
GACATTGACACTGTTGGTACAGAGGGCTGGGGAGAGGATGCAGAGCTGCAGTTGGATGAAGATGGGTTTGTGGAG
GCTACAGAAGGTTTGGGGGATGATGCTCTTGGCAAGGGACAGGAAGAAGGAGGTGGCTGGGATGTAGAAGAAGAT
CTGGAGCTCCCTCCTGAGCTGGATATATCCCTGGGGCAGCTGGTGGGGCTGAAGATGGTTTCTTTGTGCCCCA
ACCAAGGGAACAAGTCCAACCTCAGATCTGGTGAATAACTCTCAGCTTCCAGTTGATCACATCCTGGCAGGCTCT
TTGAAAACAGCCATGCGGCTCCTTCATGACCAAGTAGGGGTAATCCAGTTTGGCCCTACAAGCAACTGTTTCCTA
CAGACATACGCCCAGGGCCGCACAACCTATCAGGCTCTGCCCTGCCTACCCTCCATGTATGGCTATCCTAATCGC
AACTGGAAGGATGCAGGGCTGAAGAATGGTGTACCAGCTGTGGGCCTGAAGCTTAATGACCTCATCCAACGGTTG
CAGCTGTGCTACCAGCTCACCACAGTTGGCAAATTTGAGGAGGCTGTGGA AAAATTCGTTCCATCCTTCTCAGT

519/6881

FIGURE 483B

GTGCCACTTCTTGTGTGGACAATAAACAAGAGATTGCAGAGGCCAGCAGCTCATCACCATTGCGGTGAGTAC
ATTGTGGGTTTGTCCGTGGAGACAGAAAGGAAGAAGCTGCCCAAAGAGACTCTAGAACAGCAGAAGCGCATCTGT
GAGATGGCAGCCTATTTACCCACTCAAACCTGCAGCCTGTGCACATGATCCTGGTGCTGCGTACAGCCCTCAAT
CTGTTCTTCAAGCTCAAGAACTTCAAGACAGCTGCCACCTTTGCTCGGCGCCTACTAGAACTCGGGCCCAAGCCT
GAGGTGGCCCAACAGACCCGAAAAATCCTGTCTGCCTGTGAGAAGAATCCACAGATGCCTACCAGCTCAATTAT
GACATGCACAACCCCTTTGACATTTGTGCTGCATCATATCGGCCCATCTACCGTGGAAAGCCAGTAGAAAAGTGT
CCACTCAGTGGGGCCTGCTATTCCCCTGAGTTCAAAGGTCAAATCTGCAGGGTCACCACAGTGACAGAGATTGGC
AAAGATGTGATTGGTTTAAGGATCAGTCCTCTGCAGTTTCGCTAAGGCCCCCTTTGTGTGCATGGGTCAGTCACC
ATATGTTCCCCCAGAGAATGTGTCTATATCCTCCTTCTAACAGCACCTTCCCCCTGCAGCTACTCTTCAGATCT
GGCTCTCTGTACCCTAAAACCTAGTATCTTTTTCTCTTCTATGGAAAATCCGAAGGTCTAAACTTGACTTTTTTG
AGGTCTTCTCAACTTGACTACAGTTGTGCTCATAATTGTCCTTGCCTTTCCAGCTTAATTATTTTAAGGAACAA
TGAAAACCTCTGGGCTGGGTGGAGTGGCTCATACCTGTAATCCCAGCACCTTTGGGAGGCTACGGTGGGCAGATCAT
CTGAGGCCAGGAGTTCGAGACCTGCCTGGCCAACATGGCAACACCCCGTCTCTAATAAAAAATATAAAAATTAGCC
TGGCATGGTAGCATGCGCCTATAGTCCCAGCTGCTCAGGAGGCTGAGGCATGAGAATCGCTTGAACCTAGGAGGT
GGAGGTTGCATTCAACTGAGATCATACCACTTCATTCCAGCCTGGGTGACAGAGCAAGACTCTGTCTCAAAAAA
AAAAAAGGAAAACCTCTGTGATGGACATTTGTTTAGTAAATCCCTTCAGTATTTATCCCTCCTTTCCCCACAGCA
GCTTTCTTTCCTGTCAACTAGAAAGGAGCAGGATGTAATAAATACATTTTGGTGTGACTAGGCCACACCAACTCT
TAATCATCTCCCATTTTCCTTAGACATTTAAATTTCAAGGCAGGTACCCTCTGTGTACTCAGAAATTTGAAGAAG
TTATTTGGTTTTCCAAAATGCACACTGCGGGTTATTGATTTGTTCTTTACAACATTGTTCTCATATTTCTCACA
CTAAATAAATCTCTATGAGAGCTTCTTG

520/6881
FIGURE 484

AGCTGCGGTGTTGTGCTGTGGGGAAGGGAGAAGGATTTGTAAACCCGGAGTGAGGTTCTGCTTACCCGAGGCCG
CTGCTGTGCGGAGACCCCGGGTGAAGCCACTGTCATCATGTCTGACCAGGAGGCAAAACCTTCAACTGAGGACT
TGGGGGATAAGAAGGAAGGTGAATATATTAAACTCAAAGTCATTGGACAGGATAGCAGTGAGATTCACTTCAAAG
TGGTTCCAATGAATTCATTCAGGTTTCTCTTTGAGGGTCAGAGAATTGCTGATAATCATACTCC

521/6881
FIGURE 485

GAAGGATTTGTAAACCCCGGAGTGAGGTTCTGCTTACCCGAGGCCGCTGCTGTGCGGAGACCCCGGGTGAAGCC
ACTGTCATCATGTCTGACCAGGAGGCAAAACCTTCAACTGAGGACTTGGGGGATAAGAAGGAAGGTGAATATATT
AAACTCAAAGTCATTGGACAGGATAGCAGTGAGATTCACCTCAAAGTGAAAATGACAACACATCTCAAGAACTC
AAAGAATCATACTGTCAAAGACAGGGCGTTCCAATGAATTCATTCAGGTTTCTCTTTGAGGGTCAGAGAATTGCT
GATAATCATACTCCAAAAGAAGTGGGAATGGAGGAAGAAGATGTGATTGAAGTTTATCAGGAACAAATGGGGGGT
CATTCAACAGTTTAGATATTCTTTTTATTTTTTTCTTTCCCTCAATCCTTTCTCATTTTTAAAAATAGTTCTT
TTGTAATGTGGTGTTAAAAACGGAATTGAAACTGGCACCCCATCTCTTTGAAACATCTGGTAATCTGAATTCTA
GTGCTCATTATTCATTATTGTTTATTTTCATTGTGCTGATTTTTGGTGATCAAGCCTCAGTCCCCTTCATATTAC
CCTCTCCTTTTTATTGTGGTGATAAATAAGATTGACCAATGCAAGCGTTCATAATAACTTGCGAATTGGCCCTGA
TGTTCTAGCATGTGATTACTTCACT

522/6881
FIGURE 486

GTTTGCCAAAATCCCAGGCAGCATGGACCTCAGTCTTCTCTGGGTACTTCTGCCCCTAGTCACCATGGCCTGGGG
CCAGTATGGCGATTATGGATACCCATACCAGCAGTATCATGACTACAGCGATGATGGGTGGGTGAATTTGAACCG
GCAAGGCTTCAGCTACCAGTGTCCCCAGGGGCAGGTGATAGTGGCCGTGAGGAGCATCTTCAGCAAGAAGGAAGG
TTCTGACAGACAATGGAACCTACGCCTGCATGCCCACGCCACAGAGCCTCGGGGAACCCACGGAGTGCTGGTGGGA
GGAGATCAACAGGGCTGGCATGGAATGGTACCAGACGTGCTCCAACAATGGGCTGGTGGCAGGATTCCAGAGCCG
CTACTTCGAGTCAGTGCTGGATCGGGAGTGGCAGTTTTACTGTTGTGCTACAGCAAGAGGTGCCCATATTCCTG
CTGGCTAACAAACAGAATATCCAGGTCATATGGTGAGGAAATGGACATGATTTCTTACAATTATGATTACTATAT
CCGAGGAGCAACAACCACTTTCTCTGCAGTGGAAAGGGATCGCCAGTGGAAAGTTCATAATGTGCCGGATGACTGA
ATACGACTGTGAATTTGCAAATGTTTAGATTTGCCACATACCAAATCTGGGTGAAAGGAAAGGGGCCGGGGACAG
GAGGGTGTCCACATATGTTAACATCAGTTGGATCTCCTATAGAAGTTTCTGCTGCTCTCTTTCCTTCTCCCTGAG
CTGGTAACTGCAATGCCAACTTCCTGGGCCTTTCTGACTAGTATCACACTTCTAATAAAAATCCACAATTAAACCA
TGTTTTCTCACTTTTTCACATGTTTCATAGCAACTGCTTTATATGACTGATGATGGCTTCCTTGCACACCACATATA
CAGTGCGCATGCTTACAGCCGGGCTTCTGGAGCACCAGCTGCAGCCTGGCTACTGCTTTTTTACTGCAGAATGAAC
TGCAAGTTCAGCATAGTGGAGGGGAGAGGCAGAACTGGAGGAGAGGTGCAGTGAAGGTTCTCTACAGCTAAGCCT
GTTTGAATGATACGTAGGTTCCCCACAAAAGCAGGCTTTCTGCCCTGAGGGACATCTTCCCCTCCCCTGCTCC
ACATGAGCCATGCATGCTTAGCAATCCAAGTGCAGAGCTCTTTGCTCCAGGAGTGAGGAGACTGGGAGGTGAAAT
GGGGAAATGGAAGGGTTTGGAGGCAGAGCTGAAAACAGGGTTGGAAGGATTTCTTGAATTAGAAGACAAACGTTA
GCATACCCAGTAAGGAAAATGAGTGCAGGGGCCAGGGGAACCCGTGAGGATCACTCTCAAAATGAGATTAAAAACA
AGGAAGCAGAGAATGGTCAGAGAATGGGATTGAGATTGGGAACCTTGTGGGGATGAGAGTGACCAGGTTGAACTGG
GAAGTGGAAAAAGGAGTTTGTAGTCACTGGCACCTAGAAGCCTGCCACGATTCTTAGGAAGGCTGGCAGACACCC
TGGAACCCTGGGGAGCTACTGGCAAACCTCTCCTGGATTGGGCCTGATTTTTTTTGGTGGGAAAGGCTGCCCTGGGG
ATCAACTTTCCTTCTGTGTGTGGCTCAGGAGTTCTTCTGCAGAGATGGCGCTATCTTTCCTCCTCCTGTGATGTC
CTGCTCCCAACCATTGTACTCTTCATTACAAAAGAAATAAAAAATATTAACGTTT

523/6881
FIGURE 487

MDLSLLWVLLPLVTMAWGQYGDYGYPYQQYHDYSDDGWVNLNRQGF SYQCPQGQVIVAVRSIFSKKEGSDRQWNY
ACMP TPQSLGEPTECWWE EINRAGMEWYQTCSNNGLVAGFQSR YFESVLDREWQFYCCRYSKRCPYSCWLTTEYP
GHYGEEMDMISYNDYYIRGATTTFS AVERDRQWKFIMCRMTEYDCEFANV

524/6881
FIGURE 488

AGAGGAAGCCAAGAACGGTGAAAAGGCCAGGCGGAGTTCAGAGGAGGTGGACGGCCAGCACCCGGCCCAAGAGGA
GGTCCCGGAATCGCCCCAGACCTCTGGCCCAGAGGCAGAAAATAGGTGTGGGAGCCCCAGGGAGGAAAAGCCAGC
TGGAGAGGAAGCAGAGATGAGAAAAGGCTACAGAGGTGAAGGGGGAGAGGGTGCAAAATGAAGAGGTGGGACCTGA
ACATGACAGCCAAGAAACAAAGAAGCTGGAGGAGGGAGCTGCAGTGAAGGAGACCCCCACAGTCCCCCTGGAGG
AGTGAAGGGCGGAGATGTCCCCAAGCAGGAAAAAGGCAAGGAAAAACAACAGGAGGGGGCAGTGCTCGAGCCAGG
CTGCAGCCCCCAGACCGGCCCTGCCAGCTGGAGACCAGCAGTGAGGTCCAGAGCGAGCCAGCAGTCCCCAAGCC
GGAGGATGACACTCCTGTCCAGGACACTAAAATGTGAAGAACAGCTCATTGTGCCCCAGTGATGAAGTTGCTGGA
CACATCTCTTTGCAGGTAGCAGCAACAGTTGTAGCAGCAGCAGACGAAGCCATTGCAGAGGCAGAATATGCTGAG
TGTCTGGAGTCAGCCTGAAGACACAGGGTGGATTATTTCTGGCCTCCACACCAAACGTTCCCTTGCAGATGGAG
ACTGAATCTGAGGGCAGCAGACTTTTATCAGCTTGAGTTTATGTCAATTTGATGGACTTGGTTCAACAACAAGAAC
TTACTTAAAACAATGTACTGTGGTGATGAGTCCCAGGGGCAGTGGTCAGCCTGTGGAGCCCTGGATGCTATCCAC
ACCCACCTATCCCTGCAGCTAATTTAGCTGATCTCTAATTTAACTGAGCTCTAATTTAGCTGATCAGATTTTGCT
TGGGTAAAGTTCCTTTTTTAATGTTCTAAAGTGTTTACGGTTCCTCAATATCAGTTAAAAACTAATTTTAGGTGGC
CATAAACATAAAATAGAAACCCTGTAAGTTACAGAAGACCCTAAATTGTATCAAAAACCTAGAGACAACTTTTCA
ATTTGATCCAAATTTGAACTGGCCAACCAGTCTTTAAAACACTGGACTAGAAGAGATAATGATTGAAACATTTAA
AAAAAAAAAAGTGCTCCATTTCGAGGAGCTTTTCCTGTCTGTGGTTTTCCAGTTGGTGACCACCATGGGAGGTG
CTGGCTCGGCTCACTCCCTTCTCCACCCCTTGAGAATGTGGAGAAGTCCCATGGAGAGGCAGAATGGCAGGAGGT
TTCATGTCCCGCGTTGCATCTCCTCCTGAAAGAAAAGCAGTGATACCTGAATAATGCTGGCTCTCCGATTGATCC
TGTGAGGATGAATTTGCATTTCCAGAATCCTTGAGCATGGATTAGATGTTTCCTGGGAGGTGCCTTGAGTACCAT
TATGTGCAAGCTACATAATTTAAACATTTTTCTTAGTTTCCCTGGGAAGCTTTTCTTGACTCACAGCCAGGTT
TTCTGCCCAACACAAAAGGAGTGAGTTGGGGTCTTTAGTCTCTTCTTATTGGGTAGCTCTTGCTTTAATATTCTG
TTTGGTGAGTGTAAGGGATTCTGCAAGGGACAGGGGGCCTGACTACCCAGTCTTTGACTTGTATCCTCTCCCCTC
TTCATACACTCCTGCTGAAAAATGTTAATCCAAATACACATTTAACTTAGGGTCGGTCTTATTCTGATTTGAG
TATTTTAATGTCTCAGTGTGCTGATTTGGTAGTTGGAAGAATTATTCTTCTGGAGGTCTGTTAGACTACATCCTA
CACTGACTTCAGAAAACAGTCTGTCAGACAAAAAGGCCTTATGTCACCACTGGTACCTCAGTTTCTCATCCCAT
TTACAGTTTTTCTAACTCCAGGGTAGTGTTTAGTGTTAATATTTGGGATATATTTTTTTTCAAACCTGTTTTTAA
GTAGTTTGTAATTTGTAACAACTTGTAACCTGGTTGGGACTGATATTGTCATAGCTATGATAAACTTTGGATAT
TAGCAGAATTTGGGAAAAAAAAAAAAAAAAAAAAA

525/6881
FIGURE 489

MEKATEVKGGERVQNEEVGPEHDSQETKKLEEGAAVKETPHSPPGGVKGGDVPKQEKGKEKQQEGAVLEPGCSPQT
GPAQLETSSEVQSEPAVPKPEDDTPVQDTKM

526/6881
FIGURE 490

GGACGTTGAGAGAACGAGGAGGAAGGAGAGAAAAATGGCATCCATGGATTACAGTACCTATAGCCAAGCTGCAGCG
CAGCAGGGGCTACAGTGCTTACAACACCCAGCCCACTCAAGGATATGCACAGACCACCCAGGCATATGGGCAACAA
AGCTATGGAACCTATGGACAGCCCATTGATGTCAGCTATACCCAGGCTCAGACCACTGCAATCTATGGGCAGACC
GCCTATGCAACTTCTTATGGACAGCCTCCCACTGGTTATACTACTCCAAGTACCCCCAGGCATACAGCCAGCCT
GTCCAGGGGTATGGCACTGGTGCTTATGATACCACTGCTACAGTCACCACCACCCAGGCCTCCTATGCAGCT
CAATCTGCATATGGCACTCAGCCTGCTTATCCAGCTTATGGGCAGCAGCCAGTAGCCACTGCACCTACAAGACTG
CAGAATGGAAACAAGCCCACTGAGACTAGTCAACCTCAATCTAGCACAGGGGGTTACAACCAGCCAGCCTAGGA
TATGGACAGAGTAACTGCAGTTATCCCCAGGTACCTGGGAGCTACTCCATGCAGCCAGTCACCGCACCTCCATCC
TACCCTCCTACCAGCTATTCTCTACACAGCCAACTAGTTATGATCAGAGCAGTTACTCTCAGCAGAACACCTAT
GGGAAACCGAGCAGCTATGGACAGCAGAGTAGCTATGGTCAACAAAGCAGCTATGGGCAGCTGCCTCCCACTAGT
TACCCACCCCAAAGTGTATCCTACAGCCAAAGTCCAAGTCAGTATAGCTAACAGAGCAGCAGCTACGGGCAGCAG
AGTTTCAATCTGACAGGACCACCCCACTAGCAGTGGTGGTTTATGGGCAGGAGTCTGGAGGATTTTCCGGACTAGGA
GAGAACC GGAGCATGAGTGGCCCTGATAACTGGGGCAGGGGAAGAGGGGGATTTGATCGTGGAGGCATGAGCAGA
GGTGGGCGGGGAGGAGGATGCGGTGGAATGGGCAGCGCTGGAGAGCAAGTTGGCTTCAATAAGCCTGGTGGACCC
ATGGATGAAGGACCAGATCTTGATCTAGGCCCACCTGTAGATCCAGATGAAGACTCTGACAAACAGTGCAATTTAT
GTACAAGGATTAAATGACAATGTGACTCTAGATGATCTGGTAGACTTCTTTAAGCAGTGTGGGGTTGTTAAGATG
AACAAAGAGAAGCTGAGCAACCCATGATCCACACCTACCTGGACAAGGAAACAAGAAAAGCCCAAAGGTGATGCCACA
GTGTCTGTGAAGACTCACCTACTGCCAAAGCTGCCGTGGAATGGTTTGATGGGAAAAGATTTTCAAGGGAGCAAA
CTTAAAGTCTCTCTTGCTCGGAAGAGGCCTCCAGTGAACAGTATGCAGGGTGGTATGCCACCCCATGAGGGCAGA
GGGATGCCACCACCACTCTGCGGAGGTCCAGGAGGCCCAGGAAGTCTGGGGGACCCATGGGTACATGGGAGGC
CGTGGAGGAGATAGAGGAGGCCTCCCTCCAAGAGGACCCAGGGTTCCCGAGGGGAACACCTCTGGAGGAGGAAAC
GTCCAGCACCAAGCTGGAGACAGGCAGTGTCCAATCCGGGTGTGGAAACCAGAACTTCGCCTGGAGAACAGAG
AGCAACAAGTGTAAAGCTCCAAAGCCTGAAGGCTTCCTCCCGCCACCCTTCCACCCCGGGTGGTGTATCATGGC
AGAGGTGGCCCTGGTGGCATGTGGGGAGGAAGAGGTGGCCTCATGGATCATGGTGGTCCCGGTGGAATGTTTCTAGA
GGTGGCTGTGGTAGAGACAGAAGTGGCTTCTGTGGTGGCTGGGCATGGACCGAGGTGGCTTTGGTGGAGGAAGAC
AAGGTGGCCCTGGGGGGCCCCCGACCTTTGATGTAAACCAATGGGAGGAAGAAGAGGAGGACGTGAAGGACCTGG
AAAAACGGATAAAGGCGAGCACTGTCAGGAGCGCAGAGATCAGCCCTACTAGATGCAGAGAACCCGCAGAGCTGC
ATTGACTACCAGATTTATTTTTTAAACCAGAAAATGTTTTAAATTTATAATTCCATATTTATAATGTTGGCCACA
ACATTATGATTATTCTTTCTCTGTACTTTAGTATTTTTTACCATTTGTGAAGAAACATTAAACAAGTTAAATGG
TA

527/6881
FIGURE 491

MGVYGQESGGFSGLGENRSMSPDNWGRGRGGFDRGGMSRGGRGCGGCGMGSAGEQVGFNKPGGPMDEGPDLDLG
PPVDPDESDNSAIYVQGLNDNVTLDDLVDFFKQCGVVKMNRTEQPMIHTYLDKETRKPKGDATVSCEDSPTAK
AAVEWFDGKDFQGSKLKVSLARKRPPVNSMQGGMPPEHGRGMPPLCGGPGGPGSPGGPMGHMGGRGGDRGGLPP
RGFQGSRGNTSGGGNVQHQAQDRQCPNPGCGNQNFARWTESNKCKAPKPEGFLPPFFPPPGGDHGRGGPGGMWGG
RGGLMDHGGPGGMFRGGCGRDRSGFCGGWAWTEVALVEEDKVALGGPRTFDVTNGRKKRRT

528/6881
FIGURE 492

AACGAGGAGGAAGGAGAGAAAATGGCATCCATGGATTACAGTACCTATAGCCAAGCTGCAGCGCAGCAGGGCTAC
AGTGCTTACAACACCCAGCCCACTCAAGGATATGCACAGCGCCTATGCAACTTCTTATGGACAGCCTCCCACTGG
TTATACTACTCCAAGTGGGGGGCAGGCATACAGCCAGCCTGTCCAGGGGTATGGCACTGGTGCTTATGATACCAC
CACTGCTACAGTCACCACCACCCAGGCCTCCTATGCAGCTCAATCTGCATATGGCACTCAGCCTGCTTATCCAGC
TTATGGGCAGCAGCCAGTAGCCACTGCACCTACAAGACTGCAGAATGGAAACAAGCCCACTGAGACTAGTCAACC
TCAATCTAGCACAGGGGGTTACAACCAGCCAGCCTAGGATATGGACAGAGTAACTGCAGTTATCCCCAGGTACC
TGGGAGCTACTCCATGCAGCCAGTCACCGCACCTCCATCCTACCCTCCTACCAGCTATTCTCTACACAGCCAAC
TAGTTATGATCAGAGCAGTTACTCTCAGCAGAACACCTATGGGAAACCGAGCAGCTATGGACAGCAGAGTAGCTA
TGGTCAACAAAGCAGCTATGGGCAGCTGCCTCCCACTAGTTACCCACCCCAAACCTTGATCCTACAGCCAAGCTCC
AAGTCAGTATAGCTAACAGAGCAGCAGCTACGGGCAGCAGAGTTCATTCTGACAGGACCACCCAGTAGCATGGG
TGTTTATGGGCAGGAGTCTGGAGGATTTTCCGGACTAGGAGAGAACCGGAGCATGAGTGCCCTGATAACTGGGG
CAGGGGAAGAGGGGGATTTG

529/6881
FIGURE 493

AACGAGGAGGAAGGAGAGAAAATGGCATCCATGGATTACAGTACCTATAGCCAAGCTGCAGCGCAGCAGGGCTAC
AGTGCTTACAACACCCAGCCCACTCAAGGATATGCACAGACCACCCAGGCATATGGGCAACAAAGCTATGGAACC
TATGGACAGCCCATTGATGTCAGCTATACCCAGGCTCAGACCACTGCAATCTATGGGCAGACCGCCTATGCAACT
TCTTATGGACAGCCTCCCACTGGTTATACTACTCCAAGTGGGGGAGGCATACAGCCAGCCTGTCCAGGGGTAT
GGCACTGGTGCTTATGATACCACTGCTACAGTCACCACCACCCAGGCCTCCTATGCAGCTCAATCTGCATAT
GGCACTCAGCCTGCTTATCCAGCTTATGGGCAGCAGCCAGTAGCCACTGCACCTACAAGACTGCAGAATGGAAAC
AAGCCCACTGAGACTAGTCAACCTCAATCTAGCACAGGGGGTTACAACCAGCACCAAGCTGGAGACAGGCAGTGT
CCCAATCCGGGTTGTGAAACCAGAACTTCGCCTGGAGAACAGAGAGCAACAAGTGTAAGGCTCCAAAGCCTGAA
GGCTTCCTCCCGCCACCCTTCCACCCCCGGGTGGTGATCATGGCAGAGGTGGCCCTGGTGGCATGTGGGGAGGA
AGAGGTGGC

530/6881
FIGURE 494

GGAGGAAGGAGAGAAAATGGCATCCATGGATTACAGTACCTATAGCCAAGCTGCAGCGCAGCAGGGCTACAGTGC
TTACAACACCCAGCCCACTCAAGGATATGCACAGACCACCCAGGCATATGGGCAACAAAGCTATGGAACCTATGG
ACAGCCCATTGATGTCAGCTATACCCAGGCTCAGACCACTGCAATCTATGGGCAGACCGCCTATGCAACTTCTTA
TGGACAGCCTCCCACTGGTTATACTACTCCAAGTGGGGGGCAGGCATACAGCCAGCCTGTCCAGGGGTATGGCAC
TGGTGCTTATGATACCACCACTGCTACAGTCACCACCACCCAGGCCTCCTATGCAGCTCAATCTGCATATGGCAC
TCAGCCTGCTTATCCAGCTTATGGGCAGCAGCCAGTAGCCACTGCACCTACAAGACTGCAGAATGGAAACAAGCC
CACTGAGACTAGTCAACCTCAATCTAGCACAGGGGGTTACAACCAGCCCAGCCTAGGATATGGACAGAGTAACTG
CAGTTATCCCCAGGTACCTGGGAGCTACTCCATGCAGCCAGTCACCGCACCTCCATCCTACCCTCCTACCAGCTA
TTCCTCTACACAGCCAACTAGTTATGATCAGAGCAGTTACTCTCAGCAGAACACCTATGGGCAGCTGCCTCCAC
TAGTTACCCACCCCAAAGTTGATCCTACAGCCAAGCTCCAAGTCAGTATAGCTAACAGAGCAGCAGCTACGGGCA
GCAGAGTTTATTCTGACAGGACCACCCAGTAGCATGGGTGTTTATGGGCAGGAGTCTGGAGGATTTCCGGACT
AGGAGAGAACCGGAGCATGAGTGGCCCTGAT

531/6881
FIGURE 495

TTTCCGGTGCTATGCCCCGGAAGCGGAAGTGCGATCTTCGGGCTGTCAGAGTTGGTCTGTTACTCGGTGGTGGCG
GAGTCTACGGAAGCCGTTTTTCGCTTCACTTTTCTGGCTGTAGAGCGCTTTCCCCCTGGCGGGTGAGAGTGCAGA
GACGAAGGTGCGAGATGAGCACTATGTTTCGCGGACACTCTCCTCATCGTTTTTATCTCTGTGTGCACGGCTCTGC
TCGCAGAGGGCATAACCTGGGTCTGGTTTACAGGACAGACAAGTACAAGAGACTGAAGGCAGAAGTGAAAAAC
AGAGTAAAAAATTGAAAAAGAAGAAGGAAACAATAACAGAGTCAGCTGGTCGTCTATCAATGGTTCGAATGAAAT
CCATGTTTGCTATTGGCTTTTGTCTTACTGCCCTAATGGGAATGTTCAATTCCATATTTGATGGTAGAGTGGTGG
CAAAGCTTCCTTTTACCCCTCTTTCTTACATCCAAGGACTGTCTCATCGAAATCTGCTGGGAGATGACACCACAG
ACTGTTCCCTTCATTTTCTGTATATTCTCTGTACTATGTCGATTTCGACAGAACATTCAGAAGATTCTCGGCCTTG
CCCCCTTCACGAGCCGCCACCAAGCAGGCAGGTGGATTTCTTGGCCCACCACCTCCTTCTGGGAAGTTCTCTTGAA
CTCAAGAACTCTTTATTTTCTATCATTCTTTCTAGACACACACACATCAGACTGGCAACTGTTTTGTAGCAAGAG
CCATAGGTAGCCTTACTACTTGGGCCTCTTTCTAGTTTTGAATTATTTCTAAGCCTTTTGGGTATGATTAGAGTG
AAAATGGCAGCCAGCAAACCTTGATAGTGCTTTTGGTCCTAGATGATTTTTATCAAATAAGTGGATTGATTAGTTA
AGTTCAGGTAATGTTTATGTAATGAAAAACAAATAGCATCCTTCTTGTTTCATTTACATAAGTATTTTCTGTGGG
ACCGACTCTCAAGGCACTGTGTATGCCCTGCAAGTTGGCTGTCTATGAGCATTTAGAGATTTAGAAGAAAAATTT
ACAAGCCAAATACATGACATAAGATCAATAAAGAGGCCAAATTTTTAGCTGTTTTATGTACAAGGAGAGATCTGT
TTCATTTTGTTTTGCCGTATTTCTAGATATAAGTTTTAGCATGGGCCAGGAAGGACTAAAATAAAAGTTTTTAAG
GTACTG

532/6881
FIGURE 496

MSTMFADTLLIVFISVCTALLAEGITWVLVYRTDKYKRLKAEVEKQSKKLEKKKETITESAGRQKKKKIERQEEK
LKNNNRDLMSVRMKSMEFAIGFCFTALMGMFENSIFDGRVVAKLPFTPLSYIQGLSHRNLLGDDTTDCSFIFLYILC
TMSIRQNIQKILGLAPSRAATKQAGGFLGPPPPSGKFS

533/6881
FIGURE 497

AGACAGTTTTGAAGTTTTCAAAGACTGGCTCTGCTGTTAAGAAGTTGTACTTAAAGCGGAGGAGCTAAGCCACCT
GCCAAAATGTGCAAAGGACTTGCAGCTTTGCCCCACTCATGCCTGGAAAGGGCCAAGGAGATTAAGATCAAGTTG
GGAATTCTCCTCCAGAAGCCAGACTCAGTTGGTGACCTTGTCATTCCGTACAATGAGAAGCCAGAGAAACCAGCC
AAGACCCAGAAAACCTCGCTGGACGAGGCCCTGCAGTGGCGTGATTCCCTGGACAAACTCCTGCAGAACAACATAT
GGACTTGCCAGTTTTCAAAGTTTTCTGAAAGTCTGAATTCAGTGAGGAAAACCTTGAGTTCTGGATTGCCTGTGAG
GATTACAAGAAGATCAAGTCCCCTGCCAAGATGGCTGAGAAGGCAAAGCAAATTTATGAAGAATTCATTCAAACG
GAGGCTCCTAAAGAGGTGAATATTGACCACTTCACTAAGGACATCACAATGAAGAACCTGGTGGAACCTTCCCTG
AGCAGCTTTGACATGGCCCAGAAAAGAATCCATGCCCTGATGGAAAAGGATTCTCTGCCTCGCTTTGTGCGCTCT
GAGTTTTATCAGGAGTTAATCAAGTAGTAATTTAGCCAGGCTATGAAATCATCCTGTGAGTTATTTCCCTCCATAA
TAACCCTGCATTTCCCATTAATCTACATATCTTCCCACAGCAGCTTTGCTCAGTGATACCCACATGGGAAAAATC
CCAGGGGATGTTGCTTACTCTTTTTGCCACACTGCTTTGGATACTTATCTACTGTCCGAAGGCCTTCTTTCCCC
ACTCAATTCTTCCCTGCCCTGTTATTAATTAAGATATCTTCAGCTTGTAGTCAGACCCAATCAGAATCACAGAAAA
ATCCTGCCTAAGGCAAAGAAATATAAGACAAGACTATGATATCAATGAATGTGGGTAAAGTAATAGATTTCCAGC
TAAATTGGTCTAAAAAAGAATATTAAGTGTGGACAGACCTATTTCAAAGGAGCTTAATTGATCTCACTTGTTTTA
GTTCTGATCCAGGGAGATCACCCCTCTAATTATTTCTGAACCTTGGTTAATAAAAGTTTATAAGATTTTTATGAAG
CAGCCACTGTATGATATTTTAAGCAAATATGTTATTTAAATATTGATCCTTCCCTTGGACCACCTTCATGTTAG
TTGGGTATTATAAATAAGAGATACAACCATGAATATATTATGTTTATACAAAATCAATCTGAACACAATTCATAA
AGATTTCTCTTTTATACCTTCCCTCACTGGCCCCCTCCACCTGCCCATAGTCACCAAATCTGTTTTAAATCAATG
ACCTAAGATCAACAATGAAGTATTTTATAAATGTATTTATGCTGCTAGACTGTGGGTCAAATGTTTCCATTTTCA
AATTATTTAGAATTCTTATGAGTTTAAAATTTGTAAATTTCTAAATCCAATCATGTAAAATGAACTGTTGCTCC
ATTGGAGTAGTCTCCACCTAAATATCAAGATGGCTATATGCTAAAAAGAGAAAATATGGTCAAGTCTAAAATGG
CTAATTGTCCTATGATGCTATTATCATAGACTAATGACATTTATCTTCAAAACACCAAATTGTCTTTAGAAAAAT
TAATGTGATTACAGGTAGAGGCCTTCTAGGTGAGACACTTTTAAGGTACACTGCATTTTGCAGAAAAAAAAAAAA
AAAAGTAATCTTTTAGCAACCCCAAGTATTCCTTCACTATTTGCTTCCCTGCATTAGCAAATTTTACTTACAGTCA
AAAGTGCAGATTTATACTCCTGACGTGTCTCATTACAGCTAAATAATAGGCCATAGGACTTTTGGTAGGTTTAA
ACTTTTAATTCTGTATTTTATGATTATAAGTCTTGCTAGAATTTTTTCTAATCTTTAGTAGATTTGATTAAATAA
TGATTCACAGAATTTAGTAACAGAATCAAACCTAAGCCATGTATGAGGGTAATCGAGATGAGGATATTAACCTCAA
AGAAATAGGGTGATTTTTTAAAGGATTAATAAAATTCTGAAATGTTAAGTAG

534/6881
FIGURE 498

MCKGLAALPHSCLERAKEIKIKLGILLQKPDVGDVIPYNEKPEKPAKTQKTSLDEALQWRDSDLKLLQNNYGL
ASFKSFLKSEFSEENLEFWIACEDYKKIKSPAKMAEKAKQIYEEFIQTEAPKEVNIDHFTKDITMKNLVEPSLSS
FDMAQKRIHALMEKDSLPRFVRSEFYQELIK

535/6881
FIGURE 499

GACACCTTTTAAAATGCAGAACTAACTGAGGCATTTTCAGTAACTTTGCTTTCAAATCAATAAAAGTCAAATGTATG
GAAACATTTTGTGCCCTACTCTCCATACCTGTGTACTCAAATTCTCTACTGTATGAATTATGCTTTAAGTAGAA
TTCAGTGCCAAGGAGAACTTGGTGAAATAAATTATTTTAATTTTTTTTTTATCCTTTACAAAGCCATGGATTTTA
TTTGGTTGATGTGTGCTCTGTACACAAGCCATTTCAATAGGATGGAGCTGTTAATTATTTTCCAAAGAGTAATAG
ACATGCAAAAGTTTCAATTAATAAACTGGGCCATTAACAAATAAATTAATAAACTAATAAGCATTCCCTTCTAGGTT
TTTGCCAAACTGCCTATCCAATAACAAATTTGAGAATCGTTGAAAAAGCTAGTTATATTTTCAGAGAAATGATTTT
CATTATTGAACTGTTCTCCCTAGCAGGCCATTTTCCCTTTTTCCTGGGAGTTTAGCAAGTTTAGGAGAGAATAG
TCATGAAAAGAAAGGGAAGAAAGGGGAGAAGGGAAGAGGTTAAAAAGTAAGTGCTCAGACCTATGAACGTAATCC
CTTTGCTAGAAATATTTAAGAGCAGCTCAGCTTGGTTGAAACTGAGTTTTGTATCTTCCATATTTGCAGGAAGG
TATTTTCTGACTTGCAATGCAGCTAGATGTAATAATTTATTTTATCATCCTAGAAAAGCCTTGACTAGAAAAATGA
ATAAATATTGAGGGTTTCCCTGTCCATATCTGGCTTGCATGTGCCAGAAAGCAGAGAATAGAAAATGTAATCTCCA
ACATCCAAGCATCGAAACCCAAGGGGTAGGCAATTCTATGTAGGTTTTGGACATGAAGTTTGGTGCATCTTGGTT
TATGCTGGCTCAACTGCTATTAAACCTCTCTGGCTTATAGTCTCTTCATTCTATTAGACAAGCACGTATCGAACA
CTTGCTTCGCACAAGGCTCTTTAGTTAACAATTTAGCAGCTACTGTTTGTGTTAAACACACTTTTCACCAAATAG
GTTCTGAGGCAAACGAGAGCAATGACTATTTAAAGAAAGGCTTTCCCAGCATCACTTACACATCCCAAACTAAA
AAGATCAACTCTTCCAAGTGAAGAAAGACTCCTGGCTTTGAATGGAACTTACAGCAGAGAGTCACAGGCCACGG
CAACAACAACGACAACAACAACAAACATTTGGAATATTATTCTCAACTCACGTTTTAATAATACATCTTAATTATTT
TCTAGTAGAGAACTACAAATCAGCCTCTTCAACATTTATATACAGTTTAATAAGCCTCTTGCAAGTTACTTGTT
CTCTCACCTGAGGTATTTTTTCTCCCCACCTTGCCCTGTTCCCTCCCTTCTCTCTCCCTTTGCAAGAGGAA
ATATTTAACATATTTGGGTCCAACCTCAATAATGTAATAATTAATACATTAAAAGCATTTAACTTCCTTTCTAGA
AAAATGCACAGGCTAAGGCATAGACAAAACAAAGAGAAATGCTGAGAAATTTGCCACTGGAGACAAGCAATCTGA
ATAAATATTTGCCAAAAGTTCTTTTTATGTCATATAGTGTGAGGATTTGAAGGAGCTATTTTTTTTTAATGTTGCA
ACTAGCAACTCATCTTCGGAAGACACAGCCAGGAGAATGAAGTAGAAGTGAAGGTTTATAAATCCATTTGTAAG
CATTTATCCCATATATTTTAAATTCAAGAAAAATTGTGTTTATCTTTAGAATTTGTATTCAATACTTTATGTAC
TATGTGACTCATGCTTCTGGATAAATAAAGCACCAATATGTATCTGTAACCACAATCACACATATTATATTTAA
TATATATCTATATAACAAAAAAAAAAAAAAAAAAAAA

536/6881
FIGURE 500

MYGNILCPTLHTLCTQILYCMNYALSRIQCQGEINYNFFFIYKAMDFIWLMCALYTSHFNRMELLIIFQR
VIDMQKFQ

537/6881
FIGURE 501

AGCGGCCCCCTGCAGAGGCAGGTCCACCTGAGAGGCCGGCCGGCCTCCCAGCCCCTGTTCATCCGGGGCATCACCT
ACTATAAAGCCAAGGTCTCTGAAGAAGAGAATGACATTGAAGAGCAGCAAGATGAGTTTTTTCAGCGGTGACAATG
GAGTGGATTTGCTGATTGAAGATCAGCTCCTGAGACACAACGGCCTGATGACCAGTGTACCCCGGAGGCCTGCAG
CCACCCGTCAGGGACACAGCACTGCTGTGACAAGCGACCTGAACGCTCGGACCGCACCCCTGGTCCTCAGCACTGC
CACAGCCCTCGACCTCAGATCCCAGCATCGCCAACCATGCCTCAGTGGGACCAACACTCCAAACAACCTCGGTGT
CTCCAGATCCCACAAGGGAGTCAGTCCTGCAGCCTTCTCCTCAGGTACCAGCCACCACTGTGGCCCCACACAGCCA
CCCAGCAACCAGCAGCCCCAGCTCCTCCGGCAGTGTCTCCCAGGGAGGCATTGATGGAAGCTATGCACACAGTCC
CAGTGCCTCCCACCACAGTCAGAACAGACTCGCTGGGGAAAAGATGCTCCTGCTGGGTGGGGAACAACCCCTGCCA
GCCCCACGCTGAGCCCCGAAGAAGAAGATGACATCCGGAATGTCATAGGAAGGTGCAAGGACACTCTCTCCACAA
TCACGGGGCCGACCACCCAGAACACATATGGGCGGAATGAAGGGGCCTGGATGAAGGACCCCTGGCCAAGGATG
AGCGGATTTACGTAACCAACTATTACTACGGCAACACCCTGGTAGAGTTCCGGAACCTGGAGAACTTCAAACAAG
GTCGCTGGAGCAATTCCTACAAGCTCCCGTACAGCTGGATCGGCACAGGCCACGTGGTATACAATGGCGCCTTCT
ACTACAATCGCGCCTTCACCCGCAACATCATCAAGTACGACCTGAAGCAGCGCTACGTGGCTGCCTGGGCCATGC
TGCAATGACGTGGCCTACGAGGAGGCCACCCCTGGCGATGGCAGGGCCACTCAGACGTGGACTTTGCTGTGGACG
AGAATGGCCTATGGCTCATCTACCCGGCCCTGGACGATGAGGGCTTCAGCCAGGAGGTCATTGTCTGAGCAAGC
TCAATGCCGCGGACCTGAGCACACAGAAGGAGACCACATGGCGCACGGGGCTCCGGAGGAATTTCTACGGCAACT
GCTTCGTCATCTGTGGGGTGCTGTATGCCGTGGATAGCTACAACCAGCGGAATGCCAACATCTCCTACGCTTTTCG
ACACCCACACCAACACACAGATCGTCCCCAGGCTGCTGTTTCGAGAATGAGTATTCCTATACGACCCAGATAGACT
ACAACCCCAAGGACCGCCTGCTCTATGCCTGGGACAATGGCCACCAGGTCACCTTACCATGTTCATCTTTGCCTACT
GACACCCTTGTCCCCACAAGCAGAAGCACAGAGGGGTCACTAGCACCTTGTGTGTATGTGTGTGCGCGCACGTGT
GTGTAGGTGGGTATGTGTTGTTTAAAAATATATATTATTTTGTATAATATTGCAAATGTAAAATGACAATTTGGG
TCTATTTTTTTTATATGGATTGTAGATCAATCCATACGTGTATGTGCTGGTCTCATCCTCCCCAGTTTATATTTTT
GTGCAAATGAACTTCTCCTTTTGACCAGTAACCACCTTCCTTCAAGCCTTCAGCCCCCTCCAGCTCCAAGTCTCAG
ATCTCGACCATTTGAAAAGGTTTCTTCATCTGGGTCTTGCAGGAGGCAGGCAACACCAGGAGCAGAAATGAAAAGAG
GCAAGAAAGAAGTGCTATGTGGCGAGAAAAAAGTTTTAATGTATTGGAGAAGTTTTAAAAAACCCAGAAAAACG
CTTTTTTTTTTTAATAAAGAAGAAATTTAAAATC

538/6881
FIGURE 502

MTSVTRRPAATRQGHSTAVTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPDPTRESVLQPSPQV
PATTVAHTATQQPAAPAPPAVSPREALMEAMHTVPVPPTTVRTDSLKGDAPAGWGTTTPASPTLSPEEEDDIRNVI
GRCKDITLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYYGNTLVEFRNLENFKQGRWSNSYKLPYSWIGT
GHVVYNGAFYYNRAFTRNIIKYDLKQRYVAAWAMLHDVAYEEATPWRWQGHSDVDFAVDENGWLWLIYPALDDEGF
SQEVIVLSKLNAADLSTQKETTWRITGLRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHNTQIVPRLLFEN
EYSYTTQIDYNPKDRLLYAWDNGHQVTYHVIFAY

539/6881
FIGURE 503

GGCACGAGGGATGCAAGGAGATGAGACAGTTAGATTTACTTCCTCTTTTCTAATCTGAGAGGTTTCATGTTGAAG
AAAATCAGTGTTGGGGTTGCAGGAGACCTAAACACAGTCACCATGAAGCTGGGCTGTGTCTCATGGCCTGGGCC
CTCTACCTTTCCCTTGGTGTGCTCTGGGTGGCCAGATGCTACTGGCTGCCAGTTTTGAGACGCTGCAGTGTGAG
GGACCTGTCTGCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCTTCCAG
GTCAAGGCCTACACTTTTCAGTGAACCCCTCCACCTGATTGTGTCTATGACTGGCTGATCCTCCAAGGTCCAGCC
AAGCCAGTTTTTTGAAGGGGACCTGCTGGTCTGCGCTGCCAGGCCTGGCAAGACTGGCCACTGACTCAGGTGACC
TTCTACCGAGATGGCTCAGCTCTGGGTCCCCCGGGCCTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCA
GACAGCGGGCACTACCACTGCAGTGGCACTTCCAGAGCCCTGGTCTGGGATCCCAGAAACAGCATCTGTTGTG
GCTATCACAGTCCAAGAACTGTTTCCAGCGCCAATTCTCAGAGCTGTACCCCTCAGCTGAACCCCAAGCAGGAAGC
CCCATGACCCTGAGTTGTGACACAAAGTTGCCCTGCAGAGGTCAGCTGCCCGCCTCCTCTTCTCCTTCTACAAG
GATGGAAGGATAGTGCAAAAGCAGGGGGCTCTCCTCAGAATTCCAGATCCCCACAGCTTCAGAAGATCACTCCGGG
TCATACTGGTGTGAGGCAGCCACTGAGGACAACCAAGTTTGAAACAGAGCCCCCAGCTAGAGATCAGAGTGCAG
GGTGTCTCCAGCTCTGCTGCACCTCCCACATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAAGTCTCCT
GAGGAGGCCCTGGGCCTCTGCCTCCGCCGCCAACCCATCTTCTGAGGATCCAGGCTTTTCTTCTCCTCTGGGG
ATGCCAGATCCTCATCTGTATCACCAGATGGGCCTTCTTCTCAAACACATGCAGGATGTGAGAGTCCTCCTCGGT
CACCTGCTCATGGAGTTGAGGGAATTATCTGGCCACCAGAAGCCTGGGACCACAAAGGCTACTGCTGAATAGAAG
TAAACAGTTCATCCATGATCTCACTTAACCACCCCAATAAATCTGATTCTTTATTTTCTTCTCCTGTCTGCACA
TATGCATAAGTACTTTTACAAGTTGTCCAGTGTGTTTGTGTTAGAATAATGTAGTTAGGTGAGTGTAATAAATTTA
TATAAAGTGAGAATTAGAGTTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTCTGCTGTCTAGATCA
GGAATTTCTATCTGTTATATCGACCAGAATGTTGTGATTTAAAGAGAACTAATGGAAGTGGATTGAATACAGCAG
TCTCAACTGGGGGCAATTTTGGCCCCCAGAGGACATTGGGCAATGTTTGGAGACATTTTGGTCATTATACTTGGG
GGGTGGGGGATGGTGGGATGTGTGTGCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAAACATCCTA
TAATGCACAGGGCAGTACCCACAACGAAAAATAATCTGGCCCCAAATGTCAGTTGTACTGAGTTTGAGAAACCC
CAGCCTAATGAAACCCTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTATTATCTCTTTCCAGCCT
CATTCAGCTATTCTTACTGACATAACAGTCTTTAGCTGGTGTCTATGGTCTGTTCTTTAGTTCTAGTTTGTATCCC
CTCAAAAGCCATTATGTTGAAATCCTAATCCCCAAGGTGATGGCATTAAAGAAGTGGGCCTTTGGGAAGTGATTAG
ATCAGGAGTGCAGAGCCCTCATGATTAGGATTAGTGCCCTTATTTAAAAAGGCCCCAGAGAGCTAACTCACCCCTT
CCACCATATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCACAAAAACAGCTGTCGCCAAACACCGACTCTG
TCGTTGCCTTGATCTTGAACCTCCAGCCTCCAGAACTATGAGAAATAAAATTCTGTTGTTTGTAAAAA
AAAAA

540/6881
FIGURE 504

MKLGCVLMAWALYLSLGVLWVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQVKAYTFSEPFHLIV
SYDWLILQGPAKPVFEGDLLVLRCAWQDWPLTQVTFYRDGSALGPPGPNREFSITVVQKADSGHYHCSGIFQSP
GPGIPETASVVAITVQELFPAPILRAVPSAEPQAGSPMTLSCQTKLPLQRSAARLLFSFYKDGRIVQSRGLSSEF
QIPTASEDHSGSYWCEAATEDNQVWKQSPQLEIRVQGASSAAPPPTLNPAPQKSAAPGTAPEEAPGFLPPPPTPS
SEDPGFSSPLGMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

541/6881
FIGURE 505

AAGCAGTGGTATCAACGCAGAGTGCCCAATTACGGCCGGGGTGGCATC**ATG**TGGCAGCTGCTCCTCCCAACTGCT
CTGCTACTTCTAGTTTCAGCTGGCATGCGGACTGAAGATCTCCCAAAGGCTGTGGTGTTCTTGAGCCTCAATGG
TACAGGGTGCTCGAGAAGGACAGTGTGACTCTGAAGTGCCAGGGAGCCTACTCCCCTGAGGACAATTCCACACAG
TGGTTTCACAATGAGAGCCTCATCTCAAGCCAGGCCTCGAGCTACTTCATTGACGCTGCCACAGTCGACGACAGT
GGAGAGTACAGGTGCCAGACAAACCTCTCCACCCTCAGTGACCCGGTGCAGCTAGAAGTCCATATCGGCTGGCTG
TTGCTCCAGGCCCCCTCGGTGGGTGTTCAAGGAGGAAGACCCTATTCACCTGAGGTGTCACAGCTGGAAGAACACT
GCTCTGCATAAGGTCACATATTTACAGAATGGCAAAGGCAGGAAGTATTTTCATCATAATTCTGACTTCTACATT
CCAAAAGCCACACTCAAAGACAGCGGCTCCTACTTCTGCAGGGGGCTTGTTGGGAGTAAAAATGTGTCTTCAGAG
ACTGTGAACATCACCATCACTCAAGGTTTGGCAGTGTCAACCATCTCATCATTCTTTCCACCTGGGTACCAAGTC
TCTTTCTGCTTGGTGATGGTACTCCTTTTTTGCAGTGGACACAGGACTATATTTCTCTGTGAAGACAAACATTCTGA
AGCTCAACAAGAGACTGGAAGGACCATAAAATTTAAATGGAGAAAGGACCCTCAAGACAAA**TGA**CCCCCATCCCAT
GGGGGTAATAAGAGCAGTAGCAGCAGCATCTCTGAACATTTCTCTGGATTTGCAACCCTATCATCCTCAGGCCTC
TCTACAAGCAGCAGGAAACATAGAAGTCTCAGAGCCAGATCCCTTATCCAACCTCTCGACTTTTCCTTGGTCTCCAGT
GGAAGGGAAAAGCCCATGATCTTCAAGCAGGGAAGCCCCAGTGAGTÀGCTGCATTCTAGAAAATTGAAGTTTCAG
AGCTACACAAACACTTTTTCTGTCCCAACCGTTCCTCACAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

542/6881
FIGURE 506

MWQLLLPTALLLLVSAGMRTEDLPKAVVFLEPQWYRVLEKDSVTLKCQGAYSPEDNSTQWFHNESLISSQASSYF
IDAATVDDSGEYRCQTNLSTLSDPVQLEVHIGWLLLQAPRWVFKEEDPIHLRCHSWKNTALHKVTYLQNGKGRKY
FHHNSDFYIPKATLKDSGSYFCRGLVGSKNVSETVNITITQGLAVSTISSFFPPGYQVSFCLVMVLLFAVDTGL
YFSVKTNIRSSTRDWKDHKFKWRKDPQDK

543/6881
FIGURE 507

ATGGCGGACGGGACCTGTCAGGACGTGGCCATCGTGGGCTACAAGGACTCGCCCTCCATCTGGGCCGCCGTCCCC
GGGAAAACCTTCGCCAACATCGCGCCAGCTGAGGTTGGTGTCTGGCTGGCAAAGACAGGTCAAGATGGGGAATT
TTGCATGGATCTTCGTATACCAAGAGTACCGGTGGAGCCCCACCTTCAATGTCACTGTCACCAAGACTGACAAG
ACGCTAGTCCTGCTGATGGGCAAAGAAGGTGTCCACGGTGGTTTGATCAACAAGAAATGTTATGAAATGGCCTCC
CACCTTCGGCGTTCCCAGTACTTGA

544/6881
FIGURE 508

MADGTCQDVAIVGYKDSPSIWAAVPGKTFANIAPAEVGVLAGKDRSRWGILHGSSYTKSTGGAPTFFNVTVTKTDK
TLVLLMGKEGVHGGLINKKCYEMASHLRRSQY

545/6881
FIGURE 509

ATGGTTGTAGGATTCACTGAGTTTGAATCCTTCCACCCAGGCCTTGCTGCTGCAGCCTCTGCCAGAGCCAGCTCC
TGGTGGACCCATGTGGAAATGGGACCTCCAGATCCCATCCTGGGAGTCACTGAAGCCTTTAAGAGGGACATCAAT
AGCAAAAAGATGAATCTGGGAGTTGGGATGATAATGGGAAGCCGCTTTGCCAGTGGTGATGGTGATAAGGATGCC
TGGGCTCTGCACCACTTCATCGAACAGGGCATTAAATGTTTGTCTCTGCCAATCATATGCCAAGAACATGGGCTTA
TATGGTGAGCATGTAGGAGCCTTCACTGTGGTCTGCAAAGATGCAGATGAAGCCAAAAGGGTAGAGTCACAGTTG
AAGATCTTGATTAGTCCCATGTATTCCAACCTCTCCCCTCAATGGGGCCCAGATTGCTTCTACCATTCCAAACACC
CCAGTTGGTTTGAAGGTCTGGGTCATGGGAGGCCTACATGATCATCCTCAGGTTATGAGTGACGAGAAAGAGACA
ACACTGAGAGCAGTGGCTGTCAAGTACTGGATCAGAGTCCGGCTGTGCCACTTCCTTGAAACATTCATGTCTCCG
GACCTTACTGGCTGGAAAAAACTGCAGCAGGAAGATGGCCTTACCTCACTTCTAGCTTCCAAGTCTCACAAGAGA
GCACAGGCAGAACCGAAGCCACATCCAGGACCTGGGCTGAGAACATCTGGCACATGGAGCCTGTAG

546/6881
FIGURE 510

MVVGFTFESFHPGLAAAASARASSWWTHVEMGPPDPILGVTEAFKRDINSKKMNLGVGMIMGSRFASGDGDKDA
WALHHFIEQGINVCLCQSYAKNMGLYGEHVGAFTVVCKDADEAKRVESQLKILISPMYSNSPLNGAQIASTIPNT
PVGLKVWVMGGLHDPQVMSDEKETTLRAVAVKYWIRVRLCHFLETFMSPDLTGWKKLQQEDGLTSLASKSHKR
AQAEPKPHPGPGLRTSGTWSL

547/6881
FIGURE 511

CGGTTGCTTGCTGTCCCAGCGGCGCCCCCTCATCACCGTCGCCATGCCCCGGAGGTCTGCTTCTCGGGGACGTGGC
TCCCAACTTTGAGGCCAATACCACCGTCGGCCGCATCCGTTTCCACGACTTTCTGGGAGACTCATGGGGCATTCT
CTTCTCCCACCCTCGGGACTTTACCCCAGTGTGCACCACAGAGCTTGGCAGAGCTGCAAAGCTGGCACCAGAATT
TGCCAAGAGGAATGTTAAGTTGATTGCCCTTTCAATAGACAGTGTGAGGACCATCTTGCCTGGAGCAAGGATAT
CAATGCTTACAATTGTGAAGAGCCACAGAAAAGTTACCTTTTCCCATCATCGATGATAGGAATCGGGAGCTTGC
CATCCTGTTGGGCATGCTGGATCCAGCAGAGAAGGATGAAAAGGGCATGCCTGTGACAGCTCGTGTGGTGTGTTGT
TTTTGGTCCTGATAAGAAGCTGAAGCTGTCTATCCTCTACCCAGCTACCACTGGCAGGAACCTTGATGAGATTCT
CAGGGTAGTCATCTCTCTCCAGCTGACAGCAGAAAAAAGGGTTGCCACCCAGTTGATTGGAAGGATGGGGATAG
TGTGATGGTCCTTCCAACCATCCCTGAAGAAGAAGCCAAAAAAGCTTTTCCGAAAGGAGTCTTCACCAAAGAGCT
CCCATCTGGCAAGAAATACCTCCGCTACACACCCAGCCTTTAAGTCTCTTGGAGAAGTTGGTGCTGTGAGCCAGA
GGATGTCAGCTGCCAATTGTGTTTTCTGCAGCAATTCATAAACACATCCTGGTGTCTACAGCCAAGGTTTT
TAGGTTGCTATACCAATGGCTTATTAAATGAAAATGGCACTAAAAGTTTCTTGAGATTCTTTATACTCTCTGCCT
TCAGCAATCAATTCCATTTCATACATCAGCACTCTGCTGGTTCTGTTTGAAATATGTTCTGTATTTAAACTCAA
TCTTGTTGGATCTCTGCAGGGCTTGTGACCAATGAAGTCATATTTGTTGATGGTTGACAAAGCTTGCTTCACTCC
ATCAGAGAATGACTATCAATTTTTTTTTTAAGTGTCTATCACGTCCTCTCCTGTACCCATTTTGAAGAGTGGCA
GAAGTTGAAGTTCAACTTCCTCTGTAAATATCCAAGTATAAAGCCAGGAACCTTCTAGAATAACCCAGATGCGCT
TTAATTTTTTTTTAATATGTTTTGATCACAGAACTTCTAGAATAACCCAGATGCTCTTTCATATTCTTTAATACA
TCTTGATCACAGCTGGGGGAAAAAAGCTTTTTAATTCTGTACCTTCCTAGTAGATAAGTGAAGAGCAGGGAAAG
AGACCTTTAAATATTTTGCTATAAAAAAATTTGTGATAAGTTTCTATCAAATGGGGAGATTGCAGAAAAGGCTT
CCCTTGCTCCCAAGGAGGTGTAGCAGGTGTGAGCAATATTAGTGCCATGTGCCTTTCACACAGGGTTTGCAATT
ATCAGTCTGTTTTCCGATGATGTGTACATGAAAGAGTACACCATGTGAAGAGAAGAGAGAATGATTGAAAATGTT
TTAGTATAGAAGTCTTCTTGCAGTGGGTGCTATTTTCTAGATTTTACTTTTTAGGGAACAAAATAAAATCCTTT
GTT

548/6881
FIGURE 512

MPGGLLLGDVAPNFEANTTVGRIRFHDFLGDSWGILFSHPRDFTPVCTTELGRAAKLAPEFAKRNVKLIALSIDS
VEDHLAWSKDINAYNCEEPTKLPFFIIDDRNRELAILLGMLDPAEKDEKGMPTARVVFVFGPDKKLSILYP
ATTGRNFDEILRVVISLQLTAEKRVATPVDWKDGDSVMVLPTIPEEEAKKLFPGVFTKELPSGKKYLRYTPQP

549/6881
FIGURE 513

AGAGACCGTCCGAGGTAATTGTCTGCCACGAGTGCACATTCTGAAAACAGGAGATTTTAGTTCCTAAAAATGGGA
AGAACCTACATTGTAGAAGAGACTGTTGGCCAGTATCTTTCAAACATAAATCTCCAAGGAAAGGCTTTTGTCTCT
GGCCTTTTAATAGGACAGTGTTTCGTCACAAAAGGATTATGTGATTCTTGCCACTAGAACGCCACCCAAAGAGGAG
CAAAGTGAGAACCTCAAACATCCCAAAGCTAAGTTGGATAACTTGGATGAAGAATGGGCCACAGAACATGCCTGC
CAGGTATCCAGAAATGCTACCAGGGGGACTTTTAGTTCCTTGAGTATTTATTATTACTACTTTAGAACTGGCAAAT
GATTTTCAAAATGCCCTGCGTAGACTAATGTTTGCTGTGGAAAAGTCTATAAATAGAAAGAGATTGTGGAATTC
ACAGAGGAGGAAGTCTCAGAACGAGTGACACTTCACATTTGTGCTTCTACAAAAAAATATTTGTGCGAATTAT
GATATCCATGATCCAAAGAGTTCAGCAAGACCAGCAGATTGGAAGTATCAAAGTGGATTATCATCCTCATGGCTT
TCTTTAGAGTGTACAGTTCACATTAATATTCACATCCCACCTTCTGCTACTTCTGTGCTAGCTATACTCTGGAGAAA
AATACAAAAGATGGACTTACACGCTGGGCCAAGGAAATAGAAAATGGTGTATTATTGATTAATGGACAAGTTAA
GATGAAGATTGTGACCTATTAGAAGGACAGAAAAATCTTCTAGAGGAAATACTCAAGCAACTAGTCATTCTTTT
GATGTCAGAGTGCTAACGCAGTTGCTCCTGAATTCAGACCACAGATCCACAGCCACAGTCCAGATATGTAGCGGT
TCTGTAAACCTTAAGGGTGCTGTGAAATGCAGAGCTTATATCCACAGCAGTAAACCCAAAGTTAAAGATGCTGTG
CAGGCAGTAAAGAGGGATATATTGAACACAGTTGCTGATCGTTGTGAAATGCTATTTGAGGATCTGCTTTTGAAT
GAAATTCCAGAAAAAAAGATTCTGAAAAAGAGTTCACGTCCTCCCTTATCGAGTCTTTGTTCCCTTCCTGGA
TCCACTGTAATGTTGTGTGATTATAAATTTGACGATGAGTCAGCTGAAGAAATCAGGGACCATTTTATGGAGATG
TTGGATCACACAATTCAAATAGAAGATTTGGAAATTCAGAGGAAACAAACACAGCTTGTATGAGTTCTTCTATG
AATAGTCAAGCTTCATTGGACAACACAGATGATGAACAACCAAAACAACCAATTAAACTACAATGTTATTGAAA
ATTCAGCAAAACATAGGTGTGATTGCAGCATTTACAGTTGCAGTCCTTGCTGCGGGTATCTCCTTTCATTACTTC
AGTGATTAGGGTGAGGCACAAAGAGTTTCTTGATCATCCAGAGAACATTGACAGACAATTATGAATAATAAGAT
GTTAACAATCCATCTGTATTTAAAACACTAGCAGCCAGATCTGCTGCCATGATGCCTATTTGGTGTGTTTCTGAT
TAAATGAAATCACAAGCTGCCTTGTTTAGCCTGCTTTACATTGTAGGTGGCCCGCATTTCCAGAAATAACGTTA
TGCATCTAGATGGAAGCTGCATGTAACAAATCATTATTATCTATTTTTAAAAGCTTCAAAATGATGGGATATGAT
CATAGATTTTAGTCTTACTAATCTGAATCACATATTAATCAGGACATTAAAACTTTAACAGAGGCATGATGGCT
CACACGTATAATCCTAATGCTTTGAGAGGCTGAGGTAGGAGCATCACCTGGGGCTGGGAGGGAGTTGGAGACCAG
CCTGGATGACATAATGAGATTCTGTCTCTACTGGAAAAAAAAAAAAAAAAA

550/6881
FIGURE 514

MLPGGLLVLGVFIIITTTLELANDFQNALRRLMFAVEKSINRKRLWNFTTEEVSERVTLHICASTKKIFCRTYDIHD
PKSSARPADWKYQSGLSWLSLECTVHINIHIPLSATSVSYLEKNTKNGLTRWAKEIENG VYLINGQVKDEDC
DLLEGQKKSSRGNTQATSHSFDVRVLTQLLNSDHRSTATVQICSGSVNLKGAVKCRAYIHSSKPKVKDAVQAVK
RDILNTVADRCEMLFEDLLLNEIPEKKDSEKEFHVLPYRVFVPLPGSTVMLCDYKFDDSAEEIRDHFMEMLDHT
IQIEDLEIAEETNTACMSSSMNSQASLDNTDDEQPKQPIKTTMLLKIQQNIGVIAAFTVAVLAAGISFHYFSD

551/6881

FIGURE 515A

CGAGACGGAAGCGGGCTGGGAGGCGTCGGCGGCGGCAGCGCACGTGGTGACGTGCGAGGGGGGTGCGGCGCGAGCG
GTGCGGCGGCGGCGGAGGCAGTGTCTCCCGGTGCGCGGTGGAGGTCGGTCGCTCAGAGCTGCTGGGCGCAGTTTCT
CCGCTGCTGCTTCGGCGCGGCTGTATCGGCGAGCGAGCGAGTTCCCGCGAGTTCTCGGTGGCGCTCCCCCTTCC
TTTCAGTCTCCACGGACTGGCCCCCTCGTCTTCTACTTGACCGTCCCGTCTTCCGCCGCTTCTGGCGCTTTC
GTTGGGCCGATTCCCGCCCGCTTCTCTGCTTCCCATCGAAGCTCTAGAAATGAATGTTTCCATCTCTTCAGAG
ATGAACCAGATTATGATGCATCATTATCACAGAAGAAATTCGTGTCTATAGCTTTTAAGGACTTGATTACATCAT
TTTCAAGCCTGATAGTTTTTGAATCACCATTAGAGCTTAAGACACACCTGCCTTCATTTCAACCACCTGTCTTCA
TACCTTGACGAAGTGCACCTTTTAACTCCTTTGTCCTTGGATTACTTAAGAGTTCCCAGAAATACATTTGCCA
CCAACAGAGTAGCCAAATTTATAAGGAAAAATGATTCCCAATGGATATTTGATGTTTGAGGATGAAAATTTTATT
GAGTCTTCTGTTGCCAAATTAATGCCCCTGAGGAAAAGTGGCCAGTTCTGTGATGTTTCGACTTCAGGTCTGTGGC
CATGAAATGTTAGCACACAGAGCAGTGTAGCTTGCTGCAGTCCCTATTTATTTGAAATCTTTAATAGTGATAGT
GATCCTCATGGAATTTCTCACGTTAAATTTGATGATCTCAATCCAGAAGCTGTTGAAGTCTTGTGTAATTATGCC
TACACTGCTCAGTTGAAAGCAGATAAGGAATTGGTAAAAGATGTTTATTCTGCAGCAAAAAAGCTGAAGATGGAT
CGAGTAAAGCAGTTTGTGGTGATTATTTACTGTCTAGAATGGATGTTACCAGCTGCATCTCTTACCGAAATTTT
GCAAGTTGTATGGGAGACTCCCGTTTGTGAATAAGGTTGATGCTTATATTCAGGAGCATTGTTACAAATTTCT
GAAGAGGAGGAGTTTCTTAAGCTTCCAAGGCTAAAGTTGGAGGTAATGCTTGAAGATAATGTTTGCTTGCCGAGC
AATGGCAAATTTATATACAAAGGTAATCAACTGGGTGCAGCGTAGCATCTGGGAGAATGGAGACAGTCTGGAAGAG
CTGATGGAAGAGGTTCAAACCTTGTACTACTCAGCTGATCACAAGCTGCTTGATGGGAACCTACTAGATGGACAG
GCTGAGGTGTTTGGCAGTGATGATGACCACATTCAGTTTGTGCAGAAAAAGCCACCACGTGAGAATGGCCATAAG
CAGATAAGTAGCAGTTCAACTGGATGTCTCTCTTCTCCAAATGCTACAGTACAAAGCCCTAAGCATGAGTGGA
ATCGTTGCTTCAGAAAAGACTTCAAATAACACTTACTTGTGCCTGGCTGTGCTGGATGGTATATTCTGTGTCATT
TTTCTTCATGGGAGAAACAGCCACAGAGCTCACCACAAAGTACTCCAAAATAAGTAAGAGTTTAAGCTTTGAG
ATGCAACAAGATGAGCTAATCGAAAAGCCCATGTCTCCTATGCAGTACGCACGATCTGGTCTGGGAACAGCAGAG
ATGAATGGCAAACCTCATAGCTGCAGGTGGCTATAACAGAGAGGAATGTCTTCGAACAGTCGAATGCTATAATCCA
CATAAGATCACTGGTCTTTTCTTGCTCCCATGAGAACACCAAGAGCCCGATTTCAAATGGCTGTACTCATGGGC
CAGCTCTATGIGGTAGGTGGATCAAAATGGCCACTCAGATGACCTGAGTTGTGGAGAGATGTATGATTCAAACATA
GATGACTGGATTCTGTTCCAGAATTGAGAACTAACCGTTGTAATGCAGGAGTGTGTGCTCTGAATGGAAAGTTA
TACATCGTTGGTGGCTCTGATCCATATGGTCAAAAAGGACTGAAAAATTGTGATGTATTTGATCCTGTAACAAAG
TTGTGGACAAGCTGTGCCCTCTTAACATTCCGAGACACCAGTCTGCAGTCTGTGAGCTTGGTGGTTATTTGTAC
ATAATCGGAGGTGCAGAATCTTGGAATTGTCTGAACACAGTAGAACGATACAACTCCTGAAAATAATACCTGGACT
TTAATTGCACCCATGAATGTGGCTAGGCGAGGAGCTGGAGTGGCTGTTCTTAATGGAAAACCTGTTTGTATGTGGT
GGCTTTGATGTTTCTCATGCCATCAGTTGTGTGGAAATGTATGATCCAACCTAGAAATGAATGGAAGATGATGGGA
AATATGACTTCACCAAGGAGCAATGCTGGGATTGCAACTGTAGGGAACACCATTTATGCAGTGGGAGGATTTCGAT
GGCAATGAATTTCTGAATACGGTGGAAGTCTATAACCTTGAGTCAAATGAATGGAGCCCTATACAAAGATTTTC
CAGTTTTAACAAATTTAAGACCCCTCTCAAATAACAGGCTTAGTGATGTAATTATGGTTAGTAGAGGTACACTTG
TGAATAAAGAGGGTGGGTGGGTATAGATGTTGCTAACAGCAACACAAAGCTTTGCATATTGCATACTATTAAAC
ATGCTGTACATACTTTTTGGGTTTATTTGGAAAGGAATGCAAAGATGAAGGTCTGTTTTGTGTACTTTTAAGACT
TTGGTTATTTTACTTTTTTGGAAAAGAATAAACCAAGAATTGATTGGGCACATCATTTCAGAAGTCCCTCTCCT
CCACATTTGTTTTGCCAATTTGCACATTAAATGACTCTTCCCTCAAATGTGTACTATGGGGTAAAAGGGGTAGGG
TTTAAAGATGTAGACAGTTGGGTTTTTTAAGGGCCCTTTTTCAATAACTGGAACACTCTATAACAAAGGATACTT
ATTTAAATAGATGACATTGACTATTTTTGTTTTTATTTAAAGGAAGCTTACATGCCTACCAATATTTAATCTTTT
ATGATTGCCTTTTTTATAACTTTTTATATTTCTCAGCAGAGTGCTTTACCAATTGAAGTAAAATGTGGCAGGCTGGA
GTTATTGAAGCAGAGTGGCAGTCTTCAGTTTGCAGAGTAGGGGTCTGTCTTTTAACTCTGAGTGCAAACCTTCAG
AGTTCTTGCCCTTGGCTGCAGTTTTTTTCCCTTCAAGAATGCAGTACTAACATTTATTTGAGTGGAGTTACTGAACA
GTAACATAGCTGTGATTTTTTGGTATTTGAAACACTGGTTTTTAAATATTTTGAATGTTGAGGGTATGTTTTATAT
AGCAAGACATTATATAGCAGTAAAAAATGGTGTTTTTATCTTCTATATAATTCCTGTTTTTATTATTAACAAAACA
GTCCTAAATAGCAGCCCTCAATTGTGAAAAAATTTACTTTAACTACATTAGGTGTGTAATGCAGGTTTTATCAG
AACTATGTTTTTGTTCAGTTTATCTGTTTCATATGGATAAATATTGGTTGGGATGACTTGGTGTCTAATGTGTAGT

552/6881

FIGURE 515B

GCTACACACCTAACTTATGGGGCCAAAATAGCATGTCCTAATGCTTGCTGCTGATTTAAACACATTAAAGGTACT
TTGCAGGAAATCCTTGCACCATGGGATTAATATCCAATTGCTGCTTGCTACACTCATTCACTACTAAAAGTTTTGA
GAAATTTTTTTTTTCCAGTAATGAGCTTAAGAAATTTGTGGAAAATAACTCACCTGGCATCTTACATCTGAAATAA
GGAATGATATAAGGTTTTTTTTTCTCACAGAAGATGAAGCACACAGGAACCTAATGGGCCAACTGGGATGAGGTG
ACTATTCTGAGATGACTATTCAGTGGCTAACTTGGGTTAGGAAGAAAATAATTAGGTATTTCTCCAAATGTTCA
CTGGTACTCTGCCACTTTATTTCTCTCATCTGTTACACAAAGAACCACCAGGAAAGCAAATCAGTTTGGTTGGTA
ACTCTGTAATTCCTAACTATCACTGGTTTGGTTCTGGACTAAAACCTACATTGACAGATTGAATTTGCCTAATATG
ATGACTGTTTTTAATATGGATCTGTATGTGTTCTATTCAGCACAAAGGAAATAAAATTTTAGTTGAGGATTCAGC

553/6881
FIGURE 516

MIPNGYLMFEDENFIESSVAKLNALRKSGQFCDVRLQVCGHEMLAHRAVLACCSPYLFEIFNSDSDPHGISHVKF
DDLNPEAVEVLLNYAYTAQLKADKELVKDVYSAAKKLKMDRVKQVCGDYLLSRMDVTSCISYRNFASCMGDSRLL
NKVDAYIQEHLQISEEEFLKLPRLKLEVMLEDNVCLPSNGKLYTKVINWVQRSIWENGDSLEELMEEVQTLYY
SADHKLLDGNLLDGQAEVFGSDDDHQFVQKKPPRENGHKQISSSSTGCLSSPNATVQSPKHEWKIVASEKTSNN
TYLCLAVLDGIFCVIFLHGRNSPQSSPTSTPKLSKSLSFEMQQDELIKPMSPMQYARSGLGTAEMNGKLI AAGG
YNREECLRTVECYNPHTDHSFLAPMRTPRARFQMAVLMGQLYVVGGSNGHSDDLSCGEMYDSNIDDWIPVPELR
TNRCNAGVCALNGKLYIVGGSDPYGQKGLKNCDFDPVTKLWTSCAPLNIRRHQSAVCELGGYLYIIGGAESWNC
LNTVERYNPENNTWTLIAPMNVARRGAGVAVLNGKLFVCGGFDGSHAISCVEMYDPTRNEWKMMGNMTSPRSNAG
IATVGNTIYAVGGFDGNEFLNTVEVYNLESNEWSPYTKIFQF

554/6881
FIGURE 517

CCTTTGCCGCTGGTCGGGATTGGGATGTCGAAGAACACAGTGTCGTCGGCCCGCTTCCGGAAGGTGGACGTGGAT
GAATATGACGAGAACAAGTTCGTGGACGAAGAAGATGGGGGCGACGGCCAGGCCGGGCCCCGACGAGGGCGAGGTG
GACTCCTGCCTGCGGCAAGGAAACATGACAGCTGCCCTACAGGCAGCTCTGAAGAACCCCCCTATCAACACCAAG
AGTCAGGCAGTGAAGGACCGGGCAGGCAGCATTGTCTTGAAGGTGCTCATCTCTTTTAAAGCTAATGATATAGAA
AAGGCAGTTCAATCTCTGGACAAGAATGGTGTGGATCTCCTAATGAAGTATATTTATAAAGGATTTGAGAGCCCG
TCTGACAATAGCAGTGCTATGTTACTGCAATGGCATGAAAAGGCACTTGCTGCTGGAGGAGTAGGGTCCATTGTT
CGTGTCTTGACTGCAAGAAAACTGTGTAGTCTGGCAGGAAGTGGATTATCTGCCTCGGGAGTGGGAATTGCTGG
TACAAAGACCAAAACAACCAATGCCACCGCTGCCCTGTGGGTAGCATCTGTTTCTCTCAGCTTTGCCTTCTTGC
TTTTTCATATCTGTAAAGAAAAAATTACATATCAGTTGTCCTTAATGAAAATTGGGATAATATAGAAGAAATT
GTGTTAAAAATAGAAGTGTTCATCCTTTCAAAACCATTTTCAAGTGATGTTTATACCAATCTGTATATAGTATAATT
TACATTCAAGTTTAAATTGTGCAACTTTTAAACCCCTGTTGGCTGGTTTTTTGTTCTGTTTTGTTTTGTATTATTTT
TAACTAATACTGAGAGATTTGGTCAGAATTTGAGGCCAGTTTCCTAGCTCATTGCTAGTCAGGAAATGATATTTA
TAAAAAATATGAGAGACTGGCAGCTATTAACATTGCAAAACTGGACCATATTTCCCTTATTTAATAAGCAAAATA
TGTTTTTGGAAATAAGTGGTGGGTGAATACCACTGCCAAGTTATAGCTTTGTTTTTGCTTGCCTCCTGATTATCTG
TACTGTGGGTTTAAGTATGCTACTTTCTCTCAGCATCCAATAATCATGGCCCTCAATTTATTTGTGGTCACCCA
GGGTTTCAAGCAAGAAGTCTTGCTTTATACAAATGTATCCATAAAATATCAGAGCTTGTTGGGCATGAACATCAA
ACTTTTGTTCCACTAATATGGCTCTGTTTGAAAAAACTGCAAATCAGAAAGAATGATTTGCAGAAAGAAAGAAA
AACTATGGTGTAAATTTAACTCTGGGCAGCCTCTGAATGAAATGCTACTTTCTTTAGAAATATAATAGCTGCCTT
AGACATTATGAGGTATACAACCTAGTATTTAAGATACCATTTAATATGCCCCGTAAATGTCTTCAGTGTTCTTCAG
GGTAGTTGGGATCTCAAAGATTTGGTTCAGATCCAAACAAATACACATTCTGTGTTTTAGCTCAGTGTTTTCTA
AAAAAAGAACTGCCACACAGCAAAAAATTGTTTACTTTGTTGGACAAACCAATCAGTTCTCAAAAAATGACCG
GTGCTTATAAAAAGTTATAAATATCGAGTAGCTCTAAACAAACCACCTGACCAAGAGGGAAGTGAGCTTGTGCT
TAGTATTTACATTGGATGCCAGTTTTGTAATCACTGACTTATGTGCAAACTGGTGCAGAAATCTATAAACTCTT
TGCTGTTTTTGATACCTGCTTTTTGTTTCATTTTGTGTTTGTGTTTTGTAAAAATGATAAACTTCAGAAAATAAAAT
GTCAGTGTTGAATAAAAAAAAAAAAAAAAAAAAAA

555/6881
FIGURE 518

MSKNTVSSARFRKVDVDEYDENKFVDEEDGGDGQAGPDEGEVDSCLRQGNMTAALQAALKNPPINTKSQAVKDRA
GSIVLKVLISFKANDIEKAVQSLDKNGVDLLMKYIYKGFESP SDNSSAMLLQWHEKALAAGGVGSIVRVLTARKT
V

GCCAGGCAGAGTCTCTACTATAGGCATGCGAGCTCAGCTTGTCCTCCCTCCAATGAAGCATTGCTGTGAAAGTTCCCTTT
 CCCAGCTGCCTCCACTAATCTGCAAAAAGCACTTTCTAAAGCACTGGAAAGCCGAGATGAGGTGAAAACCAAGTG
 GGGTGTCTTCTGACTTCATCAAGGCCCTTTATTAAATTCCACGGTCATGTGTACCTGAGTAAGAGCTTGGAAAAAGTT
 GAGCCCTCTTCGAGAGAAAATTGGAAGAACAGTTTAAAGAGGCTGCTATTCCAAAAAGCTTTCAACTCTCAGCAGTT
 AGTTCATGTCACTGTCTATTAACTGTTTCAACTTCATCACCTTCGTGACTTTAGCAATGAAACCGAGCAGCACAC
 TTATAGCCAAGATGAGCAGCTATGTTGGACACAGTTGCTGGCCCTCTTTATGTCCTTTTCTTGGCATCCTGTGCAA
 GTGTCTCTACAGAATGAGTCTCAGGAGGAGTCTTACAATGCCTATCCTCTTCCAGCAGTCAAGGTCTCCATGGA
 CTGGCTAAGACTCAGACCCAGGGTCTTTCAGGAGGCAGTGGTGGATGAAAGACAGTACATTTGGCCCTGGTTGAT
 TTCTCTTCTGAATAGTTTCCATCCCCATGAAGAGGACCTCTCAAGTATTAGTGCGACACCACTTCCAGAGGAGTT
 TGAATTACAAGGATTTTTTGGCATTGAGACCTTCTTTCAGGAACCTTGGATTTTTTCCAAGGTCACCAGGGTATTAC
 AGGGGACAAAGAAGGCCAGCAACGACGAATACGACAGCAACGCTTGATCTCTATAGGCAAATGGATTGCTGATAA
 TCAGCCAAGGCTGATTCACTGTGAAAATGAGGTAGGGAAATTGTTGTTTATCACAGAAATCCCAGAATTAATACT
 GGAAGACCCCACTGAAGCCAAAGAGAACCTCATTTCTGCAAGAAACATCTGTGATAGAGTCGCTGGCTGCAGATGG
 GAGCCCAGGGCTAAAATCAGTGCTATCTACAAGCCGAAATTTAAGCAACAACCTGTGACACAGGAGAGAAGCCAGT
 GGTTACCTTCAAAGAAAACATTAAGACACGAGAAGTGAACAGAGACCAAGGAAGAAGTTTTCTCTCCAAAGAGGT
 GAGAAGGGACTATAGCAAAGGAATAACTGTAACTAAGAATGATGGAAAGAAGGACAACAACAAGAGGAAAACCTGA
 AACCAAGAAATGCACCTTAGAAAAGTTACAGGAAACAGGAAAGCAGAATGTGGCAGTGCAGGTAAAATCCCAGAC
 AGAACTAAGAAAGACTCCAGTGTCTGAAGCCAGAAAAACACCTGTAACTCAAACCCCAACTCAAGCAAGTAACTC
 CCAGTTTATCCCCATTTCATCACCTTGGAGCCTTCCCTCCTCTTCCAGCAGGCCAGGGTTTCCGCCCCCAACATA
 TGTTATCCCCCGCCTGTGGCATTCTTCTATGGGCTCAGGTTACACCTTCCAGCTGGTGTCTTCTGTCCAGGAAC
 CTTTCTTTCAGCCTACAGCTCACTCTCCAGCAGGAAACCAGGTGCAAGCTGGGAAACAGTCCCACATTCTTTACAG
 CCAGCAACGGCCCTCTGGACCAGGGCCAATGAACCAGGGACCTCAACAATCACAGCCACCTTCCAGCAACCCCT
 TACATCTTTACAGCTCAGCCAACAGCACAGTCTACAAGCCAGCTGCAGGTTCAAGCTCTAACTCAGCAACAACA
 ATCCCCCTACAAAAGCTGTGCCGGCTTTGGGGAAAAGCCCGCTCACCACCTCTGGATTCCAGCAGTATCAACAGGC
 AGATGCCTCCAAACAGCTGTGGAATCCCCCTCAGGTTCAAGGCCCATTAGGGAAAATTATGCCTGTGAAAACAGCC
 CTACTACCTTCAGACCCAAGACCCCCATAAAAAGTGTGAGCCGTCATTGCAACCTCCTGTAATGCAGCAGCAGCC
 TCTAGAAAAAAAATGAAGCCTTTTCCCATGGAGCCATATAACCATAATCCCTCAGAAGTCAAGGTCCCAGAATT
 CTACTGGGATTCTTCCCTACAGCATGGCTGATAACAGATCTGTAATGGCACAGCAAGCAAACATAGACCCGAGGGG
 CAAACGGTCACCAGGAATCTTCCGTCCAGAGCAGGATCCTGTACCCAGAATGCCGTTTGAGAAAATCCTTATTGGA
 GAAGCCCTCAGAGCTCATGTACATTATCTCTTCTGTCCTCACCAGGATTCTCTCTCAATCAGGAAAAGATA
 CCCAAATAATAGTATGTTCAATGAGGTATATGGGAAAACCTGACATCCAGCTCCAAAGCAGAACTCAGTCCCTC
 AATGGCCCCCAGGAAACATCTCTGTATTCCCTTTTTGAAGGGACTCCGTGGTCTCCATCACTTCTCTGCCAGTTC
 AGATCATTCAACACCAGCCAGCCAGTCTCCTCATTCTCTAACCACAGCAGCTACCCAGCTCTCCTCCAACACA
 CAACCATAATTCTGTTCCATTCTCCAATTTTGAGCCATTGGGACTCCAGATAACAGGGATAGAAGGACTGCAGA
 TCGGTGGAACACTGATAAGCCAGCCATGGGTGGGTTTGGCATTGATTATCTCTCAGCAACGTCATCCTCTGAGAG
 CAGTTGGCATCAGGCCAGCACTCCGAGTGGCACCTGGACAGGCCATGGCCCTTCCATGGAGGATTCTCTGCTGT
 CCTCATGGAAAGCCTAAAGTCTATCTGGTCCAGTTCCATGATGCATCCTGGACCTTCTGCTCTGGAGCAGCTGTT
 AATGCAGCAGAAGCAGAAACAGCAACGGGGACAAGGCACCATGAACCCTCCACACTGAGAGCCAAAGTGGCAACCT
 GGGAATGAAGGCTCCATAAACCATGGCATGTTGGGTTTGCAGGACTGGCCACACAGTCCCCTGCAGGTGGCAGC
 CCTCTTTTCTGTTTCTCGCTGTCAAGAGGGTGTAAGTATTCCACCAGCCCGCTGAGTGTGCACGAAATGTTTCGCA
 GTGCAACAAAAAGAAAAATCCATCAGGAACTCTCCGTCCCCCGGGGCCTTCCGGAGGGAGAGAGAGAGGAACTG
 CTGTTTATCTCACTCAGTTACTTGGTATCACCGCCTCTCACCTTCTCCATCGTGCATGTCCCCAGCCACATGGGA
 AGTGAAAGCTGAGAAGGGAAGGCAGATGGGAGAAGCCAATGGGAACCTTCTCAGTCTTTTTTCTCTTTGGGGAA
 TAAATAGGAATCCATTAATGATTGCTTTGCTGACTGAGAATGTAGTTGAAATTAACATCTTTTATTATTATTA
 CTCTCAGTAGTAAATATCACACTGAATTCTTCCATACACAGGTGTGCTTCTAGTCAGTGTGTAGCAAGGAAAGC
 CCCGTTCACTGCTCCTGTGAGAGGTTGGTGGTGACAGGATGGGGAACCGACCTCTTCAGCCAGTGGAAATGTTCC
 ATAAGGGAGAGTTCAAGGCCTGTGAGAAGGCTCTGGTAGGCCTTCTCTGGCCAGGAGACTCCAGCAGGGAATGC
 CTTTCACTCTGTAGGTGCTCGAGCCCCAATCGAGGATACAGTGTGGGIGGTGGTGTGGGCTGGACTAGCAGGTA

557/6881
FIGURE 519B

GACTGCTGTAGGATTTCAAATTACGTTTTTTGATTCTGTACATTTTACAGTCGCACAGCAAGCAGTCTCACAGAA
GGCAGGCTAGTCCATTCACAGCCTGACACGTTCTAATAGGTAGAAGCTTTCAGTGTGGTTATTTTTCTTTGGTT
GGTTTTTGTGCCCCCATTCTACTTCCCACCCCTCCTGCCCCATCTCCATCCCTTCTTTTACCCAATGCTGTATGCT
AGTAATTGTTTTTATTCCTAATGTGTGCAACATCACATCTCCCCAAGAAGCAACAGCATGGGGTCCAGCAGTTGG
GGCCCAAAAGACAGTCTGAAGAGGAAGGAAGCAGCAGTATCTGCGTAGCCACAGAGGGCCAGGCCCTGCCCA
GCTGCAGTCTCCCAGCCTCCACTTTCAGAGTGAAATTCAAGGCAGCACGGACATGTGCCCATCAGGCACAGAAGA
AAACACGACGTCGTCCATTTTGGAAGAGACGAAAGAAAGGAAAATAAACTCTTTGTATGATATTTATTAGGAGGA
AAGAGGACTGAAAATGTTCTTGTGTAGAAACAGAAGGACAGCATTTCTGTTAGTCATTTCTTGAAAAAGTAATAT
TTTAAGGGGAAATTATGGAACAATCTAATTGTTCAATTGCTGTGCTAGTGGTAGGGTTTATTTTCTGGGAGGTC
TCTCCTTTGTGTGTCTGTATGTTTGTGTACACACACGTCGCCATCTGCTGTCCCAGAGGGGAGGGGTTGTGTGTG
CGAGTGTATGGAGTTAGTGTGGAACCTTAAGAGCTGGAAGACAGCTGTAGAGCAAAGCACATCCAGGAGCCCCAGT
TGTCAGTGCAGTCTGGGCAACCCCAGCAATGAAAAGGGGTGAGATAACGCTCATTGCTCTTCAGAGAGAGTGGTT
GGAGCCCCCCCCCGCCCCGTATGCTTACATTATTGCTCTTTTAGTTTGACATGGTGTGTTGGGTTTGTGTTTTTGA
AAGGTCTGAAAAGGTGAAGCCCCCTACCCAATGGCAATATGAAACCTTTTGTGCTTCTCTTCAGCCCCCTTCCCTG
TGTCCACCTTTCTCTCCTCTTCCCAAGCCTTTTTCTACTACCTTTACCCAGTTTGTGTGTTTGAGCTCTGCATT
CAGGCAGCTGCAACATTCCAGTGTGTTGAACTGTCAGTGAATCTTGCGCCCTAGACAAGCTAACCAGGTTTACCAT
CTCACTCCCAGTAATACCCAGCTCCTATCTAAAGCCCCATTCTGCATGAGAATTTGGTGTGTTGGAATGTTTTCTG
ACTCTTGGGGCGGGATTCTCGCCTTATCATCCTCACTGTGGAGTAATGAGGGGGAGGAGAATCTTTATCAGAAA
CTGGTTTTGTGTAGTAACTTTCTTTTGTGGTTTTTTGTTTTGTTTTCTGGGTTTTGTTTTTGTGTTTTGTCTGT
GCAAGACCTGCAGCTGCTGAAAATCAGCTTTGCCTTTAATTAAACCATGTTCTCTCC

558/6881
FIGURE 520

MSFLGILCKCPLQNESQEESYNAYPLPAVKVSMDWLRLRPRVFQEAVVDERQYIWPWLISLLNSFHPHEEDLSSI
SATPLPEEFELQGFLALRPSFRNLDFSKGHQGITGDKEGQQRIRQORLISIGKWIADNQPRLIQCENEVGKLLF
ITEIPELILEDPEAKENLILQETSVIESLAADGSPGLKSVLSTSRNLSNNCDTGEKPVVTFKENIKTREVNRDQ
GRSFPPKEVRRDYSKGITVTKNDGKKDNNKRKTETKKCTLEKLQETGKQNVAVQVKSQTELKTPVSEARKTPVT
QTPTQASNSQFIP IHHPGAFFPLPSRPGFPPPTYVIPPVAFSMGSGYTFPAGVSVPGTFLOPTAHSPAGNQVQA
GKQSHIPYSQQRPSGPGPMNQGPQQSQPPSQOPLTSLPAQPTAQSTSQLQVQALTQQQQSPTKAVPALGKSPPHH
SGFQQYQQADASKQLWNPPQVQGPLGKIMPVKQPYLQTDPIKLFEPQLQPPVMQQQPLEKKMKPFMEPYNNH
PSEVKVPEFYWDSSYSMADNRSVMAQQANIDRRGKRSPGIFRPEQDPVPRMPFEKSLLEKPSELMSHSSSFLSLT
GFSLNQERYPNNSMFNEVYGKNLTSSSKAELSPSMAPQETSLSLFEFTPWSPSLPASSDHSTPASQSPHSSNPS
SLPSSPPTHNNHNSVPFSNFGPIGTPDNRDRRTADRWKTDKPAMGGFGIDYLSATSSSESSWHQASTPSGTWTGHG
PSMEDSSAVLMESLKSIIWSSSMMHPGPSALEQLLMQQKQKQQRGQGTMNPPH

559/6881
FIGURE 521A

ACCACCTGATCAAGGAAAAGGAAGGCACAGCGGAGCGCAGAGTGAGAACCACCAACCGAGGCGCGGGCAGCGAC
CCCTGCAGCGGAGACAGAGACTGAGCGGCCCCGGCCCCGCCATGCCTGCGCTCTGGCTGGGCTGCTGCCTCTGCTT
CTCGCTCCTCCTGCCCCGAGCCCCGGGCCACCTCCAGGAGGGAAGTCTGTGATTGCAATGGGAAGTCCAGGCAGTG
TATCTTTGATCGGGAACCTTCACAGACAACTGGTAATGGATTCCGCTGCCTCAACTGCAATGACAACACTGATGG
CATTCACTGCGAGAAGTGCAAGAATGGCTTTTACCGGCACAGAGAAAGGGACCGCTGTTTGCCCTGCAATTGTAA
CTCCAAAGGTTCTCTTAGTGCTCGATGTGACAACTCCGGACGGTGACAGCTGTAAACCAGGTGTGACAGGAGCCAG
ATGCGACCGATGTCTGCCAGGCTTCCACATGCTCACGGATGCGGGGTGCACCCAAGACCAGAGACTGCTAGACTC
CAAGTGTGACTGTGACCCAGCTGGCATCGCAGGGCCCTGTGACGCGGGCCGCTGTGTCTGCAAGCCAGCTGTAC
TGGAGAACGCTGTGATAGGTGTGATCAGGTTACTATAATCTGGATGGGGGGAACCCCTGAGGGCTGTACCCAGTG
TTTCTGCTATGGGCATTACAGCCAGCTGCCGACGCTCTGCAGAATACAGTGTCCATAAGATCACCTCTACCTTTCA
TCAAGATGTTGATGGCTGGAAGGCTGTCCAACGAAATGGGTCTCCTGCAAAGCTCCAATGGTCACAGCGCCATCA
AGATGTGTTTAGCTCAGCCCCAACGACTAGACCCTGTCTATTTTGTGGCTCCTGCCAAATTTCTTGGGAATCAACA
GGTGAGCTATGGTCAAAGCCTGTCTTTGACTACCGTGTGGACAGAGGAGGCAGACACCCATCTGCCCATGATGT
GATTCTGGAAGGTGCTGGTCTACGGATCACAGCTCCCTTGATGCCACTTGGCAAGACACTGCCTTGTGGGCTCAC
CAAGACTTACACATTACAGGTTAAATGAGCATCCAAGCAATAATTGGAGCCCCCAGCTGAGTTACTTTGAGTATCG
AAGGTTACTGCGGAATCTCACAGCCCTCCGCATCCGAGCTACATATGGAGAATACAGTACTGGGTACATTGACAA
TGTGACCCTGATTTACAGCCCGCCCTGTCTCTGGAGCCCCAGCACCCCTGGGTGAACAGTGTATATGTCCTGTTGG
GTACAAGGGGCAATTCTGCCAGGATTGTGCTTCTGGCTACAAGAGAGATTACAGCGAGACTGGGGCCTTTTGGCAC
CTGTATTCTTGTAACTGTCAAGGGGGAGGGGCCTGTGATCCAGACACAGGAGATTGTTATTACAGGGGATGAGAA
TCCTGACATTGAGTGTGCTGACTGCCCAATTGGTTTCTACAACGATCCGCACGACCCCCGAGCTGCAAGCCATG
TCCCTGTCATAACGGGTTACAGCTGCTCAGTGATGCCGGAGACGGAGGAGGTGGTGTGCAATAACTGCCCTCCCGG
GGTCACCGGTGCCGCTGTGAGCTCTGTGCTGATGGCTACTTTGGGGACCCCTTTGGTGAACATGGCCAGTGAG
GCCTTGTACGCCCTGTCAATGCAACAACAATGTGGACCCAGTGCCTCTGGGAATTGTGACCGGCTGACAGGCAG
GTGTTTGAAGTGTATCCACAACACAGCCGGCATCTACTGCGACCAGTGCAAAGCAGGCTACTTCGGGGACCCATT
GGCTCCCAACCCAGCAGACAAGTGTGAGCTTGCAACTGTAAACCCATGGGCTCAGAGCCTGTAGGATGTGGAAG
TGATGGCACCTGTGTTTGCAAGCCAGGATTGGTGGCCCCAACTGTGAGCATGGAGCATTACAGCTGTCCAGCTTG
CTATAATCAAGTGAAGATTACAGATGGATCAGTTTATGCAGCAGCTTCAGAGAATGGAGGGCCCTGATTTCAAAGGC
TCAGGGTGGTGTGAGTAGTACCTGATACAGAGCTGGAAGGCAGGATGCAGCAGGCTGAGCAGGCCCTTCAGGA
CATTCTGAGAGATGCCAGATTTTCAAGAGGTGTAGCAGATCCCTTGGTCTCCAGTTGGCCAAGGTGAGGAGCCA
AGAGAACAGCTACCAGAGCCGCTGGATGACCTCAAGATGACTGTGGAAGAGTTCGGGCTCTGGGAAGTCAGTA
CCAGAACCAGGTTTCGGGATACTCACAGGCTCATCACTCAGATGCAGCTGAGCCTGGCAGAAAGTGAAGCTTCCTT
GGGAAACACTAACATTCTGCTCAGACCCTACGTGGGGCCAAATGGCTTTAAAAGTCTGGCTCAGGAGGCCAC
AAGATTAGCAGAAAGCCACGTTGAGTCAGCCAGTAACATGGAGCAACTGACAAGGGAAGTTCAGGACTATTCCAA
ACAAGCCCTCTCACTGGTGCAGCAAGGCCCTGCATGAAGGAGTCGGAAGCGGAAGCGGTAGCCCGACGGTGCTGT
GGTGCAAGGGCTTGTGGAATAATGGAGAAAACCAAGTCCCTGGCCCAGCAGTTGACAAGGGAGGCCACTCAAGC
GGAAATTGAAGCAGATAGGTCTTATCAGCACAGTCTCCGCTCCTGGATTACAGTGTCTCGGCTTCAGGGAGTCAG
TGATCAGTCCTTTACAGGTGGAAGAAGCAAAGAGGATCAAACAAAAGCGGATTCACCTCAAGCCTGGTAACCAG
GCATATGGATGAGTTCAAGCGTACACAGAAGAATCTGGGAACTGGAAAGAAGAAGCACAGCAGCTCTTACAGAA
TGGAAAAAGTGGGAGAGAGAAATCAGATCAGCTGCTTTCCCGTGCCAATCTTGCTAAAAGCAGAGCACAGAAGC
ACTGAGTATGGGCAATGCCACTTTTATGAAGTTGAGAGCATCCTTAAAAACCTCAGAGAGTTTGACCTGCAGGT
GGACAACAGAAAAGCAGAAGCTGAAGAAGCCATGAAGAGACTCTCCTACATCAGCCAGAAGGTTTCAGATGCCAG
TGACAAGACCCAGCAAGCAGAAAGAGCCCTGGGGAGCGCTGCTGCTGATGCACAGAGGGCAAAGAATGGGGCCGG
GGAGGCCCTGGAAATCTCCAGTGAGATTGAACAGGAGATTGGGAGTCTGAACTTGGAAGCCAATGTGACAGCAGA
TGGAGCCTTGGCCATGGAAAAGGGACTGGCCTCTCTGAAGAGTGAGATGAGGGAAGTGGAAGGAGAGCTGGAAAG
GAAGGAGCTGGAGTTTGACACGAATATGGATGCAGTACAGATGGTGATTACAGAAGCCCAGAAGGTTGATACCAG
AGCCAAGAAGCCTGGGGTTACAATCCAAGACACACTCAACACATTAGACGGCCTCCTGCATCTGATGGACCAGCC
TCTCAGTGTAGATGAAGAGGGGCTGGTCTTACTGGAGCAGAAGCTTTCCCGAGCCAAGACCCAGATCAACAGCCA
ACTGCGGCCCATGATGTGAGAGCTGGAAGAGAGGGGCACGTACAGCAGAGGGGCCACCTCCATTTGCTGGAGACAAG

560/6881

FIGURE 521B

CATAGATGGGATTCTGGCTGATGTGAAGAACTTGGAGAACATTAGGGACAACCTGCCCCCAGGCTGCTACAATAC
CCAGGCTCTTGAGCAACAGTGAAGCTGCCATAAATATTTCTCAACTGAGGTTCTTGGGATACAGATCTCAGGGCT
CGGGAGCCATGTCATGTGAGTGGGTGGGATGGGGACATTTGAACATGTTTAATGGGTATGCTCAGGTCAACTGAC
CTGACCCCATTCCTGATCCCATGGCCAGGTGGTTGTCTTATTGCACCATACTCCTTGCTTCCTGATGCTGGGCAA
TGAGGCAGATAGCACTGGGTGTGAGAATGATCAAGGATCTGGACCCCAAAGAATAGACTGGATGGAAAGACAAAC
TGCACAGGCAGATGTTTGCTCATAATAGTCGTAAGTGGAGTCCTGGAATTTGGACAAGTGCTGTTGGGATATAG
TCAACTTATTCTTTGAGTAATGTGACTAAAGGAAAAAACTTTGACTTTGCCCAGGCATGAAATTCTTCCTAATGT
CAGAACAGAGTGCAACCCAGTCACACTGTGGCCAGTAAAATACTATTGCCTCATATTGTCTCTGCAAGCTTCTT
GCTGATCAGAGTTCCTCCTACTTACAACCCAGGGTGTGAACATGTTCTCCATTTTCAAGCTGGAAGAAGTGAGCA
GTGTTGGAGTGAGGACCTGTAAGGCAGGCCCATTGAGAGCTATGGTGCTTGCTGGTGCCCGCCACCTTCAAGTTC
TGGACCTGGGCATGACATCCTTTCTTTTAATGATGCCATGGCAACTTAGAGATTGCATTTTTATTAAAGCATTTT
CTACCAGCAAAGCAAATGTTGGGAAAGTATTTACTTTTTTCGGTTTTCAAAGTGATAGAAAAGTGTGGCTTGGGCAT
TGAAAGAGGTAAAATTCTCTAGATTTATTAGTCCTAATTCATCCTACTTTTCGAACACCAAAAATGATGCGCAT
CAATGTATTTTATCTTATTTTCTCAATCTCCTCTCTCTTTTCCATCCACCCATAATAAGAGAATGTTTCTACTCACA
CTTCAGCTGGGTACATCCATCCCTCCATTATCCTTCCATCCATCTTTCCATCCATTACCTCCATCCATCCTTC
CAACATATATTTATTGAGTACCTACTGTGTGCCAGGGGCTGGTGGGACAGTGGTGACATAGTCTCTGCCCTCATA
GAGTTGATTGTCTAGTGAGGAAGACAAGCATTTTTAAAAAATAAATTTAAACTTACAACTTTGTTTGTACACAAG
TGGTGTTTATTGCAATAACCGCTTGGTTTGCAACCTCTTTGCTCAACAGAACATATGTTGCAAGACCCTCCCATG
GGGGCACTTGAGTTTGGCAAGGCTGACAGAGCTCTGGGTGTGCACATTTCTTTGCATTCCAGCTGTCACTCTG
TGCCTTTCTACAACCTGATTGCAACAGACTGTTGAGTTATGATAACACCAGTGGGAATTGCTGGAGGAACCAGAGG
CACTTCCACCTTGGCTGGGAAGACTATGGTGCTGCCTTGCTTCTGTATTTCTTGGAATTTCTGAAAGTGTTTT
TAAATAAAGAACAATTGTTAGA

561/6881
FIGURE 522

CCCAACCGCAGTTGACTAGCACCTGCTACCGCGCCTTTTGCTTCCTGGCGCACGCGGAGCCTCCTGGAGCCTGCCA
CCATCCTGCCTACTACGTGCTGCCCTGCGCCCGCAGCCATGTGCCGCACCCTGGCCGCTTCCCCACCACCTGCC
TGGAGAGAGCCAAAGAGTTCAAGACACGTCTGGGGATCTTTCTTCACAAATCAGAGCTGGGCTGCGATACTGGGA
GTACTGGCAAGTTCGAGTGGGGCAGTAAACACAGCAAAGAGAATAGAACTTCTCAGAAGATGTGCTGGGGTGGA
GAGAGTCGTTGACCTGCTGCTGAGCAGTAAAAATGGAGTGGCTGCCTTCCACGCTTTCCTGAAGACAGAGTTCA
GTGAGGAGAACCTGGAGTTCTGGCTGGCCTGTGAGGAGTTCAAGAAGATCCGATCAGCTACCAAGCTGGCCTCCA
GGGCACACCAGATCTTTGAGGAGTTCAATTTGCAGTGAGGCCCTAAAGAGGTCAACATTGACCATGAGACCCACG
AGCTGACGAGGATGAACCTGCAGACTGCCACAGCCACATGCTTTGATGCGGCTCAGGGGAAGACACGTACCCTGA
TGGAGAAGGACTCCTACCCACGCTTCCTGAAGTCGCCTGCTTACCGGGACCTGGCTGCCCAAGCCTCAGCCGCT
CTGCCACTCTGTCCAGCTGCAGCCTGGACGAGCCCTCACACACCTGAGTCTCCACGGCAGTGAGGAAGCCAGCCG
GGAAGAGAGGTTGAGTCACCCATCCCCGAGGTGGCTGCCCCCTGTGTGGGAGGCAGGTTCTGCAAAGCAAGTGCAA
GAGGACAAAAAAAAAAAAAAAAAAAAAAAAAATGCGCTCCAGCAGCCTGTTTGGGAAGCAGCAGTCTCTCCTTCA
GATACTGTGGGACTCATGCTGGAGAGGAGCCGCCCACTTCCAGGACCTGTGAATAAGGGCTAATGATGAGGGTTG
GTGGGGCTCTCTGTGGGGCAAAAAGGTGGTATGGGGGTTAGCACTGGCTCTCGTTCTCACCGGAGAAGGAAGTGT
TCTAGTGTGGTTTtaggaaacatgtggataaaagggaaaccatgaaaatgagaggaggaaaagacatccagatcagctg
TTTTGCCCTGTGTGCTCAGTTGACTCTGATTGCATCCTGTTTTCTTAATTCCCAGACTGTTCTGGGCACGGAAGGGA
CCCTGGATGTGGAGTCTTCCCTTTGGCCCTCCTCACTGGCCTCTGGGCTAGCCCAGAGTCCCTTAGCTTGTACC
TCGTAACTCCTGTGTGTCTGTCCAGCCTTGCAGTCATGTCAAGGCCAGCAAGCTGATGTGACTCTTGCCCCAT
GCGAGATATTTATACCTCAAACACTGGCCTGTGAGCCCTTTCCAAGTCAGTGGAGAGCCCTGAAAGGAGGCTCAC
TTGAATCCAGCTCAGTGCTCTGGGTGGCCCCCTGCAGGTGGCCCTGACCCTGCGTTGCAGCAGGGTCCACCTGT
GAGCAGGCCCGCCCTGGGGCCTCTCCTGGATGTGCCCTCTCTGAGTTCTGTGCTGTCTCTTGAGGCAGGGCCC
AGGAGAACAAAGTGTGGAGGCCTCGGGGAGTGGCTTTTCCAGCTCTCATGCCCCGAGTGTGGAACAAGGCAGAA
AAGGATCCTAGGAAATAAGTCTCTTGCGGTCCCTGAGAGTCCTGCTGAAATCCAGCCAGTGTTTTTTGTGGTAT
GAGAACAGGCAAAAAGAGATGCCCCGAGATAGAAGGGGAGCCTTGTGTTTCTTTCCTGCAGACGTGAGATGAACA
CTGGAGTGGGCAGAGGTGGCCCAGGACCATGGCACCTTAGAGTGCAGAAGCTGGGGGGAGAGGCTGCTTCGAAG
GGCAGGACTGGGGATAATCAGAACCTGCCTGTCACCTCAGGGCATCACTGAACAAACATTTCTGATGGCAACTC
CTGCGGCAGAGCCCAGGCTGGGGAAAGTGAACCTACCCAGGGCAGCCCCCTTTGTGGCCCAGGATAATCAACACTGTT
CTCTCTGTACCATGAGCTCCTCCAGGAGATTATTTAAGTGTATTGTATCATTGGTTTTCTGTGATTGTCATAACA
TTGTTTTTGTATTGTTGGTGTCTGTTGTTATTTATTATTGTAATTTAGTTCAGTTGCCTCTACTGGAGAATCTCAGCA
GGGGTTTCAGCCTGACTGTCTCCCTTTCTCTACCAGACTCTACCTCTGAATGTGCTGGGAACCTCTTGAGCCTG
TCAGGAACCTCCTCACTGTTTAAATATTTATTTATTGTGACAAATGGAGCTGGTTTCCTAGATATGAATGATGTTT
GCAATCCCCATTTTCTGTTTCAGCATGTTATATTCTTATAAAATAAAAGCAAAAGTCAAATATG

562/6881
FIGURE 523

GGGTGCGGGGCTGCTGGCGGCTCTGCAGAGTCGAGAGTGGGAGAAGAGCGGAGCGTGTGAGCAGTACTGCGGCCT
CCTCTCCTCTCCTAACCTCGCTCTCGCGGCTAGCTTTACCCGCCCGCTGCTCGGCGACCAGCGGGGATCCTCC
CCCAGCCGCAAGTCCACGAAGAAAGCAACGAATGAAAATTATGAAGACAACGAGAAGTCAGACTCCTCCGGGTGCG
CGCTCCAGCTGCTTCGGCTTCGTGCGCTACTCTGTGAACTCCGGGGAGAGATCTCGAGTCAAGATTAAGACCTTA
ACCCACCAACCTGCCTGTTTCGGACACCCCCGGGCCGCGCTGTCTGTCCCCTTCTCCATCGCCCTCTCCCAGA
AAGCTCCGGTGCTTGACCAGCTAGAGTCTGAGAAAGAGGAGAGGCGCGAACGCCACTCCAAAAGAGAAGGGTT
AAAGAGGGCAACCCTAACGATACGCTTGACTTTCTGTGGCTGGGAACACCTTCCACCATGACCACCTCAGCAAGT
TCCCACCTAAATAAAGGCATCAAGCAGGTGTACATGTCCCTGCCTCAGGGTGAGAAAGTCCAGGCCATGTATATC
TGGATCGATGGTACTGGAGAAGGACTGCGCTGCAAGACCCGGACCTGGACAGTGAGCCCAAGTGTGTGGAAGAG
TTGCCTGAGTGGAAATTTTCGATGGCTCTAGTACTTTACAGTCTGAGGGTTCCAACAGTGACATGTATCTCGTGCCT
GCTGCCATGTTTCGGGACCCCTTCCGTAAGGACCCCTAACAAAGCTGGTGTATGTGAAGTTTTCAAGTACAATCGA
AGGCCTGCAGAGACCAATTTGAGGCACACCTGTAAACGGATAATGGACATGGTGAGCAACCAGCACCCCTGGTTT
GGCATGGAGCAGGAGTATACCCTCATGGGGACAGATGGGCACCCCTTTGGTTGGCCTTCCAACGGCTTCCCAGGG
CCCCAGGGTCCATATTACTGTGGTGTGGGAGCAGACAGAGCCTATGGCAGGGACATCGTGGAGGCCCATTACCGG
GCCTGCTTGTATGCTGGAGTCAAGATTGCGGGGACTAATGCCGAGGTCATGCCTGCCAGTGGGAATTTAGATT
GGACCTTGTGAAGGAATCAGCATGGGAGATCATCTCTGGGTGGCCCGTTTCATCTTGCATCGTGTGTGTGAAGAC
TTTGGAGTGATAGCAACCTTTGATCCTAAGCCATTCTGGGAACTGGAATGGTGCAGGCTGCCATACCAACTTC
AGCACCAAGGCCATGCGGGAGGAGAATGGTCTGAAGTACATCGAGGAGGCCATTGAGAACTAAGCAAGCGGCAC
CAGTACCACATCCGTGCCTATGATCCCAAGGGAGGCCTGGACAAATGCCCGACGTCTAACTGGATTCCATGAAACC
TCCAACATCAACGACTTTTCTGCTGGTGTAGCCAATCGTAGCGCCAGCATACGCATTCCCCGGACTGTTGGCCAG
GAGAAGAAGGGTTACTTTGAAGATCGTCGCCCCCTCTGCCAACTGCGACCCCTTTTTCGGTGACAGAAAGCCCTCATC
CGCACGTGTCTTCTCAATGAAACCGGCGATGAGCCCTTCCAGTACAAAATTAAGTGGACTAGACCTCCAGCTGT
TGAGCCCCCTCCTAGTTCTTTCATCCCACTCCAACCTCTTCCCCCTCTCCAGTTGTCCCATTGTAACTCAAAGGGT
GGAATATCAAGGTCGTTTTTTTTTTCATTCCATGTGCCAGTTAATCTTGCTTTCTTTGTTTGGCTGGGATAGAGGGG
TCAAGTTATTAATTTCTTTCACACCTACCCTCCTTTTTTTCCTATCACTGAAGCTTTTTAGTGCATTAGTGGGGA
GGAGGGTGGGGAGACATAACCACTGCTTCCATTTAATGGGGTGCACCTGTCCAATAGGCGTAGCTATCCGGACAG
AGCACGTTTGCAGAAGGGGTCTCTTCTTCCAGGTAGCTGAAAGGGGAAGACCTGACGTACTCTGGTTAGGTTAG
GACTTGCCCTCGTGGTGGAACTTTTCTTAAAAAGTTATAACCAACTTTTCTATTTAAAGTGGGAATTAGGAGAG
AAGGTAGGGGTGGGAATCAGAGAGAATGGCTTTGGTCTCTTGCTTGTGGGACTAGCCTGGCTTGGGACTAAATG
CCCTGCTCTGAACACGAAGCTTAGTATAAACTGATGGATATCCCTACCTTGAAAGAAGAAAAGGTTCTTACTGCT
TGGTCCTTGATTTATCACACAAAGCAGAATAGTATTTTTATATTTAAATGTAAAGACAAAAAACTATATGTATGG
TTTTGTGGATTATGTGTGTTTTGCTAAAGGAAAAAACCATCCAGGTCACGGGGCACCAAATTTGAGACAAATAGT
CGGATTAGAAATAAAGCATCTCATTTTGAGTAGAGAGCAAGGGAAGTGGTTCTTAGATGGTGATCTGGGATTAGG
CCCTCAAGACCCCTTTTGGGTTTTCTGCCCTGCCACCCCTCTGGAGAAGGTGGGCACTGGATTAGTTAACAGACAAC
ACGTTACTAGCAGTCACCTGATCTCCGTGGCTTTGGTTTAAAGACACACTTGTCCACATAGGTTTAGAGATAAG
AGTTGGCTGGTCAACTTGAGCATGTTACTGACAGAGGGGGTATTGGGGTTATTTTCTGGTAGGAATAGCATGTCA
CTAAAGCAGGCCTTTTGATATTAAATTTTTTAAAAAGCAAAATTATAGAAGTTTAGATTTTAAATCAAATTTGTAG
GGTTTCTAGGTAATTTTTACAGAATTGCTTGTTTGCTTCAACTGTCTCCTACCTCTGCTCTTGGAGGAGATGGGG
ACAGGGCTGGAGTCAAAACACTTGTAATTTTGTATCTTGATGTCTTTGTTAAGACTGCTGAAGAATTATTTTTTT
TCTTTTATAATAAGGAATAAACCCACCTTTATTCCCTTCATTTCACTACCATTTTTCTGGTTCTTGTGTTGGCTG
TGGCAGGCCAGCTGTGGTTTTCTTTTGCCATGACAACCTTCTAATTGCCATGTACAGTATGTTCAAAGTCAAATAA
CTCCTCATTGTAAACAACTGTGTAAGTGCCCAAAGCAGCACTTATAAATCAGCCTAACAT

563/6881
FIGURE 524A

GCGGGGAGGGGCGGGGCTATGGAGAGGAGGAGGAAGATGGCGGGCGGGCTGCTCTGAAGAGACCTCGGCGGGCGGC
GGAGGAGGAGAGAAGCGCAGCGCCGCGCCGCGCCGGGGCCCATGTGGGGAGGAGTCGGAGTCGCTGTTGCCGCCG
CCGCTGTAGCTGCTGGACCCGAGTGGGAGTGAGGGGGAACGGCAGGATGAAGTTCCGCCAGCACCTCTCCGCG
CACATCACTCCCGAGTGGAGGAAGCAATACATCCAGTATGAGGCTTTCAAGGATATGCTGTATTACAGCTCAGGAC
CAGGCACCTTCTGTGGAAGTTACAGATGAGGACACAGTAAAGAGGTATTTTGCCAAGTTTGAAGAGAAGTTTTTC
CAAACCTGTGAAAAAGAACTTGCCAAAATCAACACATTTTATTTCAGAGAAGCTCGCAGAGGCTCAGCGCAGGTTT
GCTACACTTCAGAATGAGCTTCAGTCATCACTGGATGCACAGAAAGAAAGCACTGGTGTTACTACGCTGCGACAA
CGCAGAAAAGCCAGTCTTCCACTTGTCCCATGAGGAACGTGTCCAACATAGAAATATTAAAGACCTTAAACTGGCC
TTCAGTGAGTTCTACCTCAGTCTAATCCTGCTGCAGAACTATCAGAATCTGAATTTTACAGGGTTTCGAAAAATC
CTGAAAAAGCATGACAAGATCCTGGAAAACATCTCGTGGAGCAGATTGGCGAGTGGCTCACGTAGAGGTGGCCCCA
TTTTATACATGCAAGAAAATCAACCAGCTTATCTCTGAACTGAGGCTGTAGTGACCAATGAACCTTGAAGATGGT
GACAGACAAAAGGCTATGAAGCGTTTTACGTGTCCCCCTTTGGGAGCTGCTCAGCCTGCACCAGCATGGACTACT
TTTAGAGTTGGCCTATTTTGTGGAATATTCATTGTACTGAATATTACCCTTGTGCTTGCCGCTGTATTTAAACTT
GAAACAGATAGAAGTATATGGCCCTTGATAAGAACTCTATCGGGGTGGCTTTCTTCTGATTGAATTCCTTTTTCTA
CTGGGCATCAACACGTATGGTTGGAGACAGGCTGGAGTAAACCATGTACTCATCTTTGAACTTAATCCGAGAAGC
AATTTGTCTCATCAACATCTCTTTGAGATTGCTGGATTCCCTCGGGATATTGTGGTGCCTGAGCCTTCTGGCATGC
TTCTTTGCTCCAATTAGTGTCTATCCCCACATATGTGTATCCACTTGCCCTTTATGGATTTATGGTTTTCTTCCTT
ATCAACCCACCAAACTTTCTACTATAAATCCCGTTTTGGCTGCTTAAACTGCTGTTTTCGAGTATTTACAGCC
CCCTTCCATAAGGTAGGCTTTGCTGATTTCTGGCTGGCGGATCAGCTGAACAGCCTGTCAGTGATACTGATGGAC
CTGGAATATATGATCTGCTTCTACAGTTTGGAGCTCAAATGGGATGAAAGTAAGGGCCTGTTGCCAAATAATTCA
GAAGAATCAGGAATTTGCCACAAATATACATATGGTGTGCGGGCCATTGTTCAAGTGCATTCCTGCTTGGCTTCGC
TTCATCCAGTGCCTGCGCCGATATCGAGACACAAAAGGGCCTTTCTCATTTAGTTAATGCTGGCAAATACTCC
ACAACCTTTCTTCATGGTGACGTTTGCAGCCCTTTACAGCACTCACAAAGAACGAGGTCCTCGGACACTATGGTG
TTCTTTTACCTGTGGATTGTCTTTTATATCATCAGTTCCTGCTATACCCTCATCTGGGATCTCAAGATGGACTGG
GGTCTCTTCGATAAGAATGCTGGAGAGAACACTTTCTCCGGGAAGAGATTGTATACCCCCAAAAGCCTACTAC
TACTGTGCCATAATAGAGGATGTGATTCTGCGCTTTGCTTGGACTATCCAAATCTCGATTACCTCTACAACCTTG
TTGCCCTCATTCTGGGGACATCATTGCTACTGTCTTTGCCCACTTGAGGTTTTCCGGCGATTTGTGTGGAACCTC
TTCCGCTGGAGAATGAACATCTGAATAACTGTGGTGAATTCGCTGCTGTGCGGGACATCTCTGTGGCCCCCTG
AACGCAGATGATCAGACTCTCCTAGAACAGATGATGGACCAGGATGATGGGGTACGAAACCGCCAGAAGAATCGG
TCATGGAAGTACAACCAGAGCATATCCCTGCGCCGGCCTCGCCTCGCTTCTCAATCCAAGGCTCGTGACACTAAG
GTATTGATAGAAGACACAGATGATGAAGCTAACACTTGAATTTTCTGAAGTCTAGCTTAACATCTTTGGTTTTCC
TACTCTACAATCCTTTCTCGACCAACGCAACCTCTAGTACCTTTCCAGCCGAAAACAGGAGAAAACACATAACA
CATTTTCCGAGCTCTTCCGGATCGGATCCTATGGACTCCAAACAAGCTCACTGTGTTTCTTTTCTTTCTCTG
TTTAATTTTAAATTTTCTATTTTCAAAACAAATATTTACTTCAATTTGCCAATCAGAGGATGTTTAAAGAAACAAAA
CATAGTATCTTATGGATTGTTTACAATCACAAGGACATAGATACCTATCAGGATGAAGAACAGGCATTGCAAGGA
CCCTCTGATGGGACGGTACTGAGATATCTCGGCTTCCGCTCAGCCCGGTTTTGACTGGTTGAAACCGGACATTGG
TTTTTAAATTTTTTGTGCTAGTTTATGTGGAGAATTTTTTCTTTCTTTCATACCCAGCGCAAAGGCACTGGCCGCA
CTTGACAGGAAAAGTGCAACTTAAAGCAGTACCTTCAATCATGAAGCTACTTTTTAATTTGATGTAACCTTTTCTTA
TTTTGGGAAGGGTTGCTGGGTGGGTGGGAAATATGATGTATTTGTTACACATAGTTTTCTCATTATTTATGAAAC
TTAACCATAACAGAATGATATAACTCCTGTGCAATGAAGGTGATAACAGTAAAGAAGGCAGGGGAAACTTACGTT
GGATGACATTTATGAGGGTCAGTCCCACATACCTCTTTCAGGAGACAACCTGCACCAGTTTGACCTTTTCTTTTC
TTTGTTTTTATTTTAAAGCCAAAGTTTCATTGCTAACTTCTTAAAGTTGCTGCTGCTTTAGAGTCTGAGCATATCT
CTCATAACAAGGAATCCCACACTTCACACCACCGGCTGAATTTTCATGGAAGAGGTTCTGATAATTTTTTTAACTT
TTTAAGGAACAGATGTGGAATACACTGGCCCATATTTCAACCTTAACAGCTGAAGCTATGCCTTATTATGCATCC
ACATGTATGGTCCCTGTAGCGTGACCTTTACTAGCTCTGAATCAGAAGACAGAGCTATTTTCAGAGGCTCTGTGTG
CCCTCACTAGATAGTTTTTCTTCTGGGTTCAACCACTTTAGCCAGAATTTGATCAAATTTAAAGTCTGTGATGGG
GAACTATATTTTTGAGCACATGGAACAAATTATACTTCCTCATTTCATATTATGTTGATACAAAAGACCTTGGA
GCCATTTCTCCCAGCAGTTTTTAAAGGATGAACATTGGATTTTCATGCCATCCCATAGAAAACCTGTTTTAAATTT

564/6881
FIGURE 524B

TAGGGATCTTTACTTGGTCATACATGAAAAGTACACTGCTTAGAAATTATAGACTATTATGATCTGTCCACAGTG
CCCATTGTCACCTTCTTTGTCTCATTTCTTCCCTTGTTCCTTAGTCATCCAAATAAGCCTGAAAACCATAAGAGA
TATTACTTTATTGAATATGGTTGGCATTAAATTTAGCATTTCATTATCTAACAAAATTAATATAAATTCAGGAC
ATGGTAAAATGTGTTTTAATAACCCCCAGACCCAAATGAAAATTTCAAAGTCAATACCAGCAGATTCATGAAAGT
AAATTTAGTCCTATAATTTTCAGCTTAATTATAAACAAAGGAACAAATAAGTGGAAGGGCAGCTATTACCATTCTG
CTTAGTCAAAACATTCGGTTACTGCCCTTTAATACACTCCTATCATCAGCACTTCCACCATGTATTACAAGTCTT
GACCCATCCCTGTCGTAACCTCAGTAAAAGTTACTGTTACTAGAAAATTTTTATCAATTAAGTACAAATAGTTT
CTTTTTAAAGTAGTTTCTTCCATCTTTATTCTGACTAGCTTCCAAAATGTGTTCCCTTTTTGAATCGAGGTTTTT
TTGTTTTGTTTTGTTTTCTGAAAAATCATACAACTTTGTGCTTCTATTGCTTTTTTGTGTTTTGTTAAGCATGT
CCCTTGGCCCAAATGGAAGAGGAAATGTTTAATTAATGCTTTTTAGTTTAAATAAATTGAATCATTATATAAAT
CAGTGTTAACAATTTAGTGACCCTTGGTAGGTTAAAGGTTGCATTATTTATACTTGAGATTTTTTCCCCTAACT
ATTCTGTTTTTTGTACTTTAAACTATGGGGGAAATATCACTGGTCTGTCAAGAAACAGCAGTAATTATTACTGA
GTTAAATTGAAAAGTCCAGTGGACCAGGCATTTCTTATATAAATAAAATTGGTGGTACTAATGTG

565/6881
FIGURE 525

AATAAATTATTTTGTAAAGGCAAGCATTGGTGTGTTCTTTAACTTGCTACTTGGAGACCTAGTGTCCAGTCTGG
ACAGAATGCACAGAGACCAGCCTCACCTGGAATGCAGCCAGACTCGATGTCCCTCAGCACACACAGCTCCTGGCC
ACAGACTGCCCATAGAACTGTCTGCACCCAAACCCCATGGCCTTTTCATGCACGGAGACAGGCCTCTGGATGTGC
AGCCTTGCCACCCCTGCCCAATCCTCCCTGAGAGCTCCTGCCTCAGTGCCCTGGGCTGGTGAGGGAGAAGCCT
GTCTGCACCTGCCTAATTCCAGCTCCTCCAGGAAGCAAGGGCTTGTGTTGTCAGAGCTGCAGGGTTGGCCACTCGG
TGGGGAGGAGTCAGCCAGGATTAGAGAGCCTGCCCCAATCCGGCCTGCTGGGTTTTACAAGGATCAGAGCTGCT
GAATGAACCTCATTAAAGGGGGAGCAGGAGCCTCAATCCGATTGTTGTTTCTCTTTGACATCTTCACTCTGCTC
AGATGGCCTGGGTGCTATGTGGAGCAGGTGGGATGCCAAGGCCACTCCTGCTATGGGGCAGCTGGGGCTGGGGAG
GGATGGCAGTCTCCCTGCAIGTTTTCCCTCGACCTCTTTAGCTGCAGCGCCTTGCTGGGCTCCTGGGTGGACTCC
CTCTCTGTGCCCTGCTCCAGGCACCCATTGGCTCCATCCTCCTGGTTGTGCTCTGCACCCCTGCTCCCTTGGG
CTGGCCCTGGCTGGGGGCTGAGAGACAGACAGGAACCCACAATCAGGAGGCAACCCTGGCCTGCAAGAGGAAGA
CAGAGGCTCCCAGGGCCGGTGCCCTGTGTGCCCACTGCACCAAGGCCGCTGAATAAGCCTGCCCTTACCCCCCTA
AGGGCTCCTTGCCCAATGCCAAGTGCTGGGGATTTCTGTGTCAGCAAGCCCTGTGGCTCCAGTGACGGTATTTCTAA
AGCCAAACTTAGTTACCTAGAATTAGCGCCATGTTGGAAACACTGTCGCAGCAGCCCGGGCTGCACAGTGTGTAG
CCCAGCCTCCAGGTCCACGGAGTGGTGTGGACCTCCACCTCACAGCTGCCTCTGGCAGCCAAGCCTCTTTTCGC
CCGGCCCCAGCCCCCTCTGGTTGATAAACGGGTGGGCCTCCTCAGCAGCGTGGCTGCCTTTACCTTGATTTCCCC
AGGGCTCTCGGCAACATCGATAAACAGCCTCGCCCCACCAGCTGGGCCCTCCCCACCCAGTCTGCCAGGCTGGG
AGCTGGAGCTTGCTGAGTCTTGAATGCCCTTCTAGATGGCTTCTCTAGAGGCTCTCCTGGCAAGAGAGGGTCCCA
AGGGGAGCCCTGCAAAGCAAAGGCTCCTTGTCTGGGGCGGGATAGAGAATCTCGCCTCTGTCTGGTGTGTTACCT
ACTGGGGGCACAGGAACAATTTCTCAAGGAGACAGTGGCATGGAGCTTTGAAAGACGAGTAGGTGTTAGCAAGG
AAATAAGGAGGAACGGGGGTACGGGCAGAGGAGAAAGCACATGCCAAGTCAGCAAAGAAAAGTAGAATTCGAAA
ACTTTTTAAAAATATTACTAAGGATTTTCACAATGCTGCACTGGGCTAGAACTGAAGCTAAAACAGATACGTGG
TCCCTGCTGCTATGGGGCTTCCGTTCTAGAGGCAAGGACAGGTTGTGATGAGGGTTCTGAAGGATAGAGACCAAG
CAGGGAGGGTGTGAGGAGGCTTCTGCGAGACCTGAAGGATGGGAAGCCAGGAAGTGGGAGGGGTGGGGTCCAG
GCTGGAGGGGCCCAATGTAGGTGTAGAGGGACTACAGCCCTGAGGGGCTGCTCCATGCGGCATTCTTGAGGTCC
AAGAGGGGCAGCGCCACCTTGGGCCAGGCTCCTCTCCAGCAGCCTTGGTATGGGGTGGGGGTGGGAAGACCCCTG
ATGCAGCCTGTCTCTGGGTGTGGGGGTGGAGGAGAGGGCTCCAGGGGACCCAGCCAGCCTTGACCTGGAGGAA
AGTCAGGTGGGCTCAGAGAGAGCCCTCAAATCTGGGCCCTGGGTGAGGTGGGGTCAAGTCCAGCCTGAAGAGA
ATGGACTCTGGAATCTGACGTCTGGGTTTGAATCCAGCTTCCAACACTCACTGGCTGTGTGACTTTGGGCAAGAT
AACTTATCCCTTGTCCCCATGTGTCAATTGGAGATAAACTACCCACCTACCAGATTGTTGTACCATGCTGGGCAA
ACACTAAGTGCTTAATAATGGTAGCCCACTGCTC

566/6881
FIGURE 526

MHRDQPHLECSQTRCPSAHTAPGHRLPIELSAPKPHGLFMHGDRPLDVQPCHP LPQSSLRAPASVPWAGEGEACL
HLPNSSSSRKQGLVCQSCRVGHSVGRSQPGLES LPLIRPAGFYKDQSC

567/6881
FIGURE 527

AGCCGGATGGTCCCGCAGCTCGGGGCCGGCCATGCCTTCGCGGTCCGTGGCGCCAGCTTTGGCTCTTTCTCCTGCT
GCTGCTCCCGGGCGCGCCTGAGCCCCGCGCGCCTCCAGGCCGTGGGAGGGAACCGACGAGCCGGGCTCGGCCTG
GGCCTGGCCGGGCTTCCAGCGCCTGCAGGAGCAGCTCAGGGCGGCGGGTGCCCTCTCCAAGCGGTACTGGACGCT
CTTCAGCTGCCAGGTGTGGCCCCGACGACTGTGACGAGGACGAGGAGGCAGCCACGGGGCCCCCTGGGCTGGCGCCT
TCCTCTGTTGGGCCAGCGGTACCTGGACCTCCTGACCACGTGGTACTGCAGCTTCAAAGACTGCTGCCCTAGAGG
GGATTGCAGAATCTCCAACAACCTTTACAGGCTTAGAGTGGGACCTGAATGTGCGGCTGCATGGCCAGCATTGTTGGT
CCAGCAGCTGGTCCTAAGAACAGTGAGGGGCTACTTAGAGACGCCCCAGCCAGAAAAGGCCCTTGCTCTGTCGTT
CCACGGCTGGTCTGGCACAGGCAAGAACTTCGTGGCACGGATGCTGGTGGAGAACCTGTATCGGGACGGGCTGAT
GAGTGACTGTGTCTAGGATGTTTCATCGCCACGTTCCACTTTCTCACCCCAAATATGTGGACCTGTACAAGGAGCA
GCTGATGAGCCAGATCCGGGAGACGCAGCAGCTCTGCCACCAGACCCTGTTTCATCTTCGATGAAGCGGAGAAGCT
GCACCCAGGGCTGCTGGAGGTCCTTGGGCCCACTTAGAACGCCGGGCCCCCTGAGGGCCACAGGGCTGAGTCTCC
ATGGACTATCTTTCTGTTTCTCAGTAATCTCAGGGGCGATATAATCAATGAGGTGGTCTAAAGTTGCTCAAGGC
TGGATGGTCCCGGGAAGAAATTACGATGGAACACCTGGAGCCCCACCTCCAGGCGGAGATTGTGGAGACCATAGA
CAATGGCTTTGGCCACAGCCGTCTTGTGAAGGAAAACCTGATTGACTACTTTCATCCCCCTTCCTGCCCTTTGGAGTA
CCGTCACGTGAGGCTGTGTGCACGGGATGCCTTCCTGAGCCAGGAGCTCCTGTATAAAGAAGAGACACTGGATGA
AATAGCCCAGATGATGGTGTATGTCCCCAAGGAGGAACAACCTCTTTTCTTCCCAGGGCTGCAAGTCTATTTCCCA
GAGGATTAACCTACTTCCCTGTCATGAAGGCTAGAGGAAGACTTCCTGGAACCTGCCTTTCTTCCACTAACAGGACCC
TGGGACCTGTAGGAGCACCCCGTTTGGGACTGTGAGGTGTTTGAGGGTGTGGACTGGCATCCAGCAGCCACTAAC
AAACACACAACCTGGTGTGTAAAAGGCAGGCCTTACATTAGAAGCCAAGCCAATCCTTTTTCTTTTTTTTGGAGGT
CCCACCGAGATAGATAGGAACCTGGATTGCTGAATTCAAAAACAGAGCCATTCTTAAGATCACTTGGTGCCTTA
AAGACACGCATTCCAAAGTGGAATGTGGTTGAAGAAAGTGGGCCAGGTGGTTGAAGAAAGCCATGTGGGAGCTCA
GCAAATCCCAAGGGCTTATTATGACACTCCAGATGGTCTCCTTAGCATCTCAGCTCTTCTGCAAGGAAGAGCTTG
GGTGTAGGCCTCAGAGGCTGTAGGGTCCTTGGGTTACAGAGCCGGGGAGAACGAAGTTCTGTGACCCAGGGGTG
GAGAATACACTCTAGGTTTGCGGGCTGGTGGGCTTTCAAATTGGTACTTCCAGAGGAAAGCCAAGCTGCTTCTGT
TGTGAGCGAATCAGCCAAGAGCCTGAGGCTGAAGGGAAAAGTACACAGAGGAAGATATTTTACAAACCAGGTCAG
TGTAGGCCAAGACTTATGGTCTACAGATTTTGGCGGGGGAGGGGGACCTTTTCAAAGACAATAGGGGGTCTTGA
CATGTTTGTGTATGTAAAGATGATAAGATTAAATTTTTGATTTTTCTAAAAAAAAAAAAAAAAAAAA

568/6881
FIGURE 528

MLRGPWRQLWLFLLLLLPGAPEPRGASRPWEGTDEPGSAWAWPGFQRLQEQQLRAAGALSKRYWTLFSCQVWPDDC
DEDEEAATGPLGWRLPLLQRYLDLLTTWYCSFKDCCPRGDCRISNNFTGLEWDLNVR LHGQHLVQQVLRLTVRG
YLETPQPEKALALSFGWSGTGKNFVARMLVENLYRDGLMSDCVRMFIATFHFPHPKYVDLYKEQLMSQIRETQQ
LCHQTLFIFDEAEKLHPGLLEVLGPHLERRAPEGHRAESPWTIFLFLSNLRGDIINEVV LKLLKAGWSREEITME
HLEPHLQAEIVETIDNGFGHSRLVKENLIDYFIPFLPLEYRHVRLCARD AFLSQELLYKEETLDEIAQMMVYVPK
EEQLFSSQGCKSISQRINYFLS

569/6881
FIGURE 529

ATTTCTCCATGTGGCAGACAGAGCAAAGCCACAACGCTTTCTCTGCTGGATTAAAGACGGCCACAGACCAGAAC
TTCCACTATACTACTTAAAATTACATAGGTGGCTTGTCAAATTCAATTGATTAGTATTGTAAAAGGAAAAAGAAG
TTCCTTCTTACAGCTTGGATTCAACGGGTCCAAAACAAAAATGCAGCTGCCATTAAAGTCACAGATGAACAAACTT
CTACACTGATTTTTTAAAATCAAGAATAAGGGCAGCAAGTTTCTGGATTCACTGAATCAACAGACACAAAAAGCTG
GCAATATAGCAACTATGAAGAGAAAAGCTACTAATAAAATTAACCCAACGCATAGAAGACTTTTTTTCTCTTCT
AAAAACAACATAAGTAAAGACTTAAATTTAAACACATCATTTTACAACCTCATTTCAAAATGAAGACTTTTACCTG
GACCCTAGGTGTGCTATTCTTCCTACTAGTGGACACTGGACATTGCAGAGGTGGACAATTCAAAATTAATAAAAT
AAACCAGAGAAGATACCCTCGTGCCACAGATGGTAAAGAGGAAGCAAAGAAATGTGCATACACATTCCTGGTACC
TGAACAAAGAATAACAGGGCCAATCTGTGTCAACACCAAGGGGCAAGATGCAAGTACCATTAAAGACATGATCAC
CAGGATGGACCTTGAAAACCTGAAGGATGTGCTCTCCAGGCAGAAGCGGGAGATAGATGTTCTGCAACTGGTGGT
GGATGTAGATGGAAACATTGTGAATGAGGTAAAGCTGCTGAGAAAGGAAAGCCGTAACATGAACTCTCGTGTTAC
TCAACTCTATATGCAATTATTACATGAGATTATCCGTAAGAGGGATAATTCATTGAACTTTCCCAACTGGAAAA
CAAAATCCTCAATGTCACCACAGAAATGTTGAAGATGGCAACAAGATACAGGGAAGTAAAGGATACGCTTC
CTTGACTGATCTTGTCAATAACCAATCTGTGATGATCACTTTGTTGGAAGAACAGTGCTTGAGGATATTTTCCCG
ACAAGACACCCATGTGTCTCCCCCACTTGTCCAGGTGGTGCCACAACATATTCCTAACAGCCAACAGTATACTCC
TGGTCTGCTGGGAGGTAAACGAGATTCAGAGGGATCCAGGTTATCCCAGAGATTTAATGCCACCACCTGATCTGGC
AACTTCTCCACCAAAAAGCCCTTTCAAGATACCACCGGTAACCTTCATCAATGAAGGACCATTCAAAGACTGTCA
GCAAGCAAAAGAAGCTGGGCATTTCGGTCAGTGGGATTTATATGATTAAACCTGAAAACAGCAATGGACCAATGCA
GTTATGGTGTGAAAACAGTTTGGACCCTGGGGGTTGGACTGTTATTTCAGAAAAGAACAGACGGCTCTGTCAACTT
CTTCAGAAATTGGGAAAAATTATAAGAAAGGGTTTGGAAACATTGACGGAGAATACTGGCTTGGACTGGAAAAATAT
CTATATGCTTAGCAATCAAGATAATTACAAGTTATTGATTGAATTAGAAGACTGGAGTGATAAAAAAGTCTATGC
AGAATACAGCAGCTTTTCGTCTGGAACCTGAAAGTGAATTCTATAGACTGCGCCTGGGAACCTTACCAGGGAAATGC
AGGGGATTCTATGATGTGGCATAATGGTAAACAATTCACCACACTGGACAGAGATAAAGATATGTATGCAGGAAA
CTGCGCCCACTTTTATAAAGGAGGCTGGTGGTACAATGCCTGTGCACATTCTAACCTAAATGGAGTATGGTACAG
AGGAGGCCATTACAGAAAGCAAGCACCAAGATGGAATTTTCTGGGCCGAATACAGAGGCGGGTCATACTCCTTAAG
AGCAGTTCAGATGATGATCAAGCCTATTGACTGAAGAGAGACACTCGCCAATTTAAATGACACAGAACCTTTGTAC
TTTTAGCTCTTAAAAATGTAAATGTTACATGTATATTACTTGGCACAATTTATTTCTACACATAAAGTTTTTAA
AATGAATTTTACCGTAACCTATAAAAGGGAACCTATAAATGT

570/6881
FIGURE 530

MKTFTWTLGVLEFFLLVDTGHCRCGGQFKIKKINQRRYPRA TDGKEEAKKCAYTFLVPEQRITGPICVNTKGQDAST
IKDMITRMDLENLKDVL SRQKREIDVLQLVVDVDGNIVNEVKLLRKESRNMNSRV TQLYMQLLHEIIRKRDNSLE
LSQLENKILNVTTEMLKMATRYRELEVKYASLTDLVNNQSVMITLLEEQLRIFSRQDTHVSPPLVQVVPQHIPP
SQQYTPGLLGNEIQRDPGYPRDLMPPPD LATSPTKSPFKIPPVTFINEGPFKDCQQA KEAGHSVSGIYMIKPEN
SNGPMLWCENSLDPGGWTVIQKRTDGSVNFFRNWENYKKGF GNIDGEYWLGLENIYMLSNQDN YKLLIELEDWS
DKKVYAEYSSFRLEPESEFYRLRLGT YQGNAGDSMMWHNGKQFTTLDRDKMYAGNCAHFHKGGW WYNACAHSNL
NGVWYRGGHYRSKHQDGIFWAEYRGGSYSLRAVQMMIKPID

571/6881
FIGURE 531

ATGGGGCTGCTCACTGGCACTGGAGGCCGAAAGAAGGTGAGGGCAAGTGAGATGCAGGGACCTCTTCTCACAGCT
GTGCTGACAAGCACAAAAAGGAGCCCCCACGTCCACACCAGGAAAGGGGGATGGTGCACAAGATCCAGAGGCG
TCAACAGACACGTCCAGCGAACAAGCACAGGGTGGGCCGTCCGGGAGCCTTGTGCCGCCAGGAGGAAAGCCGCAC
CGAGGGCAGCAGGGAGGCTCTGATGGCTGCCAAGAGGGTCTGATCCAGAAATATGGCCTCAATATGTGCCCCAG
TGTTTCCGTCAGTACGCGAAGGATATCGGTTTCATTAAATTGGACTAA

572/6881
FIGURE 532

TAGGTTTCATTTGGAAGCTTGAGTTTTATCATTGGCAACAAATGCCATCAGTTTTTTTCCAAGCTGACTTGTTCTT
TTTTGAGCAAATCTCTGCCAAAATTACCCCTAAAATATGAATAATCAATTTGTCAGGTTTTTTTCAAACATAAAAT
GTTCTGTGAAAAACAAGCAGCTAGTTCAGCITGTATCTCAAACAATTGTAACACTTTTTTCTAGGGAAAAAAAAT
CTAGACATCCATACTTTATGGCAGATGTGCTTCATGCATACCTCCCATTTTGTACACAGAATATCAAATAACG
TGTACTCAAGGTCAAGATTTACTAACAATAAAATTCAAAACCTGCTAAACAACAGAATGCTGAATAAGGTGATC
CAATTTTTTAATATTTTATTTGAGACAACATCTCACCCCTGTCACCCAGGCTGGAATCCAGTGTTGTGACACAGCTC
ACTGCATCCTCAACCTCCTGGGCTCAAGCGATCGTCCCACCTCAGTCTCATGAGTGGTTGGGACTACAGGCATGC
ACCATCATGCCCCGCTCACTTTTTTTTTTCTTTTTTTTTTTTAAATTGTAGACACAGGGTCTCACTATGTTGCCAGG
CCGGTCTTGAACCTCCTGGACTCAAGCAATCCCCCACCTTGGTTTCCCAAAGTGTGGGATTACAGGCATGAGCT
ACTACATACAACTGAAATCTTTTAATATGCTTGTCAAAAAGTTTTCTGATTCAGCAAATGGCACTTATATATAAA
AGAGAGAACAAGAAGCTGGATGCGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCTAGGTGGGCAGATCA
CGAGGTGAGGAGTTCGAGACCAGCCTGGCCAACGTGGTGAAACCCCTCTCTACTAAAAATACAAAATAGCCAG
GCATGGTGGCCACGCCTGTAATCCAGCTACTTGGGAAGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAGGTGG
AGGTTGCAGTGAGCCAAGATTGCGCCGCTACATTCCAGCCTGGGCAACACGAGCGAAACTCCGCTCTCAAAAAAAA
AAAAAAAAGAATAGAACTTGGCTGGATGCAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGGCAGGGCAG
TTGGATCACTTGAGGCCAGGAGTTCAAGACTAGCCTGGCTGACATGGTGAAACTCCATCTCTACTAAAAATACAG
AAAAAAAATTAGCTGGGAGTGGTGGCACACACCTGTATCCAGCTACTCAGGTAGTTGAGGCACAACAATCAC
TTGAGCCTAGGAGGCCAGGCTGGAGTGAGGTGGCACGATCTTGGTTCACTGCAACCTCCACCTCCAGGGTTTCAG
AGTAGCTGGGACTACAGGCCACACTACCACACCCGGCTAATTTTCGCTTTTTTTTTCAGTAGAGACCGGGTTTTGC
CATGTTGGCCAGGCTGGTCTCGAAGCCTGAGCCATAACCTGGCGAAAAGATACTTTGAAATGTAACATCGTTTTT
CACTTCAAAATCAAGGTATTTTACCAACTTGTCTTTGGTACCTCCCCAAAAACTGATCTACTACATTTGCAGTTT
CATTCATTTTTTCCAACATTAAGGAATAAACTTGAAGCGCTTACATTCTTGTGGGGGAAGTAAGAACAAAACACAT
AATAGGTCATGGTGGTCACATGAAAAGTAAAGGGTAACCGATTGGGGTAGGTGGTGGTAGTTTTGTGTGTGTGTT
TTTTTTTGAGACCAAGTCTCGCCGTTGCCAGGCTGGAGTGCGGTGGCATGATCTCAGTTCAGTCAACCTCCAC
TTCTTAGGTTCAAGCAATTTCTCCTGCCTCAGCTACTCAAGAGGCTGAGGCAGGAGAATTCCTTGAACCTGGGAGG
CAGAGGTTGCAGTGAAGTATAGTGCCGCTGCACTCCATTCTGGGCAAGAGCTAGACTCTTGTCTAAAAAAA
AAAAATACTTGAAGTGTATACCTTTGCTTCTTTAAACTTGCTCCACACAGTGTAGTCAAGCCGACTCTCCA
TACCTGTAGAAATTTAATCTCCTTTACCAATAGGTAGTAATAGGTGGATTTCTAAAAGATTTCCCAACTACTGTT
TCAGTTTAAGATTAATCTCCATTTTCTTCTCAGAGAGATTCCCATCTGCTTTAATTTTAAAATCATCACTAACA
GTAGCTCAATCAATTAACGTTAACATCAATAAAACATGTACCTTTAAAAGGTATGACAGGAAGTGTCTTCATGTC
CTTACCCAAGCAAGTCATCCATGGATAAAAACGTTACCAGGAGCTGGAATACAAATGAGGACTTCCATTAAATG
CTAAACATCATTAACCTTTTTCAAAGTTGTCTGTC

573/6881
FIGURE 533

MCFMHTSHFVTQNIKITCTQGQDLLTTKIPKLLNNRMLNKVIQFLIFYLRQHLLTLSPRLESSGVTQLTASSTSWA
QAIVPPQSHEWLGLQACTIMPGSLFFSFFF

574/6881
FIGURE 534

ATCTGTAGATGGGAGTGATTAGCTGTTTAAAAGTTAAAATGTGACTGAGAAGGAAATTGAGTAGGGCAAATTTTA
AATGGGTATTATTTTTCATCTTCAAACAGGCAGACCTGTTATCCTAAACTAGGTGAGTCAGCTTTTGGTACATGT
GATGATTTTTCAGTGTAACCAATGATGTAATGATTCTGCCAAATGAAATATAATGATATCACTGTAAAACCGTTCC
ATTTTGATTCTGAGGTTACTCTACTAACAAGCATCACACATTTGTATTTTGCCCTGATTAATATGTTGGCTTCGC
TTTCAGGGTTTTTAATGACCACAACAAGCAAGCATGCAGCTTACTGCTTGAAAGGGTCTTGCCCTCACCCAAGCTA
GAGTGCAGTGGCCTTTGAAGCTTACTACAGCCTCAAACCTCTGGGCTCAAGTGATCCTCAGCCTCCCAGTGGTCT
TTGTAGACTGCCTGATGGAGTCTCATGGCACAAGAAGATTAAAACAGTGTCTCCAATTTTAATAAATTTTGCAT
TCC

575/6881
FIGURE 535

AGTTAAACAGCTGAGCTTCTGAATGCCTGCAAGAAGCTGCCCTTTGAAATTAAGAACTTCGTGAAGAAAACAGA
GGCTCTTCGGTTGCAGTATCGCTACTTAGACTTGCGTAGTTTCCAAATGCAGTATAACCTGCGACTGAGGTCCCA
GATGGTCATGAAAATGCGGGAATATCTCTGTAATCTGCATGGGTTTGTGGATATAGAAACCCACATTGTTTAA
GAGGACCCAGGGGGTGCCAAAGAGTTTTTAGTACCATCCAGGGAACCTGGAAAGTTTTGTCTCTCCCTCAGAG
TCCTCAACAGTTTAAGCAACTTCTGATGGTTGGCGGTTTAGACAGATATTTTCAGGTTGCCCGATGTTATCGAGA
TGAAGGTTCAAGACCAGACAGACAGCCTGAGTTTACTCAGATTGACATAGAGATGTCATTTGTAGACCAGACTGG
GATCCAGAGTTTAATTGAGGGTTTGCTCCAGTATTCCTGGCCCAATGACAAAGATCCTGTGGTTGTTCCTTTTCC
TACTATGACTTTTGCTGAGGTGCTGGCCACCTATGGAACCTGATAAACCTGACACTCGCTTTGGAATGAAGATTAT
AGATATCAGTGATGTGTTTAGAAACACAGAGATTGGATTTCTTCAAGATGCACTTAGTAAGCCCCATGGAACCTGT
GAAAGCCATATGTATCCCTGAAGGAGCAAAATACTTAAAAAGGAAAGACATTGAATCCATTAGAACTTTGCAGC
TGACCATTTTAATCAGGAAATCTTACCTGTATTCTTAAACGCCAATAGAACTGGAATTCTCCAGTTGCTAATTT
CATAATGGAGTCACAAAGACTGGAATTAATCAGACTAATGGAGACCCAAGAGGAAGATGTGGTCTCTAATACTGC
TGGAGAGCACAATAAAGCATGCTCTTTGTTAGGAAAATTACGACTGGAATGTGCTGACCTTCTAGAAAACAAGAGG
AGTGGTGCTCCGTGACCCCACTCTGTTCTCTTTTCCCTTTGGGTGGTAGATTTCCCACTCTTCTGCCCCAAGGAGGA
AAGTCCCAGAGAGCTGGAATCGGCCCACCACCCATTTACTGCTCCCCACCCAGTGACATACATCTCCTGTACAC
TGAGCCCCAAAAGGCCCGTAGCCAACACTATGACTTGGTTTTAAATGGCAATGAAATAGGAGGTGGTTCAATTCTG
AATTCACAATGCAGAGCTGCAGCGTTATATCCTGGCAACCTTACTAAAGGAGGATGTGAAAATGCTCTCCCATCT
GCTCCAGGCTTTAGATTATGGGGCACCCCTCATGGAGGAATTGCCTTAGGGTTAGACAGACTGATATGCCTTGT
CACTGGATCTCCAAGCATCAGAGATGTCATAGCCTTCCCAAAGTCCTTCCGGGGACATGACCTCATGAGCAATAC
CCCAGATTCTGTCCCTCCTGAGGAAGTGAAGCCCTATCATATCCGAGTCTCCAAGCCAACAGACTCCAAAGCAGA
AAGAGCTCATTTGAATCATGCATACCATGCAGAAAGTTGAGCTTTTAGGTTTTGTCTCTTTGCTTCCCCAAGGCT
AAAGTCAGATCTAGAGTTCTGCCACAGGTCTAACAATCAAGTCTTTAGATGGAAGGAATCCAGGCAACATTCTTC
ACCACAACGAAGAAACAGATAAAAGATACCCAATTTTGAAGTTGATTTTATGCATCATTGGAATTTTTTTTGGTTA
GGACTTTTTTTGAAGTTCCTTTTTTACTTAGGTGTGAAAGATGGTTCTTTGTTGAAATAATATAGTGGTTTAGTGT
TTTCAATCATGTTTCTCATACCCAGATAGTAGATTATTCACCTAGGACAGAGGTAATCAAATTATGTGTGAAAT
GTAGGAAAATGCTTGCCCCTGTAAACTAGTGAGTTGATGGAGCATTGCTTCATCATCCTCATCAAGAGAATCAT
ATAAATTAAGCTTTATAATGACATTTCAACCATCAACATAATATAGTGAGGAGTAGCATAATATTTTTTAATAAT
GCAGAAAACATCACTGAAATGAGAGTCACAAATTTTTCTTCAGTGTTCAGCCTGAGTAAGTTACATAAACCTCG
CTTAGCCTCCCTTCTGCTAATGTGTAAAATACATACTTGCCCTGGCTACCTCACCGGGCTGTTATTGCTGGAAT
CAGAGGAGATAACATATATGGAAGATAAAGTGAATAAAAGTACTTTGAAAACT

576/6881
FIGURE 536

MQYNLRLRSQMVMKMREYLCNLHGFDIETPTLFKRTPGGAKEFLVPSREPGKFCSLPQSPQQFKQLLMVGGLDR
YFQVARCYRDEGSRPDRQPEFTQIDIEMSFVDQTGIQSLIEGLLQYSWPNDKDPVVVPFPTMTFAEVLATYGTDK
PDTRFGMKIIDISDVFRNTEIGFLQDALSKPHGTVKAICIEGAKYLKRKDIESIRNFAADHFNQEILPVFLNAN
RNWNSPVANFIMESQRLELIRLMETQEEDVVLLTAGEHKNACSLGKLRLECADLLETRGVVLRDPTLFSFLWV
DFPLFLPKESPRELESAHHPFTAPHPSDIHLLYTEPKKARSQHYDLVLNGNEIGGGSIRIHNAELQRYILATLL
KEDVKMLSHLLQALDYGAPPHGGIALGLDRLICLVTGSPSIRDVIAFPKSFRGHDLMSNTPDSVPPEELKPYHIR
VSKPTDSKAERAH

577/6881
FIGURE 537

GCCTGTCTGCATTCTACTATATAAAGCAGCAGAGACGTTGACTAGCGCATATTTGCTAAGAGCACCATGCGCGCA
GCAGCCATCTCCACTCCAAAGTTAGACAAAATGCCAGGAATGTTCTTCTCTGCTAACCCAAAGGAATTGAAAGGA
ACCACTCATTCACTTCTAGACGACAAAATGCAAAAAAGGAGGCCAAAGACTTTTGGAATGGATATGAAAGCATAC
CTGAGATCTATGATCCACATCTGGAATCTGGAATGAAATCTTCCAAGTCCAAGGATGTACTTTCTGCTGCTGAA
GTAATGCAATGGTCTCAATCTCTGGAAAACTTCTTGCCAACCAAACCTGGTCAAAATGTCTTTGGAAGTTTCCTA
AAGTCTGAATTCAGTGAGGAGAATATTGAGTTCTGGCTGGCTTGTGAAGACTATAAGAAAACAGAGTCTGATCTT
TTGCCCTGTAAAGCAGAAGAGATATATAAAGCATTGTGTCATTGATGCTGCTAAACAAATCAATATTGACTTC
CGCACTCGAGAATCTACAGCCAAGAAGATTAAAGCACCAACCCCCACGTGTTTTGATGAAGCACAAAAAGTCATA
TATACTCTTATGGAAAAGGACTCTTATCCCAGGTTCCCTCAAATCAGATATTTACTTAAATCTTCTAAATGACCTG
CAGGCTAATAGCCTAAAGTGACTGGTCCCTGGCTGAAGGGAATTAACAGATAGTATCAAGCGCAGAAGGAATGTG
CCAGTATGGCTCCCTGGGTGAACAGCTTGGCCTTTTTTGGGTGTCTTGACAGGCCAAGAAGAACAATGACTCAG
AATGGATTAAACATGAAAGTTATCCAGGCGCAGAGTTGAAGAAGCATAAGCAAGACAAAAACAGAGAGACCGCAGA
AGGAGGAAGATACTGTGGTACTGTCATAAAAAACAGTGAGCTCTGTATTAGAAAGCCCCCTCAGAACTGGGAAGG
CCAGGTAACCTCTAGTTACACAGAACTGTGACTAAAGTCTATGAACTGATTACAACAGACTGTAAGAATCAAAG
TCAACTGACATCTATGCTACATATTATTATATAGTTTGTACTGAGCTATTGAAGTCCCATTAACCTTAAAGTATAT
GTTTTCAAATTGCCATTGCTACTATTGCTTGTGCGGTGTTATTTTATTTTATTGTTTTTGAAGTGGGAGATGA
ACTGTGTATTTAACTTAAGCTATTGCTCTTAAACCAGGGAGTCAGAATATATTTGTAAGTTAAATCATTGGTGC
TAATAATAAATGTGGATTTTGTATTAAAAATATATAGAAGCAATTTCTGTTTACATGTCCTTGCTACTTTTAAAAA
CTTGCAATTTATTCTCAGATTTTAAAAATAAATAAATAATTCATT

578/6881
FIGURE 538

CTTTTCGATCCGCCATCTGCAGTGGAGCCGCCACCAAAATGCAGATTTTCGTGAAAACCTTATGGGGAAGACCA
TCACCCTCGAGGTTGAACTCTCGGATACAATAGATAATGTAAAGGCCAAGATCCAGGATAAGGAAGGAATTCCTC
CTGATCAGCAGAGACTGATCTTTGCTGGCAAGCAGTTGGAAGATGGACGTACTTTGTCTGACTACAATATTCAAA
AGGAGTCTACTCTTCATCTTGTGTTGAGACTTCGTGGTGGTGCTAAGAAAAGGAAGAAGAAGTCTTACACCACTC
CCAGGAAGAATAAGCACAAGAGAAAGAAGGTTAAGCTGGCTCTCCTGAAATATTATAAGGTGGATGAGAATGGCT
TTATGGCAAGCCACTTTGACAGACATTATTGTGGCAAATGTTGTCTGACTTACTGTTTCAACAAACCAGAAGACA
AGTAAGTGTATGACTTAATAA

579/6881
FIGURE 539

MQIFVKTLMGKTITLEVELSDTIDNVKAKIQDKEGIPPDQORLIFAGKQLEDGRTLSDYNIQKESTLHLVLRRLRG
GAKKRKKKSYYTTPRKNKHKRKKVKLALLKYYKVDENGFMASHFDRHYCGKCCLTYCFNKPEDK

580/6881
FIGURE 540

AAAACAGCCGGGGCTCCAGCGGGAGAACGATAATGCAAAGTGCTATGTTCTTGGCTGTTCAACACGACTGCAGAC
CCATGGACAAGAGCGCAGGCAGTGCCACAAGAGCGAGGAGAAGCGAGAAAAGATGAAACGGACCCCTTTTAAAAG
ATTGGAAGACCCGTTTGAGCTACTTCTTACAAAATTCCTCTACTCCTGGGAAGCCAAAACCGGCAAAAAAGCA
AACAGCAAGCTTTCATCAAGCCTTCTCCTGAGGAAGCACAGCTGTGGTCAGAAGCATTGACGAGCTGCTAGCCA
GCAAAATATGGTCTTGCTGCATTGAGGGCTTTTTTAAAGTCGGAATTCTGTGAAGAAAATATTGAATTCTGGCTGG
CCTGTGAAGACTTCAAAAAACCAAATCACCCAAAAGCTGTCCTCAAAAGCAAGGAAAATATATACTGACTTCA
TAGAAAAGGAAGCTCCAAAAGAGATAAACATAGATTTTCAAACCAAACCTCTGATTGCCCAGAATATACAAGAAG
CTACAAGTGGCTGCTTTACAACCTGCCCAGAAAAGGGTATACAGCTTGATGGAGAACAACCTTTATCCTCGTTTCT
TGGAGTCAGAATTCTACCAGGACTTGTGTAAAAAGCCACAAATCACCCACAGAGCCTCATGCTACATGAAATGTAA
AAGGGAGCCCAGAAATGGAGGACATTTCAATCTTTTTCTGAGGGGAAGGACTGTGACCTGCCATAAAGACTGAC
CTTGAATTCAGCCTGGGTGTTTCAAGAAACATCACTCAGAACTATTGATTCAAAGTTGGGTAGTGAATCAGGAAGC
CAGTAACTGACTAGGAGAAGCTGGTATCAGAACAGCTTCCCTCACTGTGTACAGAACGCAAGAAGGGGAATAGGTG
GTCTGAACGTGGTGTCTCACTCTGAAAAGCAGGAATGTAAGATGATGAAAGAGACAATGTAATACTGTTGGTCCA
AAAGCATTTAAAATCAATAGATCTGGGATTATGTGGCCTTAGGTAGCTGGTTGTACATCTTTCCCTAAATCGATC
CATGTTACCACATAGTAGTTTTAGTTTAGGATTCAAGTAACAGTGAAGTGTACTATGTGCAAGGGTATTGAAGT
TCTTATGACCACAGATCATCAGTACTGTTGTCTCATGTAATGCTAAAACCTGAAATGGTCCGTGTTTGCAATTGTTA
AAAATGATGTGTGAAATAGAATGAGTGCTATGGTGTGAAAACTGCAGTGTCCGTTATGAGTGCCAAAAATCTGT
CTTGAAGGCAGCTACACTTTGAAGTGGTCTTTGAATACTTTTAATAAATTTATTTTGATAAATAATATTG

581/6881
FIGURE 541

MQSAMFLAVQHDCREMDKSAGSGHKSEKREKMKRTLLKDWKTRLSYFLQNSSTPGKPKTGKKSKQQAFIKPSPE
EAQLWSEAFDELLASKYGLAAFRFLKSEFCEENIEFWLACEDFKKTKSPQKLSSKARKIYTDFIEKEAPKEINI
DFQTKTLIAQNIQEATSGCFTTAQKRVYSLMENNSYPRFLESEFYQDLCKKPQITTEPHAT

582/6881
FIGURE 542

TGAAGATGAAAAAGAAGATCATAAAAATGTGCGCCAACAACGGCAGGCGGCATCTAAAGCAGCTTCTAAACAGAG
AGAGATGCTCATGGAAGATGTGGGCAGTGAGGAAGAACAAGAAGAGGAGGATGAGGCACCATTCCAGGAGAAAGA
TTCCGGCAGCGATGAAGATTTCTAATGGAAGATGATGACGATAGTGAATATGGCAGTTTCGAAAAAGAAAAACAA
AAAGATGGTTAAGAAGTCCAAACCTGAAAGAAAAAGAAAAGAAAATGCCCAAACCCAGACTAAAGGCTACAGTGAC
GCCAAGTCCAGTGAAAGGCAGGAAAGTGGGTCGCCCCACAGCTTCAAAGGCATCAAAGGAAAAGACTCCTTC
TCCCAAAGAAGAAGATGAGGAACCGGAAAGCCCGCCAGAAAAGAAAACATCTACAAGCCCCCACCAGAGAAATC
TGGGGATGAAGGGTCTGAAGATGAAGCCCCCTTCTGGGGAGGATTAAAAGTGATGATGGTCTGGGGAGAGATTTTA
TTAAAAAAGAAAAAGAGGGAGGAAAAAAGAACCTACTTAAGATAGAACATGGTTTTGGCTATGGCTT
GACTCATGGGCTTTCAGTGCTTTTTTCCATTTGTTGAAAGTAACATTTCTCTCTCTCTCTCTT

583/6881
FIGURE 543

AGCCTGAGGAGCTATTTTGAGCAATGGGGAATGCTCACGGACTGTGTGGTAATGAGAGACCCAAACACCAAGTGC
TCCAGGGGCTTTGGGTTTGTACATATGCCATTGTGGAGGAGGTGGATGCAGCCATGAATGCAAGGCCACACAAG
GTGGATGGAAGAGTTGGAGAACCAGAGAGCTGTTTCAAGGGAAGATTCTCAAAGACCAGGTGCTCACTTAACT
GTGAAAAAGATATTTGTTGGCAGCATTAAAGAAGACACTGAAGAACATCACCTAAGAGATAATTTGAACAGTTTG
GAAAAACGGAAGTGATTGAAATCATGACTGACTGAGGCAGTGGCAAGAAAAGGGGCTTTGCCTTTGTAACCTTTG
ATGACCATGACTCTGTGAATAAGACTGCCATTGAGAAATACCATCCTACGAATGGCCATAACTGTGAAGTTAGGA
AAGCCCTGTCAAAGTAAGAGATGGCTAGTGCTTCATCCAGCCAAAGAAGTCGAAGTGGTTCTGGAACTTTGGTT
TGGTCGTGGAGGTGGTTTCGGTTGGCATGACAGCCGTGGTGGTGGTGGTGGATATGGTGGCAGTGAGGATGGCGA
TAATGGATTTGGTAATGATGGAAGCAATTTTGGAGGTGGTGGAGCTACAGTGATTTTGGCAACTACAATAATCA
GTCTTCAAATTTTGGACCCATGAAGGGAGGAACTTTGGAGGCAGAAGCTCTGGGCCCCATATGGCGGTGGAGGCC
AATACTCTGCCAAACCACGAAACCAAGGTGGCTATGGTGGTTTCAGTAGCAGCAGTAGCTATGGCAGTGGCAGAA
GATTTTAATTAGGAAACAAAGCTTAGCTGGAGAGGAGAGCCGGAGAAGTGACAGGGAAGCTACAGGTTACAACAG
ATTTGTGAACCTCAGCCAAGCACAGTGGTGGCAGGGCCTAACTGCTACAAAGGAGACATGTTTTAGACAAATACTC
ATGTGTATGGGCAAAAACTCGAGGACTGTATTTGTGACTAATTGTGTAAACAGGTTATTTTAGTTTCTGTTCTGT
GGAAAGCGTAAAGCATTCCAACAAAGGGTTTTAATGCAGATTTTTTTTTTTTTTGGCACCCATGCTGTTGATTGCT
AAATGTAATAGTCTGATGGTGATGCTGAATAAATGTCTT

584/6881
FIGURE 544

AGGCAGAGCCCGCGAGGAGGTGACGCGGCTGCGGAGGTGACGCGGGAGGTGCGCGCCCCCTTCCGGCGCGGGGAG
GGCGCTGAAGATCGGGGCCGCTCGGCCGCAGGCCGCTCCAGCGCCGCGGGATGTAGCGCGGGGGACCGCGGCC
CCAGCAGAGCCCGCCTGCCCGGCTTTTAGAAGACCAAACCTGGACAATGGACTTTGCTCACTATGATGACATGATC
TCCATTGACCTCCATTTGTCTACCATCAGAGGGAGATCTCTGCCCCCTGGGGCTGAGAGACCCCAACCTTTCCCC
AAGCTGAAGCTGCAGGGTATTGAGGTACCAGCCAGATGTCTTCCACAAAGGATCTGTGGTGGCACAGGGGAATG
GGGCTCCTGCCAGTAACAGGGAAGCTGACACGGTGGAACTGGCTGAACTGGGACCCCTGCTAGAAGAGAAGGGCA
AACGGGTAATCGCCAACCCACCCAAAGCTGAAGAAGAGCAAACATGCCAGTGCCCCAGGAAGAAGAGGAGGAGG
TGCGGGTACTGACACTTCCCCTGCAAGCCCACCACGCCATGGAGAAGATGGAAGAGTTTGTGTACAAGGTCTGGG
AGGGACGTTGGAGGGTCATCCCATATGATGTGCTCCCTGACTGGCTAAAGGACAACGACTATCTGCTACATGGTC
ATAGACCTCCCATGCCCTCCTTTTCGGGCTTGCTTCAAGAGCATCTTCCGCATTTCATACAGAACTGGCAACATCT
GGACCCATCTGCTTGGTTTCGTGCTGTTTCTCTTTTGGGAATCTTGACCATGCTCAGACCAAATATGTACTTCA
TGGCCCCCTCTACAGGAGAAGGTGGTTTTTGGGATGTTCTTTTGGGTGCAGTGCTCTGCCTCAGCTTCTCCTGGC
TCTTTACACCGTCTATTGTCAATTCAGAGAAAGTCTCTCGGACTTTTTCCAAACTGGACTATTCAGGGATTGCTC
TTCTAATTATGGGGAGCTTTGTCCCTGGCTCTATTATTCTTCTACTGCTCCCCACAGCCACGGCTCATCTACC
TCTCCATCGTCTGTGCTCTGGGCATTTCTGCCATCATTGTGGCGCAGTGGGACCGGTTTGCCACTCCTAAGCACC
GGCAGACAAGAGCAGGCGTGTTCCTGGGACTTGGCTTGAGTGGCGTCGTGCCACCATGCACTTTACTATCGCTG
AGGGCTTTGTCAAGGCCACCACAGTGGGGCCAGATGGGCTGGTTCTTCCTCATGGCTGTGATGTACATCACTGGAG
CTGGCCCTTTATGCTGCTCGAATTCCTGAGCGCTTCTTTCTGGAAAATTTGACATATGGTTCCAGTCTCATCAGA
TTTTCCATGTCCTGGTGGTGGCAGCAGCCTTTGTCCACTTCTATGGAGTCTCCAACCTTCAGGAATTCCGTTACG
GCCTAGAAGGCGGCTGTACTGATGACACCTTCTCTGAGCCTTCCCACCTGCGGGGTGGAGGAGGAACTTCCCAA
GTGCTTTTAAAAATAACTTCTTTGCTGAAGTGAGAGGAAGAGTCTGAGTTGTCTGTTTCTAGAAGAACTCTTA
GAGAATTCAGTACCAACCAAGCTTCAGCCCACTTTCACACCCACTGGGCAATAAACTTTCCATTTCCATTCTCCT
AGCTGGGGATGGGGCATGGTCAAACCTTAGCCATCCCCTCCTCAGCAAGGCATCTACCGGCCCTCAGAGACAG
TACTTTGAAACTCATGTTGAGATTTTACCCTCTCCTCCAACCATTTTGGGAAAATTATGGACTGGGACTCTTCAG
AAATTCTGTCTTTTCTTCTGGAAGAAAATGTCCCTCCCTTACCCCCATCCTTAACCTTTGTATCCTGGCTTATAAC
AGGCCATCCATTTTTGTAGCACACTTTTCAAAAACAATTATATACCCTGGTCCCATCTTTCTAGGGCCTGGATCT
GCTTATAGAGCAGGAAGAATAAAGCCACCAACTTTTACCTAGCCCGGCTAATCATGGAAGTGTGTCCAGGCTTCA
AGTAACTTGAGTTTTAATTTTTTTTTTTTCTTGGCAGAGTAATGTAAATTTAAATGGGGAAAGATATTTAATAT
TTAATACTAAGCTTTAAAAAGAAACCTGCTATCATTGCTATGTATCTTGATGCAAAGACTATGATGTTAATAAAA
GAAAGTACAGAAGACACTTGGCATTCAAAGATTC

[illegible]

586/6881
FIGURE 546

MARGPGPLGRPRPDTVAMPKRGKRLKFRAHDACSGRVTVADYANS DPAVVRSGRVKKAVANAVQQEVKSLCGLEA
SQVPAAEEALSGAGEPCDIIDSSDEMDAQEESIHERTVSRKKKSKRHKEELD GAGGEEYPMDIWLLLLASYIRPEDI
VNFS LICKNAWTVTCTAAFWTRLYRRHYTL DASLPLRLRPESMEKLRCLRACVIRSLYHMYEPFAARISK NPAIP
ESTPSTLKNSKCLLEFWCRKIVGNRQEP MWEFNFKFKKQSPRLKSKCTGGLQPPVQYEDVHTNPDQDCCLLQVTTL
NFI FIPIVMGMIFTLFTINVSTDMRHHRVRLVFQDSPVHGGRKLRSEQGVQVILDPVHSVRLFDWWHPQYPFSLR
A

587/6881
FIGURE 547

AGTGGAGTGGGACAGGTATATAAAGGAAGTACAGGGCCTGGGGAAGAGGCCCTGTCTAGGTAGCTGGCACCAGGA
GCCGTGGGCAAGGGAAGAGGCCACACCCTGCCCTGCTCTGCTGCAGCCAGAATGGGTGTGAAGGCGTCTCAAACA
GGCTTTGTGGTCCCTGGTGCTGCTCCAGTGCTGCTCTGCATACAACTGGTCTGCTACTACACCAGCTGGTCCAG
TACCGGGAAGGCGATGGGAGCTGCTTCCCAGATGCCCTTGACCGCTTCCTCTGTACCCACATCATCTACAGCTTT
GCCAATATAAGCAACGATCACATCGACACCTGGGAGTGGAATGATGTGACGCTCTACGGCATGCTCAACACACTC
AAGAACAGGAACCCCAACCTGAAGACTCTCTTGTCTGTCTGGAGGATGGAACCTTTGGGTCTCAAAGATTTTCCAAG
ATAGCCTCCAACACCCAGAGTCGCCGGACTTTCATCAAGTCAGTACCGCCATTTCTGCGCACCCATGGCTTTGAT
GGGCTGGACCTTGCTGGCTCTACCCTGGACGGAGAGACAAACAGCATTTTACCACCCTAATCAAGGAAATGAAG
GCCGAATTTATAAAGGAAGCCCAGCCAGGGAAAAAGCAGCTCCTGCTCAGCGCAGCACTGTCTGCGGGGAAGGTC
ACCATTGACAGCAGCTATGACATTGCCAAGATATCCCAACACCTGGATTTTATTAGCATCATGACCTACGATTTT
CATGGAGCCTGGCGTGGGACCACAGGCCATCACAGTCCCTGTTCCGAGGTCAGGAGGATGCAAGTCCCTGACAGA
TTCAGCAACACTGACTATGCTGTGGGGTACATGTTGAGGCTGGGGGCTCCTGCCAGTAAGCTGGTGATGGGCATC
CCCACCTTCGGGAGGAGCTTCACTCTGGCTTCTTCTGAGACTGGTGTGGAGCCCCAATCTCAGGACCGGGAATT
CCAGGCCGGTTACCAAGGAGGCAGGGACCCCTTGCTACTATGAGATCTGTGACTTCCTCCGCGGAGCCACAGTC
CATAGAATCCTCGGCCAGCAGGTCCCCTATGCCACCAAGGGCAACCAGTGGGTAGGATACGACGACCAGGAAAGC
GTCAAAAGCAAGGTGCAGTACCTGAAGGACAGGCAGCTGGCGGGCGCCATGGTATGGGCCCTGGACCTGGATGAC
TTCCAGGGCTCCTTCTGTGGCCAGGATCTGCGCTTCCCTCTCACCATGCCATCAAGGATGCACTCGCTGCAACG
TAGCCCTCTGTTCTGCACACAGCACGGGGGCCAAGGATGCCCCGTCCCCCTCTGGCTCCAGCTGGCCGGGAGCCT
GATCACCTGCCCTGCTGAGTCCAGGCTGAGCCTCAGTCTCCCTCCCTTGGGGCCTATGCAGAGGTCCACAACAC
ACAGATTTGAGCTCAGCCCTGGTGGGCAGAGAGGTAGGGATGGGGCTGTGGGGATAGTGAGGCATCGCAATGTAA
GACTCGGGATTAGTACACACTTGTGATTAATGGAAATGTTTACAGATCCCCAAGCCTGGCAAGGGAATTTCTTC
AACTCCCTGCCCCCAGCCCTCCTTATCAAAGGACACCATTTTGGCAAGCTCTATCACCAGGAGCCAAACATCC
TACAAGACACAGTGACCATACTAATTATAACCCCTGCAAAGCCCAGCTTGAAACCTTCACTTAGGAACGTAATCG
TGTCCCTATCCTACTTCCCCTTCCTAATTCCACAGCTGCTCAATAAAGTACAAGAGCTTAACAGTGTGTTGGCG
CTTTGCTTTGGTCTATCTTTGAGCGCCCACTAGACCCACTGGACTCACCTCCCCATCTCTTCTGGGTTCTTCC
TCTGAGCCTTGGGACCCCTGAGCTTGACAGAGATGAGGCCGCCATGT

588/6881
FIGURE 548

CAGGGTAACGCTGTCTTGTGGACCCGCACTTCCCACCCGAGACCTCTCACTGAGCCCGAGCCGCGCGGACATGA
GCCACGGGAAGGGAACCGACATGCTCCCGGAGATCGCCGCCGCCGTGGGCTTCCTCTCCAGCCTCCTGAGGACCC
GGGGCTGCGTGAGCGAGCAGAGGCTTAAGGTCTTCAGCGGGGCGCTCCAGGAGGCACTCACAGAGCACTACAAAC
ACCACTGGTTTTCCCAGAAAGCCGTCCAAGGGCTCCGGCTACCGCTGCATTTCGCATCAACCACAAGATGGACCCCA
TCATCAGCAGGGTGGCCAGCCAGATCGGACTCAGCCAGCCCCAGCTGCACCAGCTGCTGCCCAGCGAGCTGACCC
TGTGGGTGGACCCCTATGAGGTGTCTACCGCATTGGGGAGGACGGCTCCATCTGCGTCTTGTACGAGGAGGCC
CACTGGCCGCCCTCCTGTGGGCTCCTCACCTGCAAGAACCAAGTGCTGCTGGGCCGGAGCAGCCCCCTCCAAGAACT
ACGTGATGGCAGTCTCCAGCTTAGGCCCTTCCGCCCCCGCCCTGGGCGCCGCCGTGCTCATGCTGCCGTGACAACA
GGCCACCACATACCTCAACCTGGGGAAGTGTATTTTTAAATGAAGAGCTATTTATATATATATATTTTTTTTTTAAG
AAAGGAGGAAAAGAAACCAAAAGTTTTTTTTTAAGAAAAAAATCCTTCAAGGGAGCTGCTTGGAAGTGGCCTCCC
CAGGTGCCTTTGGAGAGAACTGTTGCGTGCTTGAGTCTGTGAGCCAGTGTCTGCCTATAGGAGGGGGAGCTGTTA
GGGGGTAGACCTAGCCAAGGAGAAGTGGGAGACGTTGGCTAGCACCCCAGGAAGATGTGAGAGGGAGCAAGCAA
GGTTAGCAACTGTGAACAGAGAGGTGGGATTTGCCCTGGGGGAGGAAGAGAGGCCAAGTTCAGAGCTCTCTGTC
TCCCCAGCCAGACACCTGCATCCCTGGCTCCTCTATTACTCAGGGGCATTTCATGCCTGGACTTAAACAATACTA
TGTTATCTTTTCTTTATTTTTCTAATGAGGTCTCGGGCAGAGAGTGAAGAGGCCTCTCCTGATTCCTACTGTCC
TAAGCTGCTTTTCTTGAAATCATGACTTGTTTCTAATTCACCTCAGGGGCCTGTAGATGTTGCTTTCCAGCCA
GGAATCTAAAGCTTTGGGTTTTCTGAGGGGGGGAGGAGGGAAGTGGAGGTTATTGGGGTTAGGATGGAAGGGAAC
TCTGCACAAAACCTTTGCTTTGCTAGTGCTGCTTTGTGTGTATGTGTGGCAAATAATTTGGGGGTGATTGCAAT
GAAATTTTGGGACCCAAAGAGTATCCACTGGGGATGTTTTTTGGCCAAAACCTCTTCCTTTTGGAAACCACATGAAA
GTCTTGATGCTGCTGCCATGATCCCTTTGAGAGGTGGCTCAAAAGCTACAGGGAAGTCCAGGTCCCTTTATTACTG
CCTTCTTTTCAAAAGCACAACTCTCCTCTAACCCTCCCCCTCCCCCTTCCCTTCTGGTCCGGGTCATAGAGCTACCG
TATTTTCTAGGACAAGAGTTCTCAGTCACTGTGCAATATGCCCCCTGGGTCCCAGGAGGGTCTGGAGGAAAAGT
GCTATCAGAACCTCCTGATGCCCTGGTGGGCTTAGGGAACCATCTCTCCTGCTCTCCTTGGGATGATGGCTGGCT
AGTCAGCCTTGCAATGTATTCTTGGCTGAATGGGAGAGTGCCCCATGTTCTGCAAGACTACTTGGTATTCTTGTA
GGGCCGACACTAAATAAAAGCCAAACCTTGGGCACTGTTTTTCTCCCTGGTGCTCAGAGCACCTGTGGGAAAGG
TTGCTGTCTGTCTCAGTACAATCCAAATTTGTCTGAGACTTGTGCAATATATACTGTTGTGGGTGGAGAAAAGT
GGAAAGCTACACTGGGAAGAACTCCCTTCCTTCAATTTCTCAGTGACATTGATGAGGGGTCCCTCAAAAGACCTC
GAGTTTCCCAAACCGAATCACCTTAAGAAGGACAGGGCTAGGGCATTGGCCAGGATGGCCACCTCCTGCTGTT
GCCCCCTAGTGAGGAATCTTCACCCCACTTCTCTACCCCAAGTTCTCCTCCCCACAGCCAGTCCCTTTTCTG
GATTTCTAAACTGCTCAATTTTGAATCAAAGGTGCTATTTACCAAACACTCTCCCTACCCATTCTGCCAGCTCT
GCCTCCTTTTCAACTCTCCACATTTTGTATTGCCTTCCCAGACCTGCTTCCAGTCTTTATTGCTTTAAAGTTTAC
TTTGGGCCCACAGACCCAAGAGCTAATTTTCTGGTTTGTGGGTGAAACAAAGCTGTGAATCACTGCAGGCTGTG
TTCTTGATCTTGTCTGCAACAGGTCCCTGCCTTTTTAGAAGCAGCCTCATGGTCTCATGCTTAATCTTGTCTC
TCTTCTCTTCTTTATGATGTTCACTTTAAAAACAACAAAACCCCTGAGCTGGACTGTTGAGCAGGCCTGTCTCTC
CTATTAAGTAAAAATAAATAGTAGTAGTATGTTTGTAAAGCTATTCTGACAGAAAAGACAAAGGTTACTAATTGTA
TGATAGTGTTTTTATATGGAAGAATGTACAGCTTATGGACAAATGTACACCTTTTTGTACTTTAATAAAAATGT
AGTAGGATAAAAAAAA

589/6881
FIGURE 549

MSHGKGTDMLEIAAAVGFLSSLLRTRGCVSEQRLKVFSGALQEALTEHYKHHWFPEKPSKSGYRCIRINHKMD
PIISRVASQIGLSQFQLHQLLPSELTWVDPYEVSYRIGEDGSICVLYEEAPLAASCGLLTCKNQVLLGRSSPSK
NYVMAVSS

590/6881
FIGURE 550

ATGTCCATGAGGAGCCCCATCTCTGCCAGCTGGCCCTGGATGGCGTTGGCACCATGGTGAAGTGCACCATCAAG
TCAGAGGAGAAGAAAGAGCCTTGCCACGAGGCCCCCAGGGCTCAGCCACTGCCGCTGAACCTCAGCCTGGAGAC
CCAGCCCCGGGCTCCCAGGATAGTGCTGACCCCCAAGCTCCAGCCCAGGGGAATTTTCAGGGGCTCCTGGGACTGT
AGCTCTCCAGAGGGTAATGGGTCCCAGAACCCAAGAGACCAGGAGCGTCGGAGGCTGCCTCTGGAAGCCAGGAG
AAGCTGGACTTCAACCGAAATTTGAAAGAAGTGGTGCCAGCCATAGAGAAGCTGTTGTCCAGTGACTGGAAGGAG
AGGTTTCTAGGAAGGAAGTCTATGGAAGCCAAAGATGTCAAAGGGACCCAAGAGAGCCTAGCAGAGAAGGAGCTC
CAGCTTCTGGTCATGATTACACAGCTGTCCACCCTGCGGGACCAAGCTCCTGACAGCCCACTCGGAGCAGAAGAAC
ATGGCTGCCATGCTGTTTGAGAAGCAGCAGCAGCAGATGGAGCTTGCCCGGCAGCAGCAGGAGCAGATTGCAAAG
CAGCAGCAGCAGCTGATTACAGCAGCAGCATAAGATCAACCTCCTTCAGCAGCAGATCCAGCAGGTTAACATGCCT
TATGTCTATGATCCAGCCTTCCCCCAAGCCACCAACCTCTGCCTGTACCCCTGACTCCCAGCTGGCCTTACCC
ATTCAGCCCATTCCCTGCAAACCAAGTGGAGTATCCGCTGCAGCTGCTGCACAGCCCCCTGCCCCAGTGGTGAAG
AGGCCTGGGGCCATGGCCACCCACCACCCCTGCAGGAGCCCTCCCAGCCCCTGAACCTCACAGCCAAGCCCAAG
GCCCCGAGCTGCCCAACACCTCCAGCTCCCCAAGCCTGAAGATGAGCAGCTGTGTGCCCCGCCCCCCCAGCCAT
GGAGGCCCCACGCGGGACCTGCAGTCCAGCCCCCGAGCCTGCCCTGCGGCTTCCTTGGTGAAGGGGACGCTGTC
ACCAAAGCCATCCAGGATGCTCGGCAGCTGCTGCACAGCCACAGTGGGGCCTTGATGGCTCCCCAACACCCCC
TTCCGTAAGGACCTCATCAGCCTGGACTCATCCCCAGCCAAGGAGCGGCTGGAGGACGGCTGTGTGCACCCACTG
GAGGAAGCCATGCTGAGCTGCGACATGGATGGCTCCCGCCACTTCCCCGAGTCCCGAAACAGCAGCCACATCAAG
AGGCCCATGAACGCCTTCATGGTGTGGGCCAAGGATGAGCGGAGGAAGATCCTGCAAGCCTTCCCAGACATGCAC
AACTCCAGCATCAGCAAGATCCTTGGATCTCGCTGGAAGTCCATGACCAACCAGGAGAAGCAGCCCTACTATGAG
GAACAGGCGCGGCTGAGCCGGCAGCACCTGGAGAAGTATCCTGACTACAAGTACAAGCCGCGGGCCCAAGCGCACC
TGCATCGTGGAGGGCAAGCGGCTGCGCGTGGGAGAGTACAAGGCCCTGATGAGGACCCGGCGCTCAGGATGCCCCG
CAGAGCTACGTGATCCCCCGCAGGCTGGCCAGGTGCAGATGAGCTCCTCAGATGTCTGTACCTCGGGCAGCA
GGCATGCCGCTGGCACAGCCACTGGTGGAGCACTATGTCCCTCGTAGCCTGGACCCCAACATGCCTGTGATCGTC
AACACCTGCAGCCTCAGAGAGGAGGGTGAGGGCACAGATGACAGGCACTCGGTGGCTGATGGCGAGATGTACCGG
TACAGCGAGGACGAGGACTCGGAGGGTGAAGAGAAGAGCGATGGGGAGTTGGTGGTGCTCAGAGCTGATCCCCG
CTGGGTGGGCCTGGCCCCCTTCTCCTCTGGGGAAGACCTTGTCCCAACTCGATGGGCACAGCCAGCCAACCTAAGA
CTATGTTGGTACTTGGACTTGTTCGTGCCCCAGAGATGGGCAAAGCTGTGCACTTGCAGATACATTCATGAGGGG
AGAGGCGCCCTCCCTTCTGAGGAGCTGTTGGCCTGGGTGGGCAGGAAGTGCAGTATGGCCATGGGCTGAGCAGG
CTGAGCACCTCAGCCTTTAGGGCTTATGGCCAGGGGACACTGTATGACTCTCCTCTCCTGCAGGTGTCTATCCAC
CTGGGGTATGGCATCTACCGACCTGTCTCCCTGGGGTCACATGCTTTGTTTCCATTCTTGTCTCTGGCTGGACCAG
CCACTGTGGGACCAACACCCCTCCACACTCCCCAGACTGCTCGTCTATCACCAGGATCGCTTTGTACTTTGTG
CAAAAGGGTCTGGCTGTCCCTTGCTGTTTTTCATCTCTGCCAAGCCTATTGTGCCTCTGGCTGCTGTATGTGTGCG
CGTGACGTGTGTGTGTTTCATCTGTTTCACTGCACAAGATATTTATTGAGTGCCCACTACGTGCCAGGCAC
TGTTGCTGAGTTCTGTGGGTGTGTCTCTCGATGCCACTCCTGCTTCTCTGGGGGCTCTTTCTGTGCTTCTCTT
TGTCCCCAAATTGCTACCTCTTTGTGAGTCTGGGTGTCTCAGGTTCTGTGTGTCTTGTGTGCATTTCTGTCTCT
CTCTGTCTCTGTCTCTGCAAGGCCCTCTATTTCTCTCTTCTTGGTGTCTGTCTTTGCCCCCTGTGCCCTCT
GGATTCTCTGGGTCTATGTAGGCCCTGGTCTGCCCTGGGCTCATCAGCCTTCTGACCTCCTCTGCCCTCCCC
TTCCTCCCTCCCTGGCTCTGCCAGTCGGTTCCCACGGAGCCATTTTTAGCTCTGATCAGCATGGGAATGTGCCT
CGGCCTCCAAGGGGCTTTGTCTGGTGGCCCCGCCCCCTGGTCCCAACCTGATCCCACGAGGGAGTTGGGACAGGA
GGATTGATGGTGTCTCCCTTCTGCCAGCGTCAGAGGCCCTGGAGAGGGGCTGTCCATGGCAGCTGGTCTTTATT
CCTCCCTCATGAGCACAGGCTCGGGGGGGTCCCCATTCTTGAAGAGGTTGAGAAGACTCCTGGGCTTCAGCCTC
TCCCACCCAGCCCTGCCCTCACCTGCCTGCCCTCCCCCTCCCCACTCTATACTAGGGACTGGATCTCAGCCTCT
GATCAGTTTTCAAAAGTTTGTTCCTAAGGAAATCAAATCCCATTGTACCTAACTCTGAAGATCTAAATAGCCC
TTGGATCAGTATGGGAACCCCAAATCCCACAGGGCCAGATGTGGAGTCTGTGTCTGCCCCGCTCTTCTCTCCATC
CTCAAAGCCCCCACTTCTCTCAGGCTGTTTCTTTTTTATGACTGTAAACATAGATAGTGCTTTATTTTGTAA
TAATAAGATAATGATGAGTAACTTAACCAGCACATTTCTCCTGTTTACACTCGGGGGATTTTTTGTCTTCTGAT
GACATAATAAAGACAGATCATTTTCAGAAAAA

591/6881
FIGURE 551

MSMRSPISAQLALDGVGTMVNCTIKSEEKKEPCHEAPQGSATAAEPQPGDPARASQDSADPQAPAQGNFRGSWDC
SSPEGNGSPEPKRPGASEAASGSQEKLDENRNLKEVVPAIEKLLSSDWKERFLGRNSMEAKDVKGTQESLAEKEL
QLLVMIHQSTLRDQLLTAHSEQKNMAAMLFEKQQQQMELARQQQEQAIAKQQQQLIQQQHKINLLQQQIQQVNMP
YVMIPAFPPSHQPLPVTTPDSQLALPIQPIPCPKPVEYPLQLLHSPAPVVKRPGAMATHHPLQEPSQPLNLTAKPK
APELPNTSSSPSLKMSSCVPRPPSHGGPTRDLQSSPPLPLGFLGEGDAVTKAIQDARQLLHSHSGALDGSPTNP
FRKDLISLDSSPAKERLEDGCVHPLEEAMLSCDMDGSRHFPESRNSSHIKRPMNAMVWAKDERRKILQAFPMH
NSSISKILGSRWKSMTNQEKQPYEEQARLSRQHLEKYPDYKYKPRPKRTCIVEGKRLRVGEYKALMRTRRQDAR
QSYVIPPPQAGQVQMSSSDVLYPRAAGMPLAQPLVEHYVPRSLDPNMPVIVNTCSLREEGEGTDDRHSVADGEMYR
YSEDEDSEGEKSDGELVVLTD

592/6881
FIGURE 552

AACTGCCATCTTCCAGTAATTCGCCAAAATGACGAATACAAAGGGAAAGAGGAGAGGCACCCGATGTATGTTCTC
TAGGCCTTTTAGAAAACATGGAGTTGTTTCCTTTGGCCACGTATATGCGAGTCTATAAGAAAGGTGATATTGTAGA
CATCAAGGGAATGGGTACTGTTCAAAAAGGAATGCCCCACACGCGTTACCACGGCAAAACTGGAAGAGTCTACAA
TGTTACCCAGCATGCTGTTGGCATTGTTGTAAACAAACAAGTTAAAGGCAAGATTCTTGCCAAGAGAATTAATGT
GCGTATTGAGCACATTAAGCACTCTAAGAGCCGAGATAGCTTCCTGAAACGTGTGAAGGAAAATGATCAGAAAAA
GAAAGAAGCCAAAGAGAAAGTTACCTGGATTCAACTAAAGCGCCAGCCTGCTCCACCCAGAGAAGCACACTTTGT
GAGAACCAATGGGAAGGAGCCTGAGCTGCTGGAACCTATTCCCTATGAATTCATGGCATAATAGGTGTTAAAAAA
AAAAA

593/6881
FIGURE 553A

GCTTTCAGGCGATCTGGAGAAAGAACGGCAGAACACACAGCAAGGAAAGGTCCTTTCTGGGGATCACCCCATTGG
CTGAAG**ATG**AGACCAATTCTTCCTCTTGTGTTTTGCCCTGCCTGGCCTCCTGCATGCCCAACAAGCCTGCTCCCGT
GGGGCCTGCTATCCACCTGTTGGGGACCTGCTTGTGGGAGGACCCGGTTTCTCCGAGCTTCATCTACCTGTGGA
CTGACCAAGCCTGAGACCTACTGCACCCAGTATGGCGAGTGGCAGATGAAATGCTGCAAGTGTGACTCCAGGCAG
CCTCACAACCTACTACAGTCACCGAGTAGAGAATGTGGCTTCATCCTCCGGCCCCATGCGCTGGTGGCAGTCCCAG
AATGATGTGAACCTGTCTCTCTGCAGCTGGACCTGGACAGGAGATTCCAGCTTCAAGAAGTCATGATGGAGTTC
CAGGGGCCCCATGCCCGCCGGCATGCTGATTGAGCGCTCCTCAGACTTCGGTAAGACCTGGCGAGTGTACCAGTAC
CTGGCTGCCGACTGCACCTCCACCTTCCCTCGGGTCCGCCAGGGTCGGCCTCAGAGCTGGCAGGATGTTCCGGTGC
CAGTCCCTGCCTCAGAGGCCTAATGCACGCCTAAATGGGGGGAAGGTCCAACCTTAACCTTATGGATTTAGTGTCT
GGGATTCCAGCAACTCAAAGTCAAAAAATTCAAGAGGTGGGGGAGATCACAACTTGAGAGTCAATTTACCAGG
CTGGCCCCCTGTGCCCAAAGGGGCTACCACCTCCCAGCGCCTACTATGCTGTGTCCCAGCTCCGTCTGCAGGGG
AGCTGCTTCTGTACGGCCATGCTGATCGCTGCGCACCCAAGCCTGGGGCCTCTGCAGGCCCCCTCCACCGCTGTG
CAGGTCCACGATGTCTGTGTCTGCCAGCACAACTGCCGGCCCAAATTGTGAGCGCTGTGCACCCTTCTACAAC
AACCGGCCCTGGAGACCGGCGGAGGGCCAGGACGCCCATGAATGCCAAAGGTGCGACTGCAATGGGCACCTCAGAG
ACATGTCACTTTGACCCCGCTGTGTTTGCCGCCAGCCAGGGGGCATATGGAGGTGTGTGTGACAATTGCCGGGAC
CACACCGAAGGCAAGAACTGTGAGCGGTGTGAGCTGCACTATTTCCGGAACCGGCGCCCCGGGAGCTTCCATTAG
GAGACCTGCATCTCCTGCGAGTGTGATCCGGATGGGGCAGTGCCAGGGGCTCCCTGTGACCCAGTGACCGGGCAG
TGTGTGTGCAAGGAGCATGTGCAGGGAGAGCGCTGTGACCTATGCAAGCCGGGCTTCACTGGACTCACCTACGCC
AACCCGCAGGGCTGCCACCGCTGTGACTGCAACATCCTGGGGTCCCGGAGGGACATGCCGTGTGACGAGGAGAGT
GGGCGCTGCCTTTGTCTGCCAACGTGGTGGGTCCCAAATGTGACCAGTGTGCTCCCTACCCTGGAAGCTGGCC
AGTGGCCAGGGCTGTGAACCGTGTGCCTGCGACCCGCACAACCTCCCTCAGCCACAGTGCAACCCAGTTCACAGG
GCAGTGCCCTGTGCGGAAGGCCTTTGGTGGCCTGATGTGCAGCGCTGCAGCCATCCGCCAGTGTCCAGACCGGACC
TATGGAGACGTGGCCACAGGATGCCGAGCCTGTGACTGTGATTTCCGGGGAACAGAGGGCCCCGGGCTGCGACAAG
GCATCAGGCCGCTGCCTCTGCCGCCCTGGCTTGACCGGGCCCCGCTGTGACCAGTGCCAGCGAGGCTACTGCAAT
CGCTACCCGGTGTGCGTGGCCTGCCACCCTTGCTTCCAGACCTATGATGCGGACCTCCGGGAGCAGGCCCTGCGC
TTTGGTAGACTCCGCAATGCCACCGCCAGCCTGTGGTCAGGGCCTGGGCTGGAGGACCGTGGCCTGGCCTCCCGG
ATCCTAGATGCAAAGAGTAAGATTGAGCAGATCCGAGCAGTTCTCAGCAGCCCCGAGTCACAGAGCAGGAGGTG
GCTCAGGTGGCCAGTGCCATCCTCTCCCTCAGGCGAACTCTCCAGGGCCTGCAGCTGGATCTGCCCCCTGGAGGAG
GAGACGTTGTCCCTTCCGAGAGACCTGGAGAGTCTTGACAGAAGCTTCAATGGTCTCCTTACTATGTATCAGAGG
AAGAGGGAGCAGTTTGAATAAATAAGCAGTGCTGATCCTTCCAGAGCCTTCCGGATGCTGAGCACAGCCTACGAG
CAGTCAGCCCAGGCTGCTCAGCAGGTCTCCGACAGCTCGCGCCTTTTGGACCAGCTCAGGGACAGCCGGAGAGAG
GCAGAGAGGCTGGTGGCGCAGGCGGGAGGAGGAGGACCGGCAGCCCCAAGCTTGTGGCCCTGAGGCTGGAG
ATGTCTTCGTTGCCTGACCTGACACCCACCTTCAACAAGCTCTGTGGCAACTCCAGGCAGATGGCTTGCACCCCA
ATATCATGCCCTGGTGAGCTATGTCCCCAAGACAATGGCACAGCCTGTGGCTCCCGCTGCAGGGGTGTCTTCCC
AGGGCCGGTGGGGCCTTCTTGATGGCGGGCAGGTGGCTGAGCAGCTGCGGGGCTTCAATGCCAGCTCCAGCGG
ACCAGGCAGATGATTAGGGCAGCCGAGGAATCTGCCTCACAGATTCAATCCAGTGCCAGCGCTTGGAGACCCAG
GTGAGCGCCAGCCGCTCCAGATGGAGGAAGATGTCAGACGCACACGGCTCCTAATCCAGCAGGTCCGGGACTTC
CTAACAGACCCCGACACTGATGCAGCCACTATCCAGGAGGTGAGCAGGCGCTGCTGGCCCTGTGGCTGCCACA
GACTCAGCTACTGTTCTGCAGAAGATGAATGAGATCCAGGCCATTGCAGCCAGGCTCCCCAACGTGGACTTGGTG
CTGTCCCAGACCAAGCAGGACATTGCGCGTGGCCGCGGTTGCAGGCTGAGGCTGAGGAAGCCAGGAGCCGAGCC
CATGCAGTGAGGGGCCAGGTGGAAGATGTGGTTGGGAACCTGCGGCAGGGGACAGTGGCACTGCAGGAAGCTCAG
GACACCATGCAAGGCACAGCCGCTCCCTTCGGCTTATCCAGGACAGGGTTGCTGAGGTTTCCAGGTAAGTGCAG
CCAGCAGAAAAGCTGGTGACAAGCATGACCAAGCAGCTGGGTGACTTCTGGACACGGATGGAGGAGCTCCGCCAC
CAAGCCCGGCAGCAGGGGGCAGAGGCAGTCCAGGCCAGCAGCTTGCAGGAAGGTGCCAGCGAGCAGGCATTGAGT
GCCCAAGAGGGATTTGAGAGAATAAAACAAAAGTATGCTGAGTTGAAGGACCGGTGGGTGAGGTTCCATGCTG
GGTGAGCAGGGTGCCCGGATCCAGAGTGTGAAGACAGAGGCAGAGGAGCTGTTGGGGAGACCATGGAGATGATG
GACAGGATGAAAGACATGGAGTTGGAGCTGCTGCGGGGACAGCCAGGCCATCATGCTGCGCTCGGCGGACCTGACA
GGACTGGAGAAGCGTGTGGAGCAGATCCGTGACCACATCAATGGGCGCGTGTCTACTATGCCACCTGCAAG**TGA**

594/6881
FIGURE 553B

TGCTACAGCTTCCAGCCCGTTGCCCCACTCATCTGCCGCCCTTTGCTTTTGGTTGGGGGCAGATTGGGTTGGAATG
CTTTCCATCTCCAGGAGACTTTTCATGCAGCCTAAAGTACAGCCTGGACCACCCCTGGTGTGTAGCTAGTAAGATT
ACCCTGAGCTGCAGCTGAGCCTGAGCCAATGGGACAGTTACACTTGACAGACAAAGATGGTGGAGATTGGCATGC
CATTGAAACTAAGAGCTCTCAAGTCAAGGAAGCTGGGCTGGGCAGTATCCCCGCCTTTAGTTCTCCACTGGGGA
GGAATCCTGGACCAAGCACAAAACTTAACAAAAGTGATGTAAAAATGAAAAGCCAAATAAAAATCTTTGG

595/6881
FIGURE 554

MRPFFLLCFALPGLLHAQQACSRGACYPPVGDLLVGRTRFLRASSTCGLTKPETYCTQYGEWQMKCKCDSRQPH
NYYSHRVENVASSSGPMRWWQSQNDVNPVSLQLDLDRRFQLQEVMMFEQGPMPAGMLIERSSDFGKTWRVYQYLA
ADCTSTFPRVRQGRPQSWQDVRCQSLPQRPNARLNGGKVQLNLMDLVSGIPATQSQKIQEVGEITNLRVNFTRLA
PVPQRGYHPPSAYYAVSQRRLQGSCFCHGHADRCAPKPGASAGPSTAVQVHDVCVCQHNTAGPNCERCAPFYNNR
PWRPAEGQDAHECQRCDCNHSETCHFDPAVFAASQGAYGGVCDNCRDHTEGKNCERCQLHYFRNRRPGASIQET
CISCECDPDGAVPGAPCDPVTGQCVCKEHVQGERCDLCKPGFTGLTYANPQGCHRCDCNILGSRDMPCDDEESGR
CLCLPNVVGPKCDQCAPHWKLASGQCEPCACDPHNSPQPTVQPVHRAVPCREGFGGLMCSAAAIRQCPDRTYG
DVATGCRACDCDFRGTEGPGCDKASGRCLCRPGLTGPRCDQCQRGYCNRYPVCVACHPCFQTYDADLREQALRFG
RLRNATASLWSGPGLEDRLASRILDASKIEQIRAVLSSPAVTEQEVQVASAILSLRRTLQGLQLDLPLEEET
LSLPRDLES�DRSFNGLLTMYQRKREQFEKISSADPSGAFRMLSTAYEQSAQAAQVSDSSRLLDQLRDSRREAE
RLVRQAGGGGGTGSPKLVALRLEMSSLPDLTPTFNKLCGNSRQMACTPISCPGELCPQDNGTACGSRCRGVLPRA
GGAFLMAGQVAEQLRGFNAQLQRTQRMIRAAEESASQIQSSAQRLETQVSASRSQMEEDVRRTRLLIQQVRDFT
DPDPTDAATIQEVSEAVLALWLPTDSATVLQKMNEIQAIARLPNVDLVLSQTKQDIARARRLQAEAEARSRAHA
VEGQVEDVVGNLRQGTVALQEAQDTMQGTSRSLRLIQDRVAEVQQVLRPAEKLVTSMKQLGDFWTRMEELRHQA
RQQGAEAVQAQQLAEGASEQALSAQEGFERIKQKYAELKDRLGQSSMLGEQGARIQSVKTEAEELFGETMEMMDR
MKDMELELLRGSQAIMLRSADLTGLEKRVQIRDHINGRVLYYATCK

596/6881
FIGURE 555

GCGGAGTCTCCAACCTGGGAGAGCTGCAGCTGCCGAGAGGAGGAGAACGCTGAGGTCGGTCGGACCAACGGACGCG
CTGACCGCTGCCAACTGCAGCTCGCGCTGCCTCCTGCTCGCGCCGTGCCACTAAGGTCACTCCCGCCTCCGAGAG
CCCAGAGCCGAGATGGAACGGTCCAGGAGCTGATCCCCCTGGCCAAGGAGATGATGGCCCAGAAGCGCAAGGGG
AAGATGGTGAAGCTGTACGTGCTGGGCAGCGTGCTGGCCCTCTTCGGCGTGGTGCTCGGCCTGATGGAGACTGTG
TGCAGCCCCCTTACGGCCGCCAGACGTCTGCGGGACCAGGAGGCAGCCGTGGCGGAGCTGCAGGCCGCCCTGGAG
CGACAGGCTCTCCAGAAGCAAGCCCTGCAGGAGAAAGGCAAGCAGCAGGACACGGTCCTCGGCGGCCGGGCCCTG
TCCAACCGGCAGCACGCCCTCTAGGAAGTGTGGGAGACCAGCGGAGTGGGAGGGAGACGCAGTAGACAGAGACAG
ACCGAGAAGGAAGGGAGAGACAGAGGGGGCGCGCGCACAGGAGCCTGACTCCGCTGGGAGAGTGCAGGAGCACGT
GCTGTTTTTTTATTTGGACTTAACCTTCAGAGAAACCGCTGACATCTAGAACTGACCTACCACAAGCATCCACCAA
GGAGTTTGGGATTGAGTTTTTGCTGCTGTGCAGCACTGCATTGTCATGACATTTCCAACACTGTGTGAATTATCTA
AATGCGTCTACCATTTTGCAGTAGGGAGGAAGGATAAATGCTTTTTATGTTATTATTATTAAATTATTACAATGAC
CACCATTTTGCATTTTGAAATAAAAAACTTTTTATACCAAAAAAAAAAAAAAAAAA

597/6881
FIGURE 556

METVQELIPLAKEMMAQKRKGKMKLYVLGSVLALFGVVLGLMETVCSPFTAARRLRDQEAAVAELQAALERQAL
QKQALQEKGKQQDTVLGGRALSNRQHAS

598/6881
FIGURE 557

CCCGCCTCCGAGAGCCCAGAGCCGAGATGGAAACGGTCCAGGAGCTGATCCCCCTGGCCAAGGAGATGATGGCCC
AGAAGCGCAAGGGGAAGATGGTGAAGCTGTACGTGCTGGGCAGCGTGCTGGCCCTCTTCGGCGTGGTGCTCGGCC
TGATGGAGACTGTGTGCAGCGGAGTGGGAGGGAGACGCAGTAGACAGAGACAGACCGAGAGAGGAATGGAGAGAC
AGAGGGGGCGCGCGCACAGGAGCCTGACTCCGCTGGGAGAGTGCAGGAGCACGTGCTGTTTTTTATTGGACTTA
ACTTCAGAGA

599/6881
FIGURE 558

CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTCG
CGCGGCCGAGCGTGCCCGCGGCGCTGCCCCCTCTCGGGGAGCTGCCCCGGCTGCTGCTGCTGGTGCTGTTGTGCC
TGCCGGCCCGTGTGGGGTGA CTGTGGCCTTCCCCCAGATGTACCTAATGCCAGCCAGCTTTGGAAGGCCGTACAA
GTTTTCCCGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG
TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGC
TAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGT
GCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAACTA AACTTGCCTTCAGAATTTAAAATGGTCCACAG
CAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG
GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTT
GTCTTATTTT CAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAAATTTATTGTCCAGCACCAC
CACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTA
ATAAAGGATTACCATGATTGGAGAGCACTCTATTTATTGTA CTGTGAATAATGATGAAGGAGAGTGGAGTGGCC
CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAACTTACCACAGTAAATG
TTCCA ACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAACCACCACACCAATGCTCAAGCAACAC
GGAGTACACCTGTTTCCAGGACAACCAAGCATTTTTCATGAAACAACCCCAAATAAAGGAAGTGAACCACTTCAG
GTACTACCCGTCTTCTATCTGGGCACACGTGTTT CACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCT
TGCTGAC TTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCTTAGTTTCTTAGACTTA
TCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTGTCTTTAAGATGTGTTAGG
AATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAG
AACAACTTGCAGAATTGAGAGTGATTCCTTTCCTAAAAGTGTAAAGAAAGCATAGAGATTTGTTTCGTATTTAGAAT
GGGATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTTCCACAAGATCTGTAATGTTATTTCCACTTATAAAGGAA
ATAAAAAATGAAAAACATTATTTGGATATCAAAGCAAATAAAAACCAATTCAGTCTCTTCTAAGCAAAATTGC
TAAAGAGAGATGAACCACATTATAAAGTAATCTTTGGCTGTAAAGGCATTTTCATCTTTCCTTCGGGTTGGCAAAA
TATTTTAAAGGTAAACATGCTGGTGAACCAGGGGTGTTGATGGTGATAAGGGAGGAATATAGAATGAAAGACTG
AATCTTCCTTTGTTGCACAAATAGAGTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTTGACTTAATGTCTTTAAA
AGTATCCAGAGATACTACAATATTAACATAAGAAAAGATTATATATTATTTCTGAATCGAGATGTCCATAGTCAA
ATTTGTAAATCTTATTCTTTTGTAAATATTTATTTATATTTATTTATGACAGTGAACATTCTGATTTTACATGTAA
AACAAAGAAAAGTTGAAGAAGATATGTGAAGAAAAATGTATTTTTCTAAATAGAAATAAATGATCCCATTTTTTG
GT

600/6881
FIGURE 559

MTVARPSVPAALPLLGELPRLLLLLVLLCLPAVWGDCGLPPDVPNAQPALEGRTSFPEDTVITYKCEESFVKIPGE
KDSVICLKGSQWSDIEEFCNRSCEVPTRLNSASLKQPYITQNYFPVGTVVEYECRPGYRREPSLSPKLTCLQNLK
WSTAVEFCKKKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLPECREIYC
PAPPQIDNGIIQGERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDGEWSGPPPECRGKSLTSKVPPTVQKPT
TVNVPTEVSPTSQKTTTTPNAQATRSTPVSRTTKHFHETTPNKGSGTTS GTTRLLSGHTCFTLTGLLGLTV
TMGLLT

601/6881
FIGURE 560A

GTGGATTGTCGTCTCCCTGATTCCGAGCTGCGGGCAGGGAGAGGGGCCTCGCGCCGCCCTCAGCAGCCGGCGG
CGGCCGAGGTAGACCGAGCGGGGACGGAAGGACAGACCGACGTGCGCGAGCTGGAATCATGTGAGGGCCAACCGG
GGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCTCCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCGGC
CCTGGCCCCGGGCCCTGGAGGTGGACAGCCGCTCTGTGGTCCCTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCC
CAGCAGCCGGCATGCCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACCTTCAACCACTTGACCGTCC
ACCAAGGGACGGGGGCCGTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACAGGCAACCTGACCATCCAGG
TGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTTGTTACCCGCCCTCATCGTGACGCCCTGCAGCGAAG
TGCTCACCTCACCAACAATGTCAACAAGCTGCTCATATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGGA
GCCTCTACCAGGGGGTCTGCAAGCTGCTGCGGCTGGATGACCTCTTATCCTGGTGGAGCCATCCACAAGAAGG
AGCACTACCTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGATGGCA
AGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCCTGTCCAGCCGGAAGCTGCCCGAG
ACCCTGAGTCCCTCAGCCATGCTCGACTATGAGCTACACAGCGATTTTGTCTCCTCTCTCATCAAGATCCCTTCAG
ACACCCTGGCCCTGGTCTCCCACTTTGACATCTTCTACATCTACGGCTTTGCTAGTGGGGGCTTTGTCTACTTTC
TCACTGTCCAGCCCGAGACCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATCG
TGCGGCTCTGCAAGGATGACCCCAAGTTCCACTCATACGTGTCCCTGCCCTTCGGCTGCACCCGGGCGGGGTGG
AATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCCAGGCCTTCAATATCACCAGCC
AGGACGATGTA CTCTTTGCCATCTTCTCCAAAGGGCAGAAGCAGTATCACCACCCGCCCGATGACTCTGCCCTGT
GTGCCCTTCCCTATCCGGGCCATCAACTTGCAGATCAAGGAGCGCCTGCAGTCTGCTACCAGGGCGAGGGCAACC
TGGAGCTCAACTGGCTGCTGGGGAAGGACGTCCAGTGCACCAAGGCGCCTGTCCCCATCGATGATAACTTCTGTG
GACTGGACATCAACCAGCCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCCTGTACACCACCAGCAGGGACC
GCATGACCTCTGTGGCCTCCTACGTTTACAACGGCTACAGCGTGGTTTTTGTGGGGACTAAGAGTGGCAAGCTGA
AAAAGATTCGGGCCGACGGTCCCCCCCCATGGTGGGGTCCAGTACGAGATGGTCTCTGTGCTCAAGGACGGAAGCC
CCATCCTCCGGGACATGGCCTTCTCCATTGATCAGCGCTACCTGTACGTCATGTCTGAGAGACAGGTCACCAGGG
TCCCCGTGGAGTCATGTGAGCAGTATACGACTTGTGGGGAGTGCCTGAGCTCTGGGGACCTCACTGTGGCTGGT
GTGCCCTGCACAACATGTGCTCCCGCAGGGACAAATGCCAACAGGCCTGGGAACCTAATCGATTTGCTGCCAGCA
TCAGCCAGTGTGTGAGCCTTGCAGTGCATCCCAGCAGCATCTCAGTATCTGAGCACAGCCGGTTGCTTAGCCTGG
TAGTGAGTGATGCTCCTGATCTATCTGCGGGTATCGCCTGTGCCTTTGGGAACCTGACAGAGGTGGAGGGGCAGG
TGTCCGGGAGCCAGGTCATCTGCATCTCACCTGGGCCCAAGGATGTCCCTGTCTATCCGCTGGATCAAGACTGGT
TTGGGCTGGAGCTACAGCTGAGGTCCAAGGAGACAGGGAAGATATTTGTGAGCACCAGATTCAAGTTTTACAAC
GCAGTGGCCACCAACTGTGCCTGTCTGTGTCAACAGCGCCTTCCGCTGCCATTGGTGCAAGTACCACAACCTCT
GCACTCATGACCCCAACACCTGCTCCTTCCAGGAGGGCCGGATCAATATTTAGAGGACTGTCCCCAGCTGGTGC
CCACAGAGGAGATCTTGATTCCAGTGGGGAGGTAAAGCCAATCACCTTAAGGCGGAAATCTGCCCCAGCCGC
AGTCCGGCCAGCGAGGCTATGAGTGTGTCTCAACATAACAAGGAGCCATCCACCGGGTCCCCGCTCTGCGCTTCA
ACAGCTCCAGCGTTCAGTGTGAGAACAGCTCGTACCAGTATGATGGCATGGACATCAGCAATCTGGCCGTGGATT
TCGCTGTGGTGTGGAACGGCAATTTTATCATTTGACAACCTCAGGACCTGAAAGTCCATCTCTACAAGTGTGCAG
CCCAGCGGGAGAGCTGCGGCCTCTGCCTCAAGGCCGACCGGAAGTTTGAGTGTGGCTGGTGCAGCGGCGAGCGCA
GGTGCACCTTCCACCAGCACTGTACCAGCCCTTCCAGCCCTGGCTCGACTGGTCCAGCCACAATGTCAAGTGCT
CCAACCTCAAATCACCGAGATTTTACGGTGTCTGGACCGCCGGAAGGAGGGACGCGAGTGACCATCCATGGCG
TGAACCTGGGTCTGGACTTCTCCGAGATCGCCACCATGTGCAGGTGGCTGGGGTGCCCTGCACGCCCTCCAG
GGGAATACATCATCGCTGAGCAGATTGTCTGTGAGATGGCCATGCCCTCGTGGGAACCACTCCGGGCCAGTAC
GCCTGTGTATTGGCGAGTGTAAAGCCAGAGTTTATGACGAAGTCCCATCAGCAGTACACCTTCGTGAACCTTCTG
TGCTGTCACTCAACCAATCCGAGGTCCCGAGTCAGGAGGCACTATGGTGACCATTACCGGCCATTACCTTGGGG
CTGGGAGCAGCGTGGCAGTCTACCTGGGCAACCAGACCTGCGAGTTCTACGGGAGGTCAATGAGTGAGATCGTGT
GTGTCTACCCCCATCATCAATGGCCTTGCCCCGTCCCTGTTTCTGTGAGTGTGACCGAGCCCATGTGGATA
GCAACCTGCAGTTTGTGATACATAGATGACCTCGGGTCCAGCGCATCGAGCCAGAGTGGAGCATTGCCAGTGGCC
ACACACCCCTGACCATCACAGGCTTCAACCTGGATGTCATTACAGGAGCCAAGGATCCGAGTCAAATTCAATGGCA
AAGAATCTGTCAATGTGTGTAAAGTTGTGAACACAACCAACCTCACCTGCCTGGCACCTCTCTGACCACGGACT
ACCGCCCTGGCCTGGACACTGTGGAACGCCAGATGAGTTTGGATTTGTCTTTAACAATGTCCAATCCTTGCTAA

602/6881

FIGURE 560B

TTTACAACGACACCAAGTTTATCTACTACCCCAACCCGACCTTTGAACTGCTTAGCCCTACTGGAGTCTTGGATC
AAAAGCCAGGATCGCCCATCATTCTGAAGGGCAAAAACCTCTGCCCTCCTGCCTCTGGAGGGGCCAAACTCAACT
ACACTGTGCTCATCGGAGAGACCCCTTGTGCTGTACCGTATCTGAGACCCAGCTTCTCTGCGAGCCTCCCAACC
TCACCGGGCAGCACAAGGTCATGGTTCACGTGGGCGGGATGGTGTCTCGCCTGGCTCGGTGAGTGTATCTCAG
ACAGCTTGCTGACCCTGCCAGCCATCGTCAGCATCGCGGCCGGCGGCAGCCTCCTCCTCATCATCGTCATCATCG
TCCTCATTTGCCTACAAGCGCAAGTCTCGAGAAAAATGACCTCACTCTCAAGCGGCTGCAAATGCAGATGGACAATC
TGGAGTCCCGTGTGGCCTTGGAGTGCAAGGAAGCTTTTGTGCTGAGCTCCAGACGGATATCAATGAGTTGACCAGTG
ACCTGGACCGCTCAGGAATCCCTTACCTGGACTATCGTACCTACGCTATGCGAGTCTGTTCCTGGGCATCGAGG
ACCACCCCGTCTCTGCGGGAGCTGGAGGTACAAGGAAACGGGCAGCAGCAGCTGGAGAAGGCCCTGAAGCTCTTTG
CCCAGCTCATCAACAACAAGGTGTTCTGCTGACCTTCATCCGCACCCTGGAGCTGCAGCGCAGTTTCTCCATGC
GCGACCGGGGCAACGTGGCTTCGCTCATCATGACCGGCCCTGCAGGGCCGCTGGAATATGCCACTGATGTCCTCA
AGCAGCTGCTCTCTGACCTCATCGATAAGAACCTGGAGAACAAGAACCACCCCAAGCTGCTACTCCGGAGGACAG
AGTCTGTGGCTGAAAAGATGCTGACCAATTGGTTCGCCCTTCTCCTGCAACAAGTTCTTAAAGGAGTGCGCAGGGG
AGCCACTCTTCATGCTATACTGTGCCATCAAGCAGCAGATGGAGAAGGGCCCCATTGATGCCATCACGGGCGAGG
CCCGCTACTCCCTGAGCGAGGACAAGCTCATCCGGCAGCAGATCGAGTACAAGACCTGATCCTGAAGTGCCTCA
ACCCTGACAACGAGAACAGTCCAGAGATCCCAGTGAAGGTGTTAAACTGTGACACCATCACACAGGTCAAGGAGA
AGATTCTTGATGCCGTGTATAAGAATGTGCCCTATTCCCAGCGGCCGAGGGCAGTGGACATGGACTTGGAGTGGC
GCCAAGGCCGGATCGCCCGGGTCTGTGCTGCAAGATGAGGACATCACCACCAAGATTGAGGGTGACTGGAAGCGGC
TCAACACACTGATGCATTATCAGGTGTCAGACAGGTGGTGGTGGCTCTGGTCCCCAAACAGACCTCCTCCTACA
ACATCCCTGCCTCTGCCAGCATCTCCCGGACGTCCATCAGCAGATACGGTGACTCCTCCTTCAGGTATACGGGCA
GCCCCGACAGCCTGCGGTCCCGGGCCCCGATGATCACCACAGACCTGGAAAGTGGGGTCAAGGTGTGGCATCTGG
TGAAGAACCATGACCACGGTGACCAGAAGGAGGGTGACCGGGGCAGCAAGATGGTGTCCGAGATCTACCTGACCC
GGCTACTGGCCACCAAGGGCACCCTGCAGAAGTTTGTGGACGACTTGTGAGACCTTGTTCAGCACTGTGCACC
GGGGCAGCGCTCTCCCCCTGGCCATCAAGTACATGTTTGATTTCTAGATGAGCAGGCAGACAGGCACAGCATCC
ATGACACAGATGTGCGGCACACCTGGAAAAGCAACTGCCTCCCTCTGCGCTTCTGGGTGAACGTGATTAAGAACC
CCCAGTTCTGTGTTTGACATCCACAAGGGCAGCATCACGGACGCCTGCCTCTCTGTGGTGGCCAGACCTTCATGG
ACTCTTGTTCAACGTGAGAGCACC GGCTGGGCAAGGACTCCCCCTCCAACAAGCTGCTCTATGCCAAGGACATCC
CCAGCTACAAGAGCTGGGTGGAGAGATACTACGCAGACATCGCCAAGCTCCCAGCCATCAGTGACCAGGACATGA
ATGCCTACCTCGCCGAGCAGTCCCGCCTGCACGCCGTGGAGTTCAACATGCTGAGTGCCCTCAATGAGATCTACT
CCTATGTGAGCAAGTATAGTGAGGAGCTCATCGGGGCCCTAGAGCAGGATGAGCAGGCACGGCGGCAGCGGCTGG
CTTATAAGGTGGAGCAGCTCATTAATGCCATGTCCATTGAGAGCTGAGAGGAGGAGCCTCGCATTCCTGGGAAGA
GGGACCTGTCCAAGCTGTCACTGAGGTCTCAGATGGAAGGACAAGTGATGGGGATCAGGCCCCAGAGCTTGC
TGTCCCCTGAGACCCCATCCTGGGGAGAGGGGAGGACTCCTCTCCCTACGCCAGCCAAGTTTCGTATAGCCAGT
TCCAGCTGGGAGAGACAGTGGGCGTCTCCATCCTCAGTGAGAACACCAGAGAACC CGGGGCCGGGAGAAGGTGG
TTCTTCAAGCCGAGAGGCACGAGCTGGGGACAGTTCTGCCTCTGTGACTGCTGCTTTGCATGAAAACCTATTTGA
TGTATATTGGGGAATAATGAGAACTTTATTTAATTTTTTAAGAAAAAGGGAAAAAACAGAAATAAAACAAAA
AGCCGCCCTGTTAATCCAAATTAAAAA

603/6881
FIGURE 561

ACTGAATTCAACAATTATTTATTGAGTGTCTATTATGTGCTAGATACTGAGACACATCAGAGAACAAAACCAAAA
GCCCTGCCCTCGTCGGGCTTACAGTCTAGCACTTACTGCCAGTTAACCTGGAGGCTACCTGGAACCCCGGGCAAG
TCACCGCACCTCTGTGCCTCGGTCCTCAGCTGCCTAATGGGAGAATAAGCAGACCTGGCTCAGACATGAATCATG
TGCTTGGTGTACTGCAGATGCCAACTGCATCCCCATAACCCACCACCCAGACAGTAGATAGGGCTGGAAGTTGA
TTTTTAATGATCAAGTACAATGGAGGGAGGGCAGAGGGGCTAAGCCTAGCTGTCTGGGGTGCTGTGGTGGTGGTG
GGCTGGCTACACAACTGTTGCTGCTGCTGCTGCTTCTTGGTGGCTGCCTTGCTGGCGAGGTCCTTGGCCTTCTC
TGTAGCTGCCAGTGCTGTCTCCTTTGCCTTCTCCTTGGCTTCCTTGGCTGTCTCAACAAGTGTTTTGAAGGGGC
CTCGCCTTGCAGCTTTGCCAAGATATATTCAAAACCTTCATAGTCTTGGTCACATTGCTTTTGAACCAGGCAAG
ACCAAATTCCTGGACAGCTCTGGAGACACCAAATAAGCTAGAGGAGACCCAGGCTTCCCGGCGGATTTCGGTCCG
GCCACTGTTGTCAGAGTTCACACAGTAAACACATCGTTTCTCCACCACC

604/6881
FIGURE 562

TTTCGGCCGGAACCGCCATCTTCCAGTAATTCGCCAAAATGACAAACACAAAGGGAAAGAGGAGAGGCACCCGAT
ATATGTTCTCTAGGCCTTTTAGAAAACATGGAGTTGTTCCCTTGGCCACATATATGCGAATCTATAAGAAAGGTG
ATATTGTAGACATCAAGGGAACGGGTACTGTTCAAAAAGGAATGCCCCACAAGTGTTACCATGGCAAACTGGAA
GAGTCTACAATGTTACCCAGCATGCTGTTGGCATTGTTGTAAACAAACAAGTTAAGGGCAAGATTCTTGCCAAGA
GAATTAATGTGCGTATTGAGCACATTAAGCATTCTAAGAGCCGAGATAGCTTCCTGAAACGTGTGAAGGAAAATG
ATCCTCCACCCAGAGAAGCACACTTTGTGAGAACCAATGGGAAGGAGCCTGAGCTGCTGGAACCTATTCCTATG
AATTCATGGCATAATAGGTGTT

605/6881
FIGURE 563

MTNTKGKRRGTQYMFSRPFRKHGVVALATYMQIYKKGDIVDIKGMGTVQKGMPHKCYHGKTGRVYNVPQHAVGIV
VNTQVKGKILAKRINVRIEHIKHSKS

606/6881
FIGURE 564

ATGAAGCTCTTATCTTTGGTGGCTGTGGTCGGGTGTTTGCTGGTGCCCCAGCTGAAGCCAACAAGAGTTCTGAA
GATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACATTTACAACCAGAATGTATCCAG
AAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCAGTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTG
TGCGAGTGCAGGTACGAGGAGCGCAGCACCACCACCATCAAGGTCATCATTGTCATCTACCTGTCCGTGGTGGGT
GCCCTGTTGCTCTACATGGCCTTCCTGATGCTGGTGGACCCTCTGATCCGAAAGCCGGATGCATATACTGAGCAA
CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGGGGGACCCCGAGCA
AACACAGTCCTGGAGCGTGTGGAAGGTGCCCAGCAGCGGTGGAAGCTGCAGGTGCAGGAGCAGCGGAAGACAGTC
TTCGATCGGCACAAGATGCTCAGCTAG

607/6881
FIGURE 565

MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPMPVPGHDVEAYCLL
CECRYEERSTTTIKVLIIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTEQLHNEEENEDARSMAAAAASLGGPRA
NTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

608/6881
FIGURE 566

ACCTGCACTGACTTTTTTCTCCTTTTGGAGGGAGAGCAGAGACCATGTCTGACATAGAAGAGGTGGTGGAAGAGT
ACGAGGAGGAGGAGCAGGAAGAAGCAGCTGTTGAAGAGCAGGAGGAGGCAGCGGAAGAGGATGCTGAAGCAGAGG
CTGAGACCGAGGAGACCAGGGCAGAAGAAGATGAAGAAGAAGAGGAAGCAAAGGAGGCTGAAGATGGCCCAATGG
AGGAGTCCAAACCAAAGCCCAGGTCGTTTCATGCCCAACTTGGTGCCTCCCAAGATCCCCGATGGAGAGAGAGTGG
ACTTTGÄTGACATCCACCGGAAGCGCATGGAGAAGGACCTGAATGAGTTGCAGGCGCTGATCGAGGCTCACTTTG
AGAACAGGAAGAAAGAGGAGGAGGAGCTCGTTTCTCTCAAAGACAGGATCGAGAGACGTCGGGCAGAGCGGGCCG
AGCAGCAGCGCATCCGGAATGAGCGGGGAGAAGGAGCGGCAGAACCGCCTGGCTGAAGAGAGGGCTCGACGAGAGG
AGGAGGAGAACAGGAGGAAGGCTGAGGATGAGGCCCGGAAGAAGAAGGCTTTGTCCAACATGATGCATTTTGGGG
GTTACATCCAGAAGXXXXXXXXXACAGAGCGGAAAAGTGGGAAGAGGCAGACTGAGCGGGAAAAGAAGAAGA
TTCTGGCTGAGAGGAGGAAGGTGCTGGCCATTGACCACCTGAATGAAGATCAGCTGAGGGAGAAGGCCAAGGAGC
TGTGGCAGAGCATCTATAACTTGGAGGCAGAGAAGTTCGACCTGCAGGAGAAGTTCAAGCAGCAGAAATATGAGA
TCAATGTTCTCCGAAACAGGATCAACGATAACCAGAAAGTCTCCAAGACCCGCGGGAAGGCTAAAGTCACCGGGC
GCTGGAAATAGAGCCTGGCCTCCTTCACCAAAGATCTGCTCCTCGCTCGCACCTGCCCTCCGGCCTGCACTCCCC
AGTTCCTCCGGGCCCTCCTGGGCACCCAGGCAGCTCCTGTTTGGAAATGGGGAGCTGGCCTAGGTGGGAGCCACCA
CTCCTGCCTGCCCCCACACCCACTCCACACCAGTAATAAAAAGCCACCACACACTG

609/6881
FIGURE 567

CCAGCCTTGCCCGGCAGAGGACTCTGGAGGATGAGGAGGAACAGGAGCGCGCGAXGGCGGCGGCACCGCAACCTG
AGCTCCACCACGGACGATGAGGCTCCCAGGCTCAGCAGAATGGAGACCGGCAGCCTCTGCTTCTGAGAGACTACC
GAGCGTGGAAGAAGCAGAGGTGCCCAAGCCACTGCCCCAGCCTCCAAAGATGAGGACGAGGACATCCAGAGCAT
CCTCAGAACACGGCAGGAGCGGAGGCAGAGGCGGCAGGTGGTGGAGGCTGCACAGGCCCCCATCCAGGAGAGGCT
GGAGGCAGAGGAGGGGAGGAACAGCTTGAGCCCTGTGCAGGCCACACAGAAACCCCTAGTCTCCAAGAAGGAAC
GGAAATCCCACCTCGCCGGAGACTGAGTCGGGAACAGCGGGGCCCCCTGCGCTGGAGGAGGAGAGCTTGGTGGGCA
GGGAGCCAGAAGAGAGGAAGAAAGGGGTTCCAGAAAAGTCCCCAGTCTTGAGAAAATCCTCCATGCCAAAGAAGA
CGGCACCTGAAAAGAGCCTGGTCTCCGATAAAACCTCCATCTCTGAGAAGGTGCTGGCCTCAGAGAAGACATCTC
TATCAGAGAAGATAGCAGTGTCTAGAGAAAAGAAACAGCTCAGAGAAGAAGTCTGTTCTAGAAAAAACAGTGTCT
CTGAGAAGTCGCTGGCCCCAGGGATGGCACTGGGCTCAGGAAGGAGGCTGGTGTCTGAGAAAAGCTTCCATCTTTG
AGAAGGCACTGGCCTCAGAGAAGAGCCCAACTGCAGATGCTAAGCCGGCCCCAAAGAGGCCACAGCCTCAGAGCA
GCCCTTGGCGCAGGAGCCGCCAGCCTCTGGGGGAAGCCAGCCACCACCAAGGAGCAGAGAGGAAGGGCCCTCCC
TGGGAAGAACCTGCCCTCTTTGGCAGAGCAGGGGGCTTCAGACCCTCCGACTGTGGCCTCCCGCCTCCCACCCGT
CACACTCCAGGTGAAAATCCCCAGCAAGGAGGAAGAGGCAGATATGTCCTCACCCACACAGCGAACCTACAGCAG
CTCCCTCAAACGCTCCAGCCCCAGGACCATCTCCTTTTCGGATGAAAACCAAGAAAGAAAACCTCGGAAACAACCCCT
AACTCGCAGTGCCAGCATGAAGCTCCCAGACAACACAGTGAAGTTGGGAGAGAAGCTGGAGAGATACCACACGGC
CATACGGAGATCAGAAATCTGTCAAGTCTCGGGGTCTGCCTTGCACTGAGTTATTCTGTGGCTCCTGTGGGTGTAGC
CAGCAAGCGCCACCTCTTTGAGAAGGAAGTGGCGGGCCAGAGCCGAGCAGAACAGCCTCCAGCCGGAAGGAGAA
CTTGAGGCTCTCAGGGGTTGTGACATCAAGGCTCAACCTGTGGATCAGCAGGACCCAGGAATCTGGAGATCAGGA
CCCCCAGGAGGCACAGAAAGCATCATCTGCAACCGAGAGGACTCAGTGGGGACAGAAATCTGACTCCTCGCTGGA
CGCTGAGGTGTGACAAGCCCCGCCAAGACAGACCTGCAAGTCTTCGTCTCAAGGGACCTCCCTCATGCCAGGCCC
CTGCCTCTCACAGCAGCACCCCTTTCCTCTCATTGTCCCTGTTCCCTTTTTGCCTGTGGATCTGTTTGGCCAGGGT
CCCTGGGGTCAGGAATATTTGCAAGACTCAGCCAGCTCCTTCCCAGCCCAGCCTCTTGGGGCTGGGACTTTCTCA
CCCTGCGGCAGGCACAACAGATGCTGGGACCCAGTCTCTGCCCAGGTACACAGCACAAGTGCACATCAGCACTATG
GGGCCTATGTCCTGCCCAGAGACCTCTGCTCCTTCTGCTCAGATCCACAGTCAGGGCACGGCGCCCCCTCAAGAA
CTCCAGAGTCACCTGTCTCATCGGCTCCCAGCAAGTGCCTCTTTGTCTATGATGTCCCCCTTCTCTGAGGCCTGG
ACCCACCCATCTTTGTCCCTGGGGCCTGCTCCCAGCCACTGAGGCCCGCTCTGGCCAGGGGAGAAGGAGCTGCCG
TGCGTCTTCCCTGTGCCCCGTCTCCCTGCTTGGTTCTCCCCTCCCTTCCCTGGCCGGCTGCCATGGCCAGGAGCT
AAGTGCCTTTTTGTGTGCAACCACTTACCCTTTCTCTGAAAAACCTGTTCTCAGGAAGGATCTGATAAACTCATT
TACTCTCAGGTGTAAGAGACTGATGAGACCTTAGAAGCGAATTCTCTCTGAGGCCTTGCTTTCTAGCAGAGTC
ACCTGAAGTGTGTGAGGAGGATCATCATTTTTCTCATCCCCCTCTTCTCACATTAAGGTGGTGGCTTGCCACTC
AGCAGTCCTAGCTTGGTGAAGTGGAACTGCCACATACAGGGCCAGGCCTACCCTCCTTCCCCACAAGCCCCCTCC
AACCCCCACCCCATGCTCTGGACCTCATGGCTCCTATGAGCTTGGAGCATGGTGAACCATCAGAGAATCTAGAA
CCAACCAAGCTAGGAACATCAGCCTGGTGCCTGTTAACCCTTAAAGCTGTGGTTTACAACCTTTTCAAAAATTTA
AATCATTAG

610/6881
FIGURE 568

ATTCAAGGCCTGGGGGAGCTGCGGTTCCGAGAAGCGGCAGACGGCAGCCAGAAGGCTTGGGCTGTTGAGTAAGCA
GCCCCCTCTCAGTCCCGGCCCTCCCCGCCCCGCGCCCTGCGCCTCCAGTGAGTGACTGAGCCCCGCTGCGGCC
CGCCCCCGGGGCCCTGCCGAGCTGGTGCGCGGCGCGGAGGGGAGGGCCGGCCAGGGTAGGAATGCGCTGCGGGC
GGGCGGCGCAGGAGGCGAGCGGCGGAACATGTAAGGGCACATCCCGCAGAGCTGCCGCCAGCGCGCAGACAGAGC
CCAGGGGAGCAAGAGAACGGGCGGGCGGTGGGGCTCACGGCCTAGGGAGGCGCGGAGGCATCTGGCAGAGGCGGG
TCGGGCTGGGCCAGCTGGGGTAGAGCGGAGGAGCGGGTGCCGGCTGAAGCGGGGCGGTGGGCGCGGAGCGCGCTG
GGGACACCGACACCACCTCACCGGCAGCCGGGTGCTGAGGGCCGCGGTGTGGGTGCGCGGAGCAGTCAGGGCGCA
GGTGGGCAGCGCGCACGGCCTGCCAGCCGGGGCGCCAGAATCCTGCGCTGCGGGGCCGAGAGGGGCGCCGCGCC
CGCCGCAGCCTGGAGCTTTCGCGAACCTCGGGGCGCCATGACGGCGGCGGCGACGGCTACCGTGCTCAAGGAG
GGCGTGCTGGAGAAGCGCAGCGGCGGGCTGCTGCAGCTGTGGAAGCGGAAGCGCTGCGTCCTCACCGAACGCGGG
CTGCAGCTCTTCGAGGCCAAGGGCACGGGCGGCCGCCCCAAGGAGCTCAGCTTCGCCCCGATCAAGGCCGTGGAG
TGCGTGAGAGCACCGGGCGCCACATCTACTTCACGCTGGTGACCGAAGGGGGCGGCGAGATCGACTTCGCTGC
CCCCTGGAAGATCCCGGCTGGAACGCCCAGATCACCTTAGGCCTGGTCAAGTTCAAGAACCAGCAGGCCATCCAG
ACAGTGCGGGCCCCGGCAGAGCCTCGGGACCGGGACCCCTCGTGTCCTAAACCACCGGGCGCACCATCTTTCCTTCA
TGCTACCCACCACCTCAGTGCTGAGGTCAAGGCAGCTTCGTTGTTCCCTCTGGCTTGTGGGGGCACGGCTGTGCT
CCATGTGGCAAGGTGGAAGGAATGGACGAGCCCTGGGAGGAGGGCAGAAGGCTACGCAGGGCTGAGGATGAAGAT
GCAGCCCCCTGGATGGTCCCAGACTCTCAGGACATGCCAGCTCAGGGGCTTCGAGCCACAGGCCTGGCCTCATAT
GGCATGAGGGGGAGCTGGCATAGGAGCCCCCTCCCTGCTGTGGTCTGCCCTCTGTCTGCAGACTGCTCTTAGC
CCCCCTGGCTTTGTGCCAGGCCTGGAGGAGGGCAGTCCCCCATGGGGTGCCGAGCCAACGCCTCAGGAATCAGGAG
GCCAGCCTGGTACAAAAGGAGTACCCAGGGCCTGGTACCCAGGCCCCACTCCAGAATGGCCTCTGGACTCACCTT
GAGAAGGGGGAGCTGCTGGGCCTAAAGCCCCACTCCTGGGGGTCTCCTGCTGCTTAGGTCCCTTTTGGGACCCCCAC
CCATCCAGGCCCTTTCTTTGCACACTTCTTCCCCACCTCTACGCATCTTCCCCCACTGCGGTGTTTCGGCCTGA
AGGTGGTGGGGGTGAGGGGGGGTTGGCCATTAGCATTTTCATGTCTTTCCCAA

611/6881
FIGURE 569

ATGGCGGCGGCGGCGGCAGCTGGTGCGGCCTCCGGGCTGCCGGTCCAGTGGCACAAGGATTAAAGGAAGCGTTA
GTGGATACGCTCACCGGGATCCTATCCCCAGTACAGGAGGTGCGGGCGGCTGCTGAAGAACAGATTAAAGGTGCTG
GAGGTGACGGAGGAATTTGGTGTTCACTTGGCAGAACTGACTGTAGATCCCCAGGGGGCACTGGCAATCCGTCAG
CTGGCATCAGTCATCTTGAAACAATATGTGGAGACTCACTGGTGTGCCCAATCAGAGAAATTTAGGCCTCCTGAA
ACTACAGAAAGGGCAAAAATTGTTATCCGGGAGCTATTGCCTAATGGGTTGAGAGAATCGATAAGCAAAGTGCGC
TCCAGTGTGGCCTATGCAGTGTGAGCCATTGCCCACTGGGACTGGCCTGAAGCTTGGCCCCAACTCTTCAACCTG
CTCATGGAGATGTTGGTGAGCGGAGACTTAAATGCCGTCCATGGAGCCATGCGTGTGCTGACAGAATTCACCTCGT
GAAGTTACAGACACACAGATGCCACTTGTTGCTCCTGTCACTTCTCCCAGAGATGTATAAGATCTTCACCATGGCT
GAGGTGTATGGTATTCGAACCCGTTCCCGAGCCGTGGAGATTTTTTACCCTTGTGCCCATATGATCTGTAACATG
GAGGAGCTGGAAAAGGGTGCAGCCAAAGTCCTGATCTTTCCCGTGGTACAGCAGTTCACAGAGGCCCTTTGTTTCAG
GCCCTCCAGATACCAGATGGCCCCACATCTGACAGTGGGTTTAAAGATGGAGGTCCTAAAGGCAGTGACAGCCCTA
GTGAAAACTTCCCAAAGCACATGGTGTCTCCATGCAGCAGATTCTGCCTATTGTTTGAACACCCTAACCGAG
AGTGCAGCTTTTTATGTGAGGACAGAAGTAAATTACACAGAAGAAGTAGAAGATCCTGTGGATTCTGATGGTGAA
GTCCTGGGCTTTGAAAATCTCGTCTTTAGCATTTTTGAATTTGTCCATGCTCTACTAGAAAATAGCAAATTCAAA
AGCACTGTTAAGAAAGCCTTGCCCTGAATTGATTTATTATATTATCCTGTACATGCAAATCACTGAGGAGCAGATT
AAAGTATGGACAGCCAACCCCCAACAAATTTGTAGAAGATGAAGATGATGATACATTCTCCTATACTGTTAGAATA
GCAGCTCAAGACTTGTTGCTGGCTGTGGCCACAGATTTCCAGAATGAAAGTGCAGCAGCCCTGGCTGCTGCAGCC
ACTCGACATTTACAAGAAGCTGAGCAAACCAAAAACAGTGGCACTGAGCACTGGTGAAGATCCATGAGGCATGC
ATGCTTGCCCTAGGCTCAGTGAAGGCCATCATCACTGACAGTGTGAAAAATGGCAGGATTCATTTTGACATGCAT
GGGTTCTTGACCAATGTCATCCTTGACAGACCTCAACCTCTCAGTGTCTCCTTTCTCTTGGGCCGGGCACTTTGG
GCTGCCAGTCCGTTCACTGTGTGCTATGTCCCCTGAAGTATCCAGCAGTTCCTACAGGCAACAGTTAGTGGTCTT
CACGAGACACAGCCCCCATCAGTTCGAATTTCTGCAGTGAGAGCCATCTGGGGTTATTGTGACCAACTGAAAGTC
TCAGAGAGTACCCACGTGCTCCAGCCCTTCTCCCCAGCATCCTTGATGGCTTAATTCACCTAGCAGCCCAGTTC
AGCTCAGAGGTCTCAACCTGGTGATGGAGACCTGTGCATCGTTTGTACAGTAGACCCCGAATTCACAGCAAGC
ATGGAAAGCAAATCTGCCCCCTTACCATCGCCATTTTCTTAAAGTACAGTAATGATCCCGTCGTCGCCTCACTG
GCTCAGGACATCTTCAAGGAGCTGTCCCAGATTGAAGCCTGTGAGGGCCCAATGCAAATGAGGCTGATTCCCCT
CTGGTCAGCATAATGCAGGCCCCAGCAGACAAGATTCTGTCAGGGCTTTGTGCGACAGCCATTGATATCCTGACA
ACAGTAGTACGAAATACAAAGCCTCCCTTTCCAGCTTCTCATCTGCCAAGCTTTCCCTGCTGTGGCACAGTGT
ACCCTTCACACAGATGACAATGCCACCATGCAGAATGGCGGAGAGTGCTTGCGGGCCTATGTGTGCTGACCCCTG
GAACAAGTAGCCCAGTGGCATGATGAGCAGGGCCACAATGGACTGTGGTATGTGATGCAAGTGGTGAGCCAGCTC
CTGGACCCCCGCACCTCAGAGTTCACTGCGGCCTTTGTGGGCCGCCTTGTGTTCCACCCTCATCTCCAAGGCAGGG
CGGGAACCTCGGGGAGAATCTAGACCAGATTCTTCGTGCCATCCTCAGTAAGATGCAGCAGGCAGAGACGCTCAGT
GTCATGCAGTCCCTGATCATGGTGTTCGCTCATCTGGTGCACACTCAGCTAGAACCTCTCTTGGAGTTCTGTGT
AGCCTCCAGGACCTACTGGCAAACCTGCTCTAGAGTTTGTGATGGCTGAGTGGACAAGCCGACAGCACCTGTTT
TATGGACAGTATGAAGGCAAAGTCAGCTCTGTGGCACTCTGTAAGCTGCTCCAGCATGGCATCAATGCAGATGAC
AAACGGCTACAGGATATCCGTGTGAAGGGAGAGGAGATCTACAGCATGGATGAGGGCATCCGCACCCGCTCTAAG
TCAGCCAAAAACCCAGAACGCTGGACAAACATTCTTTGCTGGTCAAGATCCTAAAGCTGATCATCAACGAGCTC
TCCAACGTCATGGAGGCTAATGCCGCTCGCCAGGCCACTCCTGCAGAGTGGAGTCAAGATGACTCCAATGATATG
TGGGAGGACCAGGAGGAGGAAGAGGAGGAGGAGGAGGAGGATGGTTTAGCTGGCCAACTTTTATCTGACATTCTTGCT
ACAAGTAAATATGAGGAGGATTACTACGAGGATGATGAGGAAGATGACCCTGATGCCCTGAAGGATCCTCTCTAT
CAGATTGATCTGCAGGCATATCTCACAGATTTCTCTGCCAGTTTGCTCAGCAGCCCTGCTACATAATGTTTTCA
GCCACCTTAATGACAATGAGAGGCGAGTTCTACAGACCATCGGCATCTAA

612/6881
FIGURE 570

MAAAAAAGAASGLPGPVAQGLKEALVDTLTGILSPVQEVRAAAEEQIKVLEVTEEFQVHLLAELTVDPQGALAIRQ
LASVILKQYVETHWCAQSEKFRPPETTERAKIVIRELLPNGLRESISKVRSSVAYAVSAIAHWDWPEAWPQLFNL
LMEMLVSGDLNAVHGAMRVLTFTTREVTDQMPVLVAPVILPEMYKIFTMAEVYGIRTRSRAVEIFTTCAHMICNM
EELEKGAACKVLIFPVVQQFTEAFVQALQIPDGPTSDSGFKMEVLKAVTALVKNFPHMVSSMQQILPIVWNTLTE
SAAFYVRTEVNYTEEVDPVDSGGEVLGFENLVFSIFEVHALLNSKFKSTVKKALPELIYYIILYMQITEEQI
KVWTANPQQFVEDEDDDTFSYTVRIAAQDLLLLAVATDFQNESAAAALAAAATRLQEAQTKNSGTEHWWKIHEAC
MLALGSKVKAIIITDSVKNGRIFDMHGFLTINVLADLNLSVSPFLLGRALWAASRFTVAMSPELIQQFLQATVSGL
HETQPPSVRISAVRAIWGYCDQLKVSESTHVLQPFPLSILDGLIHLAAQFSSEVLNLVMTLCIVCTVDPEFTAS
MESKICPFTIAIFLKYSNDPVVASLAQDIFKELSQIEACQGPMQMRLLIPTLVSIMQAPADKIPAGLCATAIDILT
TVVRNTKPPLSQLLICQAFPAVAQCTLHTDDNATMQNGGECLRAYVSVTLEQVAQWHDEQGHNGLWYVMQVVSQ
LDPRTSEFTAAFGVRLVSTLISKAGRELGENLDQILRAILSKMQQAETLSVMQSLIMVFAHLVHTQLEPLLEFLC
SLPGPTGKPALEFVMAEWTSRQHLFYGYEGKVSSVALCKLLQHGINADDKRLQDIRVKGEEIYSMDEGIRTRSK
SAKNPERWTNIPLLVKILKLIINELSNVMEANAARQATPAEWSQDDSNDMWEDQEEEEEEEEEDGLAGQLLSDILA
TSKYEEDYEDDEEDDPDALKDPLYQIDLQAYLTDFLCQFAQQPCYIMFSGHLNDNERRVLQTIGI

613/6881
FIGURE 571

AGTCAAGATGAGGAGTACGCGCGAGAGCCTTGCCCATGGCGAATTGTGGATGACTGTGGTGGGGCCTTTACGAT
GGGTACCATTGGTGGTGGTATCTTTCAAGCAATCAAAGGTTTTCGCAATTCTCCAGTGGGAGTAAACCACAGACT
ACGAGGGAGTTTGACAGCTATTAAAACCAGGGCTCCACAGTTAGGAGGTAGCTTTGCAGTTTGGGGAGGGCTGTT
TTCCATGATTGACTGTAGTATGGTTCAAGTCAGAGGAAAGGAAGATCCCTGGAATCCATCACAAGTGGTGCCTT
AACGGGAGCCATACTGGCAGCAAGAAATGGACCAGTGGCCATGGTTGGGTGAGCCGCAATGGGTGGCATTCTCCT
AGCTTTAATTGAAGGAGCTGGTATCTTGTGACAAGATTGTCCTCTGCACAGTTTCCCAATGGTCCTCAGTTTGC
AGAAGACCCCTCCCAGTTGCCTTCAACTCAGTTACCTTCCTCACCTTTTGGAGACTATCGACAATATCAGTAGGA
CTTCTTTCCTAGGATTTCTTTAACAGAACGAGTTGTGGTTCGAGAAGGATTTTCAAGATCAAGTTACAGTCTGT
TTTTAAAACCATAGGTGGGACAGCTATGGCCAATAGGCTATAAAGAGACATTTAGCACTTTTTTCTATTTAAAGG
AACAAGCGGGGAAGGGTGCTAAAAGATAATACGTTTATTTATTCACACTTGAATTGCATTTGTGATCAAAATAAA
TGTTTTAAATCGCTAAAGGAAAATACAGTAAGTGCTTGAAAGATGAAGGACCAAAAGGCCAAAAAACAGTGAAATA
TGATCATCATCTCTTGCGGACTTCTCTGCCTGGTTTTGTGTGTTCTGTTATTCAAACAATAAAAAGCTGGTGGAA
CTTACTCTTTCTTTTAAGATAAGTTGTAGACTTCGATGTTTCATGCTCATGTACTTCAAATAATGCATGTTTTAT
AGTTAGTCCCTCATCATTGAAGTGACTTCTGAGAATTATGCAGAGTCAACATGGATCATTTTACAGTGAGATGC
TTTATGGATTGAAGGATATGGTAAAATGTTTATAGTTTACTTTGAAAGTAAAATATACTATGTCTTGGTTTTGAG
GATATTGGATACAAAACCTCTCTTCCTTTAGGGCTACTGAGTCTTGATTCTGATCATCAGAAATTTACCCAGAAA
CAACTTGCTTCCAATATACCCAATTCTATATGAAGAATTCATGGAGAGTGTACTGGCACTGGAAGAGTTTAGTGT
TTCTTGATGCTTGAAAATAAAGTATGTACTGTTTTGAATGTGTTCCAAGTCCTCTGCATAAACGATGTATTTTG
GGGTCTGGTTGGGCCTGGAAAATGGATGAGCACTTCAGAACAGGTCATTTTCTGATATTGGAAGTGACATGTGG
CCCTATAGGAGGCATGATGTTAGTTAATTACACATTTGCCTACATCTGTGGGAAATGGAGAACAAAGCCATGTGG
GTACTGTAAACACACGTTTATCTTTTGGCCCAATGCCATACATATGGTAGGCATTTAATTACTGATTGTGTTTGG
ATAATTTGGGAATTTTCGACTGTGGTAAAATATACATAAAATAATACTTATTAAAAAAAAAAAAAAAAAAAAA

614/6881
FIGURE 572

MEEYAREPCPWRIVDDCGGAFTMGTIGGGIFQAIKGFRNSPVG VNHRLRGSLTAIKTRAPQLGGSFAVWGGLFSM
IDCSMVQVRGKEDPWNSITSGALTGAILAARNGPVAMVGSAA MGILLALIEGAGILLTRFASAQFFNGPQFAED
PSQLPSTQLPSSPFGDYRQYQ

615/6881
FIGURE 573

GGCCATGGCGAGCGGCGAGCATTCCCCCGGCAGCGGCGGGCCCCGGCGGCGCTGCACTCCGCGCAGGCTGTGGA
CGTGGCCTCGGCCTCCAACCTCCGGGCCTTTGAGCTGCTGCACTTGACCTGGACCTGCGGGCTGAGTTCGGGCC
TCCAGGGCCCCGGCGCAGGGAGCCGGGGGCTGAGCGGCACCGCGGTCTTGACCTGCGCTGCCTGGAGCCCCGAGGG
CGCCGCCGAGCTGCGGCTGGACTCGCACCCGTGCCTGGAGGTGACGGCGGCGGCGCTGCGGCGGGAGCGGCCCGG
CTCGGAGGAGCCGCCTGCGGAGCCCGTGAGCTTCTACACGCAGCCCTTCTCGCACTATGGCCAGGCCCTGTGCGT
GTCTTCCCCGAGCCCTGCCGCGCCGCCGAGCGCCTCCAGGTGCTGCTCACCTACCGCGTCGGGGAGGGACCCGG
GGTTTGCTGGTTGGCTCCCGAGCAGACAGCAGGAAAGAAGAAGCCCTTCGTGTACACCCAGGGCCAGGCTGTCTT
AAACCGGGCCCTTCTTCCCTTGCTTCGACACGCCTGCTGTTAAATACAAGTATTCAGCTCTTATTGAGGTCCCAGA
TGGCTTCACAGCTGTGATGAGTGCTAGCACCTGGGAGAAGAGAGGTCCAAATAAGTTCTTCTTCCAGATGTGTCA
GCCCATCCCCCTCCTATCTGATAGCTTTGGCCATCGGAGATCTGGTTTCGGCTGAAGTTGGACCCAGGAGCCGGGT
GTGGGCTGAGCCCTGCCTGATTGATGCTGCCAAGGAGGAGTACAACGGGGTGATAGAAGAATTTTGGCAACAGG
AGAGAAGCTTTTTGGACCTTATGTTTGGGGAAGGTATGACTTGCTCTTCATGCCACCGTCCCTTCCATTGGAGG
AATGGAGAACCCTTGCTGACCTTTGTACCCCTGCCTGCTAGCTGGGGACCGCTCCTTGGCAGATGTCATCAT
CCATGAGATCTCCACAGTTGGTTTGGGAACCTGGTCACCAACGCCAACTGGGGTGAATTCTGGCTCAATGAAGG
TTTCACCATGTACGCCAGAGGAGGATCTCCACCATCCTCTTTGGCGCTGCGTACACCTGCTTGGAGGCTGCAAC
GGGGCGGGCTCTGCTGCGTCAGCACATGGACATCACTGGAGAGGAAAACCCACTCAACAAGCTCCGCGTGAAGAT
TGAACCAGGCGTTGACCCGGACGACACCTATAATGAGACCCCTACGAGAAAGGTTTCTGCTTTGTTTCATACCT
GGCCCACTTGGTGGGTGATCAGGATCAGTTTGACAGTTTTCTCAAGGCCTATGTGCATGAATTCAAATTCCGAAG
CATCTTAGCCGATGACTTTCTGGACTTCTACTTGGAATATTTCCCTGAGCTTAAGAAAAAGAGAGTGGATATCAT
TCCAGGTTTTGAGTTTGATCGATGGCTGAATACCCCGGCTGGCCCCCGTACCTCCCTGATCTCTCCCCTGGGGA
CTCACTCATGAAGCCTGCTGAAGAGCTAGCCCAACTGTGGGCAGCCGAGGAGCTGGACATGAAGGCCATTGAAGC
CGTGGCCATCTCTCCCTGGAAGACCTACCAGCTGGTCTACTTCCTGGATAAGATCCTCCAGAAATCCCCTCTCCC
TCCTGGGAATGTGAAAAAAGTTGGAGACACATACCCAAGTATCTCAAATGCCCGGAATGCAGAGCTCCGGCTGCG
ATGGGGCCAAATCGTCCTTAAGAACGACCACCAGGAAGATTTCTGGAAAGTGAAGGAGTTCCTGCATAACCAGGG
GAAGCAGAAGTATACACTTCCGCTGTACCACGCAATGATGGGTGGCAGTGAGGTGGCCCAGACCCTCGCCAAGGA
GACTTTTGATCCACCGCCTCCCAGCTCCACAGCAATGTTGTCAACTATGTCCAGCAGATCGTGGCACCCAAGGG
CAGTTAGAGGCTCGTGTGCATGGCCCCCTGCCTCTTCAGGCTCTCCAGGCTTTCAGAATAATTGTTTGTTCCTCAA
TTCTGTTCCTGATCAACTTCCCTGGAGTTTATATCCCTCAGGATAATCTATTCTCTAGCTTAGGTATCTGTGA
CTCTTGGGCCTCTGCTCTGGTGGGAAGTTACTTCTCTATAGCCCACTGAGCCCCGAGACAGAGAACCTGCCACA
GCTCTCCCCGCTACAGGCTGCAGGCACTGCAGGGCAGCGGTATTCTCTCCCCACCTAAGTCTCTGGGAAGAAG
TGGAGAGGACTGATGCTCTTCTTTTTTCTCTTTCTGTCTTTTTCTTGCTGATTTTATGCAAAGGGCTGGCATTC
TGATTGTTCTTTTTTTCAGGTTTAACTCTTATTTTAAATAAAGTTTTCAAGCAAAAATT

616/6881
FIGURE 574

MASGEHSPGSGAARRPLHSAQAVDVASASNFRFELLHLHLDLRAEFGPPGPGAGSRGLSGTAVLDLRCLEPEGA
AELRLDSHPCLEVTAALRRERPGSEPPAEPVSFYTQPF SHYGQALCVSFPQPCRAAERLQVLLTYRVGEGPGV
CWLAP EQTAGKKKPFVYTQGGAVLNRAFFPCFDTPAVKYKYSALIEVPDGF TAVMSASTWEKRGPNKFFFQMCQP
IPSYLIALAIGDLVSAEVGPRSRVWAEPC LIDAAKEEYNGVIEEFLATGEKLF GPYVWGRYDLLFMPPSF PFGGM
ENPCLTFVTPCLLAGDRSLADV I IHEISHSWFGNLVTNANWGEFWLNEGFTMYAQRRISTILFGAAYTCLEAATG
RALLRQHMDITGEENPLNKL RVKIEPGVDPDDTYNETPYEKGFCFVSYLAHLVGDQDQFDSFLKAYVHEFKFRSI
LADDFLD FYLEYFPELKKKRVDIIPGFEFDRWLNTPGWPPYLPDLSPGDSL MKPAEELAQLWAAEELDMKAIEAV
AISPWKTYQLVYFLDKILQKSPLPPGNVKKLGD TYPSISNARNAELRLRWGQIVLKN DHQEDFWKVKEFLHNQ GK
QKYTLPLYHAMMGSEVAQTLAKETFASTASQLHSNVVNYVQQIVAPKGS

617/6881
FIGURE 575

AGGCTCTATTTAGAGCCGGGTAGGGGAGCGCAGCGGCCAGATACCTCAGCGCTACCTGGCGGAACCTGGATTCTC
TCCCGCCTGCCGGCCTGCCTGCCACAGCCGGACTCCGCCACTCCGGTAGGATTCCCCGCCTGTCATTCCCTAGCC
CAGCTCTTGGGAAACTGCAGAGGGGTCCAGAGGATTTGCAGTTCTGAACCTGCACACTCCAGTCTAGGATCTCCG
AGCAAGAGCGTAGCCTCATGGCTGCAACCTGTGAGATTAGCAACATTTTATAGCAACTACTTCAGTGCAGTGTACA
GCTCGGAGGACTCCACCCTGGCCTCTGTTCCCCCTGCTGCCACCTTTGGGGCCGATGACTTGGTACTGACCCTGA
GCAACCCCCAGATGTCATTGGAGGGTACAGAGAAGGCCAGCTGGTTGGGGGAACAGCCCCAGTTCTGGTCAAGA
CGCAGGTTCTGGACTGGATCAGCTACCAAGTGGAGAAGAACAAGTACGACGCAAGCGCCATTGACTTCTCACGAT
GTGACATGGATGGCGCCACCCTCTGCAATTGTGCCCTTGAGGAGCTGCGTCTGGTCTTTGGGCCCTCTGGGGGACC
AACTCCATGCCCAGCTGCGAGACCTCACTTCCAGCTCTTCTGATGAGCTCAGTTGGATCATTGAGCTGCTGGAGA
AGGATGGCATGGCCTTCCAGGAGGCCCTAGACCCAGGGCCCTTTGACCAGGGCAGCCCCCTTTGCCAGGAGCTGC
TGGACGACGGTCAGCAAGCCAGCCCCCTACCACCCCGGCAGCTGTGGCGCAGGAGCCCCCTCCCCGGCAGCTCTG
ACGTCTCCACCGCAGGGACTGGTGCTTCTCGGAGCTCCCACTCCTCAGACTCCGGTGGAAAGTGACGTGGACCTGG
ATCCCACTGATGGCAAGCTCTTCCCCAGCGATGGTTTTCTGAGACTGCAAGAAGGGGGATCCCAAGCACGGGAAGC
GGAAACGAGGCCGGCCCCGAAAGCTGAGCAAAGAGTACTGGGACTGTCTCGAGGGCAAGAAGAGCAAGCACGCGC
CCAGAGGCACCCACCTGTGGGAGTTTCAAGTTCCTGCGCTCCGAGGCTGTGGCCCAACTATGGGGCCAAAAGAAAA
AGAACAGCAACATGACCTACGAGAAGCTGAGCCGGGCCATGAGGTACTACTACAAACGGGAGATCCTGGAACGGG
TGGATGGCCGGCGACTCGTCTACAAGTTTGGCAAAAACCTCAAGCGGCTGGAAGGAGGAAGAGGTTCTCCAGAGTC
GGAAGTGAAGGTTGGAAGTATACCCGGGACCAAACTCACGGACCACTCGAGGCCTGCAAACCTTCTCGGGAGGAC
AGGCAGGCCAGATGGCCCCCTCCACTGGGGAATGCTCCAGCTGTGCTGTGGAGAGAAGCTGATGTTTTGGTGTAT
TGTCAGCCATCGTCTGGGACTCGGAGACTATGGCCTCGCCTCCCCACCCTCCTCTTGAATTACAAGCCCTGGG
GTTTGAAGCTGACTTTATAGCTGCAAGTGTATCTCCTTTTATCTGGTGCCTCCTCAAACCCAGTCTCAGACACTA
AATGCAGACAACACCTTCTCCTGCGAGACCTGGACTGAGCCAAGGAGGCCTGGGGAGGCCCTAGGGGAGCACC
GTGATGGAGAGGACAGAGCAGGGGCTCCAGCACCTTCTTTCTGGACTGGCGTTCACCTCCCTGCTCAGTGCTTGG
GCTCCACGGGCAGGGGTGAGAGCACTCCCTAATTTATGTGCTATATAAATATGTCAGATGTACATAGAGATCTAT
TTTTTCTAAAACATTCCCCTCCCCACTCCTCTCCACAGAGTGCTGGACTGTTCCAGGCCCTCCAGTGGGCTGAT
GCTGGGACCCCTTAGGATGGGGCTCCCAGCTCCTTTCTCCTGTGAATGGAGGCAGAGACCTCCAATAAAGTGCCTT
CTGGGCTTTTTCTAACCTTTGTCTTAGCTACCTGTGTACTGAAATTTGGGCCTTTGGATCGAATATGGTCAAGAG
GTTGGAGGGGAGGAAAATGAAGGTCTACCAGGCTGAGGGTGAGGGCAAAGGCTGACGAAGAGGGGAGTTACAGAT
TTCTGTAGCAGGTGTGGGCTTACAGACACATGGACTGGGCTGGGAGGCGAGCAAAGGAAGCAGCTGAGACTGTT
GGAGAACGCTTACAAGACTTCATGCAAGCAAGGACATGAACTCAGAACACTGAGGTCAGAAGCATCCTGCTGTCA
TGACACCGCTCGAGTGACCTTGACCTTGACCAAGTCTGTCTGTTTAGGACTGATTTTTCTATTAGGCTAGGGT
TTGGACCTGATGTTCTCAAGATGTCTAGAATTGCATGGCTGGCCTTGTGGAATAGATGGTTTTGCATTCCAGCCA
AGTGTGCTGTAACTGTATATCTGTAATATGAATCCAGCTTTTGAGTCTGACAAAATCAGAGTTAGGATCTTGT
AAAGGA

618/6881
FIGURE 576

CGGGTACAGGGGGCCCAAGAGCTGGGCTGGCTGTCTCCTGCTCATCCAGCCATGCGGTGGCTGTGGCCCCCTGGCT
GTCTCTCTTGCTGTGATTTTGGCTGTGGGGCTAAGCAGGGTCTCTGGGGGTGCCCCCTGCACCTGGGCAGGCAC
AGAGCCGAGACCCAGGAGCAGAGCCGATCCAAGAGGGGCACCGAGGATGAGGAGGCCAAGGGCGTGCAGCAG
TATGTGCCTGAGGAGTGGGCGGAGTACCCCCGGCCCATTACCCCTGCTGGCCTGCAGCCAACCAAGCCCCTTGGTG
GCCACCAGCCCTAACCCCGACAAGGATGGGGGCACCCAGACAGTGGGCAGGAAGTGGGGGCAATCTGACAGGG
GCACCAGGGCAGAGGCTACAGATCCAGAACCCCTGTATCCGGTGACCGAGAGCTCCTACAGTGCCTATGCCATC
ATGCTTCTGGCGCTGGTGGTGTTTGGGTGGGCATTGTGGGCAACCTGTCGGTCATGTGCATCGTGTGGCACAGC
TACTACCTGAAGAGCGCCTGGAAGTCCATCCTTGCCAGCCTGGCCCTCTGGGATTTTCTGGTCTCTTTTTCTGC
CTCCCTATTGTCTCTTCAACGAGATCACCAGCAGAGGCTACTGGGTGACGTTTCTTGTCGTGCCGTGCCCTTC
ATGGAGGTCTCCTCTCTGGGAGTCACGACTTTCAGCCTCTGTGCCCTGGGCATTGACCGCTTCCACGTGGCCACC
AGCACCCCTGCCCAAGGTGAGGCCCCATCGAGCGGTGCCAATCCATCCTGGCCAAGTTGGCTGTCTGCGGTGGGC
TCCATGACGCTGGCTGTGCCTGAGCTCCTGCTGTGGCAGCTGGCACAGGAGCCTGCCCCACCATGGGCACCCCTG
GACTCATGCATCATGAAACCCCTCAGCCAGCCTGCCCCAGTCCCTGTATTCACTGGTGATGACCTACCAGAACGCC
CGCATGTGGTGGTACTTTGGCTGCTACTTCTGCCTGCCCCATCCTCTTCACAGTCACCTGCCAGCTGGTGACATGG
CGGGTGCGAGGGCCCTCCAGGGAGGAAGTCAGAGTGCAGGGCCAGCAAGCACGAGCAGTGTGAGAGCCAGCTCAAC
AGCACCGTGGTGGGCCTGACCGTGGTCTACGCCTTCTGCACCCCTCCCAGAGAACGTCTGCAACATCGTGGTGGCC
TACCTCTCCACCGAGCTGACCCGCCAGACCCTGGACCTCCTGGGCCTCATCAACCAGTTCTCCACCTTCTTCAAG
GGCGCCATCACCCAGTGCTGCTCCTTTGCATCTGCAGGCCGCTGGGCCAGGCCTTCCTGGACTGCTGCTGCTGC
TGCTGCTGTGAGGAGTGCGGCGGGGCTTCGGAGGCCTCTGCTGCCAATGGGTGCGACAACAAGCTCAAGACCGAG
GTGTCTCTTCCATCTACTTCCACAAGCCCAGGGAGTCACCCCCACTCCTGCCCTGGGCACACCTTGCTTGAGGC
CCCAGTAGGGGTGGGGAGGGAGGGAGAGGCCGCCACCCCCGCGGTGTCTGCTGTTCTTTCCCCATAGGTCTTGC
TTTGTTCCTGTCTTGCTGTCTAGGGATGGACTTGGTTCTCTTGTCAAGGTTTGGGAATCCG

619/6881
FIGURE 577

MRWLWPLAVSLAVILAVGLSRVSGGAPLHLGRHRAETQEQQSRSKRGTEDEEAKGVQQYVPEEWA EYPRPIHPAG
LQPTKPLVATSPNPDKDGGTPDSGQELRGNLTGAPGQRLQIQNPLYPVTESSYSAYAIMLLALVVFAVGIVGNLS
VMCIVWHSYYLKS AWNSILASLALWDFLVLF FCLPIVIFNEITKQRL LGDVSCRAVPFMEVSSLGVTTFS L CALG
IDRFHVATSTLPKVRPIERCQSILAKLAVIWVGSMTLAVPELLLWQLAQEPAPTMGTLDSCIMKPSASLPESLYS
LVMTYQNARMWWYFGCYFCLPILFTVTCQLVTWRVRGPPGRKSECRASKHEQCESQLNSTVVGLTVVYAFCTLPE
NVCNIVVAYLSTELTRQTLDLLGLINQFSTFFKGAITPVLLLCICRPLGQAFLDCCCCCCEECGGASEASAANG
SDNKLKTEVSSSIYFHKPRES PPLLPLGTPC

620/6881
FIGURE 578

GCGCGCAGCGCTGGTACCCCGTTGGTCCGCGCGTTGCTGCGTTGTGAGGGGTGTCAGCTCAGTGCATCCCAGGCA
GCTCTTAGTGTGGAGCAGTGAAGTGTGTGTGGTTCCTTCTACTTGGGGATCATGCAGAGAGCTTCACGTCTGAAG
AGAGAGCTGCACATGTTAGCCACAGAGCCACCCCGAGGCATCACATGTTGGCAAGATAAAGACCAAATGGATGAC
CTGCGAGCTCAAATATTAGGTGGAGCCAACACACCTTATGAGAAAGGTGTTTTTAAGCTAGAAGTTATCATTCCCT
GAGAGGTACCCATTTGAACCTCCTCAGATCCGATTTCTCACTCCAATTTATCATCCAAACATTGATTCTGCTGGA
AGGATTTGTCTGGATGTTCTCAAATTGCCACCAAAGGTGCTTGGAGACCATCCCTCAACATCGCAACTGTGTTG
ACCTCTATTGAGCTGCTCATGTCAGAACCAACCCTGATGACCCGCTCATGGCTGACATATCCTCAGAATTTAAA
TATAATAAGCCAGCCTTCCTCAAGAATGCCAGACAGTGGACAGAGAAGCATGCAAGACAGAAACAAAAGGCTGAT
GAGGAAGAGATGCTTGATAATCTACCAGAGGCTGGTGACTCCAGAGTACACAACTCAACACAGAAAAGGAAGGCC
AGTCAGCTAGTAGGCATAGAAAAGAAATTTTCATCCTGATGTTTAGGGGACTTGTCTGGTTTCATCTTAGTTAATG
TGTTCTTTGCCAAGGTGATCTAAGTTGCCTACCTTGAATTTTTTTTTTAAATATATTTGATGACATAATTTTGTG
TAGTTTATTTATCTTGTACATATGTATTTTGAAATCTTTTAAACCTGAAAAATAAATAGTCATTTAATGTTGAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

621/6881
FIGURE 579

MQRASRLKRELHMLATEPPPGITCWQDKDQMDDLRAQILGGANTPYEKGVFKLEVIIPERYPFEPPQIRFLTPIY
HPNIDSAGRICLDVLKLPKGAWRPSLNIATVLTISIQLLMSEPNPDDPLMADISSEFKYNKPAFLKNARQWTEKH
ARQKQKADEEEMLDNLPEAGDSRVHNSTQKRKASQLVGIEKKFHPDV

622/6881
FIGURE 580A

ATGCTGCAAATGCCGAAGTTAAATGAAATACCTCCGGGGAGGGCAGGCCGCAGGGAGGCTCGGGGGGAGGGAAGA
TGGCCTGGACAAACAGGTCCTGAAGCTGCGAGGCTGGAGTGGAGGGCGCAGGGGCAGGCGGGCGGCCAGAGCT
CCATGGGACAGCTGGGGAAGCTCCAGGCTACCTACACAACCTGGCCCAGGCTGGTCACGGTGTCCCCCTCCCTG
CTCTGTGCCCTCTCCTTCCAGAAATCCACCATGGAGAGTAAGGATGAGGTGACGACACCGACAGTGGCATCATC
CTGCAGTCTGGCCCCGACAGCCCGGTCTCCCAATGAAGGAGCTGACCCATGCAGTGCACAAGCAGCAGAGGGCC
CTGGAAGCGAGGCTGGAGGCCTGCCTGGAGGAGCTGAGGAGACTCTGCCTTCGGGAAGCGGAGCTGACGGGCACC
TTGCCAGCGGAGTATCCCCTCAAACCAGGGGAAAAGGCCCCCAAGTTTCGCCGCAGGATCGGAGCGGCTTACAAA
CTGGATGACTGGGCCTTGACAGAGAGGACCCCTAAGCAGCCTGGAGCGCCAGCTGGCCCTGCAGCTGCAGATC
ACAGAGGCAGCCCGTTCGGCTGTGCCTGGAGGAGAACCTCAGCAGGCAGGCTCGGCGGCAGCGGAAGCACTCCATG
CTGCAGGAGGAGAAGAAGCTGCAGGAGCTCCAGCGCTGCCTGGTCGAGCGGCGGCGCAATAGCGAGCCACCTCCG
GCTGCTGCTCTCCCCCTGGGCGGAGAGCTCAGTGCCTCTGATGACAGCTCCCTGTGATGAGGCTCCTCCTGGAG
GAAGAGGAATCCCAAGTGCCAAAACCTCCTCCAGAGTCTCCAGCCCCACCTTCTCGGCCTCTCCCACCCCAAACC
CTTGAGGGTCTGCAGCCAACAGGACCTGAGGCTGGGAGCCAGAACGGGCTCCAGTCCAGAACAGCCCTGGAAG
GAAACCAGCCTGGACCACCCCTATGAGAAGCCAGGAAGTCTTCTGAGCCCTGGAGCGAGTCCAGCAGCCAGCC
ACCACACCACAGGATGGGCCCAGTGCCTCCAGCCTGTGGCTTCTGGAGCCTGCCTCCTACCAGTGGTTCCCATC
CGTGGTGTTCCTGGCCAGTGGCAGGGCCGCACCAAGTGCCTCCAGCCACCCCTGAGATACAGGGGAGGAGGGGCCAG
TCGCAGTCTCTGAGGGTGGATTCTTCCGGGCGGGTCTGAGGGCCGAGGTGCGAGCGCCTTTCGCCGCGCCGC
CCCACTCACTACACGGTGACAGTGCCAGATTCTGCTTTCCCGCGACCAAGCCCCGCTGCCCCACGCCGCTGC
CACTCCTGCTCAGAAGACAGTGGCTCTGACGTCTCCAGCATCTCCACCCCACTTCGCCGGGCAGCAGCAGCCCC
GACATCTCCTTTCTGCAGCCTCTCTCCCCTCCCAAGACCCATCGTCACCGCGGGGCTGGGTCCCAGCCGGCAGC
AGAGAGCTGGTCGCCACCACCCCAAGCTACTGCTGCCGCTGGCTATTTCCCGGCGGGGCGGTACGTGGTGGTG
GCTGAGAGCCCCCTGCCGCTGGCGAGTGGGAGCTGCGCCGCGCAGCCCCGGGCCCTGCTTACGAGGAGGAGGGC
ACTCCCCTGCGCTACCAGCGTCTGGTGCCCTCCCGCAGCCGCATCGTGCAGGACGCCCTCCCTGAAGGACAGCCCCG
GCAGGCCGGGGGCTCAGCAAGGCCGCCGTGTCCGAGGAGCTCAAGTGGTGGCACGAGCGTGCACGCTCCGGAGC
ACCCGCCCCCACTCACTGGACCGCCAAGGAGCTTTCGGGTGAGGAGCCTGCCCTTGGGAGAGAGGGCTTCGGA
CGAGCCCTGGGACCCCGGGCACAGGTGCCACAGTTTGTGTGCTGCGGAGATCGCCTGATGGGGCCCCCTGTGCAA
GTCTTTGTACCTGAAAAAGGAGAGATCATCAGCCAGGTGTAAGTCTGCGCCCCACGCTGGAAAAAAGTGTTCAT
AGAGGGGCTGGGCTGAGACCCCCCACCCTGAGTGCCTCTTTCAGCTCCCCATCCCCATCGCAGGCCGATGAC
CTGGAGCTGAGACCTTTTATTATTTTTTTTTTACACGACTTTTTTCAGAAGCCCTGACCTAAGGATTTATATATG
TGGATTGTCTCAATACCCCTGTGATATGATTATGTTTTATCCCCCAGAGTTTGGCCTACTGGACTTAAGGCCTT
GCCTGTCTGACTGACAGCCTCTATCTCCTTATATAAGACAAGTGGCAGGGGACGAGTGAAGCAGAGTGAGCCACC
TTGGGAGTTCTCAACGCTCTGTGCTCTGGTTCTAAGAAATCCCTGGGGAAGTGGCCCTGGCCCTCCTGTCCCA
CTATTGCTGGAGGCTGGACATGGTACATACTCATGCACATGACTCTCCCCATTTCCAGGTCTCTGGGTACCCC
AGCCTGGGCTGGGGGAGAATCTCTCCCCCTTTTCTAATGTGCTCTGTGATGCACACACCAAGTGGTAGGTCAAA
GGTCAGTATATCCCGGTGGTGTATTGTCTTGCTAGACCCTGCTATTTTCTGACCCCTAAATCCTCTTTAGGGA
CCCAGTCACTATACCCGTGTCTATGCCCTGTGGGCTCCCAGACCCCTGAGCTTTGAGTCAGTGGCATCACAGTTTG
TAGCCTCAGGGGGTCTGGCTGGGGGCTGGTCCATGCTTGTGGTTAGTGGACAGCAGCCACCCTTTGACAGCTACC
TCTGGGCATCTCAAGGGCTTGACAGCCCACTGCTCCTTCTAACATTTTGTGTTTGTGTTTGTGAGATGGAGTCTCGCTC
TGTCGCCCAGGCTGGAATGCTGTAGCAAGATTTTCGGCTCACTGCAACCCCGTCTCCCGGGTTCAAGCGAATCTC
CTGCCTCAGCCTTCCGAGTAGCTGGGATTACAGGCAAGCACCACCATGCCTGCTAATTTTTTTATTTTTTAGTAGAG
ATGGGGTTTTCATCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAAGTGATCCACCTGCCTTGGCCTTTCAA
AGTGCTGGGATTACAGGCATGAGCCACCGCACCTGGCCCTTCTAACGTTTTTTTCATCATAGTCCCAAAAACCAAT
ACTTTACAAGTGGTTTTTGAAAGGCACCACTTTTGTGGCATGTTCTGGTTGGGAGAGGGAGTCACAGTTCCTACT
CCCCCACCAGCTATGCTTCTGCTCTGAGAAGGTGGTTATTTATACAAACATGGACATACTCACTCCCAAGGGCT
GATGAGATGCTGAATTTTCTTTGGGGGCATTCAATTAATTGTCCAGCTGCAGCGACTGGAGCAAGTCTGGAAGCT
GCCTGTGCTAAGACCACCCAGCTGTCCCTGGGTCTCATCCTAGGGCCTTCTTTGCTTCCAGGTGAGGGGACCTG
CTTCAATGAGAAAGCAACTGAATTGAGGCTAGGAGAGGTAGGGAGAGCTGAGTTCTGACTTCACCTGTGCAGAAC
TCTCTGCCCCCATGTTACCTGGACTGGAACAGACTGTGAATATAGCAGAAGGTTCCAAGAACTCTGCTGTCTGAC

623/6881
FIGURE 580B

CTAGAAGAGGCACAGTTCTCTCTACTGGAAAGAAAACGATGTAGCCGATTGCACAAGGGTGCCAAGGGAAGACCC
AGGATGGCCCATCAAAGGAACCTGGGGGAGGATGCAGGAGGCTGAAGGGATGCACCTGGCATTCTCTCACTGTG
CTCTTACCGCATCAGCAACCCCCAACTTTTGGGCCTACTCTGCCCCCATGCGTGAATACCCTGCTTGGATGCTG
TGCTTTTCCGGTTTGTCTCTAAGCCCCTTTCTCCAGGGCATGTTGGTTTCCCTGGCCTCTCAGTGTCCCTAACTGG
AGCCCAGAGTGCCTTGTTCTGAGCCAGGAGACGGCTGAGCACTGGCCCTCCACACCTAAGCGTCCTTTACATTAA
CTTATTGGTCTTGTATAACACCTGGTGCCATTGCCAAGTGGCTGTGTCCTCAGCTACAGAGCTGGAATTGTGTGG
GGTTTAGTGCTAAATACTTCAATAAAGTCTGTTTTTTGTGATTGGCTG

624/6881
FIGURE 581

TCCCGGGCCGGGAGCCAGCAGGCCGGGAGCGGCTGAGGCCACACCCCGCGGGCCGGGCGCTTCCCTCCGGTGA
ATCATCGCTCGCAGCGGCGGCCCGCAGTGGCCGCAGCAGCGCGCCGGGCCCTGGCCGCGCCCCAGCCGAGCGC
AGCGCGGAGTCGCCCCGACCTTTCTCTGCGCAGTACGGCCGCGGGACCGCAGCATGGCGGGCATCGCGGCCAAG
CTGGCGAAGGACCGGGAGGCGGCCGAGGGGCTGGGCTCCCACGACAGGGCCATCAAGTACCTCAACCAGGACTAC
GAGGCGCTGCGGAACGAGTGCCTGGAGGCCGGGACGCTCTTCCAGGACCCGTCCTTCCCGGCCATCCCCTCGGCC
CTGGGCTTCAAGGAGTTGGGGCCCTACTCCAGCAAAACCCGGGGCATCGAGTGGAAGCGCCCCACGGAGATCTGC
GCTGAACCCAGTTTATCATTGGAGGAGCCACCCGCACAGACATCTGCCAAGGAGCCCTGGGTGACTGCTGGCTG
CTGGCAGCCATTGCCTCCCTCACCTTGAATGAAGAAATCCTGGCTCGAGTCGTCCCCCTAAACCAGAGCTTCCAG
GAAACTATGCAGGGATCTTTCACTTCCAGTTCTGGCAATACGGCGAGTGGGTGGAGGTGGTGGTGGATGACAGG
CTGCCCACCAAGGACGGGGAGCTGCTCTTTGTGCATTACGCCAAGGGAGCGAGTTCTGGAGCGCCCTGCTGGAG
AAGGCATACGCCAAGATCAACGGATGCTATGAAGCGCTATCAGGGGGTGCCACCACTGAGGGCTTCGAAGACTTC
ACCGGAGGCATTGCTGAGTGGTATGAGTTGAAGAAGCCCCCTCCCAACCTGTTCAAGATCATCCAGAAAAGCTCTG
CAAAAAGGCTCTCTCCTTGGCTGCTCCATCGACATCACCAGCGCCGCGGACTCGGAGGCCATCAGTTTTAGAAG
CTGGTGAAGGGGCACGCGTACTCGGTACCCGAGCCGAGGAGGTTGAAAGTAACGGAAGCCTACAGAAAAGTATC
CGCATCCGAAATCCCTGGGGAGAAGTGGAGTGGACAGGGCGGTGGAATGACAACTGCCCAAGCTGGAACACTATA
GACCCAGAGGAGAGGGAAAGGCTGACCAGACGGCATGAAGATGGAGAATTCTGGATGTCTTTCACTGACTTCCTG
AGGCACTATTCCCGCCTGGAGATCTGTAACCTGACCCCGAGACACTCTCACCAGCGATACCTACAAGAAAGTGAA
CTCACCAAAATGGATGGGAAGTGGAGGCGGGGCTCCACCGCGGGAGGTTGCAGGAAGTACCCGAACACATTCTGG
ATGAACCCCTCAGTACCTGATCAAGCTGGAGGAGGAGGATGAGGACGAGGAGGATGGGGAGAGCGGCTGCACCTTC
CTGGTGGGGCTCATTCAGAAGCACCGACGGCGGCAGAGGAAGATGGGCGAGGACATGCACACCATCGGCTTTGGC
ATCTATGAGGTTCCAGAGGAGTTAAGTGGGCAGACCAACATCCACCTCAGCAAAAAGTCTTCTCCTGACGAATCGC
GCCAGGGAGCGCTCAGACACCTTCATCAACCTCCGGGAGGTGCTCAACCGCTTCAAGCTGCCGCCAGGAGAGTAC
ATTCTCGTGCTTCCACCTTCGAACCCAACAAGGATGGGGATTTCTGCATCCGGGTCTTTTCTGAAAAGAAAGCT
GACTACCAAGCTGTGATGATGAAATCGAGGCCAATCTTGAAGAGTTCGACATCAGCGAGGATGACATTGATGAT
GGATTGAGGAGACTGTTTGCCAGTTGGCAGGAGAGGATGCGGAGATCTCTGCCTTTGAGCTGCAGACCATCCTG
AGAAGGGTTCTAGCAAAGCGCCAAGATATCAAGTCAGATGGCTTCAGCATCGAGACATGAAAATTATGGTTGAC
ATGCTAGATTTCGACGGGAGTGGCAAGCTGGGGCTGAAGGAGTTCTACATTCTCTGGACGAAGATTCAAAAATAC
CAAAAATTTTACCGAGAAATCGACGTTGACAGGTCTGGTACCATGAATTCCTATGAAATGCGGAAGGCATTAGAA
GAAGCAGGTTTCAAGATGCCCTGTCAACTCCACCAAGTCATCGTTGCTCGGTTTGAGATGACCAGCTCATCATC
GATTTTGATAATTTTGTTCGGTGTGTTGGTTCGGCTGGAAACGCTATTCAAGATATTTAAGCAGCTGGATCCCGAG
AATACTGGAACAATAGAGCTCGACCTTATCTCTTGGCTCTGTTTCTCAGTACTTTGAAGTTATAACTAATCTGCC
TGAAGACTTCTCATGATGGAAAATCAGCCAAGGACTAAGCTTCCATAGAAATACACTTTGTATCTGGACCTCAAA
ATTATGGGAACATTTACTTAAACGGATGATCATAGCTGAAAATAATGATACTGTCAATTTGAGATAGCAGAAAGTT
TCACACATCAAAGTAAAAGATTTGCATATCATTATACTAAATGCAAAATGAGTCGCTTAACCCTTGACAAGGTCAA
AGAAAGCTTTAAATCTGTAATAGTATACACTTTTTACTTTTACACACTTTCCTGTTTCATAGCAATATTAATCA
GGAAAAAATATGCAGGGAGGTATTTAAGCTGAGCAAAAACATTGAGTCACTCTCAAAGGACACGAGGCCCTT
GGCAGGGAATATTTAAAGCAACTTCAAGTTTAAATGAGCTGTTGATTCTACCAACAACAGTCCAAGATTACC
ATTTCCCATGAGCCAACTGGGAAACATGGTATATCATGAAGTAATCTTGTCAAGGCATCTGGAGAGTCCAGGAGA
GAAGACTCACCTCTGTCGCTTGGGTTAAACAAGAGACAGGTTTTGTAGAATATTGATTGGTAATAGTAAATCGTT
CTCCTTACAATCAAGTTCTTGACCTATTTCGGCTTATACATCTGGTCTTACAAAGACCAAGGGATCCTGCGCT
TGATCAACTGAACCAGTATGCCAAAACAGGCATCCAATTTGTAAACCAATTATGATAAAGGACAAAATAAGCTG
TTTGCCACCTCAAACTTTATGAACCTTACCACCCTAGTGTCTGTCCATGGAGTTAGAGGGGACATCACTTAGA
AGTTCTTATAGAAAGGACACAAGTTTGTTCCTGGCTTTACCTTGGGAAAATGCTAGCAACATTATAGAAATTTT
GCCTTGTTCCTTATCTTCTCAAATGTACTGTTAAATAAAAATAAAGGGTTACCCCATGCAATCACACCATGC
CATGTTTTCTTCTTGGAGGGCAGCCCCACAGGACGTTTTATGAGCACACAATTATAGCTTGTTCCTACTTTAAC
AAGGTATGCTGCCTCTGTAATTCATGTATTCAAAGGAAAAGACACCTTGCTATAATTAATGTGGAAGTATA
AAATTTTTTAAATCC

625/6881
FIGURE 582

TCTAATACCTATTGATCTGTTACTTTCTCCCATCACGCTCAGGTGGGAACATCCAGTTGCAGGAAAAACAAGCTTA
ACACGCCCCACTGATTCTACATTATGGTGAGTTCCATAATTATTTTATTATATATTACAGTGTAATAATGGAAATA
AAGTGCCTAATAAATGCAAAATGTGCTTACATCTTTTGGCCCAGCTCCTACCTCCCGGCAGCCTCTCCAGGCCCAG
AACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCTCAATGGCCTATTTAGGCCCATAACCCTACGTCAC
GGCAGCCTCCGCAGATGAGGCTACTGCCTCACAAACAGCCTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTT
TAGACCCAGCTCCTGCCTCCAGCCTTCTCTCCAGGCCCTGAACTTTCTCAAGTTGACCTCACCAGGCCCAGCTC
ATGCTTCTTTGCAGCCTCTCCAGGCCCAGCTCCTGCATCTTGGTGGCCCCTCCAGGCCCAGCCTCTGCCTCCCGT
CAGCCTCTACAGTCCCAACGTCTGCCTCACAGCAGATTCTTCACGCCCAGCTTCTACCTCACTTGGACCCTCCAG
ACCCAGATGGTGTCTCACTGTGGCATCCTCAGGTGAAGCTCCTGCCTTTCGGCAGCCTCTCCAGGCCCAGCTCCT
CCTGCCTCCCAGTGGCCTCTTTCGGCCCAGCCCAGCTCATGCCTCCCGGCGGCCTTCCCAAGCCCCGCTTTTGAC
TTTCGGTGGCCTCTGCAGGCCTCGACAAGGCCCCAGCCTCCTGCCTCCCGAAGGCCTGCACAGGCCCAGCCTCTGC
CTCACAGCGGACTCTC

626/6881
FIGURE 583

GGTATTTTCAGGACAGCCAGGAGGGGGCGCACATCCGCCGAGAACTGTGAGCAAGAGCGTCTGTGCTGAACCATG
GCGCCACCAGAGGGGCGCGGATCCCGCCCCAACCACTTCCCGCTGAGGTGCCAGAAGCAGCGAGGAGCTTCAGC
TTCTCAGGGCAGCAGGAGGTCGTGTTAACTTGGTGTCTTCATTGATGATGATTATTTCCCCACCTTCTAAGAG
ACAAAGACCAACGAGCCACCACAGCCACCAGTCCCAGAACCTGCCAATGCTGGGGAACGGAAAATGAGGGGAGTTC
AACTCTGGCCCTCACAATCCAGTGGAGGAGACGAACTCATCTGCCTCTGTCCCTCTGGGCACGCCTCATGCCAG
GTGCATCTGTGGACAGGGGCCATGCCCCCTGGGCTTCCAAAGTTGGAGAGAGCTGCCAGGCTCAGGTCTGAAGGCC
AGAATTCTACAGTAAGTCTTACTGAGTCAAGGTGGGAGCAGGGTCCGGTAGCTTCCGAGGCTCTGCGGGAGAATCC
GTTTCCTGGCCGTAGAGGTGGCCTGCACTCCGCAGCTTGTGCTGCCCGTCTCGAATGACTGGAGTTTCTTGCTTC
TGTCATAACCTCCACCTCTCCATCACCTGCTCTGCTCTTACAAGGATCCGAAGAAATGGAATCATCGTATC
GCTGATCTACGTAAACAACTGAAGAATTGTCTGAAAGAAAATATGACATGAACTTATGAATTCAACAGGTGAAG
ATTTACAACCTTGATAAATCAACTTTGTGAGCTCGAGCTGTAAAAGCCAAAGGTCCGGTGATGATCCCATACCTT
TTTTCCAGTCTCATGTTGAAGATTTTTATGTAGAAGGCCTTCCCAAAGGAATTTTTTTTTTTTTTTTTTTGA
GATGGAGTTTTCACTCTTATCGCCAGGCTGGGGTGCAATGGCGCAACCTTGCTGGTCACTGCAACCTCTGCCTC
CTGGGTTCAAGAAATTTCTCTGCCTTAGCCTCCCAAGTCACTGGGATTACAGGTGCCACCACCATAACCAGGCTA
ATTTTTGTATTTTTAGTGGAGATGCGGTTTTACCATGTTGGCCGGGCCAGTCTCGAACTCCTGACGTCAAGTGAT
CTTCCCGCTCGACTCCTGATATCAAGTGATCTTCCCGCTCGGCCTCCAGAGTGCTGAGATTACAGACGTGAA
CCCATGCCTGGCCAGGAATTTTTGTTTTTAGGAAGGCTTTCTACTAATGGAATTCCTGGCCTTGAGAGGATGTTA
CTTTAGAAGGAAAGGATTTTTTTGTTATTAAAAGCTGGACCTACCATGAAAGACTTCTGAATCCAGGAAGAGAAA
CTGACTGGGCAACATGTTATTAGAAACAGGACCTTGCCCTGTCACTCAGGATGGAGTTCAGTGGTCTATCATG
GCTCATTATAGCCTCAAACCTCCAGGCTCAAGCAATCCTACCATGTCAGCCTTCCAGTAGCTGGGACTACAGAT
ACCGGGTCTCACACTGTCACCCAGGCTGGAGTACAGTGGCACAACCTCTGCTCACTGCAGCCTCCACCTGCCAGG
CTCAAGCAATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGTGATTTCAGGATGTGAGCTACAATGACTCAAGCT
GCCACATACTGTTGATTGTGAAATGCCAGTTGAAGCATATGTCCTGCGAGCTTAGGGGTGCTACAAGTTGACCAC
TGCAGCAGTAAAGATGACTCTGAAGAATGGCGTGGGTTGGTTCTTTCAAATGCACTTGAGCAGCGGTCTCCAAC
CACAGGGCCACAGAGCTGGAGCTGGATCTACCATGAAAGACTTGTGAATCCAGGAAGAGAGACTGACTGGGCAAC
ATGTTATTAGAAATCTTCTGTGCCATCCAGGCTGGAGTGCAGTGATGTGATCATAGCTCACTATAGCTTTGGCC
TTCTGAGATCAAGCAATCTCCCATCTCAACCTCCCAAGTAGCTAGGACTACACACGCATGTCACCCATGCCAG
ATCATTTTTGTAGAGTCAGAGTTTACCGTGGTGGCCAGGTTGGCCATGTTGGCCAGATGGGGTCTTCTTTTGT
GCCAGGCTGGCCACAAATTCCTGGGCTCAAGTGATCTCCACCTCGTCTTGTAGAGATGAGATTTAGTTATG
TCGTCCAGGCTGATCTCAAACCTCTGGGCTAAATCGATTGTCTCACCTCAGCCTCTCAAGTATGTTATGAAGGTT
ATATGTTAGGAAGGTCCCAGGAGGTAAACCCACACAGATGGGATTTGGGCATAGGTTTGGTTTCCAGGGGGCA
GTGCTGAGCTCTTTGCCAGTGGGAAATGGGATGCTGGTGATTTCAGTAGGTGACCTCACAGTGAAGCTAC
CACTTACTGTTGATTGTGACGAAATGCCAGCTGAGGCACATGCCTTGGGAGCTAAGTGGTTGCTGCCCTTGACCA
CTGTGAAGACTGGTGTGGGAAGGTCGTTTTGGATGCACTTGAGCAGGGGTCCCCAACCCCTGAGCCATGGAGCC
GCAAGGAGCCACACAGCAGGAGGTGGGAACATCCAGTTGCAGGAAAAACAAGCTTAACACGCCCCTGATTCTACA
TTATGCTCCTACCTCCCGGCAGCCTCTCCAGGCCCAGAACCTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGA
CTCTCAATGGCCTATTTAGGCCCATACCCTACGTACGGCAGCCTCCGCAGATGAGGCTACTGCCTCACAACAGC
CTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTTTAGACCCAGCTCCTGCCTCCAGCCTTCTCTCCAGGCC
CTGAACCTTTCTCAAGTTGACCTCACCAGGCCAGCTCATGCTTCTTTGAGCCTCTCCAGGCCAGCTCCTGCAT
CTTGGTGGCCCCCTCCAGGCCAGCCTCTGCCTCCCGTCAGCCTCTACAGTCCCAACGTCTGCCTCACAGCAGATT
CTTCACGCCCAGCTTCTACCTCACTGTGGACCCCCCAAGCCAAGCTCCCAACCTTTACAGCAGCTTCTACACACCC
AGCTCCTGCCACCCAGTGCCCTTTTAGGCCAAGCTCATGCTTCACAAGGGCCTTTCCAGGCCCAACTTTTGTCT
CATGGCAACCTTCCCTGGCCAGATTCTGCTGTCTCCAGCAGCCTAGACAGGCCAGGTCTTGCTCACACTG
GCCTCTCTACATCCAGCTTATGCCTCACGGTGGCCTCTCCA

627/6881
FIGURE 584

MMIIPHLLRDKDQRATTATSPRTRQCWGTENEGVQLWPSQSSGGDETHLPLSLWARLMPGASVDRGHAPGLPKLE
KAARLRSEGQNSTVSPTESRWEQGR

628/6881
FIGURE 585

GGACGGAAGGAGCGGCGGCGACGGAGGAGGAGGATCGAGGCGGTGGTGTTCGTCTTCTCTCTCCTCGATTGTTGC
GCGCTCATCTTCCTCTCGGTCTACTTCATAATTACATTGTCTGATTTAGAATGTGATTACATTAATGCTAGATCA
TGTTGCTCAAAATTAAACAAGTGGGTAAATCCAGAATTGATTGGCCATACCATTGTCACTGTATTACTGCTCATG
TCATTGCACTGGTTCATCTTCCTTCTCAACTTACCTGTTGCCACTTGGAATATATATCGATACATTATGGTGCCG
AGTGGAACATGGGAGTGTTTGATCCAACAGAAATACACAATCGAGGGCAGCTGAAGTCACACATGAAAGAAGCC
ATGATCAAGCTTGGTTTCCACTTGCTCTGCTTCTTCATGTATCTTTATAGTATGATCTTAGCTTTGATAAATGAC
TGAAGCTGGAGAAGCCGTGGTTGAAGTCAGCCTACACTACAGTGCACAGTTGAGGAGCCAGAGACTTCTTAAATC
ATCCTTAGAACCGTGACCATAGCAGTATATATTTTCTCTTGGAACAAAAAACTATTTTGTGTATTTTACCA
TATAAAGTATTTAAAAAACAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

629/6881
FIGURE 586

MEAVVFVFSLLDCCALIFLSVYFIITLSDLECDYINARSCCSKLNKWWIPELIGHTIVTVLLLSLHWFIFLLNL
PVATWNIYRYIMVPSGNMGVFDPTTEIHNRGQLKSHMKEAMIKLGFHLLCFFMYLYSMILALIND

630/6881
FIGURE 587

CCCTAATCAAGTACCCCTCCTCCTCCACCACCTCCTGCCCCACCCCTCCCTGCATCTGGATTCTTTTTGGCATC
CATGTCAGAAGACAATCGCCCTTTAACTGGACTTGCAGCTGCAATTGCCGGAGCAAAACTTAGGAAAGTGTCACG
GATGGAGGATACCTCTTTCCCAAGTGGAGGGAATGCTATTGGTGTGAACCTCCGCCTCATCTAAAACAGATACAGG
CCGTGGAAATGGACCCCTTCCTTTAGGGGGTAGTGGTTTAATGGAAGAAATGAGTGCCCTGCTGGCCAGGAGGAG
AAGAATTGCTGAAAAGGGATCAACAATAGAAACAGAACAAAAAGAGGACAAAGGTGAAGATTAGAGCCTGTAAC
TTCTAAGGCCTCTTCAACAAGTACACCTGAACCAACAAGAAAACCTTGGGAAAGAACAAATACAATGAATGGCAG
CAAGTCACCTGTTATCTCCAGACCAAAATCCACACCCTTATCACAGCCCAGTGCCAATGGAGTCCAGACGGAAGG
ACTTGACTATGACAGGCTGAAGCAGGACATTTTAGATGAAATGAGAAAAGAATTAACAAAGCTAAAAAGAAGAGCT
CATTGATGCAATCAGGCAGGAACCTGAGCAAGTCAAATACTGCAT**TAG**AGGAACAGACTAAGGAGAGATAGGACTTT
AATCTGGAGGAAAAATATCCTACAAACAACAACCTGTTTACAAACAGCAAACCCCTACATTTATGAGCTGTAAGAAG
AAAATGGAGACAAACAGAAGGAGGGAAAAACCAACCTACTCTGAAAGCCTTCAGACATTATGACTCTGGTGATAA
GCTCTTTCCCTCTCCGTTTGCTGCTTTTTTCTGGCCTTTACAACAGAATGGAAGAGAATCATTTAAGAGTTCCTG
TAACAGTTATGCAGAAAATACTAAAACCCATCAGGCAAGATCACCACGCATTGAAATATTTTCATATCAAGATAA
AGTCGCACATTTTCCACAATACATTGCTAAAATAAAGAGGAGAAAGGCTTAGGAAGTTTTTCTGCAGAGAGTGCT
GGTAAAGAATTGAGCAAGTTTGCTATTGTATTGTAATGTTTCTCTCAGGTTTGTTCTTCCTATCATGTTTGATAT
TCCATGAATAATTGAGATCAGCCCTATGTAAGTTAAGATCATAATATGTGGAACAAATGGAATTGTAAGTGCTTT
CAAAGGGTAATATTTATAAGAAAGTGCCGAAAAATGTTTCTTCAGCTTGAGAAATTTTAGAATGATAGGAAGTT
TCTCGAGTTAGCCTTCATGCAATTTTGTAGATTAAAACATAAAATTTGTCCAGAACTTAAAGATTTAGATGCCTT
CCTAAATTGTTACAATGCTTTACCAAATCTATGACTTCTACATAACACAAACCAGTGGTCAAATGTAAACACTAT
ATTGTAGATTTACTGTAGGTTTTCAACCTTTTTTAGATTTATGCATGTGGACATTTTTTATAATGTAATTACAATC
ACCACAAGGTTAGCTTTTTTAATTGCAGACAGTAATGCATGTCACACTAATATGTAGTGGCCTTTTCAAGGCCTA
GTCCCAGGGAAAACATTTTGTAGAGTATAGGGGAGTGGGAGGAAGGGGAGGAATAATTTTTTATTTAAAGTTGAT
TTCTGCACTATCTTTTTCTCAGTTACCTGCATGAATAAATAATGAGAAATATTTTGTGACTTTAATTGGTAAATA
TGTTACAAAACCAAGTACTTAATCTTTTACATCATGTCTTCAGCTATTTGTATTTTAAACCAGTAATTTCAATGGT
CTGAAACATGATTCTGAGCTTCACATAATATCTTAACTGTGGAACCTCAAAGTTTGATCACTGAATTTGGCAGTT
ATTATTACCTAGGTACCCCGCTGTTACACAGGTGTTTAGATACGTGTTCTGAATGAAGCTGCTTTTGAATTTT
GTTATGTTGAAATGCAAGAAATAACAATGATGGCAGCAATTAAGGTCACAGAAATCATTAGGTAAAGGAAAACCA
ATGAGGAGTTCTGCAGTTTTCTTTTAATAAGTAAAGTGAGACTTGGGTGGTGGGAAGAAGGAAGGTGGGAAGAAG
GAATTAGACACTCTGCCTGCCACTCTGCGTGTGTGTGCTCTCGCGCACGTGCTGTCTATATGGAAGCCACTCCCT
TTTCTTTCCCTTTGAAACTGGTAAGGTTAAAATAGGGGAGAAATCCTACATGTTGGAATGATAGCTTTTTGGAAAA
TTTAAGAAACTCTCCAGGCTCTCCATCTTGATTTATGCTTGAGTTGTTATGTGCCATATTTGCTTTGAACTCTGA
TTATCAGAAGTTTTTACTAAAACCTTTGAAATAATTCACCTTTCATCTGCTTTCTAGATTTTGTACATCTCAGTCCAT
AAAGCAAAGCTTGTGATAGTGTAGTTTTCTAAACGCTGCAAATTTGCAGCCTTTACCCTACAAAAGAGTTTGG
ATGAGGGATTTTTTTTTTTCTTTGTCAAATAGTTCCTGTTTCTGTAGAAATTTTATTTTATAGATTAAACTGTGAT
GGATGGGCTATCATAATTCAAGTATACATTTCTTTTTTCTATCAGATATTCATTGTGCATGCAGTAGTAGTAAAAA
CATCAAAGATGCAGCAAGCTTATTAAGTATTATTTTCTAAAAGAAATAGGAGGCATTTTTCATCTTTATTATTGTA
CTTTTGGTTATGCAAACACTTTGATAATATAAACAGTTATGTCCCTATAAATCTGGTCAGCAACCTCTTTTGAT
TTTGTGGGTAAGTTAAATAGTCTGTAGTAGGTAGAGTACTGGGTACAAGTGGTCCAACTAAGATAAGAGACTA
AAATAAAATGCTAAATCTTAAAAGAACTGGGTTTATGCACTAAACGTTTTGTGCCTTGGTCTAATATTAACATG
ATGTATGTGTAACTGAC

631/6881
FIGURE 588

MSEDNRPLTGLAAAIAGAKLRKVS RMEDTSFPSSGGNAIGVNSASSKTD TGRGNGPLPLGGSGLMEEMSALLARRR
RIA EKGSTIETE QKEDKGEDSEPVTSKASSTSTPEPTRKPWERTNTMNGSKSPVISRPKSTPLSQPSANGVQTEG
LDYDRLKQDILDEM RKELTKLKEELIDAIRQELSKSNTA

632/6881
FIGURE 589

GGGGCTGCTGGGACTCGCGTCGGTTGGCGACTCCCGGACGTAGGTAGTTTGTGTTGGGCCGGGTCTGAGGCCTTGC
TTCTCTTTACTTTTCCACTCTAGGCCACGATGCCGCAGTACCAGACCTGGGAGGAGTTCAGCCGCGCTGCCGAGA
AGCTTTACCTCGCTGACCCTATGAAGGCACGTGTGTTCTCAAATATAGGCATTCTGATGGGAACCTGTGTGTTA
AAGTAACAGATGATTTAGTTTGGTGTATAAAAACAGACCAAGCTCAAGATGTAAAGAAGATTGAGAAATTCC
ACAGTCAACTAATGCGACTTATGGTAGCCAAGGAAGCCCGCAATGTTACCATGGAAACTGAGTGAATGGTTTGAA
ATGAAGACTTTGTCGTGTACTTAGGAAGTAAATATCTTTTGAATTAGAGAAAGTGTGGGACAGAAAGTACTTTA
TGTAACATAAGTGGGCTGTTTCTAGGAAGCTTAGAGGTCATTTTTTGTAAATTTCTTTTAAATTACTTTAGAGAGCTAG
GGATGCAAATGTTTTAGTTAGAAAGCCTTTATTTACTTTTGGAAATTGAACAAGAAATGCATCTGTCTTAGAAA
CTGGAGATTATTTGATGTTAGGTAAAACATGTAATTGTTTCTCTGGCAAATTTGTATCAGTAATTTGAAAATGAG
ATATTAGGAAAAACCAATTCTTCTTAAATTTAGTTCATCTTTCTTTAAAAGAACATTAAATGTAACCATTTTGTCTC
AGATCCATGTATTTTGGAGCATAAAATGTATGCTGTTGTGACCAATAAATATAAAATATGGTAATTGGAATTAAC
TCCACACCATAGTATGCATTGTTATACATACTGTGTACCTAATTATGTATAGCAGTGTAGTCTCAATTATATCTG
AAAGTAATTGTGACTAACAAGTATGCTTTGCCTTATTTCCACATTTAAACTACCTGTTAATATAAGGGATTTGTA
GTATCAGCTTGTTGAGCAATGACTTTGAATCTAGTTTTTCACTGATCAGAAGCAGCAGTATTTGAGTGTATGAAT
GGAATGATGATCACTGTGCTATAATGTACTGAAACCACCATATTACAGAAATATTTACTACATATTTTCCATCTG
TAGTTTCTCAGAAGGGCTATGGATTAGTTTGAAGTGTCAAATCCTTGACATACTTCTGTGACACCCCTGCCCATT
TCTGTCTTTAATTAACCAAGGTGTTAGGTGTGACTGTCACAACTGTTATGTTTTCCAGTAACTAGAAGTACGAT
ATTTGATAATTATATTTGTATTTTACCACCTAAATGTAATGTTGATTCTCAAGAATGAAATGAAGGCACTACAT
TGAAATATGTTTTGTATAAAATTTGTCATGTTGAACAGCATTTTAGCATGGTAAGTCCCTTAGCTATATGAATTT
TGGCATGTTTCAGAGAGATCAGTAAATAAAATATTAGAT

633/6881
FIGURE 590

MPQYQTWEEFSRAAEKLYLADPMKARVVLKYRHSDGNLCVKVTDDLVLVYKTDQAQDVKKIEKFHSQLMRLMVA
KEARNVTMETE

634/6881
FIGURE 591

GCGGCTCCCAGGAGGCGTGAACCGCGGACCATGAGCGTGGGCTTCATCGGGGCCGGCCAGCTGGCCTATGCTCTG
GCGCGGGGCTTCACGGCCGCAGGCATCCTGTGCGGCTCACAAGATAATAGCCAGCTCCCCAGAAATGAACCTGCCC
ACGGTGTCCGCGCTCAGGAAGATGGGTGTGAACCTGACACGCAGCAACAAGGAGACGGTGAAAGCACAGCGACGTC
CTGTTTCTGGCTGTGAAGCCACATATCATCCCCCTTCATCCTGGATGAGATTGGGGCCGACGTGCAAGCCAGACAC
ATCGTGGTCTCCTGTGCGGCTGGTGTACCATCAGCTCTGTGGAGAAGAAGCTGATGGCATTCCAGCCAGCCCCC
AAAGTGATTCGCTGCATGACCAACACACCTGTGGTAGTGAGGAAGGCGCTACAGTGTACGCCACGGGCACCCAT
GCCCTGGTGGAGGATGGGCAGCTCCTGGAGCAGCTCATGAGCAGCGTGGGCTTCTGCACTGAGGTGGAAGAGGAC
CTCATCGATGCCGTCACGGGGCTCAGTGGCAGCGGGCCTGCCTATGCATTATGGCTCTGGACGCATTGGCTGAT
GGTGGGGTGAAGATGGGTTTGCCACGGCGCCTGGCAATCCAACTCGGGGCCCAGGCTTTGCTGGGAGCTGCCAAG
ATGCTGCTGGACTCGGAGCAGCATCCATGCCAGCTTAAGGACAATGTCTGCTCCCCTGGGGGAGCCACCATCCAC
GCCCTGCACTTTCTAGAGAGTGGGGGCTTCCGCTCTCTGCTCATCAATGCAGTTGAGGCCTCCTGTATCCGAACA
CGAGAGCTACAGTCCATGGCCGACCAAGAAAAGATCTCCCCAGCTGCCCTTAAGAAGACCTCTTAGACAGAGTG
AAGCTGGAATCCCCACAGTCTCCACACTGACCCCTCCAGCCCAGGGAAGCTCCTCACAAGAAGCCTGGCCCTG
GGAGGCAAGAAGGACTAAGGCAGCATC

635/6881
FIGURE 592

TTTTCTTTTGA CT TGT TGTGGATGGAATGTTTACAGACATTTCTAATTACTGCTTTAATTAAATAAAATTGGATC
AAAGGCCGTTTCGAGGTATTTTTGTTTTGCCGTTTGTCTGCTCAGAATTGGCATTTTGAGAGGTGATTGATACTGCT
AACAATTTTCTAGTACTCTAGTTTGTTCAGAAGAGATTTTGGGTAGACGTAATCTTCACCCTTTCAAATTATA
TAACAATACGAACATTATTTTTTATACTGATCATAATTTCCAGATTTGGGGAGGGGGGTGATCGTGGCAGGAAAAG
TTGTATGTTTGGTAGTTGCATATGGTGATTTTTTGATTTTCAATGCTGGTAGGTAAGTAAGGAGGTCTCTGTACC
ATGGCTCGTACAAAGCAGACTGCCCGCAAATCGACCGGTGGTAAAGCACCCAGGAAGCAACTGGCTACAAAAGCC
GCTCGCAAGAGTGCGCCCTCTACTGGAGGGGTGAAGAAACCTCATCGTTACAGGCCTGGTACTGTGGCGCTCCGT
GAAATTAGACGTTATCAGAAGTCCACTGAACTTCTGATTGCGAAACTTCCCTTCCAGCGTCTGGTGCGAGAAAT
GCTCAGGACTTTAAACAGATCTGCGCTTCCAGAGCGCAGCTATCGGTGCTTTGCAGGAGGCAAGTGAGGCCTAT
CTGGTTGGCCTTTTTGAAGACACCAACCTGTGTGCTATCCATGCCAAACGTGTAACAATTATGCCAAAAGACATC
CAGCTAGCACGCCGCATACGTGGAGAACGTGCTTAAGAATCCACTATGATGGGAAACATTTTATTCTCAAAAAA
AAAAAAAATTTCTCTTCTTCTGTTATTGGTAGTTCTGAACGTTAGATATTTTTTTTTCCATGGGGTCAAAAGG
TACCTAAGTATATGATTGCGAGTGGAATAATAGGGGACAGAAATCAGGTATTGGCAGTTTTTCCATTTTCATTTG
TGTGTGAATTTTTAATAATAATGCGGAGACGTAAAGCATTAATGCAAGTTAAATGTTTCAGTGAACAAGTTTCA
GCGGTTCAACTTTATAATAATTATAATAAACCTGTTAAATTTTTCTGGACAATGCCAGCATTGATTTGGATTTTTTA
AAACAAGTAAATTTCTTATTGATGGCAACTAAATGGTGTTTGTAGCATTTTTTATCATACAGTAGATTCCATCCAT
TCACTATACTTTTCTAACTGAGTTGTCCTACATGCAAGTACATGTTTTTAATGTTGTCTGTCTTCTGTGCTGTTC
CTGTAAGTTTGCTATTAAAAATACATTAAACTAT

636/6881
FIGURE 593A

AATCTATCAGGGAACGGCGGTGGCCGGTGC GGCGTGTTCCGGTGGCGGCTCTGGCCGCTCAGGCGCCTGCGGCTGG
GTGAGCGCACGCGAGGCGGCGAGGCGGCAGCGTGTTTCTAGGTCGTGGCGTCGGGCTTCCGGAGCTTTGGCGGCA
GCTAGGGGAGGATGGCGGAGTCTTCGGATAAGCTCTATCGAGTCGAGTACGCCAAGAGCGGGCGCGCCTCTTGCA
AGAAATGCAGCGAGAGCATCCCCAAGGACTCGCTCCGGATGGCCATCATGGTGCAGTCGCCCATGTTTGATGGAA
AAGTCCCACACTGGTACCACTTCTCCTGCTTCTGGAAGGTGGGCCACTCCATCCGGCACCCTGACGTTGAGGTGG
ATGGGTTCTCTGAGCTTCGGTGGGATGACCAGCAGAAAGTCAAGAAGACAGCGGAAGCTGGAGGAGTGACAGGCA
AAGGCCAGGATGGAATTGGTAGCAAGGCAGAGAAGACTCTGGGTGACTTTGCAGCAGAGTATGCCAAGTCCAACA
GAAGTACGTGCAAGGGGTGTATGGAGAAGATAGAAAAGGGCCAGGTGCGCCTGTCCAAGAAGATGGTGGACCCGG
AGAAGCCACAGCTAGGCATGATTGACCGCTGGTACCATCCAGGCTGCTTTGTCAAGAACAGGGAGGAGCTGGGTT
TCCGGCCCGAGTACAGTGCGAGTCAGCTCAAGGGCTTCAGCCTCCTTGCTACAGAGGATAAAGAAGCCCTGAAGA
AGCAGCTCCCAGGAGTCAAGAGTGAAGGAAAAGAGAAAAGGCGATGAGGTGGATGGAGTGGATGAAGTGGCGAAGA
AGAAATCTAAAAAAGAAAAAGACAAGGATAGTAAGCTTGAAAAAGCCCTAAAGGCTCAGAACGACCTGATCTGGA
ACATCAAGGACGAGCTAAAGAAAGTGTGTTCAACTAATGACCTGAAGGAGCTACTCATCTTCAACAAGCAGCAAG
TGCCTTCTGGGGAGTCGGCGATCTTGGAACCGAGTAGCTGATGGCATGGTGTTCGGTGGCCTCCTTCCCTGCGAGG
AATGCTCGGGTCAGCTGGTCTTCAAGAGCGATGCCTATTACTGCACTGGGGACGTCACTGCCTGGACCAAGTGTA
TGGTCAAGACACAGACACCCAACCGGAAGGAGTGGGTAACCCCAAAGGAATTCCGAGAAATCTCTTACCTCAAGA
AATTGAAGGTTAAAAAACAGGACCGTATATTCCCCCAGAAACCAGCGCCTCCGTGGCGGCCACGCCTCCGCCCT
CCACAGCCTCGGCTCCTGCTGCTGTGAACTCCTCTGCTTCAGCAGATAAGCCATTATCCAACATGAAGATCCTGA
CTCTCGGGAAGCTGTCCCGGAACAAGGATGAAGTGAAGGCCATGATTGAGAAACTCGGGGGGAAGTTGACGGGGA
CGGCCAACAAAGGCTTCCCTGTGCATCAGCACCAAAAAGGAGGTGGAAAAGATGAATAAGAAGATGGAGGAAGTAA
AGGAAGCCAACATCCGAGTTGTGTCTGAGGACTTCCTCCAGGACGTCTCCGCCTCCACCAAGAGCCTTCAGGAGT
TGTTCTTAGCGCACATCTTGTCCCCTTGGGGGGCAGAGGTGAAGGCAGAGCCTGTTGAAGTTGTGGCCCCAAGAG
GGAAGTCAGGGGCTGCGCTCTCCAAAAAAGCAAGGGCCAGGTCAAGGAGGAAGGTATCAACAAATCTGAAAAGA
GAATGAAATTAACCTCTTAAAGGAGGAGCAGCTGTGGATCCTGATTCTGGACTGGAACACTCTGCGCATGTCTGG
AGAAAGGTGGGAAGGTCTTCAGTGCCACCCTTGGCCTGGTGGACATCGTTAAAGGAACCAACTCCTACTACAAGC
TGCAGCTTCTGGAGGACGACAAGGAAAACAGGTATTGGATATTAGGTCCTGGGGCCGTGTGGGTACGGTGATCG
GTAGCAACAACTGGAACAGATGCCGTCCAAGGAGGATGCCATTGAGCACTTCATGAAATTATATGAAGAAAAAA
CCGGGAACGCTTGGCACTCCAAAAATTTACGAAGTATCCCAAAAAGTTCTACCCCTGGAGATTGACTATGGCC
AGGATGAAGAGGCAGTGAAGAAGCTGACAGTAAATCCTGGCACCAAGTCCAAGCTCCCCAAGCCAGTTCAGGACC
TCATCAAGATGATCTTTGATGTGGAAGTATGAAGAAAGCCATGGTGGAGTATGAGATCGACCTTCAGAAGATGC
CCTTGGGGAAGCTGAGCAAAAAGGCAGATCCAGGCCGCATACTCCATCCTCAGTGAGGTCCAGCAGGCGGTGTCTC
AGGGCAGCAGCGACTCTCAGATCCTGGATCTCTCAAATCGCTTTTACACCCTGATCCCCCAGCACTTTGGGATGA
AGAAGCCTCCGCTCCTGAACAATGCAGACAGTGTGCAGGCCAAGGTGGAAATGCTTGACAACCTGCTGGACATCG
AGGTGGCCTACAGTCTGCTCAGGGGAGGGTCTGATGATAGCAGCAAGGATCCCATCGATGTCAACTATGAGAAGC
TCAAACTGACATTAAGGTGGTTGACAGAGATTCTGAAGAAGCCGAGATCATCAGGAAGTATGTTAAGAACACTC
ATGCAACCACACACAATGCGTATGACTTGGAAGTCATCGATATCTTTAAGATAGAGCGTGAAGGCGAATGCCAGC
GTTACAAGCCCTTTAAGCAGCTTCATAACCGAAGATTGCTGTGGCACGGGTCCAGGACCACCAACTTTGCTGGGA
TCCTGTCCCAGGGTCTTCGGATAGCCCCGCCTGAAGCGCCCGTGACAGGCTACATGTTTGGTAAAGGGATCTATT
TCGCTGACATGGTCTCCAAGAGTGCCAACCTACTGCCATACGTCTCAGGGAGACCCAATAGGCTTAATCCTGTTGG
GAGAAGTTGCCCTTGGAAACATGTATGAACTGAAGCACGCTTCACATATCAGCAAGTTACCCAAGGGCAAGCACA
GTGTCAAAGGTTTGGGCAAAAACCTACCCCTGATCCTTCAGCTAACATTAGTCTGGATGGTGTAGACGTTCTCTTG
GGACCGGGATTTTCATCTGGTGTGAATGACACCTCTCTACTATATAACGAGTACATTGTCTATGATATTGCTCAGG
TAAATCTGAAGTATCTGCTGAACTGAAATTCAATTTTAAGACCTCCCTGTGGTAATTGGGAGAGGTAGCCGAGT
CACACCCGGTGGCTCTGGTATGAATTCACCCGAAGCGCTTCTGCACCAACTCACCTGGCCGCTAAGTTGCTGATG
GGTAGTACCTGTACTAAACCACCTCAGAAAGGATTTTACAGAAACGTGTTAAAGTTTTCTCTAACTTCTCAAGT
CCCTTGTTTTGTGTTGTGTCTGTGGGGAGGGGTGTTTTGGGGTGTGTTTTGTTTTTCTTGCCAGGTAGATAAA
ACTGACATAGAGAAAAGGCTGGAGAGAGATTCTGTTGCATAGACTAGTCCTATGGAAAAACCAAGCTTCGTTAG
AATGTCTGCCTTACTGGTTTCCCCAGGGAAGGAAAAATACACTTCCACCCTTTTTTCTAAGTGTTGCTCTTAGT

637/6881
FIGURE 593B

TTTGATTTTGGAAAGATGTTAAGCATTTATTTTGTAGTTAAAAATAAAAACTAATTCATACTATTTAGATTTTCT
TTTTTAICTTGCACCTATTGTCCCCTTTTGTAGTTTTTTTTGTTTGCCTCTTGTGGTGAGGGGTGTGGGAAGACCA
AAGGAAGGAACGCTAACAATTTCTCATACTTAGAAACAAAAAGAGCTTTCCTTCTCCAGGAATACTGAACATGGG
AGCTCTTGAAATATGTAGTATTAAAAGTTGCATTG

638/6881
FIGURE 594

CGAGCGGCGGGGAGCAGGCATTTCCAGCAGTGAGGAGACAGCCAGAAGCAAGCTATTGGAGCTGAAGGAACCTG
AGACAGAAGCTAGTCCCCCTCTGAATTTTACTGATGAAGAACTGAGGCCACAGAGCTAAAGTGACTTTTCCCA
AGGTCGCCCAGCGAGGACGTGGGACTTCTCAGACGTCAGGAGAGTGATGTGAGGGAGCTGTGTGACCATAGAAA
TGACGTGTTAAAAACCAGCGCTGCCCTCTTTGAAAGCCAGGGAGCATCATTCATTTAGCCTGCTGAGAAGAAGAA
ACCAAGTGTCGGGATTCAGACCTCTCTGCGGCCCAAGTGTTCTGTGGTGCTTCCAGAGGCAGGGCTATGCTCAC
ATTCATGGCCTCTGACAGCGAGGAAGAAGTGTGTGATGAGCGGACGTCCCTAATGTCGGCCGAGAGCCCCACGCC
GCGCTCCTGCCAGGAGGGCAGGCAGGGCCCAGAGGATGGAGAGAACACTGCCCAGTGGAGAAGCCAGGAGAACGA
GGAGGACGGTGAGGAGGACCCTGACCGCTATGTCTGTAGTGGGGTTCCCGGGCGGGCCGAGGCCTGGAGGAAGA
GCTGACCCTCAAATACGGAGCGAAGCACGTGATCATGCTGTTTGTGCCTGTCACCTCTGTGCATGATCGTGGTGGT
AGCCACCATCAAGTCTGTGCGCTTCTACACAGAGAAGAATGGACAGCTCATCTACACGACATTCACTGAGGACAC
ACCCTCGGTGGGCCAGCGCCTCCTCAACTCCGTGCTGAACACCCTCATCATGATCAGCGTCATCGTGGTTATGAC
CATCTTCTTGGTGGTGCTCTACAAGTACCGCTGCTACAAGTTTCATCCATGGCTGGTTGATCATGTCTTCACTGAT
GCTGCTGTTCCCTCTTCACCTATATCTACCTTGGGGAAGTGCTCAAGACCTACAATGTGGCCATGGACTACCCAC
CCTCTTGCTGACTGTCTGGAATTCGGGGCAGTGGGCATGGTGTGCATCCACTGGAAGGGCCCTCTGGTGCTGCA
GCAGGCCTACCTCATCATGATCAGTGCCTCATGGCCCTAGTGTTTCATCAAGTACCTCCCAGAGTGGTCCGCGTG
GGTCATCCTGGGCGCCATCTCTGTGTATGATCTCGTGGCTGTGCTGTGTCCCAAAGGGCCTCTGAGAATGCTGGT
AGAAACTGCCCAGGAGAGAAAATGAGCCCATATTCCTGCCCTGATATACTCATCTGCCATGGTGTGGACGGTTGG
CATGGCGAAGCTGGACCCCTCCTCTCAGGGTGCCCTCCAGCTCCCCCTACGACCCGGAGATGGAAGAAGACTCCTA
TGACAGTTTTTGGGGAGCCTTCATACCCGAAGTCTTTGAGCCTCCCTTGACTGGCTACCCAGGGGAGGAGCTGGA
GGAAGAGGAGGAAAGGGGCGTGAAGCTTGGCCTCGGGGACTTCATCTTCTACAGTGTGCTGGTGGGCAAGGCGGC
TGCCACGGGCAGCGGGGACTGGAATACCACGCTGGCCTGCTTCGTGGCCATCCTCATTGGCTTGTGTCTGACCC
CCTGCTGCTTGCTGTGTTCAAGAAGGCGCTGCCCCGCCCTCCCCATCTCCATCACGTTGGGCTCATCTTTTACTT
CTCCACGGACAACCTGGTGCGGCCGTTTCATGGACACCCTGGCCTCCCATCAGCTCTACATCTAGAGGGACATGGTG
TGCCACAGGCTGCAAGCTGCAGGGAATTTTCATTGGATGCAGTTGTATAGTTTTTACACTCTAGTGCCATATATTT
TTAAGACTTTTCTTTCCCTTAAAAAATAAAGTACGTGTTTACTTGGTGAGGAGGAGGCAGAACAGCTCTTTGGTG
CCAGCTGTTTCATCACCAGACTTTGGCTCCCGCTTTGGGGAGCGCCTCGCTTCACGGACAGGAAGCACAGCAGGT
TTATCCAGATGAACTGAGAAGGTCAGATTAGGGCGGGGAGAAGAGCATCCGGCATGAGGGCTGAGATGCGCAAAG
AGTGTGCTCGGGAGTGGCCCTGGCACCTGGGTGCTCTGGCTGGAGAGGAAAAGCCAGTTCCTTACGAGGAGTGT
TCCAATGCTTTGTCCATGATGTCCTTGTTATTTTATTGCCTTTAGAACTGAGTCCTGTTCTTGTACGGCAGT
CACACTGCTGGGAAGTGGCTTAATAGTAATATCAATAAATAGATGAGTCCTGTTAGAAAAA

639/6881
FIGURE 595

MLTFMASDSEEEVCDERTSLMSAESPTPRSCQEGRQGPEDGENTAQWRSQENEEEDGEEDPDRYVCSGVPGRPPGL
EEELTLKYGAHVIMLFVPVTLCMIVVATIKSVRFYTEKNGQLIYTTFTEDTPSVGQRLNSVLNTLIMISVIV
VMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYLGEVLKTYNVAMDYPTLLLTVWNFGAVGMVCIHWKGPL
VLQQAYLIMISALMALVFIKYLPEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVW
TVGMAKLDPSSQGALQLPYDPEMEEDSYDSFGEPSYPEVFEPPLTGYPGEELEEEEEEERGVKLGLGDFIFYSVLVG
KAAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKKALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI

640/6881
FIGURE 596

CGAGCGGCGGCGGAGCAGGCATTTCCAGCAGTGAGGAGACAGCCAGAAGCAAGCTATTGGAGCTGAAGGAACCTG
AGACAGAAGCTAGTCCCCCTCTGAATTTTACTGATGAAGAACTGAGGCCACAGAGCTAAAGTGACTTTTCCCA
AGGTGCGCCAGCGAGGACGTGGGACTTCTCAGACGTCAGGAGAGTGATGTGAGGGAGCTGTGTGACCATAGAAAG
TGACGTGTTAAAAACCAGCGCTGCCCTCTTTGAAAGCCAGGGAGCATCATTCATTTAGCCTGCTGAGAAGAAGAA
ACCAAGTGTCCGGGATTAGACCTCTCTGCGGCCCCAAGTGTTGTTGCTTCCAGAGGCAGGGCTATGCTCAC
ATTCATGGCCTCTGACAGCGAGGAAGAAGTGTGTGATGAGCGGACGTCCCTAATGTGCGCCGAGAGCCCCACGCC
GCGCTCCTGCCAGGAGGGCAGGCAGGGCCCAGAGGATGGAGAGAACACTGCCAGTGGAGAAGCCAGGAGAACGA
GGAGGACGGTGAGGAGGACCTGACCGCTATGTCTGTAGTGGGGTTCCCGGGCGGCCGAGGCCTGGAGGAAGA
GCTGACCCCTCAAATACGGAGCGAAGCACGTGATCATGCTGTTTGTGCCTGTCACTCTGTGCATGATCGTGGTGGT
AGCCACCATCAAGTCTGTGCGCTTCTACACAGAGAAGAATGGACAGCTCATCTACACGACATTCAGTGGAGACAC
ACCCTCGGTGGGCCAGCGCTCCTCAACTCCGTGCTGAACACCCCTCATCATGATCAGCGTCATCGTGGTTATGAC
CATCTTCTTGGTGGTGTCTCTACAAGTACCGCTGCTACAAGTTCATCCATGGCTGGTTGATCATGTCTTCACTGAT
GCTGCTGTTCTCTTACCTATATCTACCTTGGGGAAGTGCTCAAGACCTACAATGTGGCCATGGACTACCCAC
CCTCTTGCTGACTGTCTGGAAGTTCGGGGCAGTGGGCATGGTGTGCATCCACTGGAAGGGCCCTCTGGTGTGCA
GCAGGCCTACCTCATCATGATCAGTGCCTCATGGCCCTAGTGTTTCATCAAGTACCTCCCAGAGTGGTCCGCGTG
GGTCATCCTGGGCGCCATCTCTGTGTATGATCTCGTGGCTGTGCTGTGTCCAAAGGGCCTCTGAGAATGCTGGT
AGAAACTGCCCAGGAGAGAAATGAGCCCATATTCCCTGCCCTGATATACTCATCTGCCATGGTGTGGACGGTTGG
CATGGCGAAGCTGGACCCCTCCTCTCAGGGTGCCCTCCAGCTCCCCTACGACCCGGAGATGGAAGACTCCTATGA
CAGTTTTTGGGGAGCCTTCATACCCCGAAGTCTTTGAGCCTCCCTTGACTGGCTACCCAGGGGAGGAGCTGGAGGA
AGAGGAGGAAAGGGGCGTGAAGCTTGGCCTCGGGGACTTCATCTTCTACAGTGTGCTGGTGGGCAAGGCGGCTGC
CACGGGCAGCGGGGACTGGAATACCACGCTGGCCTGCTTTCGTGGCCATCCTCATTGGCTTGTGTCTGACCCCTCT
GCTGCTTGCTGTGTTCAAGAAGGCGCTGCCC GCCCTCCCATCTCCATCACGTTTCGGGCTCATCTTTTACTTCTC
CACGGACAACCTGGTGC GGCCGTTTCATGGACACCCTGGCCTCCCATCAGCTCTACATCTGAGGGACATGGTGTGC
CACAGGCTGCAAGCTGCAGGGAATTTTCATTGGATGCAGTTGTATAGTTTTTACACTCTAGTGCCATATATTTTTA
AGACTTTTCTTTCCTTAAAAAATAAAGTACGTGTTTACTTGGTGAGGAGGAGGCAGAACCAGCTCTTTGGTGTCCA
GCTGTTTCATCACCAGACTTTGGCTCCCGCTTTGGGGAGCGCCTCGCTTCACGGACAGGAAGCACAGCAGGTTTA
TCCAGATGAACTGAGAAGGTGAGATTAGGGCGGGGAGAAGAGCATCCGGCATGAGGGCTGAGATGCGCAAAGAGT
GTGCTCGGGAGTGGCCCTGGCACCTGGGTGCTCTGGCTGGAGAGGAAAAGCCAGTTCCCTACGAGGAGTGTTC
CAATGCTTTGTCCATGATGTCCTTGTTATTTTATTGCCTTTAGAACTGAGTCCTGTTCTTGTACGGCAGTCAC
ACTGCTGGGAAGTGGCTTAATAGTAATATCAATAAATAGATGAGTCCTGTTAGAAAAA

641/6881
FIGURE 597

MLTFMASDSEEEVCDERTSLMSAESPTPRSCQEGRQGPEDGENTAQWRSQENEEEDGEEDPD
RYVCSGVPGRPPGL
EEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTTFTEDTPSVGQRL
LNSVLNTLIMISVIV
VMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYLGEVLKTYNVAMDYPTLLLLTV
WNFGAVGMVCIHWKGPL
VLQQAYLIMISALMALVFIKYLPEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQER
NEPIFPALIIYSSAMVW
TVGMAKLDPSSQALQLPYDPEMEDSYDSFGEPSYPEVFEPPLTGYPGEELEEEEEEER
GVKLGLGDFIFYSVLVGK
AAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKKALPALPISITFGLIFYFSTDNLVR
PFMDTLASHQLYI

642/6881
FIGURE 598A

TATACTTCGCTACTTGGCTAGAGTTGCAACTACAGCTGGGTTATATGGCTCTAATCTGATGGAACATACTGAGAT
TGATCACTGGTTGGAGTTCAGTGCTACAAAATTATCTTCATGTGATTCTTTACTTCTACAATTAATGAACTCAA
TCATTGCCTGTCTCTGAGAACATACTTAGTTGGAACTCCTTGAGTTTAGCAGATTTATGTGTTTGGGCCACCCT
AAAAGGAAATGCTGCCTGGCAAGAACAGTTGAAACAGAAGAAAGCTCCAGTTCATGTAAAACGTTGGTTTGGCTT
TCTTGAAGCCCAGCAGGCCCTTCCAGTCAGTAGGTACCAAGTGGGATGTTTCAACAACCAAAGCTCGAGTGGCACC
TGAGAAAAAGCAAGATGTTGGGAAATTTGTTGAGCTTCCAGGTGCGGAGATGGGAAAGGTTACCGTCAGATTTCC
TCCAGAGGCCAGTGGTTACTTACACATTGGGCATGCAAAGCTGCTCTTCTGAACCAGCACTACCAGGTTAACTT
TAAAGGGAAACTGATCATGAGATTTGATGACACAAATCCTGAAAAAGAAAAGGAAGATTTTGAGAAGGTTATCTT
GGAAGATGTTGCAATGTTGCATATCAAACCAGATCAATTTACTTATACTTCGGATCATTTTGAACTATAATGAA
GTATGCAGAGAAGCTAATTCAGAAGGGGAAGGCTTATGTGGATGATACTCCTGCTGAACAGATGAAAGCAGAACG
TGAGCAGAGGATAGAATCTAAACATAGAAAAACCCTATTGAGAAGAATCTACAAATGTGGGAAGAAATGAAAA
AGGGAGCCAGTTTGGTCAGTCCTGTTGTTTGGCAGCAAAAATTGACATGAGTAGTAACAATGGATGCATGAGAGA
TCCAACCCCTTTATCGCTGCAAAATTC AACCATCCAAGAACTGGAAATAAATACAATGTTTATCCAACATATGA
TTTTCCTGCCCCATAGTTGACAGCATCGAAGGTGTACACATGCCCTGAGAACACAGAATACCATGACAGAGA
TGAGCAGTTTTACTGGATTATTGAAGCTTTAGGCATAAGAAAACCATATATTGGGAATATAGTCGGCTAAATCT
CAACAACACAGTGCTATCCAAAAGAAAACCTCACATGGTTTGTCAATGAAGGACTAGTAGATGGATGGGATGACCC
AAGATTTCCTACGGTTTCGTGGTGTACTGAGAAGAGGGATGACAGTTGAAGGACTGAAACAGTTTATTGCTGCTCA
GGGCTCCTCACGTTTCAGTCGTGAACATGGAGTGGGACAAAATCTGGGCGTTTAACAAAAAGGTTATTGACCCAGT
GGCTCCACGATATGTTGCATTACTGAAGAAAGAAGTGATCCCAGTGAATGTACCTGAAGCTCAGGAGGAGATGAA
AGAAGTAGCCAAACACCCAAAGAATCCTGAGGTTGGCTTGAAGCCTGTGTGGTATAGTCCCAAAGTTTTCATTGA
AGGTGCTGATGCAGAGACTTTTTTCGGAGGGTGAGATGGTTACATTTATAAATTGGGGCAACCTCAACATTACAAA
AATACACAAAAATGCAGATGGAAAAATCATATCTCTTGATGCAAAGTTGAATTTGGAAAAACAAAGACTACAAGAA
AACCCTAAGGTCACCTTGGCTTGCAGAGACTACACATGCTCTTCCCTATTCCAGTAATCTGTGTCACTTATGAGCA
CTTGATCACAAAGCCAGTGCTAGGAAAAGACGAGGACTTTAAGCAGTATGTCAACAAGAACAGTAAGCATGAAGA
GCTAATGCTAGGGGATCCCTGCCTTAAGGATTTGAAAAAGGAGATATTATACAACCTCCAGAGAAGAGGATTCTT
CATATGTGATCAACCTTATGAACCTGTTAGCCCATATAGTTGCAAGGAAGCCCCGTGTGTTTGTATATACATTCC
TGATGGGCACACAAAGGAAATGCCAACATCAGGGTCAAAGGAAAAGACCAGTAGAAGCCACAAAAAATGAGAC
CTCTGCTCCTTTTAAGGAAAGACCAACACCTTCTCTGAATAATAATTGTACTACATCTGAGGATTCTTGGTCCT
TTACAATAGAGTGGCTGTTCAAGGAGATGTGGTTCGTGAATTAAGGAGAAAAGCAAGAAAGCACCAGGAAGATGTAGA
TGCAGCTGTAAACAGCTTTTGTCTTTGAAAGCTGAATATAAGGAGAAAAGTGGCCAGGAATATAAACCTGGAAA
CCCTCCTGCTGAAATAGGACAGAATATTTCTTCTAATTCCTCAGCAAGTATTCTGGAAAGTAAATCTCTGTATGA
TGAAGTTGCTGCACAAGGGGAGGTGGTTCGTAAGCTAAAAGCTGAAAAATCCCCTAAGXXXXXXXXXXXXXXXXXX
XX
XX
XXXXXXXXXXXXXXXXXXXXCTTCTCAAGGGGAAGTAGTTCGGAACCTTAAACTGAAAAGCCCTAAGGATCAAGT
AGATATAGCTGTTCAAGAACTCCTTCAGCTAAAGGCACAGTACAAGTCTTTGATAGGAGTAGAGTATAAGCCTGT
GTCGGCCACTGGAGCTGAGGACAAAAGATAAGAAGAAGAAAGAAAAAGAAAATAAATCTGAAAAGCAGAATAAGCC
TCAGAAACAAAATGATGGCCAAAAGGAAAGACCCCTTCTAAAAACCAAGGAGGTGGGCTCTCATCAAGTGGAGCAGG
AGAAGGGCAGGGGCCTAAGAAACAGACCAGGTGGGTCTTGAGGCAAAAAAGAAAGAAAATCTTGCTGATTGGTA
TTCTCAGGTCATCACAAAGTCAGAAATGATTGAATACCATGACATAAGTGGCTGTTATATTCTTCGTCCCTGGGC
CTATGCCATTTGGGAAGCCATCAAGGACTTTTTTGATGCTGAGATCAAGAACTTGGTGTGAAAAGTCTACTT
CCCCATGTTTGTGTCTCAAAGTGCATTAGAGAAAGAGAAGACTCATGTTGCTGACTTTGCCCCAGAGGTTGCTTG
GGTTACAAGATCTGGCAAACCGAGCTGGCAGAACCAATTGCCATTCTGCTCTACTAGTGAAACAGTAATGTATCC
TGCATATGCAAATGGGTACAATCACACAGAGACCTGCCCATCAAGCTCAATCAGTGGTGCAATGTGGTGCGTTG
GGAATTCAAGCATCTCAGCCTTTCCTACGTACTCGTGAATTTCTTTGGCAGGAAGGGCACAGTGCTTTTGCTAC
CATGGAAGAGGCAGCGGAAGAGGTCTTGACAGATACTTGACTTATATGCTCAGGTATATGAAGAACTCCTGGCAAT
TCCTGTTGTTAAAGGAAGAAAGACGGAAAAGGAAAAATTTGCAGGAGGAGACTATACAACCTACAATAGAAGCATT
TATATCTGCTAGTGGAAGAGCTATCCAGGGAGGAACATCACATCATTTAGGGCAGAATTTTCCAAAATGTTTGA

643/6881

FIGURE 598B

AATCGTTTTTGAAGATCCAAAGATACCAGGAGAGAAGCAATTTGCCTATCAAAACTCCTGGGGCCTGACAACTCG
AACTATTGGTGTATGACCATGGTTCATGGGGACAACATGGGTTTAGIATTACCACCCCGTAGCATGTGTTC
GGTGGTGATTATTCCTTGTGGCATTACCAATGCACCTTTCTGAAGAAGACAAAGAAGCGCTGATTGCAAAATGCAA
TGATTATCGAAGGCGATTACTCAGTGTTAACATCCGCGTTAGAGCTGATTTACGAGATAATTATTCTCCAGGTTG
GAAATTCAATCACTGGGAGCTCAAGGGAGTTCCTATTAGACTTGAAGTTGGGCCACGTGATATGAAGAGCTGTCA
GTTTGTAGCCGTCAGACGAGATACTGGAGAAAAGCTGACAGTTGCTGAAAATGAGGCAGAGACTAAACTTCAAGC
TATTTTGGGAAGACATCCAGGTCACCCTTTTCAACAAGGGCTTCTGAAGACCTTAAGACTCATATGGTTGTGGCTAA
TACAATGGAAGACTTTCAGAAGATACTAGATTCTGGAAAGATTGTTTCAGATTCCATTCTGTGGGGAAATTGACTG
TGAGGACTGGATCAAAAAGACCACTGCCAGGGATCAAGATCTTGAACCTGGTGCTCCATCCATGGGAGCTAAAAG
CCTTTGCATCCCCTTCAAACCACTCTGTGAACTGCAGCCTGGAGCCAAATGTGTCTGTGGCAAGAACCCTGCCAA
GTACTACACCTTATTTGGTCGCAGCTACTGAGGGATGAACGAAAGCCCCCTCTTCAACTCCTCTCACTTTTTTAA
GCATTGATATTAGTATCTTCTCAGATACAGACCGTTTTATGATTTTTTAAAAAGTAAAAGTTCTAAAATGAAGTC
ACACAGGACAATTATTCCTATGCCTAAGTTAACAGTGGATAAAAAGACTTTTCTGTAAACAACCTCCAGTAATAAAT
ATCATGAACTA

644/6881
FIGURE 599A

AGTAGCTGCGGCGCAGGGGCGGAGCGAAGGCTGCGGCGGCGTTCGGGTACGCGCACACGTTGCATCTTCTTCCTTT
CGCGGGGTCTCCGTAGTTCTGGCACGAGCCAGGCGTACTGACAGGTGGACCAGCGGACTGGTGGAGATGGCGAC
GCTCTCTCTGACCGTGAATTCAGGAGACCCCTCCGCTAGGAGCTTTGCTGGCAGTAGAACACGTGAAAGACGATGT
CAGCATTTCGGTTGAAGAAGGGAAAGAGAATATTCTTCATGTTTCTGAAAATGTGATATTCACAGATGTGAATTC
TATACTTCGCTACTTGGCTAGAGTTGCAACTACAGCTGGGTATATGGCTCTAATCTGATGGAACATACTGAGAT
TGATCACTGGTTGGAGTTCAGTGCTACAAAATTATCTTCATGTGATTCTTTACTTCTACAATTAATGAACTCAA
TCATTGCCTGTCTCTGAGAACATACTTAGTTGGAACTCCTTGAGTTTAGCAGATTTATGTGTTTGGGCCACCCCT
AAAAGGAAATGCTGCCTGGCAAGAACAGTTGAAACAGAAGAAAGCTCCAGTTCATGTAAAACGTTGGTTTGGCTT
TCTTGAAGCCCAGCAGGCCTTCCAGTCAGTAGGTACCAAGTGGGATGTTTCAACAACCAAAGCTCGAGTGGCACC
TGAGAAAAAGCAAGATGTTGGGAAATTTGTTGAGCTTCCAGGTGCGGAGATGGGAAAGGTTACCGTCAGATTTCC
TCCAGAGGCCAGTGGTTACTTACACATTGGGCATGCAAAAGCTGCTCTTCTGAACCAGCACTACCAGGTTAACTT
TAAAGGGAAACTGATCATGAGATTTGATGACACAAATCCTGAAAAAGAAAGGAAGATTTTGAGAAGGTTATCTT
GGAAGATGTTGCAATGTTGCATATCAAACCAGATCAATTTACTTATACTTCGGATCATTTTGAAACTATAATGAA
GTATGCAGAGAAGCTAATTCAGAAGGGGAAGGCTTATGTGGATGATACTCCTGCTGAACAGATGAAAGCAGAACG
TGAGCAGAGGATAGACTCTAAACATAGAAAAACCCCTATTGAGAAGAACTTACAAATGTGGGAAGAAATGAAAAA
AGGGAGCCAGTTTGGTCAGTCCGTGTTGTTTGGCAGCAAAAATTGACATGAGTAGTAACAATGGATGCATGAGAGA
TCCAACCCCTTTATCGCTGCAAAATTC AACCATCCAAGAACTGGAAATAAATACAATGTTTATCCAACATATGA
TTTTGCCTGCCCCATAGTTGACAGCATCGAAGGTGTTACACATGCCCTGAGAACAACAGAATACCATGACAGAGA
TGAGCAGTTTTTACTGGATTATTGAAGCTTTAGGCATAAGAAAACCATATATTTGGGAATATAGTCGGCTAAATCT
CAACAACACAGTGCTATCCAAAAGAAAACCTCACATGGTTTGTCAATGAAGGACTAGTAGATGGATGGGATGACCC
AAGATTTTCTACGGTTCGTGGTGTACTGAGAAGAGGGATGACAGTTGAAGGACTGAAACAGTTTATTGCTGCTCA
GGGCTCCTCACGTTCACTCGTGAACATGGAGTGGGACAAAATCTGGGCGTTTAACAAAAGGTTATTGACCCAGT
GGCTCCACGATATGTTGCATTACTGAAGAAAGAAGTGATCCAGTGAATGTACCTGAAGCTCAGGAGGAGATGAA
AGAAGTAGCCAAACACCCAAAGAATCCTGAGGTTGGCTTGAAGCCTGTGTGGTATAGTCCCAAAGTTTTTATTGA
AGGTGCTGATGCAGAGACTTTTTCGGAGGGTGAGATGGTTACATTTATAAATTGGGGCAACCTCAACATTACAAA
AATACACAAAATGCAGATGGAAAAATCATATCTCTTGATGCAAGTTGAATTTGGAAAACAAAGACTACAAGAA
AACCCTAAGGTCATTGGCTTGCAGAGACTACACATGCTCTTCTATTCCAGTAATCTGTGTCACTTATGAGCA
CTTGATCACAAGCCAGTGCTAGGAAAACAGGAGCTTTAAGCAGTATGTCAACAAGAACAGTAAGCATGAAGA
GCTAATGCTAGGGGATCCCTGCCTTAAGGATTTGAAAAAAGGAGATATTATACAACCTCAGAGAAGAGGATTCTT
CATATGTGATCAACCTTATGAACCTGTTAGCCCATATAGTTGCAAGGAAGCCCCGTGTGTTTTGATATACATTCC
TGATGGGCACACAAAGGAAATGCCAACATCAGGGTCAAAGGAAAAGACCAAAGTAGAAGCCACAAAAAATGAGAC
CTCTGCTCCTTTTAAGGAAAGACCAACACCTTCTCTGAATAATAATTGTACTACATCTGAGGATTCTTGGTCTCT
TTACAATAGAGTGGCTGTTCAAGGAGATGTGGTTCTGTAATTAAGGCAAGAAAGCACCAGGAAGATGTAGA
TGCAGCTGTAAAACAGCTTTTGTCTTTGAAAGCTGAATATAAGGAGAAAACTGGCCAGGAATATAAACCTGGAAA
CCCTCCTGCTGAAATAGGACAGAATATTTCTTCTAATTCCTCAGCAAGTATTCTGGAAAGTAAATCTCTGTATGA
TGAAGTTGCTGCACAAGGGGAGGTGGTTCTGAAGCTAAAAGCTGAAAAATCCCCTAAGGCTAAAATAAATGAAGC
TGTAAGATGCTTACTGTCCCTGAAGGCTCAGTATAAAGAAAAAACTGGGAAGGAGTACATACCTGGTCAGCCCCC
ATTATCTCAAAGTTCGGATTCAAGCCCAACCAGAAATTCGAACTGCTGGTTTAGAAACACCAGAAGCGAAAGT
ACTTTTTGACAAAGTAGCTTCTCAAGGGGAAGTAGTTTCGAAACTTAAAACTGAAAAAGCCCCCTAAGGATCAAGT
AGATATAGCTGTTCAAGAACTCCTTCAGCTAAAGGCACAGTACAAGTCTTTGATAGGAGTAGAGTATAAGCCTGT
GTCGGCCACTGGAGCTGAGGACAAAGATAAGAAGAAGAAAGAAAAAGAAATAAATCTGAAAAGCAGAATAAGCC
TCAGAAACAAAATGATGGCCAAAGGAAAGACCCCTTCTAAAACCAAGGAGGTGGGCTCTCATCAAGTGAGCAGG
AGAAGGGCAGGGGCCTAAGAAACAGACCAGGTTGGGTCTTGAGGCAAAAAAAGAAGAAAATCTTGCTGATTGGTA
TTCTCAGGTCATCACAAGTCAGAAATGATTGAATACCATGACATAAGTGGCTGTTATATTCTTCGTCCCTGGGC
CTATGCCATTTGGGAAGCCATCAAGGACTTTTTTGTGCTGAGATCAAGAACTTGGTGTGAAAACCTGCTACTT
CCCCATGTTTGTGTCTCAAAGTGCAATTAGAGAAAGAGAAGACTCATGTTGCTGACTTTGCCCCAGAGGTTGCTTG
GGTTACAAGATCTGGCAAAACCGAGCTGGCAGAACCAATTGCCATTGCTCCTACTAGTGAAACAGTAATGTATCC
TGCATATGCAAAATGGGTACAGTCACACAGAGACCTGCCCATCAAGCTCAATCAGTGGTGCATGTGGTGCCTTG

645/6881

FIGURE 599B

GGAATTCAAGCATCCTCAGCCTTTCCTACGTACTCGTGAATTTCTTTGGCAGGAAGGGCACAGTGCTTTTGCTAC
CATGGAAGAGGCAGCGGAAGAGGTCTTGCAGATACTTGACTTATATGCTCAGGTATATGAAGAACTCCTGGCAAT
TCCTGTTGTTAAAGGAAGAAAGACGGAAAAGGAAAAATTTGCAGGAGGAGACTATACAACACTACAATAGAAGCATT
TATATCTGCTAGTGGAAGAGCTATCCAGGGAGGAACATCACATCATTTAGGGCAGAATTTTCCAAAATGTTTGA
AATCGTTTTTTGAAGATCCAAAGATACCAGGAGAGAAGCAATTTGCCTATCAAAACTCCTGGGGCCTGACAACTCG
AACTATTGGTGTTATGACCATGGTTCATGGGGACAACATGGGTTTTAGTATTACCACCCCGTGTAGCATGTGTTCA
GGTGGTGATTATTCCTTGTGGCATTACCAATGCACTTTCTGAAGAAGACAAAGAAGCGCTGATTGCAAAATGCAA
TGATTATCGAAGGCGATTACTCAGTGTTAACATCCGCGTTAGAGCTGATTTACGAGATAATTATTCTCCAGGTTG
GAAATTCAATCACTGGGAGCTCAAGGGAGTTCCCATTAGACTTGAAGTTGGGCCACGTGATATGAAGAGCTGTCA
GTTTGTAGCCGTCAGACGAGATACTGGAGAAAAGCTGACAGTTGCTGAAAATGAGGCAGAGACTAACTTCAAGC
TATTTTGGGAAGACATCCAGGTCACCCTTTTCACAAGGGCTTCTGAAGACCTTAAGACTCATATGGTTGTGGCTAA
TACAAATGGAAGACTTTTCAGAAGATACTAGATTCTGGAAAGATTGTTTCAGATTCCATTCTGTGGGGAAATTGACTG
TGAGGACTGGATCAAAAAGACCACTGCCAGGGATCAAGATCTTGAACCTGGTGCTCCATCCATGGGAGCTAAAAG
CCTTTGCATCCCCTTCAAACCACTCTGTGAACTGCAGCCTGGAGCCAAATGTGTCTGTGGCAAGAACCCTGCCAA
GTACTACACCTTATTTGGTTCGCAGCTACTGAGGGATGAACGAAAGCCCCCTCTTCAACTCCTCTCACTTTTTTAA
GCATTGATATTAGTATCTTCTCAGATACAGACCGTTTTATGATTTTTTAAAAAGTAAAAAGTTCTAAAATGAAGTC
ACACAGGACAATTATTCTTATGCCTAAGTTAACAGTGGATAAAAGACTTTTCTGTAAACAACTCCAGTAATAAAT
ATCATGAACATAATATGGTTTAAAAAAAAAAAAAAAAAAAAAAGG

646/6881
FIGURE 600

CCCAGGATGTAGAGCTGGCAGTGCCTGACGGCGCGTCTGACGCGGAGTTGGGTGGGGTAGAGAGTAGGGGGCGGT
AGTCGGGGGTGGTGGGAGAAGGAGGAGGCGGCAAATCACTTATAAATGGCGCGGAAGCAGGACCCGAAGCCTAAA
TTCCAGGAGGGGTGAGCGAGTGCTGTGCTTTTCATGGGCCTCTTCTTTATGAAGCAAAGTGTGTAAAGGTTGCCATA
AAGGACAAACAAGTGAAATACTTCATACATTACAGTGGTTGGAATAAAAATTGGGATGAGTGGGTTCCGGAGAGC
AGAGTACTCAAATACGTGGACACCAATTTGCAGAAACAGCGAGAACTTCAAAAAGCCAATCAGGAGCAGTATGCA
GAGGGGAAGATGAGAGGGGCTGCCCCAGGAAAGAAGACATCTGGTCTGCAACAGAAAAATGTTGAAGTGAAAACG
AAAAAGAACAACAGAAAAACACCTGGAAATGGAGATGGTGGCAGTACCAGTGAGACCCCTCAGCCTCCTTGGAAG
AAAAGGGCCCCGGGTAGATCCTACTGTTGAAAATGAGGAAACATTCATGAACAGAGTTGAAGTTAAAGTAAAGATT
CCTGAATAGCTAAAACCGTGGCTTGTGATGACTGGGACTTAATTACCAGGCAAAAACAGCTCTTTTATCTTCCT
GCCAAGAAGAATGTGGATTCCATTCTTGAGGATTATGCAAATTACAAGAAATCTCGTGGAACACAGATAATAAG
GAGTATGCGGTTAATGAAGTTGTGGCAGGGATAAAAGAATACTTCAACGTAATGTTGGGTACCCAGCTACTCTAT
AAATTTGAGAGACCACAGTATGCCGAAATTTCTGCAGATCATCCCGATGCACCCATGTCCCAGGTGTATGGAGCG
CCACATCTCCTGAGATTATTTGTACGAATTGGAGCAATGTTGGCCTATACACCTCTGGATGAGAAGAGCCTTGCT
TTATTACTCAATTATCTTCACGATTTCTTAAAGTACCTGGCAAAGAATTCTGCAACTTTGTTTAGTGCCAGCGAT
TATGAAGTGGCTCCTCCTGAGTACCATCGGAAAGCTGTGTGAGAGGCACTCTCACTCACTTATGTTTGGATCTCC
GTAAACACATTTTTGTTCTTAGTCTATCTCTGTACAAACAATGTGCTTTGAAGATGTTAGTGTATAACAATTGA
TGTTTGTTTTCTGTTTGATTTTAAACAGAGAAAAATAAAAGGGGTAATAGCTCCTTTTTCTTTCTTTTTTTTTT
TCATTTCAAAGTTGCTGCCAGTGTTCATGATGGACAACAGAGGGATATGCTGTAGAGTGTTTTATTGCCTAG
TTGACAAAGCTGCTTTTGATGCTGGTGGTTCTATTCTTTGACACTATGCACTTTTATAATACATGTTAATGCT
ATATGACAAAATGCTCTGATTCCTAGTGCCAAAGGTTCAATTCAGTGTATATAACTGAACACACTCATCCATTTG
TGCTTTTTTTTTTTTTTTTATGGTGCTTAAAGTAAAGAGCCCATCCTTTGCAAGGCATCCATGTTGTTACTTAGG
CATTTTATCTTGGCTCAAATTGTTGAAGAATGGTGGCTTGTTTCATGGTTTTTGTATTTGTGTCTAATGCACGTT
TTAACATGATAGATGCAATGCACTGTGTAGCTAGTTTTCTGGAAAAGTCAATCTTTTAGGAATTGTTTTTCAGAT
CTTCAATAAATTTTTTCTTTAAATTC

647/6881
FIGURE 601

GAGGAGGCGGCAAATCACTTATAAATGGCGCGGAAGCAGGACCCGAAGCCTAAATTCCAGGAGGGTGAGCGAGTG
CTGTGCTTTTCATGGGCCTCTTCTTTATGAAGCAAAGTGTGTAAAGGTTGCCATAAAGGACAAACAAGTGAAATAC
TTCATACATTACAGTGGTTGGAATAAAAAATTGGGATGAGTGGGTTCCGGAGAGCAGAGTACTCAAATACGTGGAC
ACCAATTTGCAGAAACAGCGAGAACTTCAAAAAGCCAATCAGGAGCAGTATGCAGAGGGGAAGATGAGAGGGGCT
GCCCCAGGAAAGAAGACATCTGGTCTGCAACAGAAAAATGTTGAAGTGAAAACGAAAAAGAACAAACAGAAAACA
CCTGGAAATGGAGATGGTGGCAGTACCAGTGAGACCCCTCAGCCTCCTTGGAAGAAAAGGGCCCGGGTAGATCCT
ACTGTTGAAAATGAGGAAACATTCATGAACAGAGTTGAAGTTAAAGTAAAGATTCCTGAATAGCTAAAACCGTGG
CTTGTGATGACTGGGACTTAATTACCAGGCATTATGCAAATTACAAGAAATCTCGTGGAACACAGATAATAAG
G

648/6881
FIGURE 602

AATCACTTATAAATGGCGCGGAAGCAGGACCCGAAGCCTAAATTCCAGGAGGGTGAGCGAGTGCTGTGCTTTTCAT
GGGCCTCTTCTTTATGAAGCAAAGTGTGTAAAGGTTGCCATAAAGGACAAACAAGTGAAATACTTCATACATTAC
AGTGGTTTGAATAAAAAATTGGGATGAGTGGGTTCCGGAGAGCAGAGTACTCAAATACGTGGACACCAATTTGCAG
AAACAGCGAGAACTTCAAAAAGCCAATCAGGAGCAGTATGCAGAGGGGAAGATGAGAGGGGCTGCCCCAGGAAAG
AAGACATCTGGTCTGCAACAGAAAAATGTTGAAGTTACGAATTGGAGCAATGTTGGCCTATACACCTCTGGATGA
GAAGAGCCTTGCTTTATTACTCAATTATCTTCACGATTTCCCTAAAGTACCTGGCAAAGAATTCTGCAACTTTGTT
TAGTGCCAGCGATTATGAAGTGGCTCCTCCTGAGTACCATCGGAAAGCTGTGTGAGAGGCACTCTCACTCACTTA
TGTGTTGGATCTCCGTAAACACATTTTTGTTCTTAGTCTATCTCTTGTACAAACAATGTGCTTTGAAGATGTTAGT
GTATAACAATTGATGTTTGTCTTTGTTTAAACAGAGAAAATAAAAGGGGTAATAGCTCCTTTTTTCTT

649/6881
FIGURE 603

TTTTGCGCTCGGACCTTCGCCAGAGGGGSCGGGACATCATGACGGTGGGAGCCAGGCTCCGAAGCAAGGCGGAGA
GCAGCCTCCTGCGCCGCGGGCCCCGAGGGCGAGGGCGAACCGAGGGGGACGAGGAGGCGGGCCGCCATCCTGGAGC
ACCTGGAGTACGCGGACGAGGCGGAGGCGGCGGCCGAGAGCGGGACGAGCGCGGCGGACGAGCGGGGCCCGGGGA
CCCGGGGCGCGGAGGGTGCACCTTCGCCCTCCTGCCGAGCGCTACGAGCCACTGGAGGAGCCGGCGCCGAGCG
AGCAGCCCAGGAAGAGGTACCGGAGGAAGCTGAAGAAGTACGGCAAGAATGTCGGGAAGGTCATCATCAAAGGAT
GCCGCTACGTGGTCATCGGCCTGCAAGGCTTCGCTGCAGCCTACTCCGCCCCGTTTGGCGGTAGCCACCAGCGTGG
TATCCTTCGTGCGCTTAATGGGAGCTGCTGTGGCAGGTGCCCCCAGAGTGAACGGGAGCCCCCTGCTGTGGGAACCTT
TGTGAATCCTGGAGCATCTCAGACTTGAACACACAGCATATTTGGAAGAGAAAACATGCCTTTCTTTGTTGAATC
ACATTAGTATGATGAGTGAGTCATCCCTGCCCATCTGCTGAGCTTCTCACATCTCTCAGTCACACGTGGACCCAG
TGGTCAATCCTGCAGAGAATTTCGGCGGAGGTTAGGTTTGGGAGTGGAGCTAGCGTGCTAAAGCCAGAGCCTTCAC
GTGAAGGTGGCAGGCACTGGGGCGGAAGCCAACACTCAACAGATGCAAGCAGTGTGGGTGTGCAGCAGAACAGTG
ATCTTGGGGGAGGAAGAGGATGTTACTAGAGTCAGATGATTTGCTGTATTCTCCTGAAAGGTCGTAGGCTGACAG
GCGCTCACATTCTTGGCTGCCTCGGTTCTGAGGGCAGCTAAGGAGCTGTTTATTCCTCAAGTCATGCTCCCCGA
TCTCCTTCTCTACCACTCTGTCAACCAGGAGTTTAATTACAGGCTTGAGGAGAAAGAAAGGAAGAAAAGATATCTT
GATGCTTTGAAAACCTGTGTTGGCAGTGTGGCATGACTGTTTAAAGTAGATAAAAACCTTGTCATTTTACCCCATCC
CTGCATGACTGTGAAGCTGGCGAGGAAGGAGGAAGAAGGGCAAGTTTCAAGTGCAGGCTGGGTGGCTGGGACAGGT
TGGCTAAGGGACTACTCTGGAGGGCTCTTCTGCCTGGCATTGCCCACTTCGGCCCCAGCCACGTGTTTGCAGCGAC
CAGAGTCCCTGCAAAGGTGTGGCTGGCTGTGGTCAGGGTGCTACTAGCACCATCAGCGCACTCCCGCCATTGGCT
CAGCTCCTCTCTGCCAGTCCAACTAAGAGTGCTTTGTCTGGGTGGGACATAGGGGGCTGAGAGAGATGGGGGGAG
ACATAACACCCAGGAATGAAAATACAGATTTAGAGAAGGAACAGTAAGTAGGAGACAGATGTGAAGGAAATGGA
AATGAGGCAAGAGGACATTGGAAGAGAGAAGTTTGCTGTCCAGGAGCCAGGTCTGGAGCATCAGTGTGAGGGAGT
TCAGGTAGGCTGGGCCTGTGCCCTTAGGTAGGGACAAGGGAGGCTGGGTAGCCAGGGCTGGTGCTTAAACCCCT
GAGGCCATGAGCTCATTGGCTGCCCTTGTAGCATCCTGTCTTCTTCTGTGCTGCCCTGGTTTGATCTCATCTCACC
TGGATTCAAAGGGTAAGGTGGGCATGGGTCTTGGGCCTGACACCCACCAAGGATGACCTGTGGACTGCCATCGGA
TGCTGAACAGGGAGATGAAAGGAGGTCCTCTTACCATAACCCCTCTGCCAACCCCCCAGTAGGCCACTGTTCTGAC
TTTGTTCAGAAATATCCAGAAATCCAAAGGGGCTGTTGCTGAACAGTCTGCAGGACCAGTGACAGCACCTACCT
GTTGTCCCAAGGCATACAAAGGAGGCCTCAACGCTCATGCTTCTCTAATCAAGCCCTACCAAGACAGACAGAAAG
ACAGACAGAAAAAAGGAAGGGGTAGAGGAGAAGGTTGAAGCTGTGGAGCTAGACTCTGCTTCACTTCTGAAAGCT
TCAACTTCATGTGCAAGATTCACTGGGACCCAATTCCTGCATTGTTAATATTTGTGAGGAAAAGTGAACAAGTG
ATCTGGTTTTAGCCAGATGATGAAAGTGATATGGCACATTTTACACACGTGAGATAATTACAGCTTGCCCCA
CAACACTGGGTGTTGGAGAAAGGGAGAGATAGTCATAAGTGGAAGAAAAAGCCAAGCATAGTGAGTGGGAAGGAG
AGTGAGAGCCTGTGCAGGCTGTGACGAGCCCCAGGCAGCCACAAGTTTCTCGTGGGGAGATGGAGGCAGAGCC
CAGGGTAGGGGACAGAGCTGCTGGGGCCTTTCCTTGCTGGGAATCTGTCCAGGAAGAGCTTCCCCACTCCCAT
CCCCCAAATTGGA AAAACCGTACATTCAAGCCTGTTTGGCCCTGAAATCTTAAGAATCTGGTTAAGAATTAAC
CACTAATGTCAAAGTCAAAACCTCCTAGGGGTTGTCTGGGAGTCAGGTTACGGGTACAGAAGATGAATCTCA
GATGTCACCTCAACCTGAGCCGTCATTCTGTGGCAGGGCTGCCCTGGGTTTCTCTTACTCAATCCCTGGAGTGT
AAGCATTGTGATTGTGTACAGATTACCTTTTTACCTTTTCTTTCTTTTTTTTTCTTTTTTTCAATATCAGTGCC
CACACCTTACTGAGTATTGAGTTTTAGAGCTTCGCTTGATGTGCTTGACCAAGAGACTTCTTTTGTATCCTTTT
CTTGTCTATGATGTAAATAAAAAGCCTCGATTTATGT

650/6881
FIGURE 604

MTVGARLRSKAESSLLRRGPRGRGRTEGDEEAAAILEHLEYADEAEAAAESGTSADERGPGTRGARRVHFALLP
ERYEPLLEEPAPSEQPRKRYRRKLKKYGKNVGKVIKGCYVVIQGLQFAAAYSAPFAVATSVVSFVR

651/6881
FIGURE 605

TCTAATACCTATTGATCTGTCACTTTCTCCCATCACGCTCAGGTGGGACCATCCAGTTGCAGGAAAACAAGCTTA
ACATGCCCAGTGAATCTACATTATGGTGAGTTCTATAATTATTTTATTATATATTACAGTGTAATAATGGAAATA
AAGCACCTAATAAATGTAAATGTGCTTAAATCTTTTGTCCCAGCTCCTACCTCCCGGCAGCCTCTCCAGGCCAG
AACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCACAATGGCCTATTTAGGCCCATACCCTACCTCAC
GGCAGTCTCCGCAGATGAGCCTACTGCCTCACAAACAGCCTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTT
TAGACCCAGCTCCTGCCTCCCAGCCTTCTCTCCAGGCCCTGAACTTTCTCAAGTCGACCTCACCAGGCCAGTTC
ATGCTTCTTTGCAGCCTCTCCAGGCCAGCTCCTGCATCTTGGTGGCCCCTCCAGGCCAGCCTCTGCCTCCCGT
CGGCCTCTACAGTCCCAACATCTGCCTCACAGCAGATTCTTCAGGCCAGCATCTGCCTCACTGTGGACCCCCA
GACCCAGATGGTGTCTCACTGTGGCATCCTCAGGTGAAGCTCCTGCCTTTCTGCAGCCTCTCCAGGCCAGCTCC
TCCTGCCTCCCAGTGGCCTCTTTCAGCCCAGCCCAGCTCATGCCTCCTGGCGGCCTTCCAGGCCCTGCTTTTGA
CTTTTGGTGGCCTCTGCAGGCCTCGACAAGGCCCGGCCTCCTGCCTCCCGAA

652/6881
FIGURE 606

GGCACGAGGGCTCTGTGGAGCTGCGCCTGCCAACTCATTGCTTTCTGCTGTGCTGTGATCCTGCAGTCAGTTGCC
GCTGTTGCTACTGCAATCATTTGCACCAAAGTGGAGCCAGAGAAGTTCCCTCTTTTAACATAAAGAGTCAAGAAAT
TGGAGCATGGCTATGAGCAATGGAAACAATGATTTTGTGGTTCTGAGCAACAGCAGCATCGCAACCAGTGCTGCT
AACCCGAGTCCCCCTCACCCCCTGTGATGGAGACCATGCAGCCCAGCAGCTCACACCCAAAGAAGCAACAAGAACA
AAAGTGAGTCCAAATGGATGCCTGCAACTTAATGGCACGGTCAAATCATCCTTTCTGCCTTTAGACAACCAAAGA
ATGCCTCAGATGTTACCCCAATGCTGCCATCCTTGCCCATACCATCACCCCTTGACTAGCCATAGCAGTCACCAA
GAGTGCCATCCCGAGGCTGGCCCTGCAGCACCCCTCTGCTTTGGCCTCGTGTTCATGCAGCCACACTCCGAGTAT
TCTGCATCTCTTTGTCCAAATCATTACCTGTGTATCAGACTACGTGCTGTCTTCAGCCCTCTCCATCCTTCTGC
CTGCATCATCCGTGGCCTGACCATTTTCAGCATCAGCCTGTGCAACAGCACATAGCCAACATAAGACCATCCAGA
CCTTTCAAGTTGCCAAAAAGTTATGCAGCCCTGATAGCCGACTGGCCGGTGGTGGTCTTGGGCATGTGCACCATG
TTCATCGTAGTCTGTGCCTTGGTTGGAGTATTAGTGCCAGAGCTCCCTGACTTCTCTGATCCATTGCTGGGTTTT
GAACCAAGAGGAACAGCAATAGGCCAGAGATTGGTCACATGGAATAATATGGTGAAAAATACAGGATACAAAGCA
ACATTAGCAAATTATCCCTTTAAATATGCAGATGAACAAGCCAAAAGCCATCGGGATGATAGATGGTCAGATGAT
CATTATGAAAGAGAGAAAAGAGAAGTTGACTGGAACCTCCACAAGGACAGCTTTTTCTGCGACGTTCCAAGTGAC
CGATATTCCAGAGTGGTATTTACTTCATCTGGAGGGGAGACATTATGGAATTTACCTGCAATTAAATCAATGTGC
AATGTAGATAATTCCAGGATCAGATCTCATCCCCAGTTTGGTGATCTCTGCCAGAGGACCACTGCTGCCTCCTGC
TGCCCCAGCTGGACACTGGGAAACTACATCGCCATTCTGAACAATAGATCGTCCTGTCAGAAAATAGTTGAGCGA
GACGTTTCTCATACCTTGAAGCTGCTTCGGACTTGTGCCAAACACTACCAAAATGGCACTCTGGGGCCAGACTGC
TGGGACATGGCAGCCAGAAGAAAGGACCAGCTCAAGTGCACCAATGTGCCACGCAAAATGTACCAAGTACAATGCT
GTGTACCAGATCCTCCATTACTTGGTGGACAAAGACTTTATGACCCCAAAGACGGCTGACTATGCCACGCCAGCT
TTAAAATACAGCATGCTCTTCTCTCCACAGAGAAAGGGGAGAGCATGATGAACATTTACTTGGACAACCTTTGAA
AACTGGAACCTCTTCTGACGGCGTGACTACCATCACCGGGATTGAGTTTGGTATCAAACACAGTTTGTTCAGGAT
TATCTTCTAATGGATACTGTGTATCCTGCCATAGCCATTGTGATTGTCTTTTAGTTATGTGTGTCTACACCAAG
TCCATGTTTATCACTCTGATGACAATGTTTGCAATAATCAGTTCTTTGATTGTTTCCTTAAAAAAAAAAAAAAAAAAAAA
A

653/6881
FIGURE 607

MAMSNNGNDFVVLNSSSIATSAANPSPLTPCDGDHAAQQLTPKEATRTKVSPNGCLQLNGTVKSSFLPLDNQRM
QMLPQCCHPCPYHHPLTSHSSHQECHPEAGPAAPSALASCCMQPHSEYSASLCPNHSPVYQTTCCCLQPSPSFCLH
HPWPDHFQHQPVQQHIANIRPSRPFKLPKSYAALIADWPFVVVLGMCTMFIVVCALVGVLVPELPDFSDPLLGFEF
RGTAIGQRLVTWNNMVKNTRYKATLANYPFKYADEQAKSHRDDRWSDDHYEREKREVDWNFHKDSFFCDVP SDRY
SRVFTSSGGETLWNLPAIKSMCNVDNSRIRSHPQFGDLCQRTTAASCCPSWTLGNYIAILNNRSCQKIVERDV
SHTLKLRLTCAKHYQNGTLGPDWCWMAARRKDQLKCTNVPRKCTKYNAVYQILHYLVDKDFMTPKTADYATPALK
YSMLFSPTEKGESMMNIYLDNFENWNSSDGVTTITGIEFGIKHSLFQDYLLMDTVYPAIAIVIVLLVMCVYTKSM
FITLMTMFATISSLIVS

654/6881
FIGURE 608

GCTTCCGCCTCGGCTCCTCTTCTGCGGGCATCCGGGATCCCTACGTCCCGCGTCCCCGAGCGCTCGGAGCCTA
CGCGCCAGCGCTACCGAAACCCAGAGTCCTGCGCCCTGGAGTCCCCGCGCCCCGAGCCCGAGCACCCGGGAGT
CCCGAGCCTCGCGCCCCGGAGTGCCCGAGCCTGCGCCGCGCACCCGGATACCCCGGGTCCCCGCGAGCTGCCGA
GGCGCCCCGCCGCCCGCGGGACAGTACCGCCTTCTTCCCTCTGTCCGCGCCATGGCCGCCCCGACCTGTC
CACCAACCTCCAGGAGGAGGCCACCTGCGCCATCTGCCTCGACTACTTCACGGATCCGGTGATGACCGACTGCGG
CCACAACCTTCTGCCGCGAGTGCATCCGGCGCTGCTGGGGCCAGCCCCGAGGCCCGTACGCGTGCCCCGAGTGCCGC
GAGCTGTCCCCGAGAGGAACCTGCGGCCCAACCGCCGCTTGCTAAGATGGCCGAGATGGCGCGGCGCCTGCAC
CCGCCGTGCGCGGTCCCGCAGGCGTGTGCCCGCGCACCGCGAGCCACTGGCCGCCTTCTGTGGCGACGAGCTGCG
CCTCCTGTGTGCGGCCCTGCGAGCGCTCTGGGGAGCACTGGGCGCACCGCGTTGGCCGCTGCAGGACGCGGCCGAA
GACCTCAAGGCGAAGCTGGAGAAGTCACTGGAGCATCTCCGGAAGCAGATGCAGGATGCGTTGCTGTTCCAAGCC
CAGGCGGATGAGACCTGCGTCTTGTGGCAGAAGATGGTGGAGAGCAGCGGCAGAACGCTGCTGCGTGAGTTCGAGC
GTCTTCCGCGTTTGCTGGCAGAGGGAGGGACAGCAGCTGCTGCAGAGGCTGGAGAGGAGGAGCTGAAGGTGCTGC
CCCGGCTGCGGGAGGCGCAGCCACCTAGGCCAGCAGAGCGCCACCTAGCTGAGCTCATCGCCGAGCTCGAGAG
GCCGCTGCCAGCTGCCTGCGCTGGGGCTGCTGCAGGACATCAAGGACGCCCTGCGCAGGGTCCAGGATGTGAAGC
TGCAGCCCCCAGAAGTTGTGCCTATGGAGCTGAGGACCGTGTGCAGGGTCCCGGGACTGGTAGAGACACTGCGGA
GGTTTTCAGGGGGACGTGACCTTGGACCCGGACACCGCCAACCTGAGCTGATCCTGTCTGAAGACAGGCGGAGCG
TGCAGCGGGGGGACCTACGGCAGGCCCTGCCGGACAGCCAGAGCGCTTTGACCCCGGCCCTGCGTGCTGGGCC
AGGAGCGCTTACCTCAGGCCGCCACTACTGGGAGGTGGAGGTTGGGGACCGCACCACTGAGCTGGGCCCTGGGGGTGT
GCAGGGAGAACGTGAACAGGAAGGAGAAGGGCGAGCTGTCCGCGGGCAACGGCTTCTGGATCCTGGTCTTCTTG
GGAGCTATTACAATTCTCCTCGGAACGGGCCTTGGCTCCACTCCGGGACCCACCCAGGCGCGTGGGGATCTTCTTG
ACTACGAGGCTGGACATCTCTCTTTCTACAGTGCCACCGATGGGTCACTGCTATTATCTTTCCCGAGATCCCT
TCTCGGGGACGCTGCGGCCCTCTTCTACCCCTGTCCAGCAGCCCGACCCCGATGACTATCTGCCGGCCGAAAG
GTGGGTCCGGGGACACCTGGCTCCCCAGTGAAGTGGGCCCTCCTGGAGGAGTCTGTTGCCTCTCCTGCCCTC
CAGGCCACTGAGTGTTTGGCCACTTGGAGGACCTGGGAGGAGGGAGTGTGTCCTTTGAGCAAGAGGAGGAATC
CTGGTGCTTTCTGAGCCTGCGTGGGAGAACCCCAATTCTAGCACTCCAGGAACTGTGGGAGAGTGTGGGGCAG
GCTCCGTCTCCTGCGGAGACCCCTCCAGCCACCGGGTGCCACTTAATGCCAACAGCCCTTACCAAAGCTGGGAG
CCCCATTGCCCCGGCAGCTCTGGCCTGTGGTTCCAGAAGCTGAGAAAACCTCACTGGGGCTTGAGAAATCCAGGG
TTCACCTAAGCTGCACAGTTCCTGCAGCTTTGTGAGCCCCCTGAAAGTCTTGTGTACCCACCTCTGAAGATGCT
GGGGAAGGCAGCTGGGATGGGAGCCAGCCCCATGCCTGTCTGTGACCCACAGTGGGTGAGAGCCCGTCAAGTC
CTGGGTGTGGCTGCTCTGGAAGAATTAGGAGGCAGCCATAATAAGAGTCTTCAGAGAGATGATGGGAGGGGCCAG
TGAGGACAGGAACAGAGAGTAGATGTCCTATAATAAGGGGCTTCTGGGAGGTGCCTGGGCACAGATGTCTGTTT
AGCAGGTGTGTGGGCTAGAGGAGAGAGCAGAGCCAGAAATGTCTTTTGAGGCCACGTTCTGACTTGAAGCT
TTCGTGGGCATGTTGCCATTGGGTTTGGCCCTTGCAAAGGCTTCTAGGTCTCCAGTGGCCCCCTCAGGACCCAGG
GTCCAGCTGCTGCTTGGGGATGTGCACTGCTGCGCCGGCCTTGCACTCTCTTACCCTGGGGAGGAACAGTGGC
TTCTCAGAGCCTGGGGCATAAGAAAGGAGGAGTTGATTTTTGTGTTGGGTTTGGGGTTTCTTTGTCTCTCAA
GGTACTGTTCTGTTTCTCTTTACCCCTCTGCTTTATTTATTGTAAGCATTCCACGTTAAATAAACTTTGGCTGT
TGTCTAC

655/6881
FIGURE 609

MELRTVCRVPGLVETLRRFRGDVTLD PDTANPELILSEDRRSVQRGDLRQALPDSPERFDPGPCVLGQERFTSGR
HYWEVEVGDA PAGEWGCAGRT

656/6881
FIGURE 610

CCGCAGGCAGTAGAGTGAAGCGCGCAGCTGCCAGGACTTGCGCGGTGACGTGCGCCGCTGCCAGGACCTTGCAGG
TGGAGAGCATAGTTGCCAAAATCAAGGCGGAGGAGCGCACCCGCCGTAGGATCCAGGCGGAGAAGCCCACCGCGG
CCAGGACCTAAGG**ATG**CAGTACACTGCTGCCAGGATCTTGCTGTGGAGCGCAGCGCGGCCAGGACCTCCGGCTG
CAGCACACCGCTGCCAGGATCTTATCGGCAGAGCGCTCCGCGGTCCGGACCCCGCCCGTGC GCGTCCCCGACCC
CGCCCCGTGCGCGTCCCCGGCGTTGGCGTCTTCGTCTGTTGCTGGTCTCCGTCCGGTCGCCGGCCCGTCTAGGTC
TCCGGCCCTCCCCAGCCGCTCCTGCGCCCTTGCCGGCCCCGCCGCCCGCAGCCCTGGCGCTCCTGCGGGCCCCG
CCGAGGCCCGCTGCGCCCTGTGCCAGCGCGCGCCCCGGGAACCGGTGCGCGCCGACTGCGGCCACCGCTTCTGTC
GGGCGTGCGTGGTGCGCTTCTGGGCCGAGGAGGACGGGCCCTTCCCGTGCCCCGAGTGCGCCGACGACTGCTGGC
AGCGCGCCGTGGAGCCCGGCAGGCCCCCGCTCAGCCGCCGCTTCTGGCGCTCGAGGAGGCGGCCGCGCGCCCCG
CGCGCGACGGCCCGGCCAGCGAGGCCGCGCTGCAGCTGCTGTGCCGCGCCGACGCCGGCCCGCTCTGCGCCGCCCT
GCCGTATGGCTGCGGGCCCCGAGCCGCCCGAGTGGGAACCGCGCTGGAGGAAGGCGCTGCGCGGCAAGGAGAACA
AGGGGTCTGTGGAATCATGAGAAAGGACTTGA**TGA**CGCCCGGGACCTGCATGGCCAGGCAGAGTCAGCAGCTG
CAGTGTGGAAGGGACACGTGATGGACCGTAGGAAGAAGGCACTGACCGACTACAAGAAGCTGCGGGCCTTCTTTG
TGGAGGAGGAGGAGCATTTCCCTGCAGGAGGCTGAGAAGGAGGAGGGGCTCCCTGAGGACGAGCTGGCTGACCCCA
CTGAGCGGTTTCAGGTCACTGCTGCAGGCGGTCTCGGAGCTGGAGAAGAAGCATCGCAACCTGGGCCTCAGCATGC
TGCTGCAGTGATGGCGCCAACCGTGGCAGTCCAGAGCTGGAGGCAGGAGGATGGATCCTCATCTCCATGGGAA
GTGTCAGCGTGTGGCTGCCAGGGAAGCGTGGCAGGCGCCTGGCCCTGGGTCCATCTACATAGTTGCGTGTTCAA
CAATGTCCATTTATCCTTCACCCCGAGGCGTGTTTTGGGGGCTGCAAACACCTCCCTGTGCTCCACCTGCCTCCG
CAGAAGGAAGCCTCTTTCTGTGTTTCCCGGGGTGAGGGGGCTGGCAGGTGGCTAACCCATTTAGCATCTCCAGG
CCCTGCCATCGTGTCTCATCTTGCTGTTATCTCTAGCTCTTTCCCTCCTCCATTTCTTTAGTAGTTGAATTTT
GCAAAGCTTG TAGCAGTAGCTCAGTTGCCTGCAGCATCCTTGTTGTGTAGATAAATTAGTCGACAGAACTCAGCA
CTGGGGACAGGATTGCAAAGTCGGGGACATAGATGCAGACAGTTGTTGAGATTTGGGGATAGCCGGGCTTGTGAG
CGGTGCCCATTTCCAGATGAAGCCTTTAGCCCTTCTGAGTCCCCGGCCCTTGGTGCGATGTCTGTGAGTTTGAC
CTGCCCAGCGTGTGGGCTGGCTCAATGCTGAATAAAGTGGGTTTGTGTCAGCTCGTTTGCTTCGTCTCCGTGTGT
CCACCTGGCCTCTTCCCCCTGCCCTGGCCACCCTCCAGTGTCAAAGGAAACTTCCTCGTGACACGTGCTAAAGCA
TGGTGAGGAGGACTTTGATTGGGACCATTGAGATGGGTGTGGGACCCCTTCCCTTGGGGCTGGGGGGAGATGGGG
CTCCACCCCGACGTAGCAGGGCAGGGGTTGGAGGAGCGAGGAGCAGTATAGGGTCCATGGGTGGGAATGACTGTG
AGGAGACATCAGGGCTGAGGGGGCTCTGGCTAAACCCACCTCACAGAGTCCTTGCTGCAGGCAGGCAGGGCGATC
AGA

657/6881
FIGURE 611

MQYTAARILSVERSAARTSGCSTPLPGSYRQSAPRSGPRPVVPDPAPCASPALASSSCCWSPSGRRPSRSPALP
SRSCALAGPAARSPGAPCGPRRGRLRPVPARAPGTGARRLRPPLLSGVRGALLGRGGRALPVPRVRRLLAARRG
ARQAPAQPPPSGARGGGRGARARRPGQRGAAAAVPRRRRPALRRLEPYGCGPRAARVGTALEEGAARQGEQGVCG
NHEKGLE

658/6881
FIGURE 612

GGCACGAGGCGCTGGCCGGGCTGGCTGCGGCCGCCCTGGGCGGGCCCCACCGGACGGCTTGCTCTGCTCTTTAC
CTGGGGTTGCTGTCGAGGACCCTGTGCAAGACTCGGCCGGTTTTTCTTTCTCCCTGATGGACAGACCCAAACATA
GCCGCGCAGCATCGTGAAGGGCTGGGGCCTTCACTCCTCTGTGGCTCTGGAAGAGCCCGATTTCCTCAGGAGGCA
TGTCGGGCCCCAGGCCTGTGGTGCTGAGCGGGCCTTCGGGAGCTGGGAAGAGCACCCCTGCTGAAGAGGCTGCTCC
AGGAGCACAGCGGCATCTTTGGCTTCAGCGTGTCCCATACACGAGGAACCCGAGGCCCGGCGAGGAGAACGGCA
AAGATTACTACTTTGTAACCAGGGAGGTGATGCAGCGTGACATAGCAGCCGGCGACTTCATCGAGCATGCCGAGT
TCTCGGGGAACCTGTATGGCACGAGCAAGGTGGCGGTGCAGGCCGTGCAGGCCATGAACCGCATCTGTGTGCTGG
ACGTGGACCTGCAGGGTGTGCGGAACATCAAGGCCACCGATCTGCGGGCCATCTACATCTCTGTGCAGCCGCCTT
CACTGCACGTGCTGGAGCAGCGCTGCGGCAGCGCAACACTGAAACCGAGGAGAGCCTGGTGAAGCGGCTGGCTG
CTGCCCAGGCCGACATGGAGAGCAGCAAGGAGCCCGGCCTGTTTGATGTGGTCATCATTAAACGACAGCCTGGACC
AGGCCTACGCAGAGCTGAAGGAGGCGCTCTCTGAGGAAATCAAGAAAGCTCAAAGGACCGGCGCC**TGA**GGCTTGC
TGTCTGTTCTCGGCACCCCGGGCCCATACAGGACCAGGGCAGCAGCATTGAGCCACCCCTTGGCAGGCGATACG
GCAGCTCTGTGCCCTTGGCCAGCATGTGGAGTGGAGGAGATGCTGCCCTGTGGTTGGAACATCCTGGGGTGACC
CCCGACCCAGCCTCGCTGGGCTGTCCCTGTCCCTATCTCTCACTCTGGACCCAGGGCTGACATCCTAATAAAAT
AACTGTTGGATTAGAAAAAAAAAAAAAAAAAAAAA

659/6881
FIGURE 613

MSGPRPVVLSGPSGAGKSTLLKRLQEHSGIFGFSVSHTRNPRPGEENGKDYYFVTREVMQORDIAAGDFIEHAE
FSGNLYGTSKVAVQAVQAMNRCVLDVDLQGVRNIKATDLRPIYISVQPPSLHVLEQRLRQRNTETEEESLVKRLA
AAQADMESSKEPGLFDVVIINDSLDQAYAEALKEALSEEIKKAQRTGA

660/6881
FIGURE 614

GGCACGAGGTCGGGCCTGGGTCCGACGGTAGTGGGTAGCGGGTCTCGGGTTGCGGGTTGCAGGTTGCAAGCCGCA
GGCCCCAGGCCAACTGCCITTCCCGGCGCC**ATG**TTTCGGCTCCAGTCGTGGAGGCGTGCGCGGCGGGCAGGACCAGTT
CAACTGGGAGGACGTGAAGACTGACAAGCAGCGGGAGAACTACCTGGGCAACTCGCTGATGGCGCCGGTAGGCCG
CTGGCAGAAGGGCCGCGACCTCACCTGGTACGCCAAGGGCCGGGCGCCATGCGCGGGCCCGAGCCGCGAGGAGGA
ACTGGCAGCCGTGCGGGAGGCGGAGCGCGAGGCGCTGCTGGCCGCCCTTGGCTACAAGAACGTGAAGAAGCAGCC
CACGGGCCTGAGCAAGGAGGACTTCGCGGAGGTCTGCAAGCGGGAAGGAGGCGACCCCGAGGAGAAGGGCGTGGA
CCGGCTGCTGGGGCTGGGGAGCGCAAGTGGCTCCGTGGGCCGCGTGCGCATGTCCCGAGAGGACAAGGAGGCCGC
CAAACCTGGGGCTGTCTGTGTTACGCATCACCGCGTAGAGAGCGGGCGGGCCCGGGACCTCGGCAGCCTCGGCCAG
GAGGAAGCCGCGGGCGGAGGATCAGACGGAAGCAGTTGTGAGAGCCACAGGAAAAGCAAGAAGGAGAAGAAGAA
AAAGAAAAAGAGGAAACACAAGAAAGAGAAGAAGAAGAAAGACAAAGAGCACAGGCGGCCAGCTGAGGCCACCTC
CTCTCCACATCTCCTGAGAGGCCCCAGGCACCACCACCATGACTCCGACTCCAACCTCCCCCTGCTGTAAGAGGAG
GAAGCGGGGACACAGTGGGGACAGGAGGAGCCCGTCTCGCAGGTGGCATGACAGAGGCTCTGAGGCC**TGA**TGGCT
GGACCCTGCTCACTGCTGTTGTGGGACCCTGAACCCTCCCTTCACCTTGCTTGCCCTCCTGCCTCGGAAGCTCCTT
GGGTGTGGGTGAAGCCCGAGGCTGCTCCTGTGGAAGTGGCTCTGGGCACCAGCCTGTGGGGCTAAAGACTTGACA
GCTAGCTCTGGAGCAGCCGGCTTCCTGGAAAACCTCCAGGTTTCGCATACCAGGGATGGCCCCCTGGCTTGGCCTG
CGAAGGTGAACCTGCCCAGATTTATCAGTAGAGGCTGGACTCCCTCTGTGTCCTGCCCATGGTTGCAGCAGCCAT
GGGCCTATGAGCGGTCTAACTGTGGCCAAGTATGGTGACCTCTATTTTCTTTATATTGACTCTTTGTATTTCAA
TAAATATATTTTAAAGGAAGGTAAAAAAAAAAAAAAAAAAAA

661/6881
FIGURE 615

MFGSSRGGVRRGGQDQFNWEDVKTDKQRENYLGNSLMAVGRWQKGRDLTWYAKGRAPCAGPSREEELAAVREAER
EALLAALGYKNVKKQPTGLSKEDFAEVCKREGGDPEEKGVDRLLGLGSASGSVGRVAMSREDKEAAKLGLSVFTH
HRVESGGPGTSAASARRKPRAEDQTESSCESHRKSKKEKKKKKKRKHKKKKKKDKHRRPAEATSSPTSPERPR
HHHHDSDSNSPCCKRRKRGHSGDRRSPSRRWHDRGSEA

662/6881
FIGURE 616

AGGAAGCCCTGCTTGATGAGCATGAGGCTCCACGGGGGCAGTGGCTGTGACGGTGAGTGCCACACAGAGCTGCCC
ACACTGGTGGAGGGAAGGCAGGGAGATACCAGGACCATCCGGAAGGGGCTGAGTGTCAATTTGACAGGTGCCATGT
GAGCAGAGATGTGAAGGAGTGGCCCGGGACAATCAGGGCAGAATCCCTGAGGTGTCCCTGGCCAGTGTCCCTTCCA
CCTGTCCACAAGCATGGGGAACATCTTCGCCAACCTCTTCAAGGGCCTTTTTGGCAAAAAAGAAATGCGCATCCT
CATGGTGGGCCTGGATGCTGCAGGGAAGACCACGATCCTCTACAAGCTTAAGCTGGGTGAGATCGTGACCACCAT
TCCCACCATAGGCTTCAACGTGGAAACCGTGGAGTACAAGAACATCAGCTTCACTGTGTGGGACGTGGGTGGCCA
GGACAAGATCCGGCCCCCTGTGGCGCCACTACTTCCAGAACACACAAGGCCTGATCTTCGTGGTGGACAGCAATGA
CAGAGAGCGTGTGAACGAGGCCCCGTGAGGAGCTCATGAGGATGCTGGCCGAGGACGAGCTCCGGGATGCTGTCCT
CCTGGTGTTCGCCAACAAGCAGGACCTCCCCAACGCCATGAATGCGGCCGAGATCACAGACAAGCTGGGGCTGCA
CTCACTACGCCACAGGAACCTGGTACATTTCAGGCCACCTGCGCCACCAGCGGCGACGGGCTCTATGAAGGACTGGA
CTGGCTGTCCAATCAGCTCCGGAACCAGAAAGTGAACGCGACCCCCCTCCCTCTCACTCCTCTTGCCCTCTGCTTT
ACTCTCATGTGGCAAACGTGCGGCTCGTGGTGTGAGTGCCAGAAGCTGCCTCCGTGGTTTTGGTCAACCGTGTGCAT
CGCACCGTGCTGTAAATGTGGCAGACGCAGCCTGCGGCCAGGCTTTTTTATTTAATGTAAATAGTTTTTGTTCCTCA
ATGAGGCAGTTTCTGGTACTCCTATGCAATATTACTCAGCTTTTTTTTATTGTAAAAAGAAAAATCAACTCACTGT
TCAGTGCTGAGAGGGGATGTAGGCCCCATGGGCACCTGGCCTCCAGGAGTCGCTGTGTGGGAGAGCCGGCCACGC
CCTTGGCTTTAGAGCTGTGTTGAAATCCATTTTGGTGGTTGGTTTTTAACCCAAACTCAGTGCAATTTTTTAAAT
AGTTAAGAAATCCAAGTCGAGAACACTTGAACACACAGAAGGGAGACCCCGCCTAGCATAGATTTGCAGTTACGGC
CTGGATGCCAGTCGCCAGCCCAGCTGTTCCCTCGGGAACATGAGGTGGTGGTGGCGCAGCAGACTGCGATCAAT
TCTGCATGGTCACAGTAGAGATCCCCGCAACTCGCTTGTCTTGGGTACCCCTGCATTCCATAGCCATGTGCTTG
TCCCTGTGCTCCACGTTCCCAGGGGCCAGGCTGGGAGCCACAGCCACCCCACTATGCCGCAGGCCGCCCTAC
CCACCTTCAGGCAGCCTATGGGACGCAGGGCCCCATCTGTCCCTCGGTGCGCGTGTGGCCAGAGTGGGTCCGTGCG
TCCCCAACACTCGTGCTCGCTCAGACACTTTGGCAGGATGTCTGGGGCCTCACCAGCAGGAGCGCGTGCAAGCCG
GGCAGGCGGTCCACCTAGACCCACAGCCCCCTCGGGAGCACCCACCTCTGTGTGTGATGTAGCTTTCTCTCCCTC
AGCCTGCAAGGGTCCGATTTGCCATCGAAAAAGACAACCTCTACTTTTTTCTTTTGTATTTTGATAAACACTGAA
GCTGGAGCTGTAAATTTATCTTGGGGAAACCTCAGAACTGGTCTATTTGGTGTGCGTGAACCTCTTACTGCTTT
CAATACACGATTAGTAATCAACTGTTTTGTATACTTGTTTTTCAGTTTTTCATTTGACAAACAAGCACTGTAATTA
TAGCTATTAGAATAAAATCTCTTAACTATT

663/6881
FIGURE 617

MGNIFANLFGKLF GKKE MRILMVGLDAAGKTTILYKLKLGEIVTTIPTIGFNVETVEYKNISFTVWDVGGQDKIR
PLWRHYFQNTQGLIFVVD SDRERVNEAREELMRMLAEDEL RDAVLLVFANKQDLPNAMNAAEITDKLGLHSLRH
RNWYIQATCATSGDGLYEGLDWLSNQLRNQK

664/6881
FIGURE 618A

GTGGGACCATCCAGTTGCAGGAAAACAAGCTTAAACAGGCCACTGATTCTACATTATGCTCCTACCTCCCAGCAG
CCTCTCCAGGCCCAGAACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCACAATGGCCTATTTAGGCC
CATAACCTACCTACGGCAGTCTCCGCAGATGAGCCTACTGCCTCACAACAGCCTCCACAGGCACAGCTCCATCG
TTACAATGGCCTCTTTAGACCCAGCTCCTGCCTCCCAGCCTTCTCTCCAGGCCCTGAACTTTCTCAAGTCGACCT
CACCAGGCCCAGCTCATGCTTCTTTGCAGCCTCTCCAGGCCCAGCTCCTGCATCTTGGTGGCACCTCCAGGCCCA
GCCTCTGCCTCCCGTCGGCCTCTACAATCCCAACATCTGCCTCACAGCAGATTCTTCAGGCCCAGCATCTGCCTC
ACTGTGGACCCCCAAGCCAAGCTCCCAACCTTTTCAGCAGCTTCTACACACCCAACCTCCTGCCACCCAGTGGCCT
CTTTAGGCCAAGCTCATGCTTACAAGGGCCTTTCCAGGCTCAACTTTTGTCTCATGGCAACCTTTTCTGGCCAG
ATTCTGCCTGTCTCCCAGCAGCCTAGACAGGCCCAGGTCTTGCCTCACACTGGCCTCTCTACATCCAGCTCATG
CCTCACGGTGGCCTCTCCAGGCCCAACTCCTGTCCCAGGACGTATCTCCGGGCCCAAACTTACTCAAGTCAGA
CTCTCTAGTCCCAACTGCTGCCTCCTGGTGGCCTATGAAGGCCCAAAATCTCCTCAAGTGGACCTCTCCAGGCC
AGCTCCTGCCTCCTGTGAGCCTCTACAGGCCCAACCTCTGCCTCATGGGGGCTTCTCCAGGCCACCTCTTCTC
TTGGCTGGGTCTACAGGCACAACCTGCTGCCTCACAACAGCCTTTTTTGGGCCAGTTCTGTCCAGCTCATGGCGG
CCAATGTAGGCCCAAACTTCTCAAGTCAAACTCTCCAGGCCACCTTCTGCTTCCCGGTGGCATGAACAGGCC
CAGCTTTGACTTGAGAACAGCCTCTGCAGGCCCTGCTCTTGCCTCCCAGGGGCTTTTTCCAGACCCAGCTCCTGC
CTCATGGCAGCTGCCCCAGGCCAAATTTCTGCCTGCCTGCCAGCAGCCTCAACAGGCACAGCTCCTCCCTCACAG
TGGCCCATTTAGGCCCAACTCATGACTGTGGGCCATTTCCAGGCCTAGTGCCTGCCTCGTGGCTGACTCTTGAA
GCCCAAACTTCTCAAATCAGCCTTTTGGCCAACTTCTGTCTACTGTGGACTCTACAGGCCAGCCTCTGCCTC
ACAGTGGACCTCCAGACCCAGATGGTGTCTCACTGTGGCATCCTCAGGCGAAGCTCCTGCCTTTCCGCAGCCTC
TACAGGCCCAGCTCCTGCCTTGCAGTGGCCTCTTTAGGCCAAGCTCATGCCCCATGGCGACTTTTCCAGGCACAG
CTTTTGCCTTTTGCAGCCTGTGAGGCCCAGAATGTCTTAACCTCGGCATCTCCAGGATGAGCTCATCTCCAG
TGCCTCTACAGGCCCGTCTCCTGCCTCACAACAACCTCCTTTGGCCCAACTCCTGCTGAGCTGCTGGCAGCCTCT
GTAGGCCACAGAATTCTTAAGGTAAAGCTTTCCAGGCCACCTTTGGCCTCCCGGCAGGCTCAGCAATCAAATA
TTCCCTCACTGCGGCCACCGAAAGCCAAGTTTCTCCCTGCCTCAGGCATCCTCCGAAAAGTGAAGCTTTGCCTC
ACGGTGGCCTCCCCAGGCCATGAATCTGCCTGCCTCCCAGGCAGCTGCTGCCTCACAATGGTCTCTTTAGGCCCA
GCTCATGCTAAAAGATGGACTCTCCAGGCACAGCTCTTGCCTCCTGGCAGCCTCTGCAGGCCCAAAATTTCCAAA
AGTTGGCCTCTCTAACTCAGCTCCTGCCTCATGTCTGCCTACACAGGCCCAGACTCTTACCACACAGTAGACCC
TCCAGGCCCACTTGCCTGATCATAGCCTCCTAAGGCCAAGCTCCTGCCTTTCCGGCAGCCTCTACAGGCCAAG
CTCCTGCCTCGCAATTGCCTCTGTAGGCCAAGATCATGCCGTGAAGTGGCCTTCCCTAGCCTAACTTTTGCTTTT
TGACGCATACTCCAGTCCCAAACTTCTCCAGTCAGCCGGTCCAGGCCAAGCTCTTCTCCCAAGGCTTCTGC
AGGCCAAAATCATCCTGAAGTCACCCTCTGCAGGCGCAGCTCCTGCCTCCAAGTGTGTGTAGGCCAAGCTAATG
CCTCACAGCACACTTTCCAGGCTGAGCATTTCTTTTGTGCATCCTCTCCAAGCCCTGAACTTACTCCAGTTGGC
CTCTCCAGACCAAGCTCTCCCTCCAGTGGCCTCTACAGGCCCAAAATGTCTCAGGTCAGCCTCTCCAGGGCCA
ACTCCTAGCTACCGGTGGCTTCTGCAGGCCAAAATCGACCTCAAGTCAGCCTCTTACACCCAGCTCTTGCCTCT
GAGTGGCCTCTCCAGGAGCAAACTTTCTCAAGTCGGCCTCTCCAGGCCCAGCCTCCTGCTTCCCGAGGGCATGT
ACAGGCCCAGCCTCTGCCTCACAGCAGACTCTTACACCCAGCTCTTCCCTGTCTGCGGCCTCTCCAGTCCAAAG
CTGCTCCTGCCTTTTGGCAGCTTGTACAGGCCCAGCTCCTCCCTCACGGTGGCCTCTTTCCGGCCCAACTCATGCC
TCTTGCAACGTGCCCAAGTGTGAGCTCCTGCCTCACACTGGCCTGTTGAGGCCCAGCTCATGCCTCTCGTGGCCT
CAACGGGCCCATCCCTGCCTGTGCGCGGCCTCTACAGGCCCGGCCTCTACCTCACAGTGGGCTCTCCAGGCCCA
CCTCTTCCCTCACCGTGGCCTCCTGGGGCAATGCTCCTCCCTCTCGGGAGCCTCTGTGGGCCCAGCTCCTGCCTCC
CAGTGGCCTCTGTGCGCCAAGCCCGTGCCTCAGGGCAGCCTTTCCAGGCCTAGCGTTTGCTGCTTTGCATCCTCT
CCAGGCCCTGGACTTCTCCAGTCGGCCTCTCCAGGCCCAGCTCTTCTCTCGGGCGCCTCTGCAGGCCCAAGTGTCTCAAGTTG
GCCTCCCCAGGCCCAGCAACGGCCTCTCGGCGGCCTTTCCGGGTGCAAAAGTTCTCGAGTCAGCCTCTCCAGGC
CCAGCTCCTCCTGCCTCCAGTGGCCTCTTTCCGGCCAGGCCAGCTCATGCCTCCCGGCGGCCTTCCAGGCCCT
GCTTTTGAATTTCCGGTGGCCTCTGCAGGCCTCGACAAGGCCAGGCCCTCCTGCCTCCCAAGGCCTGCACAGGCC
AGCCTCTGCCTCACAGCAGACTCTCCACGCCCAGCTAGCTCTCGCCTCACTGCGGCTTCCCGAGTCCAAAGCTCC
TGCTCTCAGCCGCTTCGGCAGGCCCAGCTCCCGCCTGCCAGTGGCCTCTTCCAGGCCCATGGGGCTCATTTCTCA

665/6881
FIGURE 618B

CAACGGCCTTTCCAGGCCAGTTTTCCCTTCCGGCGGCCTCTTGGCCTCTAATTTGTTTATCTTTGGGTATAA
ATCCCAAATATTGAATTTTGAATATTTCCACCATT

666/6881
FIGURE 619

TCTAATACCTATTGATCTGTCACCTTTCTCCCATCACGCTCAGGTGGGACCATCCAGTTGCAGGAAAACAAGCTTA
ACACGCCCCACTGATTCTACATTATGGTGAGTTCTATAATTATTTTATTATATATTACAGTGTAATAATGGAAATA
AAGTGCCTAATAAATGTAAATGTGCTTAAATCTTTTGGCCCAGCTCCTACCTCCCAGCAGCCTCTCCAGGCCAG
AACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCACAATGGCCTATTTAGGCCCATACCTACCTCAC
GGCAGTCTCCGCAGATGAGCCTACTGCCTCACAACAGCCTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTT
TAGACCCAGCTCCTGCCTCCCAGCCTTCTCTCCAGGCCCTGAACTTTCTCAAGTCGACCTCACCAGGCCAGCTC
ATGCTTCTTTGCAGCCTCTCCAGGCCAGCTCCTGCATCTTGGTGGCACCTCCAGGCCAGCCTCTGCCTCCCGT
CGGCCTCTACAATCCCAACATCTGCCTCACAGCAGATTCTTCAGGCCAGCATCTGCCTCACTGTGGACCCCCA
GACCCAGATGGTGTCTCACTGTGGCATCCTCAGGCGAAGCTCCTGCCTTTCCGCAGCCTCTCCAGGCCAGCTCC
TCCTGCCTCCCAGTGGCCTCTTTCGGCCCAGCCCAGCTCATGGCTCTCGGCGGCCTTCCCAGGCCCGCTTTTGA
CTTTTGGCGGCCTCTTCAGGCC

667/6881
FIGURE 620

TTGAAGAACTTTGCCAAATACTTTCTTCACCAATCTCATGAGGAGAGGGAACATGCTGAGAAACTGATGAAGCTG
CAGAACCAACGAGGTGGCCGAATCTTCCTTCAGGATATCAAGAAACCAGACTGTGATGACTGGGAGAGCGGGCTG
AATGCGATGGAGTGTGCATTACATTTGGAAAAAAGTGTGAATCAGTCACTACTGGAAGTGCACAAACTGGCCACT
GACAAAAATGACCCCAATTTGTGTGACTTCATTGAGACACATTACCTGAATAAGCAGGTGAAAGCCATCAAAGAA
TTGGGTGAGCACGTGACCAACTTGTGCAAGATGGGAGCGCCCGAATCTGGCTCGGCGGAATACCTCTTAGACAAG
CACACCCTGGGGGACAGTGATAATGAAAGCTAAAGCCTCAGGCTAATTTCCACATAGCCGTGGGAGTGACTTCCCT
GGTCACCAAG

668/6881
FIGURE 621

MKLQNQRGGRIFLQDIKKPCDDWESGLNAMECALHLEKSVNQSLLELHKLATDKNDPHLCDFIETHYLNKQVKA
IKELGEHVTNLCKMGAPESGSAEYLLDKHTLGDSDNES

669/6881
FIGURE 622

ATGGCCGGCACAAAGATGGGGCGGGAGGACAGCGTGCTGGATACGGCGTGGGGCGGGTCCGCGGCCCGGGAGACC
CATGCTGGGGCGGCCCTGTCACTCGTCTCGCTGCCAAGCACAGGGCTGAGGTGCGGAGGGACCACTGAGAGGACT
TCGCTGCGTGTCAGCTCAGCTCTGGACGGCGTGAGGAGCCCTGGAACTTTATTTACAAAACTGACAGCAGCT
GCCCTTAGTTTGGCAGCTGGAAAATGGGAAAGAGAAAGTAAGAGGAAGGGTGGCAAAGGAGGGAGCCCATGTGGA
CAGCAGGAACGGGTACACGATAGCACAGAATCAAAACAAAGGCTCTCTGGTCGGAGTTTAGAAAGGCTGAAGGG
GATACTAAAGGAGGAGATAAAGCCCAGGTGAAGGACGAACCACAGAATAGATCCGCGAGGTTGTCTGCTAAACCT
GCTCCTCCAAAACCAGAGCCCAAGCCTAAAAAGGCCCTGCAGAGACAGTACCCAAAGGGAAAAAGGGAAAAGCT
GTTGCTGGCAAGGAGGGGAATAACCTCTGCAGAAAATGGAGATGCCAAAACAGACCAGGCACAGAAAGCTGAAGGT
GCTGGAGATGCCAAGGCAAATCTGCTGCCACGGTGTGGCAGCAAAGAAATGAAAGGAAGTGTCTGGCAGCGCAGG
GGAGAAATTGTGTTTCCTCCTTCTCCAAAGGTTACCTTTTCTATTTACCTTCATCATTGATAAGAAGGTGAAA
GGATGCCAGGAGCAAGGCGGATCTACGGGACTTTTGAAAAGAAATGTACTGACCTTTGGCTGTAAAACTGTGTC
ATGAGAACAGAAAGCCCTGAGAGAAGAAGACAGCCATTATGGGATCTATGGCGCACTCTGTGCTAGGGCAGAAT
GCCAGGGAAGAGCTGCCTGTCTTCAGCGCCCTTGCTGGGAACACACGCCAGAACCCGACCCTGCCATGCTTTGT
GCTTCAGGCAGCAGGACCCACCCCTAACAGAGTCTCAAGTCAGACACTTAA

670/6881
FIGURE 623

MAGTKMGREDSVLDTAWGGSAAARETHAGAALSLVSLPSTGLRCGGTTERTSLRVSSALDGVVEEPWKLYLQKLTA
ALSLAAGKWERESKRKGGKGGSPCGQQERVHDSRIKTKALWSEFRKAEGDTKGGDKAQVKDEPQNRSAARLSAKP
APPKPEPKPKKAPAEVTPKGKKGKAVAGKEGNNPAENGDAKTDQAQKAEGAGDAKANLLPRCGSKEMKGSVWQRR
GEIVFPPSPKVHLFYFTFIHKKVKGCQEQQGGSTGLLKRNVLTFGCKNCVMRTESPERRRQPFMGSMASVVGQN
AREELPVFSALAGNHTPEPDPAMLCASGSRTPLTESQVRH

671/6881
FIGURE 624

AAGAAGCTGCCGTTGTTCTGGGTACTACAGCAGAAGGGTATGCGGAAGCGAGCACCCAGTCTGAGATGGCTCCT
GCCGGTGTGAGCCTGAGGGCCACCATCCTCTGCCTCCTGGCCTGGGCTGGCCTGGCTGCAGGTGACCGGGTGATC
ATACACCCCTTCCACCTCGTCATCCACAATGAGAGTACCTGTGAGCAGCTGGCAAAGGCCAATGCCGGGAAGCCC
AAAGACCCACCTTCATACCTGCTCCAATTGAGGCCAAGACATCCCCTGTGGATGAAAAGGCCCTACAGGACCAG
CTGGTGTAGTCGCTGCAAACTTGACACCGAAGACAAGTTGAGGGCCGCAATGGTCGGGATGCTGGCCAACTTC
TTGGGCTTCCGTATATATGGCATGCACAGTGAGCTATGGGGCGTGGTCCATGGGGCCACCGTCCTCTCCCAACG
GCTGTCTTTGGCACCTGGCCTCTCTCTATCTGGGAGCCTTGGAACACACAGCTGACAGGCTACAGGCAATCCTG
GGTGTTCCTTGGAAGGACAAGAACTGCACCTCCCGGCTGGATGCGCACAAGGTCCTGTCTGCCCTGCAGGCTGTA
CAGGGCCTGCTAGTGGCCCAGGGCAGGGCTGATAGCCAGGCCCAGCTGCTGTCTGTCCACGGTGGTGGGCGTGTTT
ACAGCCCCAGGCCTGCACCTGAAGCAGCCGTTTGTGCAGGGCCTGGCTCTCTATACCCCTGTGGTCTCTCCACGC
TCTCTGGACTTCACAGAAGCTGGATGTTGCTGCTGAGAAGATTGACAGGTTTCATGCAGGCTGTGACAGGATGGAAG
ACTGGCTGCTCCCTGATGGGAGCCAGTGTGGACAGCACCTGGCTTTC AACACCTACGTCCACTTCCAAGGGAAG
ATGAAGGGCTTCTCCCTGCTGGCCGAGCCCCAGGAGTTCTGGGTGGACAACAGCACCTCAGTGTCTGTTCCCATG
CTCTCTGGCATGGGCACCTTCCAGCACTGGAGTGACATCCAGGACAACCTTCTCGGTGACTCAAGTGCCCTTCACT
GAGAGCGCCTGCCTGCTGCTGATCCAGCCTCACTATGCCTCTGACCTGGACAAGGTGGAGGGTCTCACTTTCCAG
CAAACTCCCTCAACTGGATGAAGAACTGTCTCCCCGGACCATCCACCTGACCATGCCCAACTGGTGCTGCAA
GGATCTTATGACCTGCAGGACCTGCTCGCCAGGCTGAGCTGCCCGCCATTCTGCACACCGAGCTGAACCTGCAA
AAATTGAGCAATGACCGCATCAGGGTGGGGGAGGTGCTGAACAGCATTTTTTTTTGTAGCTTGAAGCGGATGAGAGA
GAGCCACAGAGTCTACCCAACAGCTTAACAAGCCTGAGGTCTTGAGGTGACCCTGAACCGCCCATTCTCTGTTT
GCTGTGTATGATCAAAGCGCCACTGCCCTGCACTTCTGGGCCGCGTGGCCAACCCGCTGAGCACAGCATGAGGC
CAGGGCCCCAGAACACAGTGCCCTGGCAAGGCCTCTGCCCTGGCCTTTGAGGCAAAGGCCAGCAGCAGATAACAA
CCCCGGACAAATCAGCGATGTGTCACCCCCAGTCTCCACCTTTTCTTCTAATGAGTCGACTTTGAGCTGGAAAG
CAGCCGTTTCTCCTTGCTAAGTGTGCTGCATGGAGTGAGCAGTAGAAGCCTGCAGCGGCACAAATGCACCTCC
CAGTTTGCTGGGTTTATTTTAGAGAATGGGGGTGGGGAGGCAAGAACCAGTGTTTAGCGCGGGACTACTGTTCCA
AAAAGAATTCCAACCGACCAGCTTGTTTGTGAAACAAAAAAGTGTTCCCTTTTCAAGTTGAGAACAAAAATTGGG
TTTTAAAATTAAAGTATACATTTTTGCATTGCCTTCGGTTTGATTTAGTGTCTTGAATGTAAGAACATGACCTC
CGTGTAGTGTCTGTAATACCTTAGTTTTTCCACAGATGCTTGTGATTTTGAACAATACGTGAAAGATGCAAGC
ACCTGAATTTCTGTTTGAATGCGGAACAATAGCTGGTTATTTCTCCCTTGTTGTTAGTAATAAACGTCTTGCCAC

672/6881
FIGURE 625

MRKRAPQSEMAPAGVSLRATILCLLAWAGLAAGDRVYIHPFHLVIHNESTCEQLAKANAGKPKDPTFIPAPIQAK
TSPVDEKALQDQLVLVAAKLDTEKLRAMVGMLANFLGFRIYGMHSELWGVVHGATVLSPTAVFGTLASLYLGA
LDHTADRLQAILGVPWKDNCTSRDLAHKVLSALQAVQGLLVAQGRADSQAQLLLSTVVGVTAPGLHLKQPFVQ
GLALYTPVVLPRSLDFTELDVAAEKIDRFMQAVTGWKTGCSLMGASVDSTLAFNTYVHFQGKMKGFSLLAEPQEF
WVDNSTSVSVPMLSGMGTQHWSDIQDNFSVTQVPFTESACLLLIQPHYASDLKVEGLTFQQNSLNWMKKLSPR
TIHLTMPQLVLQGSYDLQDLLAQAEPAIHLTELNLQKLSNDRIRVGEVLNSIFFELEADEREPTTESTQQINKPE
VLEVTLNRPFLFAVYDQSATALHFLGRVANPLSTA

673/6881
FIGURE 626

GAATTCGGCACGAGCCGGGATCCTGTGTAGCGGCTGCAGAGGGTGCCGCCGCCCTAGGCGAAGTAGGGCCGTCCT
GAGCGAAAGAACCGCCCCAGCAGGAGCACCACCACGGCTTAGCAAAGAATCCCAGACCCCGCCCGGGAAGGCAG
CCGCACCATGGAGTCTTCCAGTTCATCTAACTCTTATTTCTCCGTTGGCCCAACCAGTCCCAGCGCTGTCTGTCT
CCTCTACTCGAAGGAGCTCAAAAAGTGGGATGAGTTTGAAGATATTTTAGAAGAGAGGAGGCATGTCAGTGA
GAAATTTGCAATGAAATGCTACACACCTCTTGTCTATAAGGGAATTACTCCATGTAAACCAATTGATATTAAATG
TAGTGTTCTCAATTCTGAGGAGATTCAATATGTCATTAAACAGCTTTCCAAGGAATCCCTTCAATCTGTGGATGT
CCTCCGAGAGGAAGTGAGTGAGATCTTAGATGAAATGAGTCACAACTGCGTCTTGGAGCCATTCCGGTTTGTGC
CTTCACCCTGAGCAAAGTATTTAAACAAATTTTCTCGAAGGTGTGTGTAAATGAAGAAGGTATTCAGAACTACA
AAGAGCCATCCAGGAGCATCCTGTTGTTCTGCTGCCTAGTCATCGAAGTTACATTGACTTCCTCATGTTGTCTTT
TCTTCTATACAATTATGATTTGCCTGTGCCAGTTATAGCAGCAGGAATGGACTTCCTGGGAATGAAAATGGTTGG
TGAGCTGCTACGAATGTCGGGTGCCTTTTTCATGCGGCGTACCTTTGGTGGCAATAAACTCTACTGGGCTGTATT
CTCTGAATATGTAAAACTATGTTACGGAATGGTTATGCTCCTGTTGAATTTTTCCTCGAAGGGACAAGAAGCCG
CTCTGCCAAGACATTGACTCCTAAATTTGGTCTTCTGAATATTGTGATGGAGCCATTTTTTAAAGAGAAAGTTT
TGATACCTACCTTGTCCCAATTAGTATCAGTTATGATAAGATCTTGAAGAACTCTTTATGTGTATGAGCTTCT
AGGGGTTCTTAAACCAAAGAGTCTACAAGTGGGTTGCTGAAAGCCAGAAAGATTCTCTCTGAAAATTTTGGAAG
CATCCATGTGTACTTTGGAGATCCTGTGTCACTTCGATCTTTGGCAGCTGGGAGGATGAGTCGGAGCTCATATAA
CTTGGTTCCAAGATACATTCCCTCAGAAACAGTCTGAGGACATGCATGCCTTTGTCACTGAAGTTGCCTACAAAAT
GGAGCTTCTGCAAATTGAAAACATGGTTTTGAGCCCCCTGGACCTAATAGTTGCTGTTCTGCTTCAGAACCGGCC
ATCCATGGACTTTGATGCTCTGGTGGAAAAGACTTTATGGCTAAAAGGCTTAACCCAGGCATTTGGAGGGTTTCT
CATTTGGCCTGATAATAAACCTGCTGAAGAAGTTGTCCCGCCAGCATTCTTCTGCATTCCAACATTGCCAGCCT
TGTCAAAGACCAGGTGATTCTGAAAGTGGACTCCGGAGACTCGGAAGTGGTCGATGGGCTTATGCTCCAGCACAT
CACTCTCCTCATGTGCTCAGCTTATAGGAACCAGCTGCTCAACATTTTGTGCGCCCATCCTTAGTAGCAGTAGC
ATTGCAGATGACACCAGGTTTCAAGAAAGAGGATGTCTACAGTTGCTTTCGCTTCCTACGTGATGTTTTTGCAGA
TGAGTTTCTCTTCCCTCCAGGAAACACACTAAAGGACTTTGAAGAAGGCTGTTACCTGCTTTGTAAAAGTGAAGC
CATACAAGTGACTACGAAAGACATCCTAGTTACAGAGAAAGGAAATACTGTGTTAGAATTTTGTAGTAGGACTCTT
TAAACCTTTTGTGGAAGCTATCAGATAATTTGCAAGTACCTTTTGTGAGTGAAGAAGAGGACCACTTCAGTGAGGA
ACAGTACTTTGGCTGCAGTCAGAAAATTCACAAGTCAGCTTCTCGATCAAGGTACCTCTCAATGTTATGATGTATT
ATCTTCTGATGTGCAGAAAAACGCCTTAGCAGCCTGTGTGAGGCTCGGAGTAGTGGAGAAGAAGAAGATAAATAA
TAACTGTATATTTAATGTGAATGAACCTGCCACAACCAAATTAGAAGAAATGCTTGGTTGTAAGACACCAATAGG
AAAACCAGCCACTGCAAACTTTTAATAATCAACAAATAGTTATGGAAAATTCGGTCACGTAATTACTCTCATCGA
AGGACTCATTACAACAAACAGGGAAGTAAAGGAAGAGACACATCCTCTCATACTCCCTGAGACTCTGAGAACAGT
GGACGCAGAGGGAAGAGATGATCATTGGAAGCAATCAGTTTACTCTTCCCCACCACAGTGGTTAAAGGCGTTTG
TATCTGACACTATGTGTGTGTTTTAAATAAACTTTTGGAAACATGAAAAAAAAAAAAAAAAAACTCGAG

674/6881
FIGURE 627

MESSSSSNSYFSVGPTSPSAVLLYSKELKKWDEFEDILEERRHVSDLKFAMKCYTPLVYKGITPCKPIDIKCSV
LNSEEHYVIKQLSKESLQSDVLRREEVSEILDEM SHKLR LGAIRFCAFTLSKVFKQIFSKVCVNEEGIQKLQRA
IQEHPVVLLPSHRSYIDFLMLSFLLYNYDLPVPVIAAGMDFLGKMGVGE LLRMSGAFFMRRTFGGNKLYWAVFSE
YVKTMLRNGYAPVEFFLEGTRSRSAKTLTPKFGLLNIVMEPFFKREVFDTYLPISISYDKILEETLYVYELLGV
PKPKESTTGLLKARKILSENFGSIHVYFGDPVSLRSLAAGRMSRSSYNLVPRYIPQKQSEDMHAFVTEVAYKMEL
LQIENMVLSPWTLIVAVLLQNRPSMDFDALVEKTLWLKGLTQAFGGFLIWP DNKPAEEVVPASILLHSNIASLVK
DQVILKVDSGDSEVVDGLMLQHITLLMCSAYRNQLLNIFVRPSLVAVALQMT PGFRKEDVYSCFRFLRDVFADEF
IFLPGNTLKDFEEGCYLLCKSEAIQVTTKDILVTEKGNTVLEFLVGLFKPFVESYQIICKYLLSEEDHFSEEQY
LAAVRKFTSQLLDQGTSQCYDVLSSDVQKNALAACVRLGVVEKKKINN NCIFNVNEPATTKLEEMLGCKTPIGKP
ATAKL

675/6881
FIGURE 628

CTCTTCCTAAGCCGGCGCTCGGCAAGTTCTCCCAGGAGAAGGCCATGTTTCAGTACGAGCGCCAAGATCGTGAAGC
CTAATGGCGAGAAGCCGGACGAGTTTCGAGTCCCGCATCTCCCAGGCTCTTCTGGAGCTGGAGATGAACTTGGACC
TCAAGGCTCAGCTCAGGGAGCTGAATATTATGGCAGCCAAGGAAATTGAGGTTGGTGGTGGTCAGAAAGCTATCA
TAATCTTTGTTCCCGTTCCTCAACTGAAATCTTTCCAGAAAATCCAAGTCCGGCTAGTATGTGAATTGGAGAAAA
AGTTCAGTGGGAAGCATGTTGTCTTTATCGCTTAAAGGAGAATCCTGCCTAAGCCAACCTGGAAAAGCTGTACAA
AATATAAGCAAAAGCATCCCAGGAGCCATACTCTGACAGCTGTGCACGATGCCATCCTTGAGGACTTGGTCTTCA
CAAGCAAAATTGTGGGCAAGAGAATCCGCGTGAAACTAGATGGCAGCCGGCTCATGAAGGTTCAATTTGGACAAAG
CACAGCAGAACAATGTGGAACACAAGGTTGAAACTTTTTCTGGTGTCTATAAGAAGCTCATGGGCAAGGATGTTA
ATTTTGAATTCCCAGAGTTTCAATTGTAAACAAAAATGACTAAATAAAAAATATATATTCACAGT

676/6881
FIGURE 629

MFSTSAKIVKPNGEKPDEFESRISQALLELEMNLDLKAQLRELNIMAAKEIEVGGGQKAIIFVVPVQLKSFQKI
QVRLVCELEKKFSGKHVVFIARRILPKPTWKSCTKYQKHPRSHLTAVHDAILEDLVFTSKIVGKRIRVKLDG
SRLMKVHLDKAQQNNVEHKVETFSGVYKKLMGKDVNFEPFQQL

677/6881
FIGURE 630

GTCGCGACCCCTGGTCCGGACCTGACCTGAATTGCGACCCCAACCTGGACTGCTCCCCTGACCGCAACCCCTACCC
CCGCCCACCAGTATGCCCCGGCACGTGTTCTTAACGGGGCCCCCAGGAGTTGGAAAAACAACATTGATCCATAAA
GCCAGTGAGGTTTTAAAAATCCTCTGGTGTGCCTGTTGATGGATTTTATACCGAAGAAGTCAGACAGGGAGGGAGA
AGAATAGGATTGATGTCGTCACGTTGTCCGGCACCCGGGGGCCTTTATCGAGAGTTGGGTTAGAGCCTCCACCT
GGAAAACGTGAATGCCGAGTTGGGCAGTATGTGGTCGACCTGACTTCTTTTGAGCAGTTGGCACTACCCGTCTTG
AGGAATGCCGACTGCAGCAGTGGCCCAGGGCAAAGAGTGTGCGTCATCGATGAGATTGGGAAGATGGAGCTCTTC
AGTCAGCTTTTCATTCAAGCTGTTTCGTCAGACGCTGTCTACCCCAGGGACTATAATCCTTGGCACAATCCCAGTT
CCTAAAGGAAAGCCACTGGCTCTTGTAGAAGAAATCAGAAACAGAAAGGATGTGAAGGTGTTTAATGTCACCAAG
GAAAACAGAAACCACCTTCTGCCAGATATCGTGACGTGCGTGCAGAGCAGCAGGAAGTGAAGACACGTGCATTCC
TGCCTTCCGTGAAGGAGTGCCAGTTCAAGAGGAGCCTGATGGAGCCCTGCCTGTGAGGCTGTATGCCTATGGG
GTTATGGAACCTTGTGGGCTTTTCTAGAGAAAACCTCAACAGCTGTTTCCCATAAAATGTTTAAAAGATCAAATTA
GCCTTAATGCTGGATTGTCTGTACAAGATTAACCTATCCATTGTGGCTTATCTATGCTTAAAGATTTCCTGTTTAT
TTAAAAAAAAAAAAAAAAAAAAAAAAA

678/6881
FIGURE 631

MARHVFLTGPPGVGKTTLIHKASEVLKSSGVPVDGFYTEEVRQGGRIGFDVVTLSGTRGPLSRVGLEPPPGKRE
CRVGQYVVDLTSFEQLALPVLARNADCSSGPGQRCVIDEIGKMELEFSQLFIQAVRQTLSTPGTIILGTIPVPKGK
PLALVEEIRNRKDVKVFNVTKENRNHLLPDIVTCVQSSRK

679/6881
FIGURE 632

GCAAGATGGCAGAAGTAGAGCAGAAGAAGAAGCGGACCTTCCGCAAGTTCACCTACCGCGGCGTGGACCTGGACC
AGCTGCTGGACATGTCCTACGAACAGCTGATGCAGCTGTACAGTGC GCGCCAGCGGCGGCGGCTGAACCGGGGCC
TGCGGCGGAAGCGGCACTACCTGCTGAAGCGCCTGCGCAAGGCCAAGAAGGAGGCGCGCCCATGGAGAAGCCGG
AAGTGGTGAAGACGCACCTGAGGGACGTGATCATCCTGCCCCGAGGTGGTGGGCAGCATGGTGGGCGTCCACAACG
GCAAGACCTTCACCTACAAGCCCGTAAAGCAATGCCGGTCCGGCATCGGCGCCACCCACTCCTTCTGCTTCATCC
CTCTCAAGTAGTGGCTCAGCTAATAAAGGCGCACATG

680/6881
FIGURE 633

MAEVEQKKKRTFRKF⁶⁸⁰TYRGVDLDQLLDMSYEQLMQLYSARQRRRLNRGLRRKRHYLLKRLRKAKKEAPPMEKPEV
VKTHLRDVIIILPEVVGSMVGVHNGKTF⁶⁸⁸¹TYKPVKQCRSGIGATHSFCFIPLK

681/6881
FIGURE 634

ACCATGTCTATTCTCAAGATCCATGCCAGGGAGCTCTTTGACTCTCGTGGGAATCCCACTGTTGAGGTTGATCTC
TTCACCTCAGAAGGTCTCTTCAGAGCTGCTGTGCCCAGTGGTGCTTCAACTGGTATCTATGAGGTCCTAGAGCTC
CAGGACAATGATAAGACTCGCTATATGGGGAAGGGTGTCTCAAAGCCTGTTGAGCCCATCAATAAACTATTGCA
CCTGTCCTGGTTAGCAAGAACTGAACGTACAGAACTTCTACAGAAGCCAAGCTCCCTGGAGCCCTGTTGGCAG
CTCTAGCCTTGCAGTCATGTAATTGGCCAAATCACCGGAGCCACGTGACCCTCCAGTGTCATCTCCGGGGTGGC
CACAGGCAAGATCCCCAGTGATTTTGTGCTCAAATAAAAAGCCTCATTGACCCATGAG

682/6881
FIGURE 635

MSILKIHARELFD SRGNPTVEVDLFTSEGLFRAAVPSGASTGIYEVLELQDNDKTRYMGKGVSKPVEPINKTIAP
VLVSKKLNVTPELLQKPSSLEPCWQL

683/6881
FIGURE 636

CCCAGAAATTCTACCCAAGCTCCCTCAGCACCAATGTACCGAGCACTTCGGCTCCTCGCGCGCTCGCGTCCCCCTCG
TGCGGGCTCCAGCCGAGCCTTAGCTTCGGCTCCCGGCTTGGGTGGCGCGGCCGTGCCCTCGTTTTGGCCTCCGA
ACGCGGCTCGAATGGCAAGCCAAAATTCCTTCGGGATAGAATATGATACCTTTGGTGAACATAAAGGTGCCAAATG
ATAAGTATTATGGCGCCCAGACCGTGAGATCTACGATGAACTTTAAGATTGGAGGTGTGACAGAACGCATGCCAA
CCCCAGTTATTAAAGCTTTTGGCATCTTGAAGCGAGCGGCCGCTGAAGTAAACCAGGATTATGGTCTTGATCCAA
AGATTGCTAATGCAATAATGAAGGCAGCAGATGAGGTAGCTGAAGGTAAATTAAATGATCATTTCCTCTCGTGG
TATGGCAGACTGGATCAGGAATCAGACAAATATGAATGTAAATGAAGTCATTAGCAATAGAGCAATTGAAATGT
TAGGAGGTGAACTTGGCAGCAAGATACCTGTGCATCCCAACGATCATGTTAATAAAAGCCAGAGCTCAAATGATA
CTTTTCCACAGCAATGCACATTGCTGCTGCAATAGAAGTTTCATGAAGTACTGTTACCAGGACTACAGAAGTTAC
ATGATGCTCTTGATGCAAAATCCAAAGAGTTTGCACAGATCATCAAGATTGGACGTACTCATACTCAGGATGCTG
TTCCACTTACTCTTGGGCAGGAATTTAGTGTTATGTTCAACAAGTAAAATATGCAATGACAAGAATAAAAGCTG
CCATGCCAAGAATCTATGAGCTCGCAGCTGGAGGCACTGCTGTTGGTACAGGTTTAAATACTAGAAATTGGCTTTG
CAGAAAAGGTTGCTGCAAAAGTGGCTGCACTTACAGGCTTGCCTTTTGTCACTGCTCCGAATAAAATTTGAAGCTC
TGGCTGCTCATGACGCTCTGGTTGAGCTCAGTGGAGCCATGAACACTACTGCCTGCAGTCTGATGAAGATAGCAA
ATGATATTTCGATTTTTTGGGTTCTGGTCCTCGGTCAGGTCTGGGAGAATTGATCTTGCCTGAAAATGAACCAGGAA
GCAGTATCATGCCAGGCAAGGTGAACCCTACTCAGTGTGAAGCAATGACCATGGTTGCAGCCCAAGTCATGGGGA
ACCATGTTGCTGTCACTGTCTGGAGGCAGCAATGGACATTTTGAGTTGAATGTTTTCAAGCCAATGATGATTAAAA
ATGTGTTACACTCAGCCAGGCTGCTGGGGGATGCTTCAGTTTCCTTTACAGAAAACCTGCGTGGTGGGAATCCAGG
CCAATACAGAAAGGATCAACAAGCTGATGAATGAGTCTCTAATGTTGGTGACAGCTCTCAATCCTCATATAGGGT
ATGACAAGGCAGCAAAGATTGCTAAGACAGCACACAAAAATGGATCAACCTTAAAGGAACTGCTATCGAACTTG
GCTATCTCACAGCAGAGCAGTTTGACGAATGGGTAAAACCTAAGGACATGCTGGGTCCAAAGTGAATTACATAAA
TTTATAATGAAAATAAACATGTATAAAATTTAAAAAACAGACTCCCATTTCTTAAAAACGGATAAGTTTGAAAG
GAAACTGCTATTGAACCTAAGCATCTCTAGCAGAGCAATTTGATCAGTATATAAAACCTAGGATGTGCTAGGTC
TAAGATGGATTAAACAAGTATAAAATAAAATACATTTATAAAATAAAAGGAAAACAGACTTAAAA

684/6881
FIGURE 637

MYRALRLLARSRLVRAPAAALASAPGLGGAAVPSFWPPNAARMASQNSFRIEYDTFGELKVPNDKYYGAQTVRS
TMNFKIGGVTERMPTPVIKAFGILKRAAAEVNQDYGLDPKIANAIMKAADEVAEGKLNDHFPLVVWQTGSGTQTN
MNVNEVISNRAIEMLGGEELGSKIPVHPNDHVNKSQSSNDTFPTAMHIAAAIEVHEVLLPGLQKLHDALDAKSKEF
AQIIKIGRTHQTQDAVPLTLGQEFSGYVQQVKYAMTRIKAAMPRIYELAAGGTAVGTGLNTRIGFAEKVAAKVAAL
TGLPFVVTAPNKFEEALAAHDALVELSGAMNTTACSLMKIANDIRFLGSGPRSGLGELILPENEPGSSIMPGKVNPT
QCEAMTMVAAQVMGNHVAVTVGGSNHGFELNVFKPMMIKNVLHSARLLGDASVSFTENCVVGIQANTERINKLMN
ESLMLVTALNPHIGYDKAAKIAKTAHKNGSTLKETAIELGYLTAEQFDEWVKPKDMLGPK

685/6881
FIGURE 638

GGGXTCGGCCCCCTCCCCCTCTTCTGCGCTCTCTTCGGGATACACGTGGGCTTCGGGCCTGGGCCGCGCAGTTTTT
CTTTGGCTTTCTCGAATCATCGAGGAGACTGGCAAAATTAGTAATGTCTTTAGACTGCGTCACTAGCGCCAATCG
AATTTCGTAGTTGATTGTTCTTTGAATTCACATTTGAGTCCTCGGTTAAAACCTCAGTTAAAAAGCAGGATAAAGT
CGAGCTGCTTTGGTTCTCGGAACGGAAAAGCGTTTTTTTGTGTGTTAGAGGCTTGGCCTTTATGGGGCTCGTGTG
TGTTTTAGGGGACGGCAAAACAGAACAGAAAGGCGGAGATAAAAAGAGGGGTGTTAAAAGACCACGAGAAGATCA
TGGCCGTGGATATTTTGAGTACATTGAAGAGAACAGTATAGCAGAGCCAAATCTCCTCAGCCACCTGTTGAAGA
AGAAGATGAACACTTCGATGACACAGTGGTTTGTCTTGATACTTATAATTGTGATCTACATTTTAAAAATATCAAG
AGATCGTCTCAGTGCTTCTTCCCTTACAATGGAGAGTTTTGCTTTTCTTTGGGCTGGAGGAAGAGCATCCTATGG
TGTGTCAAAAAGGCAAAGTGTGTTTTGAGATGAAGGTTACAGAGAAGATCCCAGTAAGGCATTTATATACAAAAGA
TATTGACATACATGAAGTTCGTATTGGCTGGTCACTAACTACAAGTGAATGTTACTTGGTGAAGAAGAATTTTC
TTATGGGTATTCTCTAAAAGGAATAAAAAACATGCAACTGTGAGACTGAAGATTATGGAGAAAAGTTTTGATGAAAA
TGATGTGATTACATGTTTTGCTAACTTTGAAAGTGATGAAGTAGAACTCTCGTATGCTAAGAATGGACAAGATCT
TGGCGTTGCCTTCAAAATCAGTAAGGAAGTTCTTGCTGGACGGCCACTGTTCCCGCATGTTCTCTGCCACAACCTG
TGCAGTTGAATTTAATTTTGGTCAGAAGGAAAAGCCATATTTTCCAATACCTGAAGAGTATACTTTTCATCCAGAA
CGTCCCCCTTAGAGGATCGAGTTAGAGGACCAAAGGGGCTGAAGAGAAGAAAGATTGTGAAGTTGTGATGATGAT
TGGCTTGCCAGGAGCTGGAAAACTACCTGGGTTACTAAACATGCAGCAGAAAATCCAGGGAAAATATAACATTCT
TGGCACAAATACTATTATGGATAAGATGATGGTGGCAGGTTTTAAGAAGCAAATGGCAGATACTGGAAAACCTGAA
CACACTGTTGCAGAGAGCCCCCAGTGTCTTGGGAAATTTATTGAGATTGCTGCCCCGAAAGAAGCGAAATTTTAT
TCTGGATCAGACAAATGTGTCTGCTGCTGCCCAGAGGAGAAAAATGTGCCTGTTTGCAGGCTTCCAGCGAAAAGC
TGTTGTAGTTTGGCCAAAAGATGAAGACTATAAGCAAAGAACACAGAAGAAAGCAGAAGTAGAGGGGAAAGACCT
ACCAGAACATGCGSTCCTCAAAATGAAAGGAACTTTACCCTCCCAGAGGTAGCTGAGTGCTTTGATGAAATAAC
CTATGTTGAACTTCAGAAGGAAGAAGCCCCAAAACCTCTTGGAGCAATATAAGGAAGAAAGCAAAAAGGCTCTTCC
ACCAGAAAAGAAACAGAACACTGGCTCAAAGAAAAGCAATAAAAATAAGAGTGGCAAGAACCAGTTTAACAGAGG
TGGTGGCCATAGAGGACGTGGAGGATTCAATATGCGTGGTGGAAATTTTCAAGGAGGAGCCCCCTGGGAATCGTGG
CGGATATAATAGGAGGGGCAACATGCCACAGAGAGGTGGTGGCGGTGGAGGAAGTGGTGGAAATCGGCTATCCATA
CCCTCGTGCCCTGTTTTTCTGGCCGTGGTAGTTACTCAAACAGAGGGAACCTACAACAGAGGTGGAATGCCCAA
CAGAGGGAACCTACAACCAGAACCTCAGAGGACGAGGAAACAATCGTGGCTACAAAAATCAATCTCAGGGCTACAA
CCAGTGGCAGCAGGGTCAATTCTGGGGTCAGAAGCCATGGAGTCAGCATTATCACCAAGGATATTATTGAATACC
CAAATAAAACGAACTGATACATATTTCTCCAAAACCTTCACAAGAAGTCGACTGTTTTCTTTAGTAGGCTAACTT
TTTAAACATTCCACAAGAGGAAGTGCCTGCGGGTTCCTTTTTTTAGAAGCTTTGTGGGTGATTTTTTTTTCTTTTC
TTTTTTGTACATTTTTTAATTGCAGTTTAAAAGTGAATCGTAAGAGAACCTCAGCATTGTGCACGATAAGAGAATG
TGTCAGTATTTTCAAGGTTCTACATTTTATCTGTAAAAATGTGACTTTTTTTTTTTTTTATCACAAACAGAAGTAAAA
TGTTGCTTTGTACCTGGTGTCTTTTATTAAGAATTTACTCCCCCATTTCTCACAGAGAATAACAGTCGGGAGTC
ATTGTCACAAATATAATAGAAATGTTAGCAACCAGATTTCATGTAAGGACTAAGTGGTCTCATGAATTGCATTAAG
ACTCTGTACTGCTCATATTACACTCCATCCTCTCTGTAGTTTGCTGGGTAGTGGAGGGGGTAAGCTAAATCATAG
TTTCTGACAATAACTGGGAAGGTTTTTTCTTAAAAATAACAATGGAATTGGTATAATTGGGATTGAAAACATAAAC
TTGGAACATAAGATAGAGAAGATGGAGTGTATGTAGAAGGGCTGTAAAAATGTAAAACTTGGTTGCATTATTTGT
GGAGGCTCAAACCTGTGAAGGTTAATACCATAATTTTCCATTTGTTCTGCATTTTGATTCTGAAAAGAAAGCTG
GCTTTGCCCATTTCTTATTAAAAAACTTGTGTAAATCCAGTTGTCTAATGGGATCTATATGAAGTTAGCCATG
TCTGTATGCCCTTCTCCACAAAATACTGTATAACTAGTGTGCTTGTAGTAGTTAACTCCACCATCTTTGTAAGC
TAATGAAATTGTGAGTCACCCATTTATATCTTAATTTTTAATCATGTTCAGTTCTTGAATGGGTATCTCCTTAGCC
TGCTGATTTCTTTTTCTTTCTAAAGAAAGTGGGTGGAGAAATTAATTTAGACGTTTGTGTGCAATAAAAAGAATT
CATTTT

686/6881
FIGURE 639

GGCGTTGCCGGCCGTGGGTGCTCTGGCCACAGTGAGTTAGGGGCGTCGGAGCGGGTTTCTCCAACCGCAATCGGC
TCCGCTCAAGGGGAGGAGAGAGTCCCTTCTCGGAAGGCCTAAGGAAACGTGTCGTCTGGAATGGGCTTGGGGGC
CACGCCTGCACATCTCCGCGAGACAGAGGGATAAAGTGAAGATGGTGCTGTTATTGTTACCTCGAGTGCCACATG
CGACCTCTGAGATATGTACACAGTCATTCTTACTATCGCACTCAGCCATTCTTACTACGCTAAAGAAGAAATAAT
TATTCGAGGATATTTGCCTGGCCCAGAAGAACTTATGTAAATTTTCATGAACTATTATATCCGTTTTCTCTCGGAG
TGAGAGAAAACCTCTTTTGTAGATATCATCTGAGAGAACTAGTGAATCCCAGTCACTGAGTGGAGTTGAGAGTCTAA
GAACCTCTGAAATTTGAGAACTGCTGGACCAGAGCCTTTAGAGCTCTGATAAGGTGTCAACAGGGTAGTTAATTT
GGCACC**ATC**GGGATACAGGGATTGCTACAATTTATCAAAGAAGCTTCAGAACCCATCCATGTGAGGAAGTATAAA
GGGCAGGTAGTAGCTGTGGATACATATTGCTGGCTTCACAAAGGAGCTATTGCTTGTGCTGAAAACTAGCCAAA
GGTGAACCTACTGATAGGTATGTAGGATTTTGTATGAAATTTGTAAATATGTTACTATCTCATGGGATCAAGCCT
ATTCTCGTATTTGATGGATGTACTTTACCTTCTAAAAAGGAAGTAGAGAGATCTAGAAGAGAAAGACGACAAGCC
AATCTTCTTAAAGGGAAAGCAACTTCTTCGTGAGGGGAAAGTCTCGGAAGCTCGAGAGTGTTCACCCGGTCTATC
AATATCACACATGCCATGGCCACAAAGTAATTAAGCTGCCCGGTCTCAGGGGGTAGATTGCCTCGTGGCTCCC
TATGAAGCTGATGCGCAGTTGGCCTATCTTAACAAAGCGGGAATTGTGCAAGCCATAATTACAGAGGACTCGGAT
CTCCTAGCTTTTGGCTGTAAAAAGGTAATTTTAAAGATGGACCAGTTTGAAATGGACTTGAAATTGATCAAGCT
CGGCTAGGAATGTGCAGACAGCTTGGGGATGTATTACGGAAGAGAAGTTTCGTTACATGTGTATTCTTTCAGGT
TGTGACTACCTGTCTACTGCGTGGGATTGGATTAGCAAAGGCATGCAAAGTCCTAAGACTAGCCAATAATCCA
GATATAGTAAAGGTTATCAAGAAAATTGGACATTATCTCAAGATGAATATCACGGTACCAGAGGATTACATCAAC
GGGTTTATTCGGGCCAACAAATACCTTCTCTATCAGCTAGTTTTTGATCCCATCAAAGGAAACTTATTCCTCTG
AACGCCTATGAAGATGATGTTGATCCTGAAACACTAAGCTACGCTGGGCAATATGTTGATGATTCCATAGCTCTT
CAAATAGCACTTGAAAATAAAGATATAAATACTTTTGAACAGATCGATGACTACAATCCAGACACTGCTATGCCT
GCCCATTCAAGAAGTCATAGTTGGGATGACAAAACATGTCAAAGTCAGCTAATGTTAGCAGCATTGCGCATAGG
AATTACTCTCCAGACCAGAGTCGGGTACTGTTTCAGATGCCCCACAATTGAAGGAAAATCCAAGTACTGTGGGA
GTGGAACGAGTGATTAGTACTAAAGGGTTAAATCTCCCAAGGAAATCATCCATTGTGAAAAGACCAAGAAGTGCA
GAGCTGTGAGAAGATGACCTGTTGAGTCAGTATTCTCTTTCATTTACGAAGAAGACCAAGAAAAATAGCTCTGAA
GGCAATAAATCATTGAGCTTTTCTGAAGTGTTTGTGCTGACCTGGTAAATGGACCTACTAACAAAAAGAGTGTA
AGCACTCCACCTAGGACGAGAAATAAATTTGCAACATTTTACAAAGGAAAAATGAAGAAAGTGGTGCAGTTGTG
GTTCCAGGGACCAGAAGCAGGTTTTTTTTGTCAGTTCAGATTCTACTGACTGTGTATCAAACAAAGTGAGCATCCAG
CCTCTGGATGAAACTGCTGTACAGATAAAGAGAAACATCTGCATGAATCAGAGTATGGAGACCAAGAAGGCAAG
AGACTGGTTGACACAGATGTAGCACGTAATTCAAGTGATGACATTCCGAATAATCATATTCCAGGTGATCATATT
CCAGACAAGGCAACAGTGTTTACAGATGAAGAGTCTACTCTTTTGAGAGCAGCAAATTTACAAGGACCATTTC
CCACCCACTTTGGGAACACTAAGAAGTTGTTTTAGTTGGTCTGGAGGTCTTGAGATTTTTTCAAGAACGCCGAGC
CCCTCTCCAAGCACAGCATTGCAGCAGTTCCGAAGAAAAGAGCGATTCCCCCACCTCTTTGCCTGAGAATAATATG
TCTGATGTGTCGCAGTTAAAGAGCGAGGAGTCCAGTGACGATGAGTCTCATCCCTTACGAGAAGGGGCATGTTCT
TCACAGTCCCAGGAAAGTGGAGAATTCTCACTGCAGAGTTCAAATGCATCAAAGCTTTCTCAGTGCTCTAGTAAG
GACTCTGATTGAGAGGAATCTGATTGCAATATTAAGTTACTTGACAGTCAAAGTGACCAGACCTCCAAGCTATGT
TTATCTCATTTCTCAAAAAAAGACACACCTCTAAGGAACAAGGTTCCCTGGGCTATATAAGTCCAGTTCTGCAGAC
TCTCTTTCTACAACCAAGATCAAACCTCTAGGACCTGCCAGAGCCAGTGGGCTGAGCAAGAAGCCGGCAAGCATC
CAGAAGAGAAAGCATCATAATGCCGAGAACAAGCCGGGTTACAGATCAAACCTCAATGAGCTCTGGAAAACTTT
GGATTTAAAAAAGATTCTGAAAAGCTTCTCTTGTAAAGAAACCCCTGTCCCAGTCAGAGATAACATCCAACCTA
ACTCCAGAAGCGGAAGAGGATATATTTAACAAACCTGAATGTGGCCGTGTTCAAAGAGCAATATTCAGT**TAA**ATG
CAGACTGCTGCAAAGCTTTTGCCTGCAAGAGAATCTGATCAATTTGAAGTCCCTGTTTGGGAATGAGGCACTTAT
CAGCATGAAGAATTTTTCTCATTCTGTGCCATTTTAAAAATAGAATACATTTTGTATATTGACTTTAAAAAAA
AAAAAAAAAAAAA

687/6881
FIGURE 640

MGIQGLLQFIKEASEPIHVRKYKGQVVAVDTYCWLHKGAIACAELAKGEPTDRYVGFCMKFVNMLLSHGKPIIL
VFDGCTLP SKKEVERSRERRRQANLLKGKQLLREGKVSEARECFTRSINITHAMAHKVIKAARSQGVDCLVAPYE
ADAQLAYLNKAGIVQAIITEDSDLLAFGCKKVILKMDQFGNGLEIDQARLGMCRLGDVFTTEKFRYMCILSGCD
YLSSLRGIGLAKACKVRLANNPDIVKVIKKIGHYLMKNITVPEDYINGFIRANNTFLYQLVFDPIKRKLIPLNA
YEDDVDPETLSYAGQYVDDSIQIALGNKDINTFEQIDDYNPD TAMP AHSRSHSWDDKTCQKSANVSSIWHRNY
SPRPESGTVSDAPQLKENPSTVGVERVISTKGLNLPRKSSIVKRPRSAELSEDDLLSQYSLSFTKKTKKNSSEGN
KSLSFSEVFVPDLVNGPTNKKSVSTPPRTRNKFATFLQRKNEESGAVVPGTRSRFFCSDSTDCVSNKVS IQPL
DETA VTDKENNLHESEYGDQEGKRLVDTDVARNSSDDIPNNHIPGDHIPDKATVFTDEESYSFESSKFTRTISPP
TLGTLRSCFSWSGGLGDFSRTSPSPSPSTALQQFRKSDSPTSLPENNMSDVSQKSEESSDDESHPLREGACSSQ
SQESGEFSLQSSNASKLSQCSSKSDSEESDCNIKLLDSQSDQTSKLCLSHFSKKDTPLRNKVPGLYKSSSADSL
STTKIKPLGPARASGLSKKPASIQKRKHHNAENKPGQLIKLNLWKNFGFKKDSEKLPPCKKPLSPVRDNIQLTP
EAEEDIFNKPECGRVQRAIFQ

688/6881
FIGURE 641

TCTAATACCTATTGATCTGTCACCTTTCTCCCATCACGCTCAGGTGGGACCATCCAGTTGCAGGAAAACAAGCTTA
ACACGCCCCACTGATTCTACATTATGGTGAGTTCTATAATTATTTTATTATATATTACAGTGTAATAATGGAAATA
AAGTGCCTAATAAAATGCAAATGTGCTTACATCTTTTGGCCCAGCTCCTACCTCCTGGCAGCCTCTCCAGGCCAG
AACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCACAATGGCCTATTTAGGCCCATACCCTACGTCAC
GGCAGTCTCCGCAGATGAGGCTACTGCCTCACAACAGCCTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTT
TAGACCCAGCTCCTGCCTCCCAGCCTTCTCTCCAGGCCCTGAACTTTCTCAAGTCGACCTCACCAGGCCAGCTC
ATGCTTCTTTGCAGCCTCTCCAGGCCAGCTCCTGCATCTTGGTGGCCCCTCCAGGCCAGCCTCTGCCTCCCGT
CGGCCTCTACAGTCCCAACATCTGTCTCACAGCAGATTCTTCAGGCCAGCATCTGCCTCACTTGGACCCTCCAG
ACCCAGATGGTGTCTCACTGTGGCATCCTCAGGTGAAGCTCCTGCCTTTCGGCAGCCTCTCCAGGCCAGCTCCT
CCTGCCTCCCAGTGGCCTCTTTTCGGCCCAGCCCAGCTCATGCCTCCCGGCGGCCTTCCCAAGCCCCGCTTTTGAC
TTTCCACCGAAAGTCCCAGCCTCCTGCCTCCCGAAGGCCTGCACAGGCCCA

689/6881
FIGURE 642

GTCCACATGCAGAGGCTCGCTACAGAAGCTACAGAAGAAGATGGTTACATTTCAAGTGGGCAGGTGCCGTTTGCT
TATGAGCACCATCAGCCACATCAGCCACGGTTCTTTGAATTTTACCTAATTGTCTCTAATTCTTAACAATTCTTT
GAGGTGATCTGCAACTCTTTCACCATCTGTAATGCGGAGATGCAGGAAGTTGGTGTGGCCTATATCCCAGTATC
TCTTTGCTCAATCACAGCTGTGACCCCACTGTTTCGATTGTGTTCAATGGGCCCCACCTCTTACTGCGAGCAGTC
CGAGACATCGAGGTGGGAGAGGAGCTCACCATCTGCTACCTGGATATGCTGATGACCAGTGAGGAGCGCCGGAAG
CAGCTGAGGGACCAGTACTGCTTTGAATGTGACTGTTTCCGTTGCCAAACCCAGGACAAGGATGCTGATATGCTA
ACTGGTGATGAGCAAGTATGGAAGGAAGTTCAAGAATCCCTGAAAAAAATTGAAGAACTGAAGGCACACTGGAAG
TGGGAGCAGGTTCTGGCCATGTGCCAGGCAATCATAAGCAGCAATTCTGAACGGCTTCCCGATATCAACATCTAC
CAGCTGAAGGTGCTCGACTGCGCCATGGATGCCTGCATCAACCTCGGCCTGTTGGAGGAAGCCTTGTTCTATGGT
ACTCGGACCATGGAGCCATACAGGATTTTTTTCCAGGAAGCCATCCCGTCAGAGGGGTTCAAGTGATGAAAGTT
GGCAAACCTGCAGCTACATCAAGGCATGTTTCCCAAGCAATGAAGAATCTGAGACTGGCTTTTGATATTATGAGA
GTGACACATGGCAGAGAACACAGCCTGATTGAAGATTTGATTCTACTTTTAGAAGAATGCGACGCCAACATCAGA
GCATCCTAAGGGAACGCAGTCAGAGGGAAATACGGCGTGTGTCTTTGTTGAATGCCTTATTGAGGTCACACACTC
TATGCTTTGTTAGCTGTGTGAACCTCTCCTATTGGAAATTCTGTTCCGTGTTTGTGTAGGTAAATAAAGGCAGAC
ATGGTTTGCAAACCACAAGAATCATTAGTTGTAGAGAAGCACGATTATAATAAATTCAAAACATTTGGTTGAGGA
TGCC

690/6881
FIGURE 643

CTTGCTTCGGACGCCGGATTTTGACGTGCTCTCGCGAGATTGGGTCTCTTCCTAAGCCGGCGCTCGGCAAGTTC
TCCCAGGAGAAAGCC**ATG**TTTCAGTTCGAGCGCCAAGATCGTGAAGCCCAATGGCGAGAAGCCGGACGAGTTCGAG
TCCGGCATCTCCCAGGCTCTTCTGGAGCTGGAGATGAACTCGGACCTCAAGGCTCAGCTCAGGGAGCTGAATATT
ACGGCAGCTAAGGAAATTGAAGTTGGTGGTGGTTCGGAAAGCTATCATAATCTTTGTTCCCGTTCCTCAACTGAAA
TCTTTCCAGAAAATCCAAGTCCGGCTAGTACGCGAATTGGAGAAAAAGTTCAGTGGGAAGCATGTCGTCTTTATC
GCTCAGAGGAGAATTCTGCCTAAGCCAACTCGAAAAAGCCGTACAAAAAATAAGCAAAAGCGTCCCAGGAGCCGT
ACTCTGACAGCTGTGCACGATGCCATCCTTGAGGACTTGGTCTTCCCAAGCGAAATTGTGGGCAAGAGAATCCGC
GTCAAACTAGATGGCAGCCGGCTCATAAAGGTTCAATTTGGACAAAGCACAGCAGAACAAATGTGGAACACAAGGTT
GAAACTTTTTCTGGTGTCTATAAGAAGCTCACGGGCAAGGATGTTAATTTTGAATTTCCAGAGTTTCAATTG**TAA**
ACAAAAATGACTAAATAAAAAGTATATATTCACAGTAAAAAAAAAAAAAAAAAAAA

691/6881
FIGURE 644

MFSSSAKIVKPNGEKPDEFESGISQALLELEMNSDLKAQLRELNITAAKEIEVGGGRKAIIFVVPVQLKSFQKI
QVRLVRELEKKFSGKHVVFIAQRRILPKPTRKSRTKNKQKRPRSRTLTA VHDAILEDLVFPSEIVGKRIRVKLDG
SRLIKVHLDKAQQNNVEHKVETFSGVYKKLTGKDVNFEFFPEFQL

692/6881
FIGURE 645

GGCACGAGGCGGGGCCAGCGACGGGCAGGACGCCCCGTTGCGCTAGCGCGTGCTCAGGAGTTGGTGTCTGCCTGCCTGC
GCTCAGGATGAGGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCACTGCTGCCATCTGG
ACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTCGTCCCTGGCCTCAAAGGGGATGCGGGAGA
GAAGGGAGACAAAGGCGCCCCCGGACGGCCTGGAAGAGTCGGCCCCACGGGAGAAAAAGGAGACATGGGGGACAA
AGGACAGAAAGGCAGTGTGGGTCGTTCATGGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGG
TGACATAGGACCCCCCTGGTCCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGG
GGAGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTGCGCGGTGTGCGCGA
GACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGACGCCCAGCTGTCCTGCCAGGGCCG
CGGGGGCACGCTGAGCATGCCCAAGGACGAGGCTGCCAATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCT
GGCCCCGTGTCTTCATCGGCATCAACGACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCCATGCG
GACCTTCAACAAGTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGGAGATGGTGGCCTC
GGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAGGAGAACATGTGAGC
CTCAGGCTGGGGCTGCCCATTGGGGGCCCCACATGTCCCTGCAGGGTTGGCAGGGACAGAGCCCAGACCATGGTG
CCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAGGCTCACTGAGTAGAGGGCTGTTGTCTAAACTGAGAAAATG
GCCTATGCTTAAGAGGAAAATGAAAGTGTTCCTGGGGTGCTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATT
GTAGCCCCAATGTCATTATGTAATTATTACCCAGAATTGCTCTTCATAAAGCTTGTGCCTTTGTCCAAGCTATA
CAATAAAATCTTTAAGTAGTGCAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

693/6881
FIGURE 646

MRGNLALVGVLISLAFLSLLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGRVGPTGEKGDMDKGQ
KGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLRKAIGEMDNQVSQLTSELKFIKNAVAGVRETE
SKIYLLVKEEKRYADAQLSCQGRGGTLSMPKDEAANGLMAAYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTF
NKWRSGEPNNAIDEEDCVEMVASGGWNDVACHTTMYFMCEFDKENM

694/6881
FIGURE 647

GGCACGAGGGGCTTCTGTACCTTCCTCACGGACCTTGGTACGGCCGCAGGTGACCCCTTAGCCCAGCTCCAGT
GGGCGGGTGGCAGGGTCATGGAGGACGCTGGCGGCGGCGAGGAGACCCGGCCCCGGAGGCCCCGCACCCCCCTC
AGCTCGCGCCTCCGGAGGAGCAGGGTTGCTCTTCCAGGAGGAAACCATCGATCTTGGCGGAGATGAGTTTGGAT
CCGAAGAGAACGAGACCGCATCGGAAGGCTCGAGTCCTCTCGCGGACAAGCTGAACGAACACATGATGGAGAGCG
TCCTCATCTCTGACTCCCCAACAGCGAGGGCGACGCGGGCGACCTGGGGCCGAGTGCGGGACGAAGCTGAGCCCC
GAGGGGAAGGCGACCCAGGCCCGGAGCCCGCGGGCACCCGAGTCCCAGCGGCGAGGCCGACGGCGACTGTGCCC
CCGAGGACGCGGCACCCAGTAGCGGAGGGGCCCCGAGGCAGGACGCGGCCCGCGAGGTCCCAGGCAGCGAAGCCG
CGCGCCCGGAGCAGGAGCCTCCCGTTGCGGAGCCGGTCCCGGTGTGCACCATCTTCAGCCAGCGCGCGCCCCAG
CCTCCGGGGACGGCTTCGAGCCGCAGATGGTGAAGTCGCCCAGCTTCGGTGGCGCCAGCGAGGCCTCGGCCAGGA
CACCGCCCCAGGTTCGTGCAGCCCAGCCCCAGCCTCAGCACGTTCTTCGGAGACACGGCCGCCAGCCACTCCTTGG
CCTCGGACTTCTTCGACTCCTTTACTACCTCCGCCTTCATTTCCGTGACCAATCCCGGCGCGGGCTCCCCGGCCC
CCGCCAGCCCGCCTCCCTTCGCTGTGCCGGGACCGAGGGGCGCCCCGAACCCGTGGCCATGCGAGGGCCCCAGG
CAGCTGCGCCCCCGGCGTCGCCAGAGCCTTTCGCGCACATCCAGGCAGTGTTCGAGGGAGTGACGACCCCTTTG
CCACCGCCCTGAGCATGAGCGAGATGGACCGGAGGAACGACGCCTGGCTTCCCGGCGAGGCTACGCGTGGAGTCC
TGCGGGCCGTGGCCACCCAGCAGCGCGGCGCCGTGTTTCGTGGACAAGGAGAACCTCACCATGCCGGGCCTCAGGT
TCGACAACATCCAGGGAGATGCAGTTAAAGACTTGATGCTTCGCTTTCTGGGTGAAAAAGCTGCAGCAAAGAGAC
AAGTCCTAAATGCCGACTCAGTGGAAACAATCTTTTGTTGGATTGAAACAGCTAATCAGCTGCAGAACTGGAGGG
CAGCAGTGGACCTGTGCGGACGTCTCCTCACAGCCACGGCCAGGGCTACGGCAAGAGCGGGCTGCTCACCAGCC
ACACGACAGATTCACTGCAGCTCTGGTTTGTTCAGGCTGGCACTACTAGTGAAGTTGGGCCTTTTCCAGAATGCTG
AGATGGAATTTGAACCCCTTCGGAAATCTTGATCAGCCAGATCTTTATTACGAGTACTACCCGCACGTGTACCCTG
GGCGCAGGGGCTCCATGGTCCCCCTTCTCGATGCGCATCTTGACGCGGAGCTTCAGCAGTACCTGGGGAACCCAC
AGGAGTCGCTGGATAGACTGCACAAGGTGAAGACTGTCTGCAGCAAGATCCTGGCCAATTTGGAGCAAGGCTTAG
CAGAAGACGGCGGCATGAGCAGCGTGACTCAGGAGGGCAGACAAGCCTCTATCCGGCTGTGGAGGTACAGTCTGG
GCCGGGTGATGTACTCCATGGCAAACGTCTGTCTCCTGATGAAGGATTATGTGCTGGCCGTGGATGCGTATCATT
CGGTTATCAAGTATTACCCAGAGCAAGAGCCCCAGCTGCTCAGCGGCATCGGCCGGATTTCCCTCCAGATTGGAG
ACATAAAAACAGCTGAAAAGTATTTTCAAGACGTTGAGAAAGTAACACAGAAATTAGACGGACTACAGGGTAAAA
TCATGGTTTTTGATGAACAGCGCGTTCCCTTCACCTCGGGCAGAATAACTTTGCAGAAGCCCACAGGTTCTTCACAG
AGATCTTAAGGATGGATCCAAGAAACGCAGTGGCCAACAACAACGCTGCCGTGTGTCTGCTCTACCTGGGCAAGC
TCAAGGACTCCCTGCGGCAGCTGGAGGCCATGGTCCAGCAGGACCCCAGGCACTACCTGCACGAGAGCGTGCTCT
TCAACCTGACCACCATGTACGAGCTGGAGTCCCTCACGGAGCATGCAGAAGAAACAGGCCCTGCTGGAGGCTGTGCG
CCGGCAAGGAGGGGGACAGCTTCAACACACAGTGCCTCAAGCTGGCCTAGCTGCCTCCAACACACTACGTGAGAA
GGACCCGGGTCTTTGAAACTGTGTCTTGAAGCTAATGTATTAATGTGACATGGAGGAACTCAATAAACTCCTGC
TTCAAAAAAAAAAAAAAAAAAAAAA

695/6881
FIGURE 648

MLRFLGEKAAAKRQVLNADSVEQSFVGLKQLISCRNWRAAVDLCGRLLTAHGQGYGKSGLLTSHTTDSLQLWFVR
LALLVKLGFLFQNAEMEFEPFGNLDQPDLYEYYPHVYPGRRGSMVPFMRILHAELQQYLGNPQESLDRHLHKVKT
VCSKILANLEQGLAEDGGMSSVTQEGRQASIRLWRSRLGRVMYSMANCLLLMKDYVLAVDAYHSVIKYYPEQEPQ
LLSGIGRISLQIGDIKTAEKYFQDVEKVTQKLDGLQGKIMVLMNSAFLHLGQNNFAEAHRFFTEILRMDPRNAVA
NNNAVCLLYLGKCLKDSLRLQLEAMVQDPRHYLHESVLFNLTMYELESSRSMQKKQALLEAVAGKEGDSFNTQC
LKLA

696/6881
FIGURE 649

AATTCGGCACGAGAAGACTTCCAGTTTGGAGTCGTTTGCTGCGGGGAGGGAATGAATGGGCGCTGGGAACACGCC
CGCGAGGTGGGGACGCGCCGGCCGTAGCGAGGTCCTTAGCGTGTGAGTGGCCGGGGTCGGGTCGCTTCCCCGCAG
CATGGAGGACGATGCACCAGTGATCTACGGGCTGGAGTTCAGGCACGTGCCTTAACACCTCAAACCTGCAGAAAC
AGATGCCATTTCGGTTTTTGGTTGGGACGCAGTCTCTTAAATATGATAATCAGATCCATATCATAGATTTTGACGA
TGAAAACAACATTATAAATAAAAAATGTCTCTCCATCAAGCGGGTGAAATCTGGCATATTAGCGCTAGCCCTGC
AGACAGAGGTGTGCTGACGACCTGCTACAACAGAACTTCAGACAGCAAAGTCCTGACATGTGCAGCCGTGTGGAG
GATGCCGAAGGAATTGGAATCAGGCAGCCACGAGTCCCCTGATGATTCATCCAGCACTGCACAGACCCCTGGAGCT
GCTCTGTACCTTGACAACACAGCCCATGGCAACATGGCCTGTGTCTGTGGGAGCCAATGGGAGATGGGAAGAA
AATCATTTCTTGGCTGATAACCATATCTGTGTGGGATTTACAGGAAAGCTCGAGCCAGGCTGTGCTGGCCAG
CTCAGCGTCCCTGGAAGGGAAGGGACAACCTGAAGTTCACCTCAGGACGGTGGAGCCACATCATAACTGCACCCA
GGTGGCCACAGCGAACGACACCACCTCCGTGGCTGGGACACCCGGAGCATGAGCCAGATCTACTGCATAGAGAA
TGCCACAGGACAGCTGGTGCGGGACCTTGACTTTAATCCCAATAAGCAGTACTACTTGGCCAGCTGCGGAGACGA
CTGTAAGGTGAAGTTCTGGGACACCCGAAATGTACCCGAACCCGTGAAGACCCTGGAGGAGCACTCCCACTGGGT
GTGGAACGTCCGCTACAACCACTCTCATGACCAGCTGGTCCCTCACGGGCAGCAGTGACAGCAGAGTCATCCTTTC
CAACATGGTGTCCATCTCGTCGGAGCCCTTCGGCCACTTGGTAGACGACGATGACATCAGTGACCAGGAGGACCA
CCGTTCTGAAGAGAAGAGCAAGGAGCCCTGCAGGACAACGTGATCGCCACCTACGAGGAGCACGAGGACAGCGT
CTATGCCGTGGACTGGTCCCTCGGCTGACCCGTGGCTGTTTGCTCCCTGAGCTATGACGGGAGGCTCGTGATCAA
CAGGGTGCCAGGGCCCTGAAGTACCACATCCTGCTATTGACTCCCGGGCCTGGGTTATCCAGGTCCCATTGAGTG
GTTTTCTCTTGGCAGATTCTCAAACAGTCGCAGCTCTTTGGAGGTGACTCGTGTTCCAGGTGGATCCCTCTCTG
GGAGAGCCGCTGTTCCCTTCTGTAGCAGCAGCATTTATGAATGGGGTGAATGGGGCTATTGTGACGGCACAGC
TAATGCCCCGAACCCAGCCCTGTGCGCAGAGACAGAGCCCCACATTATTATGTGAATAACAATGTTTTCTGTTTT
AAGGGTGTGAGGAGTTTCGCTTTTTAAAAAATGTCTGTTCTGTCAGTAGTAACCTCTTCTTCTCTTGAGAGTAA
AAAATGAAATAAAATAAATCCACGCTGACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

697/6881
FIGURE 650

MEDDAPVIYGLEFQARALTPQTAETDAIRFLVGTQSLKYDNQIHIIDFDDENNIINKNVLLHQAGEIWHISASPA
DRGVLTTTCYNRTSDSKVLTCAAVWRMPKELESGSHESPDDSSSTAQTLELLCHLDNTAHGNMACVVWEPMGDGKK
IISLADNHILLWDLQESSSQAVLASSASLEGKGQLKFTSGRWSPHHNCTQVATANDTTLRGWDTRSMSQIYCIEN
AHGQLVRDLDFNPNKQYYLASCDDCKVKFWDTRNVTEPVKTL EEHSHVWVNVRYNHS HDQLVLTGSSDSRVILS
NMVSISSEPFGLVDDDDISDQEDHRSEEKSKEPLQDNVIATYEEHEDSVYAVDWSSADPWLFASLSYDGRLVIN
RVPRALKYHILL

698/6881
FIGURE 651

CCCAGGCGCAGCCAATGGGAAGGGTCGGAGGCATGGCACAGCCAATGGGAAGGGCCGGGGCACCAAAGCCAATGG
GAAGGGCCGGGAGCGCGCGGGGAGATTTAAAGGCTGCTGGAGTGAGGGGTCGCCCCGTGCACCCTGTCCCAG
CCGTCTGTCTTGGCTGCTCGCTCTGCTTCGCTGCGCCTCCACTATGCTCTCCCTCCGTGTCCCCTGCGCGCCA
TCACGGACCCGACAGCTGCAGCTCTCGCCGCTGAAGGGGCTCAGCTTGGTCGACAAGGAGAACACGCCGCGCGG
CCCTGAGCGGGACCCGCGTCTTGCCAGCAAGACCGCGAGGAGGATCTTCCAGGAGCCCACGGAGCCGAAAACCTA
AAGCAGCTGCCCCCGCGTGGAGGATGAGCCGCTGCTGAGAGAAAACCCCGCCGCTTTGTTCATCTTCCCCATCG
AGTACCATGATATCTGGCAGATGTATAAGAAGGCAGAGGCTTCCTTTTGGACCGCCGAGGAGGTTGACCTCTCCA
AGGACATTACAGCACTGGGAATCCCTGAAACCCGAGGAGAGATATTTTATATCCCATGTTCTGGCTTTCTTTGACG
CAAGCGATGGCATAGTAAATGAAAACCTTGGTGGAGCGATTTAGCCAAGAAGTTCAGATTACAGAAGCCCGCTGTT
TCTATGGCTTCCAAATTGCCATGGAAAACATACATTCTGAAATGTATAGTCTTCTTATTGACACTTACATAAAAG
ATCCCAAAGAAAGGGAATTTCTCTTCAATGCCATTGAAACGATGCCTTGTGTCAAGAAGAAGGCAGACTGGGCCT
TGCGCTGGATTGGGGACAAAGAGGCTACCTATGGTGAACGTGTTGTAGCCTTTGCTGCAGTGGAAGGCATTTTCT
TTTCCGGTTCTTTTTCGCTCGATATTCTGGCTCAAGAAACGAGGACTGATGCCTGGCCTCACATTTTCTAATGAAC
TTATTAGCAGAGATGAGGGTTTACACTGTGATTTTGTCTTGCCTGATGTTCAAACACCTGGTACACAAACCATCGG
AGGAGAGAGTAAGAGAAAATAATTATCAATGCTGTTTCGGATAGAACAGGAGTTCCTCACTGAGGCCTTGCTGTGA
AGCTCATTGGGATGAATTGCACTCTAATGAAGCAATACATTGAGTTTGTGGCAGACAGACTTATGCTGGAAGTGG
GTTTTAGCAAGGTTTTTCAGAGTAGAGAACCCATTTGACTTTATGGAGAATATTTCACTGGAAGGAAAGACTAACT
TCTTTGAGAAGAGAGTAGGCGAGTATCAGAGGATGGGAGTGATGTCAAGTCCAACAGAGAATTCTTTTACCTTGG
ATGCTGACTTCTAAATGAAGTGAAGATGTGCCCTTACTTGGCTGATTTTTTTTTTCCATCTCATAAGAAAAATCA
GCTGAAGTGTTACCAACTAGCCACACCATGAATTGTCCGTAATGTTTCAATTAACAGCATCTTTAAACTGTGTAGC
TACCTCACAAACAGTCCTGTCTGTTTATAGTGCTGGTAGTATCACCTTTTGCCAGAAGGCCTGGCTGGCTGTGAC
TTACCATAGCAGTGACAATGGCAGTCTTGGCTTTAAAGTGAGGGGTGACCTTTAGTGAGCTTAGCACAGCGGGA
TTAAACAGTCCTTTAACCAGCACAGCCAGTTAAAGATGCAGCCTCACTGCTTCAACGCAGATTTTAAATGTTTAC
TTAAATATAAACCTGGCACTTTACAAACAAATAAACATTGTTTTGTACTCACGGCGGCGATAATAGCTTGATTTA
TTTGGTTTTCTACACCAAATACATTCTCCTGACCACTAATGGGAGCCAATTCACAATTCCTAAGTGAAGTAAAGTA
AGTTAACTTGTGTAGACTAAGCATGTAATTTTTTAAGTTTTATTTTAAATGAATTAAATATTTGTTAACCAACTT
TAAAGTCAGTCCTGTGTATACCTAGATATTAGTCAGTTGGTGCCAGATAGAAGACAGGTTGTGTTTTTATCCTGT
GGCTTGTGTAGTGTCTGGGATTCTCTGCCCCCTCTGAGTAGAGTGTTGTGGGATAAAGGAATCTCTCAGGGCAA
GGAGCTTCTTAAAGTTAAATCACTAGAAAATTTAGGGGTGATCTGGGCCTTCATATGTGTGAGAAGCCGTTTCATTT
TATTTCTCACTGTATTTTCTCAACGTCTGGTTGATGAGAAAAAATCTTGAAGAGTTTTTCATATGTGGGAGCTA
AGGTAGTATTGTAAATTTCAAGTCATCCTTAAACAAAATGATCCACCTAAGATCTTGCCCTGTAAAGTGGTGA
AATCAACTAGAGGTGGTTTCTACAAGTTGTTTCAATTCTAGTTTTTGGTTGGTGAAGTAGGTTGTGTGAGTTAATTC
ATTTATATTTACTATGTCTGTAAATCAGAAAATTTTTATTATCTATGTTCTTCTAGATTTTACCTGTAGTTTCAT
AAAAAAAAAAAAAAAAAAAAAAAAA

699/6881
FIGURE 652

MLSLRVPLAPITDPQQQLQLSPLKGLSLVDKENTPPALSGTRVLASKTARRIFQEPTTEPKTKAAAPGVEDEPLLRE
NPRRFVIFPIEYHDIWQMYKKAEASFWTAEVDLSKDIQHWESLKPEERYFISHVLAFFAASDGIVNENLVERFS
QEVQITEARCFYGFQIAMENIHSEMYSLIDITYIKDPKEREFLFNAIETMPCVKKKADWALRWIGDKEATYGERV
VAFAAVEGIFFGSGSFASIFWLKKRGLMPGLTFSNELISRDEGLHCDFACLMFKHLVHKPSEERVREIIINAVRIE
QEFLTEALPVKLI GMNCTLMKQYIEFVADRLMLELGF SKVFRVENPFDFMENISLEGKTNFFEKRVGEYQRMGVM
SSPTENSFTLDADF

700/6881
FIGURE 653

GTGCTGAGGCGCCCATGGCCTTCGCCCCGCGGCTCCTGCGCGGGCCACTGTGCGGGCCGCTGCTCGGGCGGGCGC
GGGGTCTGCGCTGGGGCCATGGCTCCGCCGCGCCGCTTCGTCTTGAGCTTCCCGACTGCACCCCTGGCTCACTTC
GCCCTAGGCGCCGACGCCCCGCGACGCAGACGCCCCGACCCCGCCTGGCGGGCGCTGCTGGGGCCCCCGGAG
CGCAGCTACTCGCTGTGCGTGCCCGTGACCCCGGACGCCGGCTGCGGGGGCCGGGTCCGGGCGGCGCGGCTGCAC
CAGCGCCTGCTGCACCAGCTGCGCCGCGGCCCCCTCCAGCGGTGCCAGCTGCTCAGGCTGCTCTGCTACTGCCCCG
GGCGGCCAGGCCGGCGGGCGCACAGCAAGGCTTCCTGCTGCGCGACCCCTGGATGACCCTGACACCCGGCAAGCG
CTGCTCGAGCTGCTGGGCGCCTGTGAGGAGGCACACGCCCGCACTTGGGCGAGTTCGAGGCCGACC¹CGCGCGGC
CAGCTGTGGCAGCGCCTCTGGGAGGTGCAAGACGGCAGGCGGCTGCAGGTGGGCTGCGCACAGGTCGTGCCCGTC
CCGGAGCCCCCGCTGCACCCGGTGGTGCCAGACTTGCCAGTTCCTGTTGTTCTCCCGGACCGGGAAGCCGCCCGG
GCCGTTTTTGGAGGAGTGACCTCCTTTATTCTTGAAGCCCGGCAGTGCTTGACCTGGTCGACCAAGTGCCTCAAA
CAGATCCAGAAAGGAAAGTTCCAGGTTGTTGCCATCGAAGGACTGGATGCCACGGGTAAACCACGGTGACCCAG
TCAGTGGCAGATTCACTTAAGGCTGTCTCTTAAAGTCACCACCCTCTTGCAATTGGCCAGTGGAGGAAGATCTTT
GATGATGAACCAACTATCATTAGAAGAGCTTTTTACTCTTTGGGCAATTATATTGTGGCCTCCGAAATAGCTAAA
GAATCTGCCAAATCTCCTGTGATTGTAGACAGGTACTGGCACAGCACGGCCACCTATGCCATAGCCACTGAGGTG
AGTGGGGGTCTCCAGCACCTGCCCCAGCCCATCACCTGTGTACCAGTGGCCAGAGGACCTGCTCAAACCTGAC
CTTATCCTGCTGCTCACTGTGAGTCTTGAGGAGAGGTTGCAGAGGCTGCAGGGCCGGGGCATGGAGAAGACCAGG
GAAGAAGCAGAACTTGAGGCCAACAGTGTGTTTCGTCAAAGGTAGAAATGTCTACCAGCGGATGGAGAATCCT
GGCTGCCATGTGTTGATGCCAGCCCCCTCCAGAGAAAAGTCTGCAGACGGTATTAAGCCTAATCCAGAATAGT
TTTAGTGAACCGTAGTACTCTGGCCAGGTGCCACGTCTAACTAGATTAGATGTTGTTTGAACATCTACATCCA
CCATTTGTTATGCAGTGTTCCCAAATTTCTGTTCTACAAGCATGTTGTGTGGCAGAAAACCTGGAGACCAGGCATC
TTAATTTTACTTCAGCCATCGTACCCTCTTCTGACTGATGGACCCGTATCACAAAGGTCCCTCTCATCATGTTT
CAGTGAGAGGCCAGCGATTGCTTTCTTCTGGCATACTAAACATTTTCTTGGAAACATATGTTTCACTTAATCACT
ACCAAATATCTGGAAGACCTGTCTTACTCAGACAGCACCAGGTGTACAGAAGCAGCAGACAAGATCTTCCAGATC
AGCAGGGAGACCCCGGAGCCTCTGCTTCTCCTACACTGGCATGCTGATGAGATCGTGACATGCCACATTGGCTT
CTTCCACATCTGGTTGCACTCGTCATGATGGGCTCGCTGCATCTCCCTCAGTCCCAAATTCAGAGCCAAGTGTT
CCTGCAGAGGCTGTCTATGTGTCTGGCTGCCCAAGGACACTCCTGCAGAGCCATTTTGGGTAAGGAACACTTA
CAAAGAAGGCATTGATCTTGTGTCTGAGGCTCAGAGCCCTTTTGATAGGCTTCTGAGTCATATATAAAGACATTC
AAGCCAAGATGCTCCAAGTCAAAATATACCAACCTTCTCTGAATTATATTTTGCTTATTTATATTTCTTTCTTT
TTTTCTAAAGTATGGCTCTGAATAGAATGCACATTTTCCATTGAACTGGATGCATTTCAATTTAGCCAATCCAGTA
ATTTATTTATATTAATCTATACATAATATGTTTCTCAGCATAGGAGCTATGATTCATTAATTTAAAGTGGAGTC
AAAACGCTAAATGCAATGTTTGTGTGATTTTCATTACACAACTTAATTTGTCTTGTAAATAAGTACAGTGG
ATCTTGGAGTGGGATTTCTTGGTAAATTATCTTGCACTTGAATGTCTCATGATTACATATGAAATCGCTTTGACA
TATCTTTAGACAGAAAAAAGTAGCTGAGTGAGGGGGAAATTATAGAGCTGTGTGACTTTAGGGAGTAGGTTGAAC
CAGGTGATTACCTAAAATTCCTTCCAGTTCAAAGGCAGATAAATCTGTAAATTATTTATCCTATCTACCATTTT
TTAAGAAGACATTACTCCAAAATAATTAAATTTAAGGCTTTATCAGGTCTGCATATAGAATCTTAAATTTCTAATA
AAGTTTCATGTTAATGTCATAGGATTTTAAAAGAGCTATAGGTAATTTCTATATAATATGTGTATATTTAAATG
TAATTGATTTAGTTGAAAGTATTTTAAAGCTGATAAATAGCATTAGGGTCTTTGCAATGTGGTATCTAGCTGT
ATTATGGTTTTATTTACTTTAAACATTTTGAAGCTTATACTGGCAGCCTAGAAAAACAAACAATTAATGTAT
CTTTATGTCCCTGGCACATGAATAAACTTTGCTGTGGTTTACT

701/6881
FIGURE 654

MAFARRLLRGPLSGPLLGRRGVCAGAMAPRRFVLELPDCTLAHFALGADAPGDADAPDPRLAALLGPPERSYSL
CVPVTPDAGCGARVRAARLHQRLRHQLRRGPFQRCQLLRLLCYCPGGQAGGAQQGFLLRDPDDPDTRQALLELL
GACQEAPRPHLGFEADPRGQLWQRLWEVQDGRRLQVGCAQVVPVPEPPLHPVVPDLPSSVVFPDREAARAVLEE
CTSFIEARAVLDLVDQCPKQIQKGKFQVVAIEGLDATGKTTVTQSVADSLKAVLLKSPPSCIGQWRKIFDDEPT
IIRRAFYSLGNYIVASEIAKESAKSPVIVDRYWHSTATYAIATEVSGGLQHLPPAHHPVYQWPEDLLKPDLLLL
TVSPEERLQRLQGRGMEKTREEAELEANSVFRQKVEMSYQRMENPGCHVVDASPSREKVLQTVLSLIQNSFSEP

702/6881
FIGURE 655

GTGGTGGGACTCGCGTCGCGGCCGCGGAGACGTGAAGCTCTCGAGGCTCCTCCCGCTGCGGGTCTGGCGCTCGCCC
TCGCTCTCCTCGCCCTCCGCCCCGGCCCCGGCCCCGCGCCCGCCATCGGAGAAGACTGAGCTGATCCAGAAGGCCA
AGCTGGCCGAGCAGGCCGAGCGCTACGACGACATGGCCACCTGCATGAAGGCAGTGACCGAGCAGGGCGCCGAGC
TGTCCAACGAGGAGCGCAACCTGCTCTCCGTGGCCTACAAGAACGTGGTCTGGGGGCCGAGGTCCGCCTGGAGGG
TCATCTCTAGCATCGAGCAGAAGACCGACACCTCCGACAAGAAGTTGCAGCTGATTAAGGACTATCGGGAGAAAG
TGGAGTCCGAGCTGAGATCCATCTGCACCACGGTGTGGAATTGTTGGATAAATATTTAATAGCCAATGCAACTA
ATCCAGAGAGTAAGGTCTTCTATCTGAAAATGAAGGGTGATTACTTCCGGTACCTTGCTGAAGTTGCGTGTGGTG
ATGATCGAAAACAAACGATAGATAATTCCCAAGGAGCTTACCAAGAGGCATTTGATATAAGCAAGAAAGAGATGC
AACCACACACCCAATCCGCCTGGGGCTTGCTCTTAACTTTTCTGTATTTTACTATGAGATTCTTAATAACCCAG
AGCTTGCTGCACGCTGGCTAAACGGCTTTTGATGAGGCCATTGCTGAACCTTGATACACTGAATGAAGACTCAT
ACAAAGACAGCACCTCATCATGCAGTTGCTTAGAGACAACCTAACACTTTGGACATCAGACAGTGCAGGAGAAG
AATGTGATGCGGCAGAAGGGGCTGAAAACTAAATCCATACAGGGTGTCTCCTTCTTTCCTTCAAGAAACCTTTT
TACACATCTCCATTCTTATTCCACTTGGAATTCCTATAGCAAAGAAACCCATTTCATGTGTATGGAATCAACTGT
TTATAGTCTTTTACACTGCAGCTTTGGGAAAACCTTATTCCTTGATTTGTGTTTGTCTTGGCCTTCCTGGTGTG
CAGTACTGCTGTAGAAAAGTATTAATAGCTTCATTTTCATATAAACATAAGTAACTCCCAAACACTTATGTAGAGG
ACTAAAAATGTATCTGGTATTTAAGTAATCTGAACCAGTTCTGCAAGTGAAGTGTGTTTGTATTACTGTGAAAAT
AAGAAAATGTAGTTAATTACAATTTAAAGAGTATTCACATAACTTCTTAATTTCTACATTCCCTCCCTTACTCT
TCGGGGGTTTTCTTTTCAGTAAGCAACTTTCCATGCTCTTAATGTATTCTTTTTTAGTAGGAATCCGGAAGTATT
AGATTGAATGGAAAAGCACTTGCCATCTCTGTCTAGGGGTCACAAATTGAAATGGCTCCTGTATCACATACGGAG
GTCTTGTGTATCTGTGGCAACAGGGAGTTTCCTTATTCACTCTTTATTTGCTGCTGTTTAAGTTGCCAACCTCCC
CTCCCAATAAAAAATTCACTTACACCTCCTGCCTTTGTAGTTCTGGTATTCACTTTACTATGTGATAGAAGTAGCA
TGTGCTGCCAGAATACAAGCATTGCTTTTGGCAAATTAAAGTGCATGTCATTTCTTAATACTAGAAAGGGGA
AATAAATTAAAGTACACAAGTCCAAGTCTAAAACCTTTAGTACTTTTCCATGCAGATTTGTGCACATGTGAGAGGG
TGTCCAGTTTGTCTAGTGATTGTTATTTAGAGAGTTGGACCACTATTGTGTGTTGCTAATCATTGACTGTAGTCC
CAAAAAAGCCTTGTGAAAATGTTATGCCCTATGTAACAGCAGAGTAACATAAAAATAAAAGTACATTTTATAAACC
ATTTACTATGGCTTTGTAAACAATTGCATACCCATATTTTAAAGGGACAGGTGAATTTACTACTTTCTAAAGTTTAT
TGATACTTCCCTTTTATGTAAAATGTAGTAGTGATACCTATATTTCCACATTGTGCATTGTGACACACTTGTCTA
GGGATGCCCTGGAAGTGATAAAAATTGGACTGCATTTCTTAGAGTGTTTTACTATAGATCAGTCTCATGGGCCATC
TCTTCCTCAGATGTAAATGATATCTGGTTAAGTGTTATATGGAATAAAGTGGACATTTTAAACTA

703/6881
FIGURE 656

MEKTELIQKAKLAEQAERYDDMATCMKAVTEQGAELSNEERNLLSVAYKNVVGRRSAWRVISSIEQKTDTSDDK
LQLIKDYREKVESELRSICTTVLELLDKYLIANATNPESKVLYLKMGDYFRYLAEVACGDDRKQTDNSQGAYQ
EAFDISKKEMQPTHPIRLGLALNFSVFYYEILNPNELACTLAKTAFDEAIAELDTLNEDSYKDSTLIMQLLRDNL
TLWTSDSAGEECDAAEGAEN

704/6881
FIGURE 657

GGCACGAGGCTCCGGTGTGTCTGTCTGGTTGCAGTGTGGAGGTCGGCGCCGGCCCCCGCCTTCCGCGCCCCCCAC
GGGAAGGAAGCACCCCCGGTATTAAAACGAACGGGGCGGAAAGAAGCCCTCAGTCGCCGGCCGGGAGGCGAGCCG
ATGCCGAGCTGCTCCACGTCCACCATGCCGGGCATGATCTGCAAGAACCCAGACCTCGAGTTTGACTCGCTACAG
CCCTGCTTCTACCCGGACGAAGATGACTTCTACTTCGGCGGCCCCGACTCGACCCCCCGGGGGAGGACATCTGG
AAGAAGTTTGAGCTGCTGCCCACGCCCCCGCTGTGCGCCAGCCGTGGCTTCGCGGAGCACAGCTCCGAGCCCCCG
AGCTGGGTACGGAGATGCTGCTTGAGAACGAGCTGTGGGGCAGCCCCGGCCGAGGAGGACGCGTTCGGCCTGGGG
GGACTGGGTGGCCTCACCCCCAACCCGGTCACTCTCCAGGACTGCATGTGGAGCGGCTTCTCCGCCCCGCGAGAAG
CTGGAGCGCGCCGTGAGCGAGAAGCTGCAGCACGGCCGCGGGCCGCCAACCGCCGGTTCCACCGCCCAGTCCCCG
GGAGCCGGCGCCGCCAGCCCTGCGGGTGC GGGCACGGCGGGGCTGCGGGAGCCGGCCGCGCCGGGGCCGCCCTG
CCCGCCGAGCTCGCCACCCGGCCGCCGAGTGCCTGGATCCCGCCGTGGTCTTCCCTTTCCCGTGAACAAGCGC
GAGCCAGCGCCCGTGCCTGCAGCCCCGGCCAGTGCCTCGGCGGGCGGGCCCTGCGGTGCGCTCGGGGGCGGGTATT
GCCGCCCCAGCCGGGGCCCCGGGGGTGCCCCCTCCGCGCCAGGCGGGCCGCCAGACCAGCGGCGGCGACCACAAG
GCCCTCAGTACCTCCGGAGAGGACACCTTGAGCGATTGAGATGATGAAGATGATGAAGAGGAAGATGAAGAGGAA
GAAATCGACGTGGTCACTGTGGAGAAGCGGCGTTCTCTCCAACACCAAGGCTGTCACCACATTCACCATCACT
GTGCGTCCCAAGAACGCAGCCCTGGGTCCCGGGAGGGCTCAGTCCAGCGAGCTGATCCTCAAACGATGCCTTCCC
ATCCACCAGCAGCACAACTATGCCGCCCTCTCCCTACGTGGAGAGTGAGGATGCACCCCCACAGAAGAAGATA
AAGAGCGAGGCGTCCCCACGTCCGCTCAAGAGTGTCTATCCCCCAAAGGCTAAGAGCTTGAGCCCCGAAACTCT
GACTCGGAGGACAGTGAGCGTCGCAGAAACCACAACATCCTGGAGCGCCAGCGCCGCAACGACCTTCGGTCCAGC
TTTCTCACGCTCAGGGACCACGTGCCGGAGTTGGTAAAGAATGAGAAGGCCGCAAGGTGGTCATTTTGAAAAAG
GCCACTGAGTATGTCCACTCCCTCCAGGCCGAGGAGCACCAGCTTTTGCTGGAAAAGGAAAAATTGCAGGCAAGA
CAGCAGCAGTTGCTAAAGAAAAATTGAACACGCTCGGACTTGCTTAGACGCTTCTCAAACTGGACAGTCACTGCCA
CTTTGCACATTTTGATTTTTTTTTTAAACAAACATTGTGTTGACATTAAGAATGTTGGTTTACTTTCAAATCGGT
CCCCTGTCGAGTTTCGGCTCTGGGTGGGCAGTAGGACCACCAGTGTGGGGTCTGCTGGGACCTTGAGAGCCCTGC
ATCCCAGGATGCTGGGTGGCCCTGCAGCCTCCTCCACCTCACCTCCATGACAGCGCTAAACGTTGGTGACGGTTG
GGAGCCTCTGGGGCTGTTGAAGTCACCTTGTTGTGTTCCAAGTTTCCAAACAACAGAAAGTCATTCTTTCTTTTA
AAATGGTGCTTAAGTTCCAGCAGATGCCACATAAGGGGTTTGCCATTTGATACCCCTGGGGAACATTTCTGTAAA
TACCATTGACACATCCGCCTTTTGTATACATCCTGGGTAAATGAGAGGTGGCTTTTGCGGCCAGTATTAGACTGGA
AGTTCATACCTAAGTACTGTAATAATACCTCAATGTTTGAGGAGCATGTTTTGTATACAAATATATTGTTAATCT
CTGTTATGTACTGTACTAATTCTTACACIGCCTGTATACTTTAGTATGACGCTGATACATAACTAAATTTGATAC
TTATATTTTCGTATGAAAATGAGTTGTGAAAGTTTTGAGTAGATATTACTTTATCACTTTTTGAACTAAGAACT
TTGTAAAGAAATTTACTATATATATATGCCTTTTTCTAGCCTGTTTCTTCTGTTAATGTATTTGTTCATGTT
TGGTGATAGAACTGGGTAAATGCAAAGTTCTGTGTTAATTTCTTCAAAATGTATATATTTAGTGCTGCATCTT
ATAGCACTTTGAAATACCTCATGTTTATGAAAATAAATAGCTTAAATTAATAAAAAAAAAAAAAAAAAA

705/6881
FIGURE 658

MPSCSTSTMPGMICKNPDLEFDSLQPCFYDDEDDFYFGGPDSTPPGEDIWKKFELLPTPPLSPSRGFAEHSSEPP
SWVTEMLLENELWGSPAEEDEFGLGGLGGLTPNPFVILQDCMWSGFSAREKLERAVSEKLQHGRGPPTAGSTAQSP
GAGAASPAGRGHGGAAGAGRAGAALPAELAHFAAECVDFAVVFPPVKNREPAPVPAAPASAPAAGPAVASGAGI
AAPAGAPGVAPPRPGGRQTSGGDHKALSTSGEDTILSDSDDDEDEEEDEEEEIDVVTVEKRRSSNTKAVTTFTIT
VRPKNAALGPGRQSSELILKRCLPIHQHNYAAPSPYVESEDAPPQKKIKSEASPRPLKSVIPPKAKSLSPRNS
DSEDSERRRNHNILERQRRNDLRSSFLLTRDHPPELVKNEKAAKVVLKKATEYVHSLQAEHQLLLEKEKLQAR
QQLLKKIEHARTC

706/6881
FIGURE 659

GTCAGTCCCTCCTGTAGCCGCCGCCGCCGCCGCCGCCGCCCTCTGCCAGCAGCTCCGGCGCCACCTCGGGCCG
GCGTCTCCGGCGGGCGGGAGCCAGGCGCTGACGGGCGCGCGGGGGCGGCCGAGCGCTCCTGCGGCTGCGACTCA
GGCTCCGGCGTCTGCGCTTCCCCATGGGGCTGGCCTGCGGCGCCTGGGCGCTCTGAGATTGTCACTGCTGTTCCA
AGGGCACACGCAGAGGGATTGGAATTCCTGGAGAGTTGCCTTTGTGAGAAGCTGGAAATATTTCTTTCAATTCC
ATCTCTTAGTTTTCCATAGGAACATCAAGAAATC**ATGA**ACAACCTTTGGTAATGAAGAGTTTGAAGTCCACTTCCT
CGATGAAGTTTTACTGCCAAGGACATTCTGGACCAGAAAATTAATGAAGTTTCTTCTCTGATGATAAGGATGC
CTTCTATGTGGCAGACCTGGGAGACATTCTAAAGAAACATCTGAGGTGGTTAAAAGCTCTCCCTCGTGTACCCCC
CTTTTATGCAGTCAAATGTAATGATAGCAAAGCCATCGTGAAGACCTTGCTGCTACCGGGACAGGATTTGACTG
TGCTAGCAAGACTGAAATACAGTTGGTGCAGAGTCTGGGGGTGCCTCCAGAGAGGATTATCTATGCAAATCCTTG
TAAACAAGTATCTCAAATTAAGTATGCTGCTAATAATGGAGTCCAGATGATGACTTTTGATAGTGAAGTTGAGTT
GATGAAAGTTGCCAGAGCACATCCCAAAGCAAAGTTGGTTTTGCGGATTGCCACTGATGATTCCAAAGCAGTCTG
TCGTCTCAGTGTGAAATTCGGTGCCACGCTCAGAACCAGCAGGCTCCTTTTGGAACGGGCGAAAGAGCTAAATAT
CGATGTTGTTGGTGTGAGCTTCCATGTAGGAAGCGGCTGTACCGATCCTGAGACCTTCGTGCAGGCAATCTCTGA
TGCCCGCTGTGTTTTTGACATGGGGGCTGAGGTTGGTTTTACGATGTATCTGCTTGATATTGGCGGTGGCTTTCC
TGGATCTGAGGATGTGAAACTTAAATTTGAAGAGATCACCGGCGTAATCAACCCAGCGTTGGACAAATACTTTCC
GTCAGACTCTGGAGTGAGAATCATAGCTGAGCCCGGCAGATACTATGTTGCATCAGCTTTCACGCTTGCAAGTAA
TATCATTGCCAAGAAAATTGTATTAAAGGAACAGACGGGCTCTGATGACGAAGATGAGTCGAGTGAGCAGACCTT
TATGTATTATGTGAATGATGGCGTCTATGGATCATTTAATTGCATACTCTATGACCACGCACATGTAAAGCCCCCT
TCTGCAAAGAGACCTAAACCAGATGAGAAGTATTATTATCCAGCATATGGGGACCAACATGTGATGGCCTCGA
TCGGATTGTTGAGCGCTGTGACCTGCCTGAAATGCATGTGGGTGATTGGATGCTCTTTGAAAACATGGGCGCTTA
CACTGTTGCTGCTGCCTCTACGTTCAATGGCTTCCAGAGGCCGACGATCTACTATGTGATGTGAGGCGCTGCGTG
GCAACTCATGCAGCAATTCCAGAACCCCGACTTCCACCCGAAGTAGAGGAACAGGATGCCAGCACCCCTGCCTGT
GTCTTGTGCCTGGGAGAGTGGGATGAAACGCCACAGAGCAGCCTGTGCTTCCGGCTAGTATTAATGTG**TAG**ATAGC
ACTCTGGTAGCTGTAACTGCAAGTTTAGCTTGAATTAAGGGATTTGGGGGGACCATGTAAGTAACTTAATTACTGCTA
GTTTTGAAATGTCTTTGTAAGAGTAGGGTCGCCATGATGCAGCCATATGGAAGACTAGGATATGGGTACACTTA
TCTGTGTTCCATGGAACTATTTGAATATTTGTTTTATATGGATTTTTATTCACTCTTCAGACACGCTACTCAA
GAGTGCCCTCAGCTGCTGAACAAGCATTTGTAGCTTGTACAATGGCAGAATGGGCCAAAAGCTTAGTGTTGTGA
CCTGTTTTTAAAATAAAGTATCTTGAAATAATTAGGC

707/6881
FIGURE 660

MNNEFGNEEFDCHEFLDEGFTAKDILDQKINEVSSSSDDKDAFYVADLGDILKKHLRWLKA
LPRVTPFFYAVKCND
SKAIVKTLAATGTGFD
CASKTEIQLVQSLG
VPPERIIYANPCKQ
VSQIKYAANNGVQ
MMTFDSEVELMKV
ARAH
PKAKLVLRIATDDSKAV
CRLSVKFGATLRT
SRLLLERAKELNID
VVGVSFHVGS
GCTDPETFVQAIS
DARCVFDMGAEV
GFSMYLLDIGGGF
PGSEDVKLKFE
EITGVINPALDKY
FSPDSGVRIIAEP
GRYYVASAFTLAV
NIIAKKIVLKEQ
TGSDDEDESSE
QTFMYVNDGVYGS
FNCILYDHAHV
KPLLQKRPKPDE
KYYSSSIWGPTC
DGLDRIVERCDL
PEMHVGDWMLFEN
MGAYTVAAASTF
NGFQRPTIYYVM
SGPAWQLMQQFQ
NPDPPEVEEQD
ASTLPVSCAWES
GMKRHRAACAS
ASINV

708/6881
FIGURE 661

ATGAGTCAGCAGCGGCCGCGAGGAAGTTACCCAGTCTCCTCCTGGACCCGACGGAGGAGACGGTTCGCCGTCGG
TGCCGAGACCCCATCAACGTGGAGGGCCTGCTGCCATCAAAAATAAGGATTAATTTAGAAGATAATGTACAATAT
GTGTCCATGAGAAAAGCTCTAAAAGTGAAGAGACCTCGTTTTGATGTATCGCTGGTTTATTTAACTCGAAAATTT
ATGGATCTTGTGAGATCTGCTCCCGGGGTATTCTTGACTTAAACAAGGTTGCAACGAAACTGGGAGTCCGAAAG
CGGAGAGTGTATGACATCACCAATGTCTTAGATGGAATCGACCTCGTTGAAAAGAAATCCAAGAACCATATTAGA
TGGATAGGATCTGATCTTAGCAATTTTGGAGCAGTTCCCCAACAAAAGAAGCTACAGGAGGAACTTTCTGACTTA
TCAGCAATGGAAGATGCTTTGGATGAGTTAATTAAGGATTGTGCTCAGCAGCTGTTTGAGTTAACAGATGACAAA
GAAAATGAAAGACTAGCATATGTGACCTATCAAGACATTTCATAGCATTTCAGGCCTTCCATGAACAGATCGTCATT
GCAGTTAAAGCTCCAGCAGAAACCAGATTGGATGTTCCAGCTCCCAGAGAAGACTCTATCACAGTGCACATAAGG
AGCACCAACGGACCTATCGATGTCTATTTGTGTGAAGTGGAGCAGGGTCAGACCAGTAACAAAAGGTCTGAAGGT
GTCGGGACCTCTTCATCTGAGAGCACTCATCCAGAAGGCCCTGAGGAAGAAGAAAATCCTCAGCAAAGTGAAGAA
TTGCTTGAAGTAAGCAACTGATGGCATTGTGAGAATTTATGTATCACTGAGTTTTTTTGGGAATATCTTCGTGGAGA
ATTACGCATCAAATTTGATTCTCAGAGCAATAAATTATCCATGAAGTGCTCTCGTTCTCAGTAGCGGCATCATGG
CCAGTAGTGCTTTTGAGGAGTTCACCACTTAGATTACTGAGTAATTGTGGTTTCCACATTTGAAAACAACCTCCTT
TTATAATTATTCAGTGCTTTTTGTGAGTGAATAGACATCTTGCCCTCTGAAGTAGCTTCATCACAGAGTGTCAT
GAAGACAGACAGTCAGGCTGAAATGGACAGTTCTTTGTGGACTCTACCCTTCCCTTCAAGGAGTATGTCATATAT
CACAAAAGAAATTGCCTTACACTGGTTCATGTTTGAGTTACTGTTGTACATTGCATAGATGTACACACGAATTT
AAATGTGATGTCTTTGTATATATCTGTATAATGTTGAGATTACTTACGAAATATGTCTGAGTGACACTTTTCACC
CTTGATACAGCCAAAATAATGTATATATGGAAGTGACAGACAAATCTCTAATCTCTTTGGTACCTATAACTTAT
TAGAATCCTCTGGATGAGGGTTAGAAGAGACTTTTTCCAACTTCTACATGTAGAAGTATCATAAATGTGCTACA
CATTTATGTTTGTGGATTTAATTAAAGTATTTTAATATGGTTTTTCAGTGCTAAAATTGGAGTCAGATACTTCTTG
GTTTTAAGCTGTCTACCTAATTGCTGTCTCCAGCAGACTGGTGGCATGCCAGTGGCTTTGGGGGCAAGGATAG
AAATGCCATCAGGAAATAGCTGAATTCATTGTGAAACATGAATTCAGTCATGGTGATAATTGGAAACTCCTTTCA
GGTTTTTGCAAGTAGATTTTGTAAATGTTTGTGTATGCAGCCTTGCTGTTGAGTCAGTCCAAGGGGTTTTACTTAG
GACAAGTTGTACCTTGCCCTCTCTCCAGCTCTGCTCCACATTTTACATACCTAGCTGTTTCTACCTCATTGGG
TAAGTCATTTACCACTCTGTGCCTCAGTTTACTCTGTAGTTTACCATTAGACTGTGAGCTCCTTGAGGGACTTTG
TCATAATCACTGTTACATCCCAGTGCCTCACACCATGCCTGGCCCTTAAGAAGTGCTCAATAAATGTCTGAACAA
ATAA

709/6881
FIGURE 662

CTCTGTAGCTGTGACCCTGATACCGCGTGGTGTGCTCCGAACACATGGTGCCAGAACGAAGGCGGCGTCCAGAA
GCCCTAGGTCCCAGAGGTCCGCTCAGCGGCAGGCGCATAAGGCGGGGCGGCGCGGGCCTTTCCCTCCATCGGAA
CCGTTCTCCCGGGGCTGAGTCCCTGCCCGGACTCCGAACGCCGAAGACCAGGGGCCGGAAGCGCGCGCCGCACT
GCCACGCCGTGTGAGTCGGGAGGGAGGGAGCGAGCAGGCGAAGCCGCGGAGGACGGGGTGAAGATGCGGCCTTC
TCCGAGATGGGTGTAATGCCTGAGATTGCACAAGCTGTGGAAGAGATGGATTGGCTCCTCCCAACTGATATCCAG
GCTGAATCTATCCCATTTGATCTTAGGAGGAGGTGATGTACTTATGGCTGCAGAAACAGGAAGTGGCAAACTGGT
GCTTTTAGTATCCAGTTATCCAGATAGTTTATGAAACCTCTGAAAGACCAACAGGAAGGCAAAAAGGAAAAACA
ACAATTAAAACTGGTGTTCAGTGTGCTGAACAAATGGCAGATGAACCCATATGACAGAGGATCTGCTTTTGCAATT
GGGTGAGATGGTCTTTGTTGTCAAAGCAGAGAAGTAAAGGAATGGCATGGGTGTAGAGCTACTAAAGGATTAATG
AAAGGGAAAACTACTATGAAGTATCCTGTGATGACCAAGGGTTATGCAGGGTCGGGTGGTCTACCATGCAGGCC
TCTTTGGACCTAGGTACTGACAAGTTTGGATTTGGCTTTGGTGGAAACAGGAAAGAAATCCCATAACAAACAATTT
GATAATTATGGAGAGGAATTCATATGCATGATACCATTTGGATGTTACCTGGATATAGATAAGGGACATGTCAAG
TTCTCCAAAAATGGAAAAGATCTTGGTCTGGCATTGAAATACCACCACATATGAAAAACCAAGCCCTCTTTCCCT
GCCTGTGTTTTGAAGAATGCTGAACTGAAATTTAACTTCGGTGAAGAGGAATTTAAGTTTCCACCAAAAGATGGC
TTTGTGCTCTTTCCAAGGCACCGGATGGTTACATTGTCAAATCACAGCACTCAGGTAATGCACAGGTGACACAA
ACAAAGTTTCTCCCAATGCTCCGAAAGCTCTCATTGTTGAACCTTCCCGGGAGTTAGCTGAACAACTTTGAAC
AACATCAAGCAGTTTAAGAAATACATTGATAATCCTAAATTAAGGGAGCTTCTGATAATTGGAGGTGTTGCAGCC
CGGGATCAGCTCTCTGTTTTGGAAGATGGAGTAGATATAGTTGTAGGTACTCCGGGAAGACTAGATGACTTGGTG
TCAACTGGAAGCTGAACTTATCTCAAGTTAGATTCTTGGTCTGATGAAGCTGATGGGCTTCTTTCTCAAGGT
TATTCTGATTTTATAAATAGGATGCACAATCAGATTCTCAGGTTACCTCTGATGGAAAAAGACTTCAGGTGATT
GTTTGCTCTGCCACTTTGCATTCTTTGATGTAAAGAACTGTCCGAGAAGATAATGCATTTTCTTACATGGGTT
GACTTAAAAGGAGAAGACTCTGTTCCAGATACTGTACACCATGTTGTTGTCCAGTAAATCCCAAACTGACAGA
CTCTGGGAAAGGCTTGGAAGAGCCACATTAGAAGTATGATGTACATGCAAAAGATAACACAAGACCTGGTGCT
AATAGTCCAGAGATGTGGTCTGAAGCTATTAATAATCCTGAAAGGGGAGTATGCTGTCCGGGCAATCAAGGAACAT
AAGATGGATCAAGCAATTATCTTCTGTAGAACCAAAATTGACTGTGATAACTTGGAGCAGTACTTTATACAACAA
GGAGGAGGACCTGATAAAAAAGGACACCAGTTCTCATGTGTTTGTCTTCATGGTGACAGAAAGCCTCATGAGAGA
AAGCAAACTTGGAAGATTTAAGAAAGGAGATGTAAGATTCTTGATTTGCACAGATGTAGCTGCTAGAGGAATT
GATATCCACGGTGTTCTTATGTTATAAATGTCACTCTGCCCGATGAAAAGCAAACTACGTACATCGAATTGGC
AGAGTAGGAAGAGCTGAAAGGATGGGTCTGGCAATTTCCCTGGTGGCAACAGAAAAAGAAAAGGTTTGGTACCAT
GTATGTAGCAGCCGTGGAAGGGTGTATAACACAAGACTCAAGGAAGATGGAGGCTGTACCATATGGTACAAC
GAGATGCAGTTACTATCTGAGATAGAAGAACACCTGAACTGTACCATTTCTCAGGTTGAGCCGGATATAAAGGTA
CCAGTGGATGAATTTGATGGGAAAGTTACCTACGGTCAGAAAAGGGCTGCTGGTGGTGGAAAGCTATAAAGGCCAT
GTGGATATTTTGGCACCTACTGTTCAAGAGTTGGCTGCCCTTGAAAAGGAGGCGCAGACATCTTTCTGCTCTT
GGCTACCTTCCTAACAGCTGTTTCAAGACCTTCTGATTTTTTACATTTACTGAATAAGATTTGAGTAATGAAAGTC
TGATGCTTTAAACTCTAAAACAGTTGTACTGCTTCCAAGCAGCAGTATTTATAGTAACGTAAGCTATTAATGCT
AACTCTTGCATGTCAAGAAACATTAGTCTTAGGAATCTTCAAAAAATGGCATCCCAATGAAAATAAATTTGATG
ACTATA

710/6881
FIGURE 663

MAAFSEMGMPEIAQAVEEMDWLLPTDIAESIPLILGGGDVLMMAETGSGKTGAFSIPVIQIVYETLKDQQEGK
KGKTTIKTGASVLNKWQMNPYDRGSAFAIGSDGLCCQSREVKEWHGCRATKGLMKGKHYYEVSCHDQGLCRVGWS
TMQASLDLGTDKFGFGFGGTGKKSHNKQFDNYGEEFTMHDTIGCYLDIDKGHVKFSKNGKDLGLAFEIPPHMKNQ
ALFPACVLKNAELKFNFGEFEFKFPPKDGVALSKAPDGYIVKSQHSNAQVTQTKFLPNAPKALIVEPSRELAE
QTLNNIKQFKKYIDNPKLRELLIIGGVAARDQLSVLENGVDIVVGTPGRLDDLSTGKLNLSQVRFLVLDEADGL
LSQGYSDFINRMHNQIPQVTS DGKRLQVIVCSATLHSFDVKKLSEKIMHFPTWVDLKGEDSVPDTVHHVVVPEVNP
KTDRLWERLGKSHIRTD DVHAKDNTRPGANSPPEMWSEAIKILKGEYAVRAIKEHKMDQAIIFCRTKIDCDNLEQY
FIQGGGPDKKGHQFSCVCLHGDRKPKHERKQNLERFKKGDVRF LICTDVAARGIDIHGVPYVINVTLPDEKQNYV
HRIGRVGRAERMGLAISLVATEKEKVWYHVCSSRGKGCYNTRLKEDGGCTIWYNEMQLLSEIEEHLNCTISQVEP
DIKVPVDEFDGVITYGQKRAAGGGSYKGHVDILAPTVQELAALEKEAQT SFLHLGYLPNQLFRTF

711/6881
FIGURE 664A

GAACATGGCGGCCCCCGAGTCAGGGCCGGCTTTGAGTCCAGGCACTGCAGAGGCCTAGAGGCAACCAAAAACATG
GTGCATCCTTTATCATCACGAAAGCAATTCGAGATCGTTTATTATTTTTACGCCAATACATCTGGTACAGCCCCG
CACCTTTTTTGCTCCCTGATGGACTGGTTCGCTTGGTTAATAAACAGATAAACTGGCATTGTTGGTACTTGCAAGCA
ATAGCACTAGAGTGCATCTATACCTGTGAACGAAATGATCAACTCTGTCTTTGCTATGACCTACTAGAATGTCTG
CCAGAAAGAGGATATGGTGATAAGACAGAGGCAACCACAAAGCTTCATGACATGGTAGACCAACTGGAACAAATT
CTCAGTGTGTGACAGCTTTTGAAAAACATGGACTCGAGAAACCAATTTTCAATTTGTTAAAAACACTCAATCTAGC
TCAGAAGAGGCACGCAAGCTGATGGTTAGATTGACGAGGCACACTGGCCGGAAGCAGCCTCCTGTGCTGAGTCT
CATTGGAGAACGTTGCTGCAAGACATGTTAACTATGCAGCAGAATGTATACACATGTCTAGATTCTGATGCCTGC
TATGAGATATTTACAGAAAGCCTTCTGTGCTCTAGTCGCCTTGAAAACATCCACCTGGCTGGACAGATGATGCAC
TGCAGTGCTTGTTCAGAAAATCCTCCAGCTGGTATAGCCATAAAGGGAAACCCCACTACAGGGTCAGCTACGAA
AAGAGTATTGACTTGGTTTTGGCTGCCAGCAGAGAGTACTTCAATTCCTTCTACCAACCTCACTGATAGCTGCATG
GATCTAGCCAGGTGCTGCTTACAACCTGATAACAGACAGACCCCTGCCATTCAAGAGGAGCTAGATCTTATCCAA
GCCGTTGGATGTCTTGAAGAATTTGGGGTAAAGATCCTGCCTTTGCAAGTGCATTGTGCCCTGATCGGATCAGT
CTCATCAAGGAGTGTATTTCCAGTCCCCACATGCTATAAACAATCCACCAAGCTTCTGGGCCTTGCTGAGCTG
CTGAGGGTTGCAGGTGAGAACCCAGAAGAAAGGCGGGACAGGTTCTAATCCTTTTAGTGGAGCAGGCACCTTCGC
TTCCATGACTACAAAGCAGCCAGTATGCATTGTGAGGCTGATGGCCACAGGTTATCCTAAAAGTTGGGATGTT
TGTAAGTAGGTGTTCCAGGTAGCAATTCAGCTGACCTATTGCGCTGGACCACTGCTACCACCATGAAAGTCCTT
CATTGCCCTCCTAGCAGCATTGAACCTCTTTTGGCAGCTAGCAGCTCTCTGCAGACAGAAATTCTTTATCAAAGA
GTGAATTTCCAGATCCATCATGAAGGAGGGGAAAATATCAGTGCTTCACCATTAACTAGTAAAGCAGTACAAGAG
GATGAAGTAGGTGTTCCAGGTAGCAATTCAGCTGACCTATTGCGCTGGACCACTGCTACCACCATGAAAGTCCTT
TCCAACACCACAACCACCACCAAAGCGGTGCTGCAGGCCGTCAGTGATGGGCAGTGGTGAAGAAGTCTTTAACT
TACCTTCGACCCCTTCAGGGGCAAAAATGTGGTGGTGATATCAAATCGGAACTACAGCCAATGAAGATCTAGAG
AAACAAGGGTGTGATCCTTTTTATGAATCTGTGCTCTCAAATCCTTTTGTGCTGAGTCTGAAGGGACCTATGAC
ACCTATCAGCATGTTCCAGTGGAAGCTTTGCAGAAGTATTGCTGAGAAGTGAAGAAATGGCAGAGGCTAAAAAT
AAAGGAGAAGTATTTCCAACAAGTGAAGTTCTCTTGCAACTAGCAAGTGAAGCCTTGCCAAATGACATGACCTTG
GCTCTTGCTTACCTTCTTGCTTACCACAAGTGTTAGATGCTAACC GGTTGCTTTGAAAAGCAGTCCCCCTCTGCA
TTATCTCTCCAGCTGGCAGCGTATTACTATAGCCTCCAGATCTATGCCCGATTGGCCCCATGTTTCAGGGACAAG
TGCCATCCTCTTTACAGGGCTGATCCCAAAGAACTAATCAAGATGGTCACCAGGCATGTGACTCGACATGAGCAC
GAAGCCTGGCCTGAAGACCTTATTTCACTGACCAAGCAGTTACACTGCTACAATGAACGTCTCCTGGATTTCCT
CAGGCGCAGATCCTTCAGGGCCTTCGGAAGGGTGTGGACGTGCAGCGGTTTACTGCAGATGACCAGTATAAAGG
GAACTATCCTTGGTCTGGCAGAACTCTAGAGGAAAGCGTCTACAGCATTGCTATTTCTCTGGCACAACGTTAC
AGTGTCTCCCGCTGGGAAGTTTTTATGACCCATTTGGAGTTCCCTTTCACGGACAGTGGTTTTGTCCACACTAGAA
ATTGAAAATAGAGCCCAAGACCTTCATCTCTTTGAGACTTTGAAGACTGATCCAGAAGCCTTTCACCAGCACATG
GTCAAGTATATTTACCCTACTATTGGTGGCTTTGATCACGAAAGGCTGCAGTATTATTTCACTCTTCTGGAAGC
TGTGGCTGTGCAGATTTGGGGAAGTGTGCCATTAAACCAGAAACCCACATTGCTGCTGAAGAAGTTTAAGGTT
GTTGCATCAGGTCTTAATTACAAAAAGCTGACAGATGAAAACATGAGTCCTCTTGAAGCATTGGAGCCAGTTCTT
TCAAGTCAAATATCTTGTCTATTTCCAAACTTGTTCCCAAAATCCCTGAAAAGGATGGACAGATGCTTTCCCCA
AGCTCTCTGTACACCATCTGGTTACAGAAGTTGTTCTGGACTGGAGACCCTCATCTCATTAAACAAGTCCCAGGC
TCTTCACCGGAGTGGCTTCATGCCTATGATGTCTGCATGAAGTACTTTGATCGTCTCCACCCAGGTGACCTCATC
ACTGTGGTAGATGCAGTTACATTTCTCCAAAAGCTGTGACCAAGCTGTCTGTGGAAGCCCGTAAAGAGATGACT
AGAAAGGCTATTAAGACAGTCAAACATTTTATTGAGAAGCCAAGGAAAAGAACTCAGAAGACGAAGCTCAAGAA
GCTAAGGATTCTAAAGTTACCTATGCAGATACTTTGAATCATCTGGAGAAATCACTTGCCACCTGGAAACCCCTG
AGCCACAGCTTCATCCTTTCTCTGAAGAATAGTGAGCAGGAAACACTGCAAAAATACAGTCACCTCTATGATCTG
TCCCGATCAGAAAAAGAGAACTTCATGATGAAGCTGTGGCTATTTGTTTAGATGGTCAGCCTCTAGCAATGATT
CAGCAGCTGCTAGAGGTGGCAGTTGGCCCTCTTGACATCTCACCCAAGGATATAGTGCAGAGTGAATCATGAAA
ATAATTTCTGCATTGAGTGGTGGCAGTGTGACCTTGGTGGGCCAAGGGACCCACTGAAGGTCTGGAAGGTGTT
GTTGCAGCAGTCCACGCCAGTGTGGACAAGGGTGAGGAGCTGGTTTACCTGAGGACCTGCTGGAGTGGCTGCGG
CCTTTCTGTGCTGATGACGCCTGGCCGGTGC GGCCCGCATTACGTGCTGCAGATTTTGGGGCAATCATTTTAC

712/6881
FIGURE 664B

CTGACTGAGGAGGACAGCAAGCTCCTCGTGTTCTTTAGAACTGAAGCCATTCTCAAAGCCTCCTGGCCCCAGAGA
CAGGTAGACATAGCTGACATTGAGAATGAAGAGAACCGCTACTGTCTATTTCATGGAACCTCCTGGAATCTAGTCAC
CACGAGGCTGAATTTACGCACTTGGTTTTACTTTTGCAAGCTTGGCCACCTATGAAAAGTGAATATGTCATAACC
AATAATCCATGGGTGAGACTAGCTACAGTGATGCTAACCAGATGTACGATGGAGAACAAGGAAGGATTGGGGAAT
GAAGTTTGAAGTGTGTCGCTCTTTGTATAACACCAAGCAGATGCTGCCTGCAGAGGGTGTGAAGGAGCTGTGT
CTGCTGCTGCTTAACCACTCCCTCCTGCTTCCATCTCTGAACTTCTCCTCGAGAGCCGAGATGAGCATCTGCAC
GAGATGGCACTGGAGCAAATCACGGCAGTCACTACGGTGAATGATTCCAATTGTGACCAAGAACTTCTTTCCCTG
CTCCTGGATGCCAAGCTGCTGGTGAAGTGTGTCTCCACTCCCTTCTATCCACGTATTGTTGACCACCTCTTGGCT
AGCCTCCAGCAAGGGCGCTGGGATGCAGAGGAGCTGGGCAGACACCTGCGGGAGGCCGCCATGAAGCCGAAGCC
GGGTCTCTCCTTCTGGCCGTGAGGGGGACTCACCAGGCCTTCAGAACCTTCAGTACAGCCCTCCGCGCAGCACAG
CACTGGGTGTGAGGGCCACCTGTGGCCCTGCTCCTTAGCAGAAAAAGCATCTGGAGTTGAATGCTGTTCCCAGAA
GCAACATGTGTATCTGCCGATTGTTCTCCATGGTTCCAACAAATTGCAAATAAAACTGTATGGAAACG

713/6881
FIGURE 665

ATGAGATCTCGGCTGCGAAGTGTGTCATCAGCATCTGGCTTTCTGGGTTATGATGTGGTCAGGGATGTGTCTTCT
GGCCCATTTTGGAGGCGCAAAAATGGTGATCCATGTTTGGATTTATGTGGAAGGGACAGTTCCACAGTATGGAAA
AGGGGAGACAGTCCCAGGAAGCGTGAAGAGGAAAGGTCATTGGGAATCTCTCAGTACCTCTGCCCTAATCTCTTC
TCTCCTACGGAGGCAGTTAAGTCTAAAGCCATTTGTCTGGTTTCCATATCTGAACTTCAAGCAGCATCTTCTGGA
CTTAGTTCTTGGTGGCTGGAGCAGGGAAAGTGTGGCCTCATTGAAATGGGATCAGGTTTCAGGATGTTTCATGTG
TCTGTGTCTTTCTCACACATTGTGAGGAACAGGACAGTCCCTCTGATGCGCTGGTACCTGGCCGCCATGCAGATC
ATGAGGGGAGAGAAGCAGGCTGCTTCGGGGAATCCTGCCATAGAGGCTGGAGCTTCATGTGCATCTCAGCCAGCC
CTGCAGCAGCCCTCAGCAGCCCTTCTGTGGGGCTGGGGTATCTGTTGCCAGGAAATCACTGGGCTGAGGAAGTA
GGAGATGAATGGCTCTGTGCTATCACACCATCTTCTGCATTGAGTCTTCTTCGCTTTCTTATCATCGTCATCATG
ATTATCATCAATAAAATTTGTAAGGAAGGAAACAGGACTGCTTATTGATTTTCATTTCTATGCTACTGAGAGCCAA
GGCTACGGATTTCTTTCCCCAGGAATGGAGAGAGGAAAGAGATGTGAGATTGGCTACCCAAGTGTGCATCAGTA
CCCCATTCTATCATCAACGGGTACAAACGAGTCCTGGCCTTGTCTGTGGAGACGGATTACACCTTCCCCTCGCT
GAAAAGGTCAAGGCCTTCTTGGCTGATCCATCTGCCTTTGAGATGGAGGAGTGGAGGGGTGATGATAAAATGGAA
GCTCCCGTGTCAAGAGATCAGGCAAATGGGGAGACTCCGTGGGATCCTCTGAAGAATCTACATGCACGTACTTAC
GAGAATCAGATTAGGGATGCCTACCACACAGGAGTACCAATGTTTAGTATTAGCCCGTAA

714/6881
FIGURE 666

MRSRLRSVSSASGFLGYDVVRDVSSGPFWRRKNGDPCLDLCGRDSSTVWKRGDSPRKREEERSLGISQYLCPNLF
SPTEAVKSKAICLVSISELQAASSGLSSWWLEQGKCGLIEMGSGFRMFHVSVSFSHIVRNRTVPLMRWYLAAMQI
MRGEKQAASGNPAIEAGWERTGAQM

715/6881
FIGURE 667

CGCGAAGAAGCTGGCAGGGGCACGAGCCGGGGCGGGTTTGAAGACGCGTCGTTGGGTTTTGGAGGCCGTGAAAC
AGCCGTTTTGAGTTTGGCTGCGGGTGGAGAACGTTTGTGAGGGGCCCGCCAAGAAGGAGGCCCGCCTGTTACGAT
GGTGTCCATGAGTTTCAAGCGGAACCGCAGTGACCGGTTCTACAGCACCCGGTGCTGCGGCTGTTGCCATGTCCG
CACCGGGACGATCATCCTGGGGACCTGGTACATGGTAGTAAACCTATTGATGGCAATTTTGCTGACTGTGGAAGT
GACTCATCCAAACTCCATGCCAGCTGTCAACATTCACTATGAAGTCATCGGTAATTACTATTTCGTCTGAGAGAAT
GGCTGATAATGCCTGTGTTCTTTTTGCCGTCTCTGTTCTTATGTTTATAATCAGTTCAATGCTGGTTTTATGGAGC
AATTTCTTATCAAGTGGGTTGGCTGATTCCATTCTTCTGTTACCGACTTTTTGACTTCGTCTCAGTTGCCTGGT
TGCTATTAGTTCTCTCACCTATTTGCCAAGAATCAAAGAATATCTGGATCAACTACCTGATTTTCCCTACAAAGA
TGACCTCCTGGCCTTGGACTCCAGCTGCCTCCTGTTTATTGTTCTTGTGTTCTTTGCCCTTATTCATCATTTTTAA
GGCTTATCTAATTAACCTGTGTTTGGAACTGCTATAAATACATCAACAACCGAAACGTGCCGGAGATTGCTGTGTA
CCCTGCCTTTGAAGCACCTCCTCAGTACGTTTGGCAACCTATGAAATGGCCGTGAAATGCCTGAAAAAGAACC
ACCACCTCCTTACTTACCTGCCCTGAAGAAATTCTGCCTTTGACAATAAATCCTATACCAGCTTTTTGTTTTGTTTA
TGTTACAGAATGCTGCAATTCAGGGCTCTTCAAACCTTGTGTTGATATAAAATATGTTGTCTTTGTTTAAGCATTT
ATTTTCAAACACTAAGGAGCTTTTTGACATCTGTTAAACGTCCTTTTTGTTTTTTGTTAAGTCTTTTACATTTTA
ATAGTTTTTGAAGACAATCTAGGTTAAGCAAGAGCAAAGTGCCATTGTTTGCCTTTAATTGGGGGGTGGGAAGGG
AAAGAGGGTACTTGCCACATAGTTTCCTTTTTTAACCTGCATTTCTTTATATAATCGTTTGCATTTTGTACTTGC
TACCCTGAGTACTTTTCAAGGAAGACTGACTTAAATATTGCGGGTGAGTAAGTAGTTGGGTATAAGATCTGAACCTT
TCATCTGCAGAGGCAAGAAAAATATTTGACATTGTGACTTGACTGTGGAAGATGATGGTTGCATGTTTCTAGTTT
GTATATGTTTCCATCTTTGTGATAAGATGATTTAATAAATCTCTTTAAATACTT

716/6881
FIGURE 668

MVSMSEFKRNRSDRFYSTRCCGCCHVRTGTIILGTWYMVVNLLMAILLTVEVTHPNSMPAVNIQYEVIGNYYSSER
MADNACVLFAVSVMFIISSMLVYGAIQVGVLIPIFFCYRLFDFVLSCLVAISSLTYLPRKEYLDQLPDFPYK
DALLALDSSCLLFIVLVFFALFIIFKAYLINCWNCYKYINNRNVPEIAVYPAFEAPPQYVLPTYEMAVKMPEKE
PPPPYLPA

717/6881
FIGURE 669

GCGGCTTGCGGGGACCACAGCTCCCGAAAGCGACGTTTCGGCCACCGGAGGAGCGGGAGCCAAGCAGGCGGAGCTC
GGCGGGAGAGGTGCGGGCCGAATCCGAGCCGAGCGGAGAGGAATCCGGCAGTAGAGAGCGGACTCCAGCCGGCGG
ACCCTGCAGCCCTCGCCTGGGACAGCGGCGCGCTGGGCAGGCGCCCAAGAGAGCATCGAGCAGCGGAACCCGCGA
AGCCGGCCCCGAGCCGCGACCCGCGCAGCCTGCCGCTCTCCCGCCGCCGGTCCGGGCAGCATGAGGCGCGCGGCG
CTCTGGCTCTGGCTGTGCGCGCTGGCGCTGAGCCTGCAGCCGGCCCTGCCGCAAATTGTGGCTACTAATTTGCC
CCTGAAGATCAAGATGGCTCTGGGGATGACTCTGACAACTTCTCCGGCTCAGGTGCAGGTGCTTTGCAAGATATC
ACCTTGTCACAGCAGACCCCTCCACTTGGAAGGACACGCAGCTCCTGACGGCTATTCCACGTCTCCAGAACCC
ACCGGCCTGGAGGCTACAGCTGCCTCCACCTCCACCCTGCCGGCTGGAGAGGGGCCCAAGGAGGGAGAGGCTGTA
GTCCTGCCAGAAGTGGAGCCTGGCCTCACCGCCCCGGGAGCAGGAGGCCACCCCCGACCCAGGGAGACAGCATCA
GGGTAAAGAAGACTTTTTTTTTTTTTTTTTTAAACTAGGAGAACCAAATCTGGAAGCCAAAATGTAGGCTTAGTTT
GTGTGTTGTCTCTTGAGTTTGTGCTCATGTGTGCAACAGGGTATGGACTATCTGTCTGGTGGCCCCGTTTCTGG
TGGTCTGTTGGCAGGCTGGCCAGTCCAGGCTGCCGTGGGGCCGCCGCTCTTTCAAGCAAGGCCAGAGGCCCCCA
GCCAGGGCTCCTGCACTTACTTGCTTATTTGACAACGTTTCAGCGACTCCGTTGGCCACTCCGAGAGGTGGGCC
AGTCTGTGGATCAGAGATGCACCACCAAGCCAAGGGAACCTGTGTCCGGTATTCGATACTGCGACTTTCTGCCTG
GAGTGTATGACTGCACATGACTCGGGGTGGGGAAAGGGTTCGGCTGACCATGCTCATCTGCTGGTCCGTGGGAC
GGTGCCCAAGCCAGAGGCTGGGTTCATTTGTGTAACGACAATAAACGGTACTTGTCAATTCGGGC

718/6881
FIGURE 670

ACTGCGCGCCCCGCCCCGGAGTCCCCGCCGCGTCATGCAGTCCCCGGCGGTGCTCGTCACCTCCAGGCGACTTCA
GAATGCCCCACACTGGCCTCGACCTGACTGTGCCCCAGCACCAGGAGGTACGGGGCAAGATGATGTCTGGACACGT
GGAGTACCAGATCCTGGTGGTGACCCGTCTGGCTGCGTTCAAGTCGGCCAAGCACAGGCCCGAGGATGTCTGCTCCA
GTTCTTGGTCTCCAAAAAGTACAGCGAGATTGAGGAGTTTTACCAGAAACTGAGCAGTCGTTATGCAGCAGCCAG
CCTCCCCCCTACTACCCAGGAAGGTCTGTTTGGTGGGGAGTCTGACATCCGGGAGAGGAGAGCCGTGTTCAATGA
GATCCTGCGCTGTGTCTCCAAGGATGCCGAGTTGGCAGGCAGCCCAGAGCTGCTAGAGTTCCTAGGTACCAGATC
CCCAGGGGCTGCAGGGCTCACCAGCAGAGATTCTCTGTCTGGATGGCACAGACAGTCAGACAGGGAATGATGA
AGAGGGCTTTCGACTTTTTTTGAGGAGCAAGACCAAGTGGCAGAAGAGGGTCCGCCCCGTCCAGAGCCTGAAGGGCGA
GGATGCTGAGGAATCCTTGGAGGAGGAGGAGGCGCTGGACCCTCTGGGCATTATGCGCTCCAAGAAGCCCAAGAA
ACATCGGTGTGAAGGGAAGGGACTGGGCCCTGCAGGGTCAGAACCTCCCCACCCCCAGGGGAGGCCAGGCAGAAG
CCTGGGTACACAGCACCCAGAACTGCATGGTTCCATTTCTCCGGGGCTGTGGGGCCAAAGTAGAAGCCTGCGGGC
TGCGGGAGCGGCTCTCACCTAGGAGCCAGAGCCCAATGTGTCTTATTCCCCGTGGACATGAAGGGGAGGGAGGG
TGTGGGGATGCCTTGCCAACCAGAAGCCCAGCCCCAAGGATGAAGCAAGACATGTGGGGCCGTAGCGAGGTGTCA
CATGGGGCAGGGAAGCTTCATGCCCCACGGGTTCTGCCAGCCCCAGCACAGACCCAACTGGGGCTGGGCCTCTAT
CCCTCCTCTGCCTCTGTTTCGCATAGTAAGAAGGAGTGACCGGTATCCTCCCCCTTCCCCTACCCTAAGCTGTAGCC
TGGGTGACTGACTGGCCTGGGCCTGGGGTGGGGACGTCCCAAGCCAAATTACTCCAGGGCCTCTGCTCCTCGTG
GCTGCCAGGGGCTGCAGGGTCTGGGTGGGTCTCCAGGAGAGGAATACTGAGTGGGAGATCGGCTGTCTGGAGT
GTTCTGATGCAAGTCTCTCTCTCCTGAGCCTCCTCTTGATGCAAGCTCTAAAGGGAGAAGTCAGGCCCTGCCTCT
CCAGGGTATAGACGGCCCTGCTAGGCCCCAGTTCTTCCTCCTTCCCCCTTCCCAGGAAAGGCCAGCCCAGTCCA
TGGCCTTCTTGGGCCTCTGGGCACAGAGCCAATGTTTCGTATTGCAGCTCTCAGCAAACCTGGGTCTATAGCTTTCC
CCACAGCTCAGCCTGGGGCCTGGGCAGGGCTCCAGCCTGCACCGCCTCCCACTGCCAGTGGGGCATGATTCTCT
CAGGCTTCTGCCCCGAGGCCTTCGTCTCTCCTCAGGGTCTGGACTTGGTCAGTGGCCTTTACCAGTGGAGCTGCC
TTCCAGGGAGAAGGAGCCGTGCGCCAGGGCAGGGCCCGTGCCTTAGACTTCTCCCGACCCCCAGAGCGCTGGTA
CACAGGTCTAGGCACCACACAGTGCTTTGGAAATTCTCAGTGAATGATGTTTAATAAAGCAAAAAATGTC

719/6881
FIGURE 671

MQSPAVLVTSRRLQNAHTGLDLTVPHQEVRGKMMSGHVEYQILVVTRLAAFKSAKHPEDVVQFLVSKKYSEIE
EFYQKLSSRYAAASLPPLPRKVL FVGESDIRERRAVFNEILRCVSKDAELAGSPELLEFLGTRSPGAAGLTSRDS
SVLDGTDSTGNDEEAFDFFEEQDQVAEEGPPVQSLKGEDAEESLEEEALDPLGIMRSKKPKKHRCEGKGLGPA
GSEPPHPQGRPGRSLGHSTQNCMVPFSPGLWGQSRSLRAAGAALT LGARAQCVLFPVDMKGREGVGMPCQPEAQP
QG

720/6881
FIGURE 672

ATGGGTCAAAGTCAGAGTGGTGGTCATGGTCCTGGAAGTGGCAAGAAGGATGACAAGGACAAAAAAGAAATAT
GAACCTTCTGTACCAACTAGAGTGAGGAAAAAGAAGAAAACAAAGGGACCAGATGCAGTCAGCAAAC TGCCA
CTGGTGACACCTCACACTCAGTGCCGGTTAAAATTACTGACATTAGAGAGAATTAAAGACTATCTTCTCATGGAG
GAAGAATTCATTAGAAATCAGGAACAGATGAAACCATTAGAAGAAAAGCAAAAGGAGGAAAGATCAAAAGTGGAT
GATCTGAGGGGGGACCCCGATACAAGGATCTTCTGGAAGTGGCTGCTCGGTCTGCTCAACCACAAGGTGCATGC
CGTGATGGGGTGCTGATGGATGACACGGATCCCCTGGTCACAGTGATGAAGATGGAAAAGACCCCCCAGGAGACC
TATGCCAATATTGGGGGGCTGGACAACCAAATTCAGGAAATAAAGGAAGCTGTGGAGTTTCCTCTCACCCATCCT
GAATATTATGAAGAGATGGGTAAAAAGCCTCCTAAGGGGGTCATTCTCTATGGTCCACCTGGCACAGGCAAAACC
TTGTTATCCAAAGCAGTAGCAAACCAAACCTCAGCCACTTCTTGAGAGTGGTTGGCTCTGAACTTATT CAGAAG
TACCTAGTTGCTGAAGAGCATGAACTATCCATCATGTTTACTGATGAAATTGGAGCCATTGGGACAAAAAGATAT
GACTCAAATTCCTGGTGGCCGCATTGACAGGAAGATCAAGTTCTCCCTGCCTGATGAAAGGACTAAGAAGCGTATC
TTTCAGAATCACACAAGCAGGATGACACTGGCCGATGAAGTAACCCCTGGACGACTTGATCATGGTTAAAGATGAC
CTCTCTGGTGCTGACATCAAGGCAATCTGTACAGAAGCTGGTCTGATGGCCTCAAGAGAACGTAGAATGAAAGTA
ACGAATGAATTCTTCAAAAAATATAAAGAAATGTTCTTTATAAGAAACAGGAAGGCACCCCTGAGGGGCTCTATC
TCTAGTGAACCACAGCTGCCATCAGGAAAATGGTTGGGCGATTCCCTCGACCCCTGAAAAGGATGAGCAACTTGTT
CCCAAAGCTGGAGAAGACACTCCTGAGGGCTATTTAGGACAAC TTATGACTCAGCTCTTTGAGCAGAAAGAGGCC
AAAAAGTTCAGCAGAAAAAGCCCTGAACTCTTGGAAGAGCTGGCTTCAAGCCTGGCTTAG

721/6881
FIGURE 673

MGQSQSGGHGPGSGKKDDKDKKKKYEPSVPTVRKKKKKTKGPDVSKLPVTPHTQCRLKLLTLERIKDYLLME
EEFIRNQEQMKPLEEKQKEERSKVDDLRGTPIQSSGNWLLGPAQPQGACRDGVLMDDDTDLVTVMKMEKTPQET
YANIGGLDNQIQEIKEAVEFPLTHPEYYEEMGKKPPKGVILYGPPGTGKTLLSKAVANQTSATFLRVVGSELIQK
YLVAEEHEL SIMFTDEIGAIGTKRYDSNSGGRIDRKIKFSLPDERTKKRIFQNHTSRMTLADEVTLDDLIMVKDD
LSGADIKAICTEAGLMASRERRMKVTNEFFKKYKEMFFIRNRKAPLRGSISSEPQLPSGKWLGDSSSTPEKDEQLV
PKAGEDTPEGYLGQLMTQLFEQKEAKKFSRKSPELLEELASSLA

722/6881
FIGURE 674

GACGGCGCCTTCGCGAAACACT**ATG**CTAATGGCATGGTGCCGCGGTCCTGTCTTGCTGTGCCTGCGGCAGGGGCT
CGGAACCAATTCATTCCTGCACGGCCTGGGGCAGGAGCCCTTCGAGGGAGCTCGGTCACTGTGTTGCAGGTCCTC
GCCTAGAGACCTGCGAGATGGAGAAAGAGAGCACGAGGCGGCACAAAGGAAAGCCCCAGGAGCAGAGTCTTGCCC
ATCTCTCCCTCTGAGCATCTCGGACATTGGGACTGGATGTCTTTTCGTCACTGGAAAACCTCAGACTGCCGACGCT
GCGGGAAGAGTCATCACCTCGAGAGCTCGAGGACTCGAGCGGAGACCAGGGCCGGTGCGGTCCACACACCAGGG
ATCCGAGGATCCTTCGATGCTCTCGCAGGCCCCAGTCCGCTATCGAGGTCTGAAGAGCGTCACGTCTCCCCTTCTTG
TTCAACTTCCAGAGAGAGACCCTTTTCAGGCTGGGGAGCTGATTTTAGCTGAGACTGGGGAGGGAGAAACAAAATT
TAAGAAATTATTTAGGTTGAACAACCTTCGGACTCTTAAATAGTAACTGGGGGCGAGTCCCGTTCGGCAAGATCGT
GGGGAAGTTCCCCGGCCAGATACTGAGGAGTTCCTTCGGTAAGCAGTACATGCTGAGGAGGCCAGCCTTGGAAGA
CTATGTAGTATTGATGAAAAGAGGGGACTGCCATAACATTCCCAAAGGATATTAATATGATTCTCTCAATGATGGA
TATCAACCCAGGTGATACTGTTTTGGAAGCTGGCTCAGGCTCTGGTGGAATGAGCTTATTTTTATCCAAAGCAGT
TGGATCACAAGGACGAGTCATAAGTTTTGAGGTACGAAAAGACCACCATGATCTGGCTAAGAAGAATTACAAACA
CTGGCGTGATTTCATGGAAATTAAGTCATGTAGAAGAGTGGCCAGACAATGTGGATTTTATTCATAAGGACATTTT
AGGAGCAACCGAAGACATAAAATCTTTAACATTTGACGCAGTAGCTTTGGATATGTTAAATCCTCATGTTACTTT
GCCTGTTTTTTACCCACATCTTAAGCATGGTGGTGTATGTGCTGTATATGTAGTAAACATCACACAGGTTATTGA
ACTTTTAGATGGAATTCGCACCTGTGAACCTGCTCTTTTCATGTGAAAAGATAAGCGAGGTCATTGTCTAGAGATTG
GTTGGTTTGCCTTGCAAAACAGAAAAATGGAATTTTAGCTCAAAAAGTAGAATCTAAATCAACACAGATGTACA
ACTAGATTCTCAAGAGAAAATTGGAGTTAAAGGTGAGCTGTTTCAAGAGGATGACCATGAAGAATCGCATTCTGA
TTTTCCATATGGATCATTTCCCTATGTTGCTAGACCAGTACACTGGCAACCTGGTCATACAGCTTTTCTTGTCAA
GTTGAGGAAGGTCAAACCACAACCTTAAC**TGAG**TACTCCAGATGACAGTAACTGACTTGAAGATGGAAAAATATCA
AAATAGAACTTTATATTGAAAATCACTGCTTCCATAGATTGGCATTTTTAGCTATTACTATGACTTATATAACTT
ATACATATAATTTTGAAAATAACAATAAAAGATGTATAACATAGCAAACTGCTTAAACATCCCATTTTGACAC
TTGTCTTGCAAGTTAGTTTGACATTTTGTAGTTAATGATTCCAAATTGGTTTAGTTGGGCCATCTCATTCTTCACT
TCCTGTAAACCACTCCATAGATTTGTCTTTCTTCAAGAAATTAGTTTTCTTCTTTATTTGATTGATGGTCATT
GACTACTGAAATAAAATATGCATTTTAAGATAAAAAAAAAAAAAA

723/6881
FIGURE 675

MLMAWCRGPVLLCLRQGLGTNSFLHGLGQEPFEGARSLCCRSSPRDLRDGEREHEAAQRKAPGAESCPSLPLSIS
DIGTGCLSSLENLRLPTLREESSPRELEDSSGDQGRCGPTHQGSSEDPMSLSQAQSAIEVEERHVSPSCSTSRERP
FQAGELILAETGEGETKFKKLFRLNNFGLLNSNWGAVPFGKIVGKFPGQILRSSFGKQYMLRRPALEDYVVLTKR
GTAITFPKDINMILSMMDINPGDTVLEAGSGSGGMSLFSLKAVGSQGRVISFEVRKDHHDLAKKNYKHWRDSWKL
SHVEEWPDNVDFIHKDISGATEDIKSLTFDAVALDMLNPHVTLVPFYPHLKHGGVCAVYVVNITQVIELLDGIRT
CELALSCEKISEVIVRDWLVCLAKQKNGILAQKVESKINTDVQLDSQEKIGVKGELFQEDDHEESHSDFPYGSFP
YVARPVHWQPGHTAFLVKLRKVKPQLN

724/6881
FIGURE 676

ATGCAACAAGCTTCCTACCCCCAACCCGGCCAGACAAAGCCCCGGCAGCAGGGCCGGCACTTCCGAGCCTCCGGA
CTCGGGACGCCGCGCTCTTACCCTGGCCTCATCCAGAGTGACGCCGGCGCCACCGCTTCCCCCGGCTTTGGCGGC
GGGGCAGCTGGCGGCGCGGGTCTTGGAGGAGCGGGTCCGAGAGGAGATGAAATGGCTGCTGCCTCCGGTCGCCCC
AGGCTCTGCTCCGGCCCCAGGCCCAGGCCCCGGGACCAGGAGACTTGGACCCGAGAAGGCGGAGAGAGCTCTTCCG
GGTGTTCACCATGGTCCAGCCAGGGGGACGGAGTCCACGCCGCGCCCGGGAGAGCCGAGCAAGGCCGGCCCCGCCG
GCCGCTGCCCCGCCCCCGGCGCGGCGTCAGCGCTCGGCGGCCGGGGAGCGACGCTCTAGGCTGTCAGCTCGGTGG
TTTCCAGCTCTCCCCGACCGCAGGGCTGGGGCGACCAGAAAAGCCAGACTAATCAGGACGAGTTCGGGCGTGGA
TTGGGCCTGAAGCCCTCATGCCCAGCCAGGCCTGAATGCCCCAGACCCACCGTCACCCCCGTGGCCTGGATGGA
GCAGGGGACGGCCGGCGAAGGCGCGGGTGAAGGGGAGCGGCGACGAAGGCGCGAGGAGCTGACTGGGAATCCC
CAAGCTACCCGAGGCAAGACACTGAACTTGAGTCGCACTTTTTCATGCCTGTAGAAATGAGAATGACAGCTGTGAT
AAAAAAAAAATTCTGCGCGGTATCTGGAACCTTGGGCGTTCCGAAACTTACAGTTATGCGCAACACAATGTTT
CTATTTTCAAAGGCGAACGCTGCACGATCGCAGTCCAGTGATACAAATAATAAAAGAGTTTATTACTTGTCAGCA
ATGATGAATGTTTCGTGTGGCATCCAGCGTTGAGTTCCTATTCTTACTTGGAACCTATTGGTCCCTGTGTCTGGGG
CCAGCACTGATGGACACAATAAGTTTGCACTCGTCTTCCCTCTCATGTATCATACCTGGAATGGGATCCAACAC
TTGATGTGGGACCTAGGAAAAGGCCTGAAGATTCCCCAGCTATACCAGTCTGGAGTGGTTGTCCTGGTTCTTACT
GTGTTATTTGTAGGGCTGGCAGCTGTGTGA

725/6881
FIGURE 677

MQQASYPQPGQTKPRQQGRHFRASGLGTPRSYPGLIQSDAGATASPGFGGGAAGGAGLGGAGPRGDEMAAASGRP
RLCSGPRPRPGTRRLGPEKAERALPGVHHGPARGTESTPRPGEPSKAGPPAAAPPPARRQRSAAGERRSRLSARW
FPALPDRRAGATRKARLIRTSSGVELGLKPSCPARPECPRPHRHPRGLDGAGDGRRRRRGVEGERRRRRREELTGNP
QATRGTNLNLSRTFHACRNENDSCDKKKIHLGGIWNLGVPKLTVMRNTMFLFSKANAARSQSSDTNNKRVYYLSA
MMNVRVASSVEFLFLLGTHWSLCLGPALMDTTKFALVFPLMYHTWNGIQHLMWDLGKGLKIPQLYQSGVVVLVLT
VLFVGLAAV

726/6881
FIGURE 678A

ACAGAGAGATTGGTGTGTTTTGTGAGGCAGTGAGACCTAAGGTAACCTTTATCAAAAGGATCGAGTTGGGAAAAGG
AAAAC TACTCAGGACTGGACTGAATGCGTTGCATCAAGCAGTGCATCCGATCCATGGCCTTGCTGGACCGATGG
GAATCAAGTTGTCTTAAC TGATTTGCGGCTTCACAGTGGAGAGGTCAAGTTTGGGGACTCCAAAGTCATTGGACA
GTTTGAATGTGTCTGTGGGTTGTCTGGGCCCCACCTGTTGCAGATGATACACCTGTTCTACTCGCTGTCCAGCA
TGAGAAGCATGTCACTGTGTGGCAGCTGTGTCCCAGCCCTATGGAGTCAAGCAAATGGCTGACGTCTCAGACTTG
TGAGATTAGAGGATCACTACCTATCCTTCCCCAGGGCTGTGTGTGGCACCCAAAATGTGCTATTCTGACTGTGTT
GACTGCTCAGGATGTCTCCATTTTCCCTAATGTTCACTCTGATGATTCCCAGGTAAAGGCAGACATCAACACCCA
GGGCCGCATTCACTGTGCATGTTGGACCCAGGATGGCCTGAGGCTGGTGGTGGCAGTAGGCAGCAGCCTGCATT
TTATATTTGGGACAGCGCTCAGAAGACTCTTCACAGGTGCTCCTCCTGCCTGGTGTGTTGATGTGGACAGCCACGT
CTGCTCCATCACAGCAACTGTGGACTCACAGGTTGCTATAGCTACTGAGCTTCCATTGGATAAGATCTGTGGCTT
AAATGCATCTGAAACCTTTAATATCCCACCTAACAGTAAAGACATGACTCCGATGCTTTACCAGTTATTGGTGA
AGTACGCTCTATGGATAAAGAGGCAACTGATTCTGAAACAAATTCTGAAGTATCAGTTTCTTCTTCTTCTATTAG
ACCTCTGGATCTAACTCACATACATTTCAATCAACATAAGTCTGAGGGTAATTCTCTTATTTGTCTAAGAAAAA
GGACTACTTGACAGGAACTGGCCAAGATTCTTCACATTTGGTCCCTGTGACCTTTAAGAAGGCAGTTACCATGAC
GAGAAAAGTCACTATTCCAGGCATTCTGGTTCCTGATCTGATAGCATTTAATCTTAAAGCCCACGTAGTGGCAGT
GGCTTCCAACACTTGTAATATAATTTTGATCTACTCTGTCAATTCCATCTTCAGTCCCAAACATCCAGCAAATTCG
ATTAGAGAACTGAAAGACCAAAGGGATATGTTTCTTGACAGACCAACTATTACTAATTTTGGTAGGAAAAA
AAAAC TCACTGATACAACATTTCTTCCCTTCTTCAAAGTCTGATCAGTATGCCATTAGCTTGATTGTTAGAGAAAT
AATGTTGGAAGAAGAACCTTCAATAACATCAGGTGAAAGCCAGACTACCTACTCTACTTTTCAGTGTCCGTTAAA
TAAAGCAAATAGAAAAAGTTAATTGAAAGTCTTTCCCAGATTTTGTCAACAAACAAAGGGCTGTTGCTGAC
AGTTAATACCAGTAGTCAGAATGGAAGGCCTGGAAGAACACTTATTAAAGAAATCCAGAGTCTCTGTCTAGTAT
CTGTGATGGCTCCATAGCTCTAGATGCTGAGCCTGTTACCCAGCCAGCATCGCTGCCAGACACAGCAGCACACC
AGACCACACCAGCACACTGGAGCCTCCTCGTTTGCCTCAAAGAAAGAACTTACAAAGTGAAAAGGAACTTATCA
GCTGTCTAAGGAGGTGGAATTTTATCTAGGAACCTGGTTGAAATGCAACGGTGTCTTTCTGAACCTACAAACCG
TCTGCATAATGGGAAGAAATCCTCTTCAGTGTATCCACTCTCTCAAGATCTTCCCTATGTTTACATCATTTACCA
GAAACCTTATTATCTAGGTCTGTGTTGAAAAAGAGCGGTGCTTCTCTGTGATGGTAACTAAGGCTCAGTAC
AGTTCAGCAGACTTTTGGCCTTTCTCTCATTGAAATGCTACATGATTCCCACTGGATTCTTCTCTCTGCTGACAG
TGAGGGCTTTATCCCGTTAACCTTCACAGCCACACAGGAAATAATCATAAGAGATGGCAGCCTGTCCAGGTGAGA
TGTCTTCAGAGACTCTTTTTCTCACAGTCCAGGTGCTGTTTCTTCTTAAAGTCTTTACAGGCCTTGCTGCCCC
CAGTTTAGATACCACTGGCTGTTGTAACCATGTAGATGGCATGGCTTGATATCTGCAGTGTCTTGGCTGTGTAGC
TCTTCAGATGAGACCATTACAAACAAGGCCTGCTTGACACTGGACACTCGCCAATGAGACTCCCACTGCACTCAG
GCGAAGCGCTTGCCATGGTGGCTCTCCTGGTTTCCCCCTGTTTCCCCTGAGCTGAGGCTCGCTGCTGTGTAGCA
GAGCTCAGTCTTTATTAGATGGCTCCGAAAGTGTTGTTAIGTATTGATGACTGTGTGGTTTTGACTAAGGGCAG
AATTCTCAGAACAAAACAATATTATGGTGCCATATGGATGGTGTGTTTATGGTTTCTCTGAGGCTTTGTGTCCCTT
GTCCAAAGCTGCATTGAAGCTGTCTTAGGAGCACCTAAAAGATACCTTGGCATTGTTATAGGTCTTTTTCTTGCC
TTCAAGAGGAGGTTGAGGAGTCTGCTGGGGGGCATGTGCTCTAGCATATTAACCTCAAACCAGCAAGAATTAGCA
GAGCTCCAAGGAGGACCAGAGACCCACTGGCTTCTGCTCTCAGGAACAGGAAGTGGCTCTGATGTTGCCTGGACC
TCCCAGAATTTAAACCAAACCTCTTGCTTCCCTAACAAATTCTGGCTGACGAAGGTCCAGGTACTCTTAAAAAC
TGGCCCTGGGAAAATTTTGAATGAAATTTCAAGGGAATTTGTCCCCTCTGGGTTCCACTGAGGTTGTGCCGATG
CTGCTACCACACTGTGAGCCCAGGTAAGTCTACTGCAGGATTTTGTGCTGTGGCCACTCATGAGTGTCCCTGA
AATAACTTTTTTTTTTTTTTAAATCCAGTTTTGGGATCACGCAACTTCCCTATTTTTCTCCCAGTAGTCAGCTCCC
TTAGTTAACTTGTCACCTTTAATTTGATATTTTTATTTTCTCTCCTTTTAAAGTCTTAGAGACCAGCAGAGAATCTG
TGAGAGAAAGTATTTAGGAAGTTAGAAATTCAACCGAATCTGAGGTAGTCCTAAAAAGTGCCATTTTGTTCAC
TTATGGGCTAAAGTACCAGCTTAGTCAGGTAAGAGCCCTGACCCACTTCAGATGGTAACACCACCTTCTCACTGCC
TTCAGATGGAATCACAGATTTCACTCACGGCGCATAACAAATTGATCAGTGAGTGGCTAGGCATCTGCAGATAAA
TTGTTTCAGCCATAGAAGCTCCATTAGCACATATGCTTCCCTTTCCCCCTTCCCTTTAAAAATCATCTGGAAAGAA
ACTATTTTGTGCCCTTGGGGACTCCTGTCTGTCTGTTACAGTTTACCAAGATGGAGCTGGGTTAGGAAAGAAGTG
AGGGCCCATTTTGTGGTTCAGTGCCTAGACAGCTGCTGGGGTAGGAAGCACAGGCAATGTCTGCAATCAGCTG

727/6881
FIGURE 678B

TGGGAGAGCGGTGACTGAGAACAGTCTGAGGCCTGGCTCCACTTGGAAGTATCTGGGGTGCGATGAAATCACAAT
TATCTTGAAGCCTAAAGAGGGAACTACAAGACTGTAACTAAGATCAATGTGGGCACCTAAAAGGGTATGTTAAA
ATCACCATTCTCAGGTCAAATACTGTGAAATAAAAAATGGAAACGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAA

728/6881
FIGURE 679

MELGKGKLLRTGLNALHQAVHPIHGLAWTDGNQVVLTDLRLHSGEVKFGDSKVIQFECVCGLSWAPPVADDTPV
LLAVQHEKHVTVWQLCPSPMESSKWLTSQTCEIRGSLPILPQGCVWHPKCAILTVLTAQDVSIIPNVHSDDSQVK
ADINTQGRIHCACWTQDGLRLVVAVGSSLSHSYIWDQAQKTLHRCSSCLVFDVDVSHVCSITATVDSQVAIATELPL
DKICGLNASETFNIPPNSKDMTPYALPVICEVRSMDEATDSETNSEVSVSSSYLEPLDLTHIHFNQHKSEGNLS
ICLRKKDYLTTGTGQDSSHLVLVTFKKAVTMTTRKVTIPGILVPDLIAFNLKAHVAVASNTCNIIILIYSVIPSSVP
NIQQIRLENTERPKGICFLTDQLLLILVGKQKLTDTTFLPSSKSDQYAISLIVREIMLEEEPSITSGESQTTYST
FSAPLNKANRKKLIESLSPDFCHQNKGLLLTVNTSSQNGRPGRTLKEIQSPLSSICDGSIALDAEPVTQPASLP
RHSSTPDHTSTLEPPRLPQRKNLQSEKETYQLSKEVEILSRNLVEMQRCLSELTNRLHNGKKSSSVYPLSQDLPY
VHIIYQKPYLGPVVEKRAVLLCDGKLRLSTVQQTFLGLSLIEMLHDSHWILLSADSEGFIPLTFTATQEIIIRDG
SLSRSDVFRDSF SHSPGAVSSLKVFTGLAAPSLDTTGCCNHVDGMA

729/6881
FIGURE 680

TTCTCTTAGCAGCACCCAGCTTGCCACCCATGCTCAAGATGGGCGGGATGCCAGCCTGTTACATAAAATGTGCCA
AAAGCCTGGCCATGCCTGGAAAATGGACCAATCCGCCCAGCAAGAGGTTGGGTCTCGTTCCCTAGAGAGAAGGAA
GTTTCCTCTCCTTGAAGTGAGAGCTAGAATCGCACTTTCTGTCAAGCTGAGAGAAAGACTCTTTTCCAGAGGCTA
AAAGGACAAGAAAATCTGATTTGCTTGCTTCTAACTTTGCGTTTTAAAGGGGGAAGGAGGAAAGGAAAAGAGGGGG
AGGGTGGTTCTGCTTAGCCCCACCCCTCCGGCTACCCAGGTCCAGCCGTCCATTCCGGTGGAGGCAGAGGCAGT
CCTGGGGCTCTGGGGCTCGGGCTTTGTACCGGGACCCGAGGAGCCAGAACCACTCGGCGCCGCTGGTGCATG
GGAGGGGAGCCGGGCCAGGAACAATATGTTAGCCGTGCACCTTGACAAGCCGGGAGGACCGGAAAACCTCTACGT
GAAGGAGGTGGCCAAGCCGAGCCCGGGGAGGGTGAAGTCTCTGAAGGTGGCGGCCAGCGCCCTGAACCGGGC
GGACTTAATGCAGAGACAAGGCCAGTATGACCCACCTCCAGGAGCCAGCAACATTTTGGGACTTGAGGCATCTGG
ACATGTGGCAGAGCTGGGGCTGGCTGCCAGGGACACTGGAAGATCGGGGACACAGCCATGGCTCTGCTCCCCGG
TGGGGGCCAGGCTCAGTACGTCACTGTCCCCGAAGGGCTCCTCATGCCTATCCCAGAGGGATTGACCCTGACCCA
GGCTGCAGCCATCCCAGAGGCCTGGCTCACCGCCTTCCAGCTGTTACATCTTGTGGGAAATGTTACAGGCTGGAGA
CTATGTGCTAATCCATGCAGGACTGAGTGGTGTGGGCACAGCTGCTATCCAACCTACCCGGATGGCTGGAGCTAT
TCCTCTGGTCACAGCTGGCTCCCAGAAGAAGCTTCAAATGGCAGAAAAGCTTGGAGCAGCTGCTGGATTCAATTA
CAAAAAAGAGGATTTCTCTGAAGCAACGCTGAAATTCACCAAAGGTGCTGGAGTTAATCTTATTCTAGACTGCAT
AGGCGGATCCTACTGGGAGAAGAACGTCAACTGCCTGGCTCTTGATGGTCGATGGGTTCTCTATGGTCTGATGGG
AGGAGGTGACATCAATGGGCCCTGTTTTCAAAGCTACTTTTTAAGCGAGGAAGTCTGATCACCAGTTTGCTGAG
GTCTAGGGACAATAAGTACAAGCAAATGCTGGTGAATGCTTTCACGGAGCAAATCTGCCTCACTTCTCCACGGA
GGGCCCCCAACGTCTGCTGCCGGTCTGGACAGAATCTACCCAGTGACCGAAATCCAGGAGGCCCATAGTACAT
GGAGGCCAACAAGAACATAGGCAAGATCGTCCTGGAAGTCCCCAGTGAAGGAGGATGGGGCAGGACAGGACGCG
GCCACCCAGGCCTTTCCAGAGCAAACCTGGAGAAGATTACAATAGACAGGCCAAGAAACCCGGTGCTTCTCTCC
AGAGCCGTTTAAAGCTGATATGAGGAAATAAAGAGTGAAGTGG

730/6881
FIGURE 681

GGCACGAGGGTCCCGTTACCGCCTCCTGCTCCTGCCGCGCGCACCCCCGGGGCTTCGGCTCCGGCACGGGTCCGCG
CCCAGCTTTTCTGACCTGAGGCCGCCGGCCAGCCGCCGCCATGGGTGCCTACCTCTCCCAGCCCAACACGGTGA
AGTGCTCCGGGGACGGGGTCGGCGCCCCGCGCCTGCCGCTGCCCTACGGCTTCTCCGCCATGCAAGGCTGGCGCG
TCTCCATGGAGGATGCTCACAACCTGTATTCTGAGCTGGACAGTGAGACAGCCATGTTTTCTGTCTACGATGGAC
ATGGAGGGGAGGAAGTTGCCTTGTACTGTGCCAAATATCTTCTGATATCATCAAAGATCAGAAGGCCTACAAGG
AAGGCAAGCTACAGAAGGCTTTAGAAGATGCCTTCTTGGCTATTGACGCCAAATTGACCACTGAAGAAGTCATTA
AAGAGCTGGCACAGATTGCAGGGCGACCCACTGAGGATGAAGATGAAAAAGAAAAAGTAGCTGATGAAGATGATG
TGGACAATGAGGAGGCTGCACTGCTGCATGAAGAGGCTACCATGACTATTGAAGAGCTGCTGACACGCTACGGGC
AGAACTGTCAAGGGCCCTCCCCACAGCAAATCTGGAGGTGGGACAGGCGAGGAACCAGGGTCCCAGGGCCTCA
ATGGGGAGGCAGGACCTGAGGACTCAACTAGGGAACTCCTTCACAAGAAAATGGCCCCACAGCCAAGGCCTACA
CAGGCTTTTCTCTCAACTCGGAACGTGGGACTGAGGCAGGCCAAGTTGGTGAGCCTGGCATTCCCACTGGTGAGG
CTGGGCCTTCTGCTCTTCAGCCTCTGACAAGCTGCCTCGAGTTGCTAAGTCCAAGTTCTTTGAGGACAGTGAGG
ATGAGTCAGATGAGGCGGAGGAAGAAGAGGAAGACAGTGAGGAATGCAGCGAGGAAGAGGATGGCTACAGCACTG
AGGAGGCAGAGAATGAGGAAGATGAGGATGACACCGAGGAGGCTGAAGAGGACGATGAAGAAGAAGAAGAAGAGA
TGATGGTGCCAGGGATGGAAGGCAAAGAGGAGCCTGGCTCTGACAGTGGTACAACAGCGGTGGTGGCCCTGATAC
GAGGGAAGCAGTTGATTGTAGCCAACGCAGGAGACTCTCGCTGTGTGGTATCTGAGGCTGGCAAAGCTTTAGACA
TGTCTATGATCACAAACCAGAGGATGAAGTAGAACTAGCACGCATCAAGAATGCTGGTGGCAAGGTCACCATGG
ATGGGCGAGTCAACGGGGGCCTCAACCTCTCCAGAGCCATTGGGGACCACTTCTATAAGAGAAACAAGAACCTGC
CACCTGAGGAACAGATGATTTTCAGCCCTTCTGACATCAAGGTGCTGACTCTCACTGACGACCATGAATTCATGG
TCATTGCCTGTGATGGCATCTGGAATGTGATGAGCAGCCAGGAAGTTGTAGATTTTATTCAATCAAAGATCAGCC
AGCGTGATGAAAATGGGGAGCTTCGGTTATTGTCTCATTCATTGTGGAAGAGCTGCTGGATCAGTGCCTGGCACCAG
ACACTTCTGGGGATGGTACAGGGTGTGACAACATGACCTGCATCATCATTTGCTTCAAGCCCCGAAACACAGCAG
AGCTCCAGCCAGAGAGTGGAAGCGAAAACCTAGAGGAGGTGCTCTCTACTGAGGGGGCTGAAGAAAATGGCAACA
GCGACAAGAAGAAGAAGGCCAAGCGAGACTAGCAGTCATCCAGACCCCTGCCCACCTAGACTGTTTTCTGAGCCC
TCCGGACCTGAGACTGAGTTTTGTCTTTTTCTTTAGCCTTAGCAGTGGGTATGAGGTGTGAGGGGGAGCTGGG
TGGCTTCACTCCGCCCATTCCAAAGAGGGCTCTCCCTCCACACTGCAGCCGGGAGCCTCTGCTGTCTTCCCAGC
CGCCTCTGCTCCTCGGGCTCATCACCGGTTCTGTGCTGTGCTCTGTTGTGTTGGAGGGAAGGACTGGCGGTTCT
GGTTTTTACTCTGTGAACCTTATTTAAGGACATTCTTTTTTATTGGCGGCTCCATGGCCCTCGGCCGCTTGCACC
CGCTCTCTGTTGTACACTTTCAATCAACACTTTTTTCAGACTAAAGGCCAAAACCTAAAAAAAAAAAAA

731/6881
FIGURE 682

MGAYLSQPNTVKCSGDGVGAPRLPLPYGFSAMQGWRVSMEDAHNCIPELDSETAMFSVYDGHGGEEVALYCAKYL
PDIIKDQKAYKEGKLQKALEDAFLAIDAKLTTEEVIKELAQIAGRPTEDEDEKEKVADEDDVDNEEAALLHEEAT
MTIEELLTRYGQNCHKGPPHSKSGGGTGEEPGSQGLNGEAGPEDSTRETPSQENGPTAKAYTGFSSNSERGT
EAGQVGEFGIPTGEAGPSCSSASDKLPRVAKSKFFEDSEDESDEAEEDSEECSEEDGYSSEEAENEDEDDTEE
AEEDDEEEEEEMVPGMEGKEEPGSDSGTTAVVALIRGKQLIVANAGDSRCVVSEAGKALDMSYDHKPEDEVELA
RIKNAGGKVTMDGRVNGGLNLSRAIGDHFYKRKNLPPPEQMSALPDIKVLTLTDDHEFMVIACDGIWNVMSSQ
EVDVFIQSKISQDENGELRLLSSIVEELLDQCLAPDTSGDGTGCDNMTCTIIICFKPRNTAELQPESGKRKLEEV
LSTEGAEENGNSDKKKKAKRD

732/6881
FIGURE 683

CCACTGCCGCTGCCGCCGCTCTCCTTAGTCGCCGGCATGACGACCGCGTCTACCTCGCAGGTGCGCCAGAACTT
GCTGAGAAATTGATGAAGCTGTAGAACCAACGAGGTGGCCGAATCTTCCTTCAGGATATCAAGAAACCAGACTGT
GCGGGGAGAATGCGATGGGAGAGCGGGCTGAATGCGATGGATTACATTTGGAAAAAATTGTGCATTTTGCATTAC
ATTTGGAAAAAATGTGAATCAGTCACTACTGGAAGTGCACAACTGGCCACTGACAAAAATGACCCCCATTGT
GTGACTTCATTGAGACACATTACCTGAATGAACAAGTGAAGGCCATCAAAGAATTGGGTGACCACGTGACCAACA
TGCACGAGATGGGAGCGCCCGAATCTGGCGTGGCAGAATACCTCTTTGACAAGCACACCCTGGGAGACAGTGATA
ATGAAAGCTAAGCCTCAGGCTAATTTCCCATAGCCATAGGGTGACTTACCTTGTCACCAAGGCAGCGCATGTAT
GTTGGGGTTTCTTTACCTTTTCTATAAGTTGTTCCAAGACACCCACTTAAGTTCTTTGATTTGTACCATTCCTT
CAAATAAATAAATTGGTACCC

734/6881
FIGURE 685

MHFSIPETESRSGDSGGSAYVAYNIHVNGVLHCRVRYSQLLGLHEQLRKEYGANVLP AFPPKKLFSITPAEVEQR
REQLEKYMQAVRQDPLLGSSETFNSFLRRAQQETQQVPTEEVSLEVLLSNGQKVLVNVLTSDQTEDVLEAVAAKL
DLPDDLIGYFSLFLVREKEDGAFSFVRKLQEFELPYVSVTSLRSQEYKIVLRKSYWDSAYDDDVMENRVGLNLLY
AQTVSDIERGWILVTKEQHRQLKSLQEKVSKKEFLRLAQLRHYGYLRFDACVADFPEKDCPVVVSAGNSELSLQ
LRLPGQQLREGSFRVTRMRCWRTSSVPLPSGSTSSPGRGRGEVRLELAFEYLMKDRLOQWVTITSPQAIMMSIC
LQSMVDELMVKKSGGSIRKMLRRRVGGTLRRSDSQQAVKSPPLLESPDATRESMVKLSSKL SAVSLRGIGSPSTD
ASASDVHGNFAFEGIGDEDL

735/6881
FIGURE 686

GATGGCTGCTGTGGCCGTGGCTGTTTCGCGAGGACTCGGGATCCGGGATGAAGGCGGAGCTTCCCCCTGGGCCTGG
GGCAGTGGGGAGGGAAATGACCAAAGAAGAAAAGCTGCAGCTTCGGAAGGAAAAGAAACAGCAGAAGAAGAAACG
GAAGGAAGAAAAGGGGGCAGAACCAGAGACTGGCTCTGCTGTATCTGCAGCCCAATGTCAAGTAGGCCCAACCAG
AGAACTGCCAGAATCGGGCATTTCAGTTGGGCACTCCTCGGGAGAAAGTTCCAGCTGGTCGGAGTAAGGCCGAAC
TCGGGCTGAGCGTCGAGCCAAGCAGGAGGCCGAGCGGGCCCTGAAACAGGCAAGAAAAGGGGAACAAGGAGGACC
ACCTCCTAAGGCCAGCCCCAGCACAGCTGGAGAAAACCCCTCAGGAGTGAAGCGTCTCCCTGAGTACCCTCAGGT
TGATGACCTACTTCTGAGAAGGCTTGTTAAAAAACAGAGCGTCAACAGGTTCTTACACGAAAGGATTATGGATC
CAAAGTCAGTCTCTTCTCTCACCTACCCAGTACAGCAGACAAAACCTCTCTGACCCAGTTTATGAGCATCCCATC
CTCTGTGATCCACCCAGCCATGGTGCGACTCGGCCTGCAGTACTCCCAGGGCCTGGTCAGTGGCTCCAATGCCCG
GTGTATTGCCCTGCTTCGTGCCTTGCAGCAGGTGATTTCAGGATTACACAACACCGCCTAATGAAGAACTCTCCAG
GGATCTAGTGAATAAACTAAAACCCCTACATGAGCTTCCTGACTCAGTGCCGTCCCCTGTCAGCGAGCATGCACAA
CGCCATCAAGTTCCTTAACAAGGAAATCACCAGTGTGGGCAGTTCCAAGCGGGAAGAGGAGGCCAAGTCAGAACT
TCGAGCAGCCATTGATCGGTATGTGCAAGAGAAGATTGTGCTAGCAGCTCAGGCAATTTACGCTTTTGCTTACCA
GAAGATCAGTAATGGAGATGTGATCCTGGTATATGGATGCTCATCTCTGGTATCACGAATTTCTTCAGGAGGCTTG
GACAGAGGGCCGGCGGTTTTCGGGTGGTAGTGGTGGACAGCCGGCCATGGCTGGAAGGAAGGCACACACTACGTTT
TCTAGTCCATGCTGGTGTCCCAGCCTCCTACCTGCTGATTCTGTCAGCCTCCTATGTGCTCCCAGAGGTTTCCAA
GGTGCTATTGGGAGCTCATGCACTCTTGGCCAACGGGTCTGTGATGTACGGGTAGGGACAGCACAGTTAGCCCT
GGTGGCTCGAGCCCATAATGTACCAGTGCTGGTTTGCTGTGAAACATACAAGTTCTGTGAGCGTGTGCAGACTGA
TGCTTTTGTCTCTAATGAGCTAGATGACCCTGATGATCTGCAATGTAAGCGGGGAGAACATGTTGCGCTGGCTAA
CTGGCAGAACCACGCATCCCTACGGTTGTTGAATCTAGTCTATGATGTGACTCCCCAGAGCTTGTGGATCTGGT
GATCACGGAGCTGGGGATGATCCCTTGCACTTCTGTACCTGTTGTTCTACGAGTCAAGAGCAGTGACCAGTGACG
GGGGAACACAGGGTTAATAAATGCCATACTCCCTACCCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAC

736/6881
FIGURE 687

MAAVAVAVREDSGSGMKAELPPGPGAVGREMTKEEKLQLRKEKKQQKKRKEEKGAEPETGSAVSAAQCQVGPTR
ELPESGIQLGTPREKVPAGRSKAELRAERRAKQEAERALKQARKGEQGGPPPKASPSTAGETPSGVKRLPEYPQV
DDLLLRRLVKKPERQQVPTRKDYGSKVSLFSLPQYSRQNSLTQFMSIPSSVIHPAMVRLGLQYSQGLVSGSNAR
CIALLRALQQVIQDYTTTPNEELSRDLVNKLKPYMSFLTQCRPLSASMHNAIKFLNKEITSVGSSKREEEAKSEL
RAAIDRYVQEKIVLAAQAISRFAYQKISNGDVILVYGCSLVSRILQEAWTEGRRFRVVVDSRPWLEGRHTLRS
LVHAGVPASYLLIPAASYVLPEVSKVLLGAHALLANGSVMSRVGTAQLALVARAHNPVVLVCCETYKFCERVQTD
AFVSNELDDPDDLQCKRGEHVALANWQNHASLRLNLVYDVTPELVDLVITELGMIPCSSVPVVLRVKSSDQ

737/6881
FIGURE 688

AGGACTTTGGCGAGGGGGCAGCCATTTTGGGGGGTGCTGATCGATACCTGCGGGGTCGGCTATGTTGCCCTGGGG
GAGGCCGGCCCCGTGGGGAACATGACTGTGGTAGACTCTCCTGGACAAGAGGTGCTAAATCAGCTTGATGTCAAG
ACCTCTTCAGAAATGACCAAGTGCAGAGGCTTCCGTAGAGATGTCATTACCTACCCCTTTGCCTGGATTGAGGAT
TCTCCTGATCAGAGGAGGCTCCCTCCAGAGCAGGAAAGCCTCTCCAGACTGGAACAGCCAGATCTTCTTCAGAG
ATGTCAAAGGTCTCAAAGCCTAGGGCCTCAAAGCCTGGCCGGAAGAGAGGTGGTAGGACACGAAAAGGCCCAA
AGGCCCCAACAGCCTAATCCTCCATCAGCCCCACTGGTTCTTGGTCTCTTAGATCAATCCAACCTCTGTCCACC
CCCATGCTTAAGAAACGAGGTGCAAGTCCAAGGCAGAGCTGCTGCTGCTGAAGTTGTCAAAGACCTAGATCGG
CCAGAATCTCAATCTCCAAAGAGGCCCCCTGAGGACTTTGAGACCCCTTCTGGGGAACGACCCCGCCGAAGGGCT
GCCCCAAGTGGCACTTCTGTATCTTCAGGAACTGGCTGAAGAGCTCTCAACAGCCCTGCCTGCCCCGTGTCTCTGT
CCTGAGGGCCCCAAGGTGAGCAGCCCCACCAAACCGAAGAAGATCCGGCAGCCAGCAGCCTGTCCAGGTGGAGAA
GAGGTGGATGGTGCTCCACGGGATGAAGACTTTTTTCTCCAGGTTGAGGCTGAAGATGTGGAAGAAAGTGAGGGC
CCAAGTGAGAGCTCATCTGAACCTGAGCCTGTAGTGCCCCGAAGCACCCACGAGGATCTACTTCAGGGAAACAG
AAACCACACTGCCGAGGAATGGCTCCCAATGGCTTACCAAATCATATCATGGCTCCTGTTTGGAAAGTGCCCTCCAT
CTCACCAGGACTTCCGAGAGCAGAAACATTCATACTGGGAGTTTGCTGAGTGAGATTCTTTAGCCTGGAAGTGG
CACTTGTTATCTGAGCTTGAGGCGCTCCCTACCTGCCCCAGGAGGAGAAGTCTCCATTGTTTTCTGTACAACGT
GAAGGGCTACCTGAAGATGGCACCCCTCTACCGAATAAACAGATTTAGCTCGATCACAGCACATCCAGAGCGCTGG
GATGTGTCTTCTTCACGGGGGGACCGCTCTGGGCTCTGGACTGGTGCCAGTGCCAGAGGGGGCAGGAGCCTCG
CAATATGTGGCTCTTTTCTCCAGCCCTGACATGAATGAGACACACCCACTGAGCCAGCTTCATTTCGGGTCTGGG
CTGCTCCAGCTCTGGGGCCTTGGGACCTTGCAGCAAGAAAGCTGTCTGGCAACAGGGCCCCACTTTGTCTATGGG
ATTGCTTGAGACAACGGCTGCATCTGGGACCTCAAGTTCTGCCCCAGTGAGCATGGGAACCTCCAGGCACCCCT
CGGAAGGCTCCTCTCTGCCCCGGTTGGGTCTCTTGGCTCTGGCCTGCTCAGACGGGAAAGTACTGCTATTCACT
CTACCCCATCCGGAGGCCCTGTCTGGCTCAGCAACCCCCAGATGCAGTGAAGCCTGCCATATATAAGGTACAATGT
GTGGCAACTCTGCAGGTGGGGTCTATGCAAGCTACAGACCCCTCTGAGTGTGGTCAGTGCCCTTAGCCTGGCCTGG
ATGCCCTACCAGGCCCCACCAACACCTAGCTGCTGGATATTATAATGGCATGGTGGTTTTCTGGAACCTTCCCACT
AACTCACCCCTGCAGCGGATACGGCTCTCTGATGGCTCCTTAAAGCTCTACCCCTTCCAGTGTTTCTAGCCCAT
GACCAGGCTGTGCGTACCCTTCAATGGTGCAAAGCTAACAGCCATTTCTTGTCTCTGCGGGGAGTGACCGGAAA
ATCAAATTTCTGGGACCTTCGACGTCTTACGAACCCATAAACTCTATCAAGCGCTTCTTGAGTACAGAACTGGCC
TGGCTGCTTCCCTACAATGGTGTCACTGTGGCTCAGGACAACCTGCTATGCCTCTTATGGACTCTGTGGGATTCTAT
TATATTGACGCTGGTTACCTTGGTTTTCAAGGCCCTACTTCACTGCTCCTCGAAAAGGCACCGTTTTGGAGTCTTTCA
GGATCCGACTGGCTTGGGACAATAGCTGCAGGAGATATATCCGGGGAGCTCATTGCTGCTATATTACCAGATATG
GCACTGAATCCAATAAATGTCAAGCGACCTGTAGAGCGAAGATTTCTATATATAAAGCAGATCTGATACCGTAT
CAGGACAGTCTGAAGGTCCAGACCATTCTTCTGCTTCACTGCGGTCCCCAACCCCTCCCAAGGCTCGAACTTAC
ACTGAAACTGTCAACCATCACTACTTGCTCTTTCAAGACACAGATTTGGGTTTCACTCCATGATCTGCTCCGTAGA
GAACCAATGCTGCGCATGCAGGAGGGAGAGGGGCATTCTCAACTCTGCCTGGACAGGCTGCAGCTGGAGGCTATT
CATAAGGTACGTTTTAGCCCCAACCTGGACTCCTATGGATGGCTGGTATCTGGGGGGCAGTCAGGGCTGGTTCTGA
ATCCATTTTGTCCGTGGACTCGCTCCCCACTGGGGCCACCGTATGCAGCTTGAAAGCCGAGCCCACTTCAATGCT
ATGTTCCAACCATCTCCCCCACTAGACGGCCTGGCTTCTCTCCAACAGCCATCGCCTTCTGCCCCACTCCCTAG

CCTTGGCCCCACACCAGATCCTTGGAGTGAAGTCGGTCAAGAACAAATGGCCCCCTATGCACAGAGCCATAGGAACT
GGGGGCCCTTCCCTGGACAGTGATCATGCCAGGCCTGGACCTTTAGGCCTGCCTCCCCAGGACTCCTTAGATCCCA
CTCTTTCTACAGACTTCTGTGATCACAGCCCCCTGCGGGCAGGGGGGCTCTCCCTCCACCAACTCTCAAGGCTCC
TCAGCCTAAGACTATGGCTCATGAGAAACACTCAGGCCTGACCTAGGCTTGGGAGTCAAAGTCTCATATTGAGC
ATATTGTTAAGTGGGTAAAGCCAAGTAAAGGTACTGGGTGTTTTTGTGACCACTTGTGAATGGGTGTATGGAGAA
CTGAAAAGGGTATCTGCATGAAGGCTCCGTCTGACTATTCCAGGATCCAATATTACTGCCTTCTGAAACTTCTT
CTTTAGGGTAACCATCATGTATGCCCACGAGGGTGATAGTAATTTCGTGAGACTGAAGTTGCTTAGAGTACTTCTT
TGACCAAGGAATACCACAGACACCCCTACCGATAGAACAGTGGCTCAGATCTTACTTGCTCCTGCTTACGAAGTAT
TCCCAATCACTGGTCATCTGACCCCTACTTGAACACTCCTGAACAGTCATGTTTTTAAATCTTCTTTTATATCA
AGTCAGAGAGTATACTTCTATAAATTTCACTCATGGATGTTAGGAAATCTAGTCATCTTCCCTGTGATTGCCCTG
TTAAGTATTTAACCATAGCTATCATGTGTTTCCCAATCTTCTCTAGATTAAATATCTTCAGTTACTTC

738/6881
FIGURE 689

MDTCGVGYVALGEAGPVGNMTVVDS PGQEV LNQLDV KTSSEMTSAEASVEMSLPTPLPGFEDSPDQRRLPPEQES
LSRLEQPDLSSEMSKVS KPRASKPGRKRGGRTRKGPKRPQQPNPPSAPLVPGLLDQSNPLSTPMPKKRGRKSKAE
LLLLKL SKDLDRPESQSPKRPPEDFETPSGERPRRRAAQVALLYLQELAEELSTALPAPVSCPEGPKVSSPTKPK
KIRQPAACPGGEEVDGAPRDEDFFLQVEAEDVEESEGPSESSSEPEPVVPRSTPRGSTSGKQKPHCRGMAPNGLP
NHIMAPVWKCLHLTKDFREQKHSYWEFAEWIPLAWKWHLLSELEAAPYLPQEEKSP LFSVQREGLPEDGTLYRIN
RFSSITAHPERWDVSFFTGGPLWALDWCPVPEGAGASQYVALFSSPDMNETHPLSQLHSGPGLLQLWGLGTLQQE
SCPGNRAHFVYGIACDNGCIWDLKFCPSGAWELPGTPRKAPLLPRLGLLALACSDGKVLLFSLPHPEALLAQQPP
DAVKPAIYKVQC VATLQVGSMQATDPSECGQCLSLAWMPTRPHQH LAAGYYNGMVVFWNLPTNSPLQIRIRLSDGS
LKLYPFQCF LAHDQAVRTLQWCKANSHFLVSAGSDRKIKFWDLR RPYEPINSIKRFLSTELAWLLPYNGVTVAQD
NCYASYGLCGIHYIDAGYLGFKAYFTAPRKGTVWSLSGSDWLGTIAAGDISGELIAAILPDMALNP INVKREVER
RFPIYKADLIPYQDSPEGPDHSSASSGVPNPPKARTYTET'VNHHYLLFQD TDLG SFHDL LRREPMLRMQEGEGHS
QLCLDRLQLEAIHKVRFSPNLDSYGWLVS GGQSGLVRIHFVRGLASPLGHRMQLESRAHFNAMFQPSSPTRRPGF
SPTSHRLLPTP

739/6881
FIGURE 690

GAGGGACGGTGGGGGTGACCCCTCTCCTCTTGGCTTGACAGGAAGCATGGCACTCTGGCGGGCATAACCAGCGGG
CCCTGGCCGCTCACCCGTGGAAAGTACAGGTCCTGACAGCTGGGTCCCTGATGGGCCTGGGTGACATTATCTCAC
AGCAGCTGGTGGAGAGGCGGGGTCTGCAGGAACACCAGAGAGGCCGACTCTGACCATGGTGTCCCTGGGCTGTG
GCTTTGTGGGCCCTGTGGTAGGAGGCTGGTACAAGGTTTTGGATCGGTTTCATCCCTGGCACCACCAAAGTGGATG
CACTGAAGAAGATGTTGTTGGATCAGGGGGGCTTTGCCCCGTGTTTTCTAGGCTGCTTTCTCCCACTGGTAGGGG
CACTTAATGGACTGTCAGCCCAGGACAACCTGGGCCAACTACAGCGGGATTATCCTGATGCCCTTATCACCAACT
ACTATCTATGGCCTGCTGTGCAGTTAGCCAACTTCTACCTGGTCCCCCTTCATTACAGGTGGCCGTTGTCCAAT
GTGTTGCTGTTATCTGGAACCTCTACCTGTCCTGGAAGGCACATCGGCTCTAAGCCTGCCTCACTCCATCGTTTC
CACCTTGCACTGATGCAGCTTGACCCTGGAACGGTCAGACAACCTCCTCAAAGTGGGCATAACCAGTTTCCACGGG
GTTGGGTTGCCGGTCAGAGCTTAAGAGGACTAGCACCTGCAATGCCCTCTTCACTCTAAAATGTACACTGACT
GCTTTAGAGCCCTTGATAATAGTCTTATTTCCACCACATACTAGGCACTCCATAAATATCTGTTGAACCTTCATG
ACCTTATCAACTTTACACCCATATCCCAGCAAATGCCACTCATCCCCACTCTTCATAGACACATTTGTTACTCTA
ACCTGCCTAGGCTTCTTGTAGCTCCAGCTCTTTAGAGACTCCCGGAACCCTTTATATGGTGCCTCAGTAAATAT
GTTATTAAATATGTAATCCGG

740/6881
FIGURE 691

MALWRAYQRALAAHPWKVQVLTAGSLMGLGDIISQQLVERRGLQEHQGRITLTMVSLGCGFVGPVVGGWYKVLDR
FIPGTTKVDALKKMLLDQGGFAPCFLGCFPLVVGALNGLSAQDNWAKLQRDYPDALITNYYLWPAVQLANFYLP
LHYRLAVVQCVAVIWNSYLSWKAHRL

741/6881
FIGURE 692A

CGCCCCCGCCTCTGAGCTCCCTTCCCATGGCGGCCCTAGTGTGGAGGACGGGTCCGTCTGCGGGGCCAGCCCT
TTGGGGCCGCGTGTGACTGCCGGGGAAGTGGTGTTCAAACCGGCATGGTCGGCTACCCCGAGGCCCTCACTG
ATCCCTCCTACAAGGCACAGATCTTAGTGCTCACCTATCCTCTGATCGGCAACTATGGCATCCCCCAGATGAAA
TGGATGAGTTCGGTCTCTGCAAGTGTTTGAATCCTCGGGCATCCACGTAGCAGCACTGGTAGTGGGAGAGTGCT
GTCCTACTCCCAGCCACTGGAGTGCCACCCGCACCCTGCATGAGTGGCTGCAGCAGCATGGCATCCCTGGCTTGC
AAGGAGTAGACACTCGGGAGCTGACCAAGAAGTTGCGGGAACAGGGGTCTCTGCTGGGGAAGCTGGTCCAGAATG
GAACAGAACCTTTCATCCCTGCCATTCTTGGACCCCAATGCCCGCCCCCTGGTACCAGAGGTCTCCATTAAGACTC
CACGGGTATTCAATACAGGGGGTGCCCTCGGATCCTTGCTTTGGACTGTGGCCTCAAGTATAATCAGATCCGAT
GCCTCTGCCAGCGTGGGGCTGAGGTCACTGTGGTACCCTGGGACCATGCACTAGACAGCCAAGAGTATGAGGGTC
TCTTCTTAAGTAATGGGCCTGGTGACCCTGCCTCCTATCCCAGTGTGCTATCCACACTGAGCCGTGTTTTATCTG
AGCCTAATCCCCGACCTGTCTTTGGGATCTGCCTGGGACACCAGCTATTGGCCTTAGCCATTGGGGCCAAGACTT
ACAAGATGAGATATGGGAACCGAGGCCATAACCAGCCCTGCTTGTGGTGGGCTCTGGGCGCTGCTTTCTGACAT
CCCAGAACCATGGGTTTGCTGTGGAGACAGACTCACTGCCAGCAGACTGGGCTCCTCTCTTACCAACGCCAATG
ATGGTTCCAATGAAGGCATTGTGCACAACAGCTTGCTTTCTTCAGTGTCCAGTTTCACCCAGAGCACCAAGCTG
GCCCTTCAGATATGGAAGTCTTTTCGATATCTTTCTGAAACTGTGAAAGAGGCCACAGCTGGGAACCTGGGG
GCCAGACAGTTAGAGAGCGGCTGACTGAGCGCTCTGTCCCCCTGGGATTCCCACTCCCGGCTCTGGACTTCCAC
CACCACGAAAGGTTCTGATCCTGGGCTCAGGGGGCCTCTCCATTGGCCAAGCTGGAGAATTTGACTACTCGGGCT
CTCAGGCAATTAAGGCCCTGAAGGAGGAAAACATCCAGACGTTGCTGATCAACCCCAATATTGCCACAGTGCAGA
CCTCCCAGGGGCTGGCCGACAAGGTCTATTTTCTTCCATAACACCTCATTATGTAACCCAGGTGATACGTAATG
AACGCCCCGATGGTGTGTTACTGACTTTTGGGGGCCAGACTGCTCTGAACTGTGGTGTGGAGCTGACCAAGGCCG
GGGTGCTGGCTCGGTATGGGGTCCGGTCTGGGCACACCAGTGGAGACCATTGAGCTGACCGAGGATCGACGGG
CCTTTGCTGCCAGAATGGCAGAGATCGGAGAGCATGTGGCCCCGAGCGAGGCAGCAAATTTCTTGAACAGGCC
AGGCAGCCGCTGAACGGCTGGGGTACCCTGTGCTAGTGCCTGCAGCCTTTGCCCTGGGTGGCCTGGGCTCTGGCT
TTGCCCTCTAACAGGGAGGAGCTCTCTGCTCTCGTGGCCCCAGCTTTTGCCCATACCAGCCAAGTGCTAGTAGACA
AGTCTCTGAAGGGATGGAAGGAGATTGAGTACGAGGTGGTGAGAGACGCCTATGGCAACTGTGTACGGTGTGTA
ACATGGAGAACTTGACCCACTGGGCATCCACACTGGTGAGTCCATAGTGGTGGCCCCCTAGCCAGACACTGAATG
ACAGGGAGTATCAGCTCCTGAGGCAGACAGCTATCAAGGTGACCCAGCACCTGGGAATTGTTGGGGAGTGCAATG
TGCAGTATGCCTTGAACCCCTGAGTCTGAGCAGTATTACATCATTGAAGTGAATGCCAGGCTCTCTCGCAGCTCTG
CCCTGGCCAGTAAGGCCACAGGTTATCCACTGGCTTATGTGGCAGCCAAGCTAGCATTGGGCATCCCTTTGCCTG
AGCTCAGGAACTCTGTGACAGGGGGTACAGCAGCCTTTGAACCCAGCGTGGATTATTGTGTGGTGAAGATTCCCTC
GATGGGACCTTAGCAAGTTTCTGCGAGTCAGCACAAAGATTGGGAGCTGCATGAAGAGCGTTGGTGAAGTCATGG
GCATTGGGCGTTTCAATTTGAGGAGGCCCTCCAGAAGGCCCTGCGCATGGTGGATGAGAACTGTGTGGGCTTTGATC
ACACAGTGAAACCAGTCAGCGATATGGAGTTGGAGACTCCAACAGATAAGCGGATTTTGTGGTGGCAGCTGCTT
TGTGGGCTGGTTATTCAGTGGACCGCTGTATGAGCTCACACGCATCGACCGCTGGTTCTTGCACCGAATGAAGC
GTATCATCGCACATGCCCAGCTGCTAGAACAACACCGTGGACAGCCTTTGCCGCCAGACCTGCTGCAACAGGCCA
AGTGTCTTGGCTTCTCAGACAAACAGATTGCCCTTGCACTTCTGAGCACAGAGCTGGCTGTTGCAAGCTGCGTC
AGGAACTGGGGATCTGTCCAGCAGTGAAACAGATTGACACAGTTGCAGCTGAGTGGCCAGCCCAGACAAATTACC
TATACCTAACGTATTGGGGCACCAACCATGACCTCACCTTTCGAACACCTCATGTCCTAGTCCTTGGCTCTGGCG
TCTACCGTATTGGCTCTAGCGTTGAATTTGACTGGTGTGCTGTAGGCTGCATCCAGCAGCTCCGAAAGATGGGAT
ATAAGACCATCATGGTGAACATAACCCAGAGACAGTCAGCACCGACTATGACATGTGTGATCGACTCTACTTTG
ATGAGATCTCTTTTGGAGTGGTGTATGGACATCTATGAGCTCGAGAACCCTGAAGGTGTGATCCTATCCATGGGTG
GACAGCTGCCCCAACACATGGCCATGGCGTTGCATCGGCAGCAGTGCCGGGTGCTGGGCACCTCCCCTGAAGCCA
TTGACTCGGCTGAGAACCCTTTCAAGTTTCCCGGCTCCTTGACACCATTGGTATCAGCCAGCCTCAGTGGAGGG
AGCTCAGTGACCTCGAGTCTGCTCGCCAATTCTGCCAGACCGTGGGGTACCCCTGTGTGGTGCGCCCTCCTATG
TGCTGAGCGGTGCTGCTATGAATGTGGCCTACACGGATGGAGACCTGGAGCGCTTCTGAGCAGCGCAGCAGCCG
TCTCCAAAGAGCATCCCGTGGTCATCTCCAAGTTCATCCAGGAGGCTAAGGAGATTGACGTGGATGCCGTGGCCT
CTGATGGTGTGGTGGCAGCCATCGCCATCTCTGAGCATGTGGAGAATGCAGGTGTGCATTAGGTGATGCGACGC
TGGTGACCCCCCACAAGATATCACTGCCAAAACCTGGAGCGGATCAAAGCCATTGTGCATGCTGTGGGCCAGG

742/6881
FIGURE 692B

AGCTACAGGTCACAGGACCCCTTCAATCTGCAGCTCATTGCCAAGGATGACCAGCTGAAAGTTATTGAATGCAACG
TACGTGTCTCTCGCTCCTTCCCCCTTCGTTTCCAAGACACTGGGTGTGGACCTAGTAGCCTTGGCCACGCGGGTCA
TCATGGGGGAAGAAGTGGAACTGTGGGGCTAATGACTGGTTCTGGAGTCGTGGGAGTAAAGGTGCCTCAGTTCT
CCTTCTCCCGCTTGGCGGGTGTGACGTGGTGTGGGTGTGGAAATGACCAGTACTGGGGAGGTGGCCGGCTTTG
GGGAGAGCCGCTGTGAGGCATACCTCAAGGCCATGCTAAGCACTGGCTTTAAGATCCCCAAGAAGAATATCCTGC
TGACCATTGGCAGCTATAAGAACAAAAGCGAGCTGCTCCCACTGTGCGGCTACTGGAGAGCCTGGGCTACAGCC
TCTATGCCAGTCTCGGCACAGCTGACTTCTACACTGAGCATGGCGTCAAGGTAACAGCTGTGGACTGGCACTTTG
AGGAGGCTGTGGATGGTGAAGTGGCCACCACAGCGGAGCATCCTGGAGCAGCTAGCTGAGAAAACTTTGAGCTGG
TGATTAACTGTCAATGCGTGGAGCTGGGGGCCGGCGTCTCTCTTCTTTGTACCAAGGGCTACCGCACCCGAC
GCTTGGCCGCTGACTTCTCCGTGCCCCCTAATCATCGATATCAAGTGCACCAAACCTCTTTGTGGAGGCCCTAGGCC
AGATCGGGCCAGCCCTCCTTTGAAGGTGCATGTTGACTGTATGACCTCCCAAAGCTTGTGCGACTGCCGGGAT
TGATTGATGTCCATGTGCACCTGCGGGAACAGGTGGGACACATAAGGAGGACTTTGCTTCAGGCACAGCCGCTG
CCCTGGCTGGGGGTATCACCATGGTGTGTGCCATGCCTAATACCGGGCCCCCATCATTGACGCCCTGCTCTGG
CCCTGGCCAGAAAGCTGGCAGAGGCTGGCGCCCGGTGCGACTTTGCGCTATTCTTGGGGCCTCGTCTGAAAATG
CAGGAACCTTGGGCACCGTGGCCGGGTCTGCAGCCGGGTGAAGCTTTACCTCAATGAGACCTTCTCTGAGCTGC
GGCTGGACAGCGTGGTCCAGTGGATGGAGCATTTTCGAGACATGGCCCTCCCACCTCCCCATTGTGGCTCACGCAG
AGCAGCAAACCGTGGCTGCTGTCTCATGTTGGCTCAGCTCACTCAGCGCTCAGTGCACATATGTCACGTGGCAC
GGAAGGAGGAGATCCTGCTAATTAAAGCTGCAAAGGCACGGGGCTTGCCAGTGACCTGCGAGGTGGCTCCCCACC
ACCTGTTCTTAAGCCATGATGACCTGGAGCGCTGGGGCCTGGGAAGGGGGAGGTCCGGCCTGAGCTTGGCTCCC
GCCAGGATGTGGAAGCCCTGTGGGAGAACATGGCTGTCTCATCGACTGCTTTGCCTCAGACCATGCTCCCCATACCT
TGGAGGAGAAGTGTGGGTCCAGGCCCCACCTGGGTTCAGGGTTAGAGACCATGCTGCCACTACTCCTGACGG
CTGTAAGCGAGGGCCGGCTCAGCCTGGACGACCTGCTGCAGCGATTGCACCACAATCCTCGGCGCATCTTTCACC
TGCCCCCGCAGGAGGACACCTATGTGGAGGTGGATCTGGAGCATGAGTGGACAATCCCAGCCACATGCCCTTCT
CCAAGGCCCACTGGACACCTTTTGAAGGGCAGAAAGTGAAGGGCACCGTCCGCCGTGTGGTCTGCGAGGGGAGG
TTGCCTATATCGATGGGCAGGTTCTGGTACCCCCGGGCTATGGACAGGATGTACGGAAGTGGCCACAGGGGGCTG
TTCTCAGCTCCCACCCCTCAGCCCCCTGCCACTAGTGAGATGACCACGACACCTGAAAGACCCCGCCGTGGCATCC
CAGGGCTTCTGATGGCCGCTTCCATCTGCCGCCCGAATCCATCGAGCCTCCGACCCAGGTTTGCCAGCTGAGG
AGCCAAAGGAGAAGTCTCTCGGAAGGTAGCCGAGCCAGAGCTGATGGGAACCCCTGATGGCACCTGCTACCCCTC
CACCACCAGTACCGAGACAGGCATCTCCCCAGAACCTGGGGACCCCTGGCTTGCTGCACCCCCAGACCTCACCCC
TGCTGCACTCATTAGTGGGCCAACATATCCTGTCCGTCCAGCAGTTACCAAGGATCAGATGTCTCACCTGTTCA
ATGTGGCACACACACTGCGTATGATGGTGCAGAAGGAGCGGAGCCTCGACATCCTGAAGGGGAAGGTATGGCCT
CCATGTTCTATGAAGTGAACACACGACCAGCAGCTCCTTTGCAGCAGCCATGGCCCGGTGGGAGGTGCTGTGC
TCAGCTTCTCGGAAGCCACATCGTCCGTCCAGAAGGGCGAATCCCTGGCTGACTCCGTGCAGACCATGAGCTGCT
ATGCCGACGTGCTGCTGCTCCGGCACCCCCAGCCTGGAGCAGTGGAGCTGGCCGCCAAGCACTGCCGGAGGCCAG
TGATCAATGCTGGGGATGGGGTCCGAGAGCACCCCCACCCAGGCCCTGCTGGACATCTTACCATCCGTGAGGAGC
TGGGAACCTGTCAATGGCATGACGATCACGATGGTGGGTGACCTGAAGCACGGACGCACAGTACATTCCCTGGCCT
GCCTGCTCACCCAGTATCGTGTGAGCCTGCGCTACGTGGCACCTCCCAGCCTGCGCATGCCACCCACTGTGCGGG
CCTTCGTGGCCTCCCGCGGCACCAAGCAGGAGGAATTCGAGAGCATTGAGGAGGCGCTGCCTGACACTGATGTGC
TCTACATGACTCGAATCCAGAAGGAACGATTTGGCTCTACCCAGGAGTACGAAGCTTGCTTTGGTCAGTTTCATCC
TCACTCCCCACATCATGACCCGGGCCAAGAAGAAGATGGTGGTGTGACCCGATGCCCCGTGTCAACGAGATAA
GCGTGGAAGTGGACTCGGATCCCCGCGCAGCCTACTTCCGCCAGGCTGAGAACGGCATGTACATCCGCATGGCTC
TGTTAGCCACCGTGCTGGGCCGTTTCTAGGGGCCTGGCTTCCTCAGCCTCTTCTCTTTAGGCCAGCTGCTGGGC
AAGGAATTCCAGTGCTCCTACGGGGGCAGCACACTTAGATATTCCTGGACATCCAGATTGCTCACATGTGCTGA
CCACACTTCAGGCTCTGGACTGGAGCTCTCTGGCATGGGGGTGGGGCCTCAGATGCTGGGGCCAGTCTGCCCA
TCTTCATTCTGCACCTTAAACCTGTACAGTCATTTTTCTACTGACTTAATAAACAGCCGAGCTGTCCCTTG

743/6881
FIGURE 693

MAALVLEDGSLVRGQPFGAAVSTAGEVVFQTMGVGYPEALTDPSYKAQILVLTYPLIGNYGIPPDEMDEFGLCKW
FESSGIHVAALVVGECPTPSHWSATRTLHEWLQOHGIPGLQGVDTRELTKKLREQGSLGKLVQNGTEPSSLPF
LDPNARPLVPEVSIKTPRVFNTGGAPRILALDCGLKYNQIRCLCQRGAEVTVPWDHALDSQEYEGFLSNGPGD
PASYPVSVSTLSRVLSEPNRPVFGICLGHQLLALAIGAKTYKMRYGNRGHNQPCLLVGSGRCFLTSQNHGFAVE
TDSLPAWAPLFTNANDGSNEGIVHNSLPFFSVQFHPEHQAGPSDMELLFDIFLETVKEATAGNPGGQTVRERLT
ERLCPPGIPTPGSGLPPPRKVLILGSGGLSIGQAGEFDYSGSQAICALKEENIQTLINPNIAITVQTSQGLADKV
YFLPITPHYVTQVIRNERPDGVLLTFGGQTALNCGVELTKAGVLARYGVRVLGTPVETIELTEDRRAFAARMAEI
GEHVAPSEAANSLEQAQAAAERLGYPVLVRAAFALGGLGSGFASNREELSALVAPAFHAITSQVLVDKSLKGWKEI
EYEVVRDAYGNCVTVCNMENLDPLGIHTGESIVVAPSQTLNDREYQLLRQTAIKVTQHLGIVGECNVQYALNPES
EQYYIIIEVNARLSRSSALASKATGYPLAYVAACKLALGIPLPELRNSVTGGTAAFEPSVDYCVVKIPRWDLKFLR
VSTKIGSCMKSVGEVMGIGRSFEEAFQKALRMVDENCVGFDHTVKPVSDMELETPTDKRIFVVAALWAGYSVDR
LYELTRIDRWFLHRMKRIIAHAQLLEQHRGQPLPPDLLQQAACLGFSQKQIALAVLSTELAVRKLRLQELGICPAV
KQIDTVAAEWPAQTNYLYLTWGTTHDLTFRTPHVLVLGSGVYRIGSSVEFDWCAVGCIIQQLRKMGYKTIMVNYN
PETVSTDYDMCDRLYFDEISFEVMDIYELENPEGVILSMGGQLPNNMAMALHRQQCRVLGTSPEAIDSAENRFK
FSRLDITIGISQPPQWRELSDESARQFCQTVGYPCVVRPSYVLGAAMNVAYTDGDLERFLSSAAAVSKEHPVVI
SKFIQEAKEIDVDAVASDGVVAAIAISEHVENAGVHSGDATLVTPPDITAKTLERIKAIHVAVGQELQVTGPFN
LQLIAKDDQLKVIENVRVRSRFPFVSKTLGVDLVALATRVIMGEEVEPVGLMTGSGVGVKVPQFSFSLAGAD
VVLGVEMTSTGEVAGFGESRCEAYLKAMLSTGFKIPKKNILLTIGSYKNKSELLPTVRLLESGLYSLYASLGTAD
FYTEHGKVTAVDWHFEEAVDGECPQRSILEQLAEKNFELVINLSMRGAGGRRLSSFVTKGYRTRRLAADFSVP
LIIDIKCTKLFVEALGQIGPAPPLKVHVCMTSQKLVRPLGLIDVHVHLREPGGTHKEDFASGTAAALAGGITMV
CAMPNTRPPIIDAPALALAQKLAEAGARCDFALFLGASSENAGTLGTVAGSAAGLKLYLNETFSELRLDSVVQWM
EHFETWPSHLPVIVAHAEQQTVAAVLMVAQLTQRSVHICHVARKEEILLIKAAKARGLPVTCEVAPHHLFLSHDDL
ERLGP GKGEVRPELGSRDVEALWENMAVIDCFASDHAPHTLEEKCSRPPPGFPGLTMLPLLLTAVSEGRLSL
DDLQRLHNNPRRIHFLPPQEDTYVEVDLEHEWTIPSHMPFSKAHWTPFEGQKVKGTVRRVVLGRGEVAYIDGQVL
VPPGYGQDVRKWPQGAVPQLPPSAPATSEMTTTTPERPRRGIPGLPDGRFHLPPRIHRASDPGLPAEEPKEKSSRK
VAEPELMGTPDGTCTYPPPPVPRQASPQNLGTPGLLHPQTSPLLHSLVGGHILSVQQFTKDQMSHLFNVAHTLRMM
VQKERSLDILKGKVMASMFYEVSTRTSSSFAAAMARLGGAVALSFSEATSSVQKGESLADSVQTMSCYADVVLRRH
PQPGAVELAAKHCRRPVINAGDGVGEHPTQALLDIFTIREELGTVNGMTITMVGDLKHGRTVHSLACLLTQYRVS
LRYVAPPSLRMPPTVRAFVASRGTKQEEFESIEEALPDTDVLYMTRIQKERFGSTQEYECFGQFILTIPHIMTRA
KKKMVMVMPMPRVNEISVEVDSDPRAAYFRQAENGYIRMAALLATVLRGF

744/6881
FIGURE 694

GGAGCACCAAGGGAACGGAAAAATGGCGCCTCACGGCCCCGGGTAGTCTTACGACCCTGGTGCCCTGGGCTGCCGCC
CTGCTCCTCGCTCTGGGCGTGGAAGGGCTCTGGCGCTACCCGAGGTACAGAAGCAAGTTTGAGGTCGGGCTGAA
GCAGGGTCACTGGCCAGCCGTGCGTCTGCGCTCGCCAGCGGCTCCCCCTTCTCCTCGGCGGGCCTGCGGTTCTGAT
TTCGTCCCTGACGCTTCCCGACCCTGCCCAGCCAGATATGCACCCAATGTCCAGGGAGCGTGCAAAATTTGTCAA
AAGTGGCCTTTTATTGTAAAACGACACGAGAGCTAATGCTGCATGCCCCGTTGCTGCCTGAATCAGAAGGGCACCA
TCTTGGGGCTGGATCTCCAGAACTGTTCTCTGGAGGACCCTGGTCCAACTTTCATCAGGCACATACCACTGTCA
TCATAGACCTGCAAGCAAACCCCTCAAAGGTGACTTGGCCAACACCTTCCGTGGCTTTAÇTCAGCTCCAGACTC
TGATACTGCCACAACATGTCAACTGTCCTGGAGGAATTAATGCCTGGAATACTATCACCTCTTATATAGACAACC
AAATCTGTCAAGGGCAAAGAACCTTTGCAATAACACTGGGGACCCAGAAATGTGTCCTGAGAATGGATCTTG TG
TACCTGATGGTCCAGGTCTTTTGCAGTGTGTTTGTGCTGATGGTTTCCATGGATACAAGTGTATGCGCCAGGGCT
CGTTCTCACTGCTTATGTTCTTCGGGATTCTGGGAGCCACCACTCTATCCGTCTCCATTCTGCTTTGGGCGACCC
AGCGCCGAAAAGCCAAGACTTCATGAACTACATAGGTCTTACCATTGACCTAAGATCAATCTGAACCTATCTTAGC
CCAGTCAGGGAGCTCTGCTTCCCTAGAAAGGCATCTTTCGCCAGTGGATTGCGCTCAAGGTTGAGGCCGCCATTGG
AAGATGAAAAATTGCACTCCCTTGGTGTAGACAAATACCAGTTCCATTGGTGTGTTGCCTATAATAAACACTT
TTTCTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

745/6881
FIGURE 695

MLHARCCLNQKGITILGLDLQNCSEDPGPNFHQAHTTVIIDLQANPLKGLANTFRGFTQLQTLILPQHVNCPPG
INAWNTITSYIDNQICQGQKNLCNNTGDPEMCPENGSCVPDGPGLLQCVCADGFHGYKCMRQGSFSLMFFGILG
ATTLSVSILLWATQRRKAKTS

746/6881
FIGURE 696

GGAGCACCAAGGGAACGGAAAATGGCGCCTCACGGCCCGGGTAGTCTTACGACCCTGGTGCCCTGGGCTGCCGCC
CTGCTCCTCGCTCTGGGCGTGGAAGGGCTCTGGCGCTACCCGAGATATGCACCCAATGTCCAGGGAGCGTGCAA
AATTTGTCAAAAGTGGCCTTTTATTGTAAAACGACACGAGAGCTAATGCTGCATGCCCGTTGCTGCCTGAATCAG
AAGGGCACCATCTTGGGGCTGGATCTCCAGAACTGTTCTCTGGAGGACCCTGGTCCAACTTTCATCAGGCACAT
ACCACTGTCAATCATAGACCTGCAAGCAAACCCCTCAAAGGTGACTTGGCCAACACCTTCCGTGGCTTTACTCAG
CTCCAGACTCTGATACTGCCACAACATGTCAACTGTCCTGGAGGAATTAATGCCTGGAATACTATCACCTCTTAT
ATAGACAACCAAATCTGTCAAGGGCAAAAGAACCTTTGCAATAACACTGGGGACCCAGAAATGTGTCCTGAGAAT
GGATCTTGTGTACCTGATGGTCCAGGTCTTTTGCAGTGTGTTTGTGCTGATGGTTTCCATGGATACAAGTGTATG
CGCCAGGGCTCGTTCFCACIGCTTATGTTCTTCGGGATTCTGGGAGCCACCACTCTATCCGTCTCCATTCTGCTT
TGGGCGACCCAGCGCCGAAAAGCCAAGACTTCATTGAACTACATAGGTCTTACCATTGACCTAAGATCAATCTGAA
CTATCTTAGCCAGTCAGGGAGCTCTGCTTCCTAGAAAGGCATCTTTCGCCAGTGGATTCCGCTCAAGGTTGAGG
CCGCCATTGGAAGATGAAAAATTGCACTCCCTTGGTGTAGACAAATACCAGTTCCCATTTGGTGTGTTGCCTATA
ATAAACACTTTTTCTTTTTAAAA

747/6881
FIGURE 697

MLHARCCLNQKGTILGLDLQNCSEDPGPNFHQAHTTVIIDLQANPLKGDLANTFRGFTQLQTLILPQHVNCPPG
INAWNTITSYIDNQICQGQKNLCNNTGDPFEMCPENGSCVPDGPGLLQCVCADGFHGYKCMRQGSFSLLMFFGILG
ATTLSVSILLWATQRRKAKTS

748/6881
FIGURE 698

GCGCCCTAGCCCTCTTTTCGGGGATACTGGCCGACCCCTCTTCCTTTTCCCCTTTAGTGAAGGCCTCCCCCGTCG
CCGCGCGGCTTCCCGGAGCCGACTGCAGACTCCCTCAGCCCGGTGTTCCCGCGTCCGGACGCCGAGGTTCGCGGC
TTCGCAGAACTCGGGCCCCCTCCATCCGCCCTCAGAAAAGGGAGCGATGTTGATCTCAGGAAGCACAAAGGGACC
TTCCTAGCTCTGACTGAACCACGGAGCTCACCTTGGACAGTATCACTCCGTGGAGGAAGACTGTGAGACTGTGGC
TGGAAGCCAGATTGTAGCCACACATCCGCCCTGCCCTACCCAGAGCCCTGGAGCAGCAACTGGCTGCAGATCA
CAGACACAGTGAGGATATGAGTGTAGGGGTGAGCACCTCAGCCCTCTTTCCCCAACCTCGGGCACAAGCGTGGG
CATGTCTACCTTCTCCATCATGGACTATGTGGTGTTCGTCTGTGCTGCTGGTTCTCTCTCTTGCCATTGGGCTCTA
CCATGCTTGTCTGTGGCTGGGGCCGGCATACTGTTGGTGAGCTGCTGATGGCGGACCGCAAAATGGGCTGCCTTCC
GGTGGCACTGTCCCTGCTGGCCACCTTCCAGTCAGCCGTGGCCATCCTGGGTGTGCCGTGAGAGATCTACCGATT
TGGGACCCAATATTGGTTCCTGGGCTGCTGCTACTTTCTGGGGCTGCTGATACCTGCACACATCTTCATCCCCGT
TTTCTACCGCTGCATCTCACCAGTGCCTATGAGTACCTGGAGCTTCGATTCAATAAAACTGTGCGAGTGTGTGG
AACTGTGACCTTCATCTTTTACAGATGGTGATCTACATGGGAGTTGTGCTCTATGCTCCGTCAATTGGCTCTCAATGC
AGTGAAGTGGCTTTGATCTGTGGCTGTCCGTGCTGGCCCTGGGCATTGTCTGTACCGTCTATACAGCTCTGGGTGG
GCTGAAGGCCGTCTATCTGGACAGATGTGTTCCAGACACTGGTCAATGTTCCCTCGGGCAGCTGGCAGTTATCATCGT
GGGGTCAGCCAAGGTGGGCGGCTTGGGGCGTGTGTGGGCCGTGGCTTCCCAGCACGGCCGCATCTCTGGGTTTGA
GCTGGATCCAGACCCCTTTGTGCGGCACACCTTCTGGACCTTGGCCTTCGGGGGTGTCTTCATGATGCTCTCCTT
ATACGGGGTGAACCAGGCTCAGGTGCAGCGGTACCTCAGTTCCCGCACGGAGAAGGCTGCTGTGCTCTCCTGTTA
TGCAGTGTTCCTTCCAGCAGGTGTCCCTCTGCGTGGGCTGCCTCATTGGCCTGGTCAATGTTCCGTATTACCA
GGAGTATCCCATGAGCATTACAGCAGGCTCAGGCAGCCCCAGACCAGTTTCGTCTGTACTTTGTGATGGATCTCCT
GAAGGGCCTGCCAGGCTGCCAGGGCTCTTCATTGCCTGCCTCTTCAGCGGCTCTCTCAGCACTATATCCTCTGC
TTTTAATTCAATTGGCAACTGTTACGATGGAAGACCTGATTGACCTTGGTTCCTGAGTTCTCTGAAGCCCGGGC
CATCATGCTTTCCAGAGGCTTGCCTTTGGCTATGGGCTGCTTTGTCTAGGAATGGCCTATATTTCTCTCCAGAT
GGGACCTGTGCTGCAGGCAGCAATCAGCATCTTTGGCATGGTTGGGGACCGCTGCTGGGACTCTTCTGCCTTGG
AATGTTCTTTCCATGTGCTAACCTCTCTGGTGTGTGTGGGCTGTGGCTGGGCTCGTCATGGCCTTCTGGAT
TGGCATCGGGAGCATCGTGACCAGCATGGGCTTCAGCATGCCACCCTCTCCCTCTAATGGGTCCAGCTTCTCCCT
GCCCACCAATCTAACCGTTGCCACTGTGACCACACTGATGCCCTTGACTACCTTCTCCAAGCCCACAGGGCTGCA
GCGGTTCTATTCTTGTCTTACTTATGGTACAGTGCTCACAACCTCCACCACAGTGATTGTGGTGGGCTGATTGT
CAGTCTACTCACTGGGAGAATGCGAGGCCGGTCCCTGAACCCTGCAACCATTTACCCAGTGTGCGCAAAGCTCCT
GTCCCTCCTTCCGTGTCTGTGCTGAGAAGCGGCTCCACTGCAGGAGCTACGGCCAGGACCACCTCGACACTGGCCT
GTTTCCTGAGAAGCCGAGGAATGGTGTGCTGGGGGACAGCAGAGACAAGGAGGCCATGGCCCTGGATGGCACAGC
CTATCAGGGGAGCAGCTCCACCTGCATCCTCCAGGAGACCTCCCTGTGATGTTGACTCAGGACCCCGCCTCTGTCT
CTCACTGTGCCAGGCCATAGCCAGAGGCCACCCTGTAGTACAGGGATGAGTCTTGGTGTGTCTGTCAGGGACAGG
CCTGGATGATCTAGCTCATACCAAAGGACCTTGTCTGAGAGGTTCTTGCCTGCAGGAGAAGCTGTACATCTCA
AGCATGTGAGGCACCGTTTTTCTCGTCTGCTTGCCAACTGTGTTTTTAAAGGATCAGGCTCGTAGGGAGCAGGATC
ATGCCAGAAATAGGGATGGAAGTGCATCCTCTGGGAAAAAGATAATGGCTTCTGATTCAACATAGCCATAGTCCT
TTGAAGTAAGTGGCTAGAAACAGCACTCTGGTTATAATTGCCCCAGGGCCTGATTCAGGACTGACTCTCCACCAT
AAAAGTGAAGCTGCTTCCCCTGTAGTCCCCATTTAGTACCAGTTCTGCCAGCCACAGTGAGCCCTATTATTA
CTTTCAGATTGTCTGTGACACTCAAGCCCCCTCTCATTTTTATCTGTCTACCTCCATTCTGAAGAGGGAGGTTTTG
GTGTCCCTGGTCTCTGGGAATAGAAGATCCATTTGTCTTTGTGTAGAGCAAGCACGTTTTCCACCTCACTGTCT
CCATCCTCCACCTCTGAGATGGACACTTAAGAGACGGGGCAAATGTGGATCCAAGAAACCAGGGCCATGACCAGG
TCCACTGTGGAGCAGCCATCTATCTACCTGACTCCTGAGCCAGGCTGCCGTGGTGTCAATTTCTGTCTATCCGTGCT
CTGTTTCTTTTGGAGTTTCTTCTCCACATTATCTTTGTTCTGGGGAATAAAAACTACCATTGGACCTAAAAAA
AAAAAAAAAAAA

749/6881
FIGURE 699

MSVGVSTSAPLSPTSGTSVGMSTFSIMDYVVFVLLLVLSLAIGLYHACRGWGRHTVGELLMADRKMGCLEPVALSL
LATFQSAVAILGVPSEIYRFGTQYWFLGCCYFLGLLIPAHIFIPVFYRLHLTSAYEYLRLRFNKTVRVCGTVTFI
FQMVIYMGVVLYAPSLALNAVTGFDLWLSVLALGIVCTVYTALGGLKAVIWTDFQTLVMFLGQLAVIIVGSAKV
GGLGRVWAVASQHGRI SGFELDPDPFVRHTFWTLAFGGVFMMLSLYGVNQAQVQRYLSSRTEKAAVLSCYAVFPF
QQVSLCVGCLIGLVMFAYYQEYPMISIQQAAAPDQFVLYFVMDLLKGLPGLPGLFIACLFSGSLSTISSAFNSLA
TVTME DLIRPWFPEFSEARAIMLSRGLAFGYGLLCLGMAYISSQMGPVLQAAISIFGMVGGPLLGLFCLGMFFPC
ANPPGAVVGLLAGLVMAFWIGIGSIVTSMGFSMPSPSNGSSFSLPTNLTVATVTTLMPLTTFSKPTGLQRFYSL
SYLWYSAHNSTTVIVVGLIVSLLTGRMRGRSLNPATIPVLPKLLSLLPLSCQKRLHCRSYGQDHLDTGLFPEKP
RNGVLGDSRDKEAMALDGTAYQGSSSTCILQETSL

750/6881
FIGURE 700

GCCTGCGCGGAGGGAGCCGCGAGACAGGTGCGCATGCGCAGTGC GCGTCTGCGAGACCGACTTGGACGGAGCCGA
GCTGAGGGCTCGGCTTCCTGCTGATGGTCAGGGTTTTGGCAACTCCCCGGTGTGAGAGGGGTAGGGAGTGCTCCCG
GCGGCGACGGGGCCGAGTTACACAGCCGCGGGGCGAGTAGTCGAAGGCCCGGCGCGGCATGTCCTGGGTGCCGCG
GTGCGGGCAGTGAACGCGCGCCGGGCGGGATGGGCGGGCGCCGGGCGCCAGAGCTGTACCGGGCTCCGTTCCCGT
TGTACGCGCTTCAGGTCGACCCAGCACTGGGCTGCTCATCGCTGCGGGCGGAGGAGGCGCCGCCAAGACAGGCA
TAAAGAATGGCGTGCACTTTCTGCAGCTAGAGCTGATTAATGGGCGCTTGAGTGCCTCCTTGCTGCACTCCCATG
ACACAGAGACACGGGCCACCATGAACTTGGCACTGGCTGGTGACATCCTTGCTGCAGGGCAGGATGCCCCACTGTC
AGCTCCTGCGCTTCAGGCACATCAACAGCAGGGGCAACAAGGCAGAGAAGGCCGGTTCCAAGGAGCAGGGGCGCTC
GACAAAGGAAGGGAGCAGCCCCAGCAGAGAAGAAATGTGGAGCGGAAACCCAGCACGAGGGGCTAGAACTCAGGG
TAGAGAATTTGCAGGCGGTGCAGACAGACTTTAGCTCCGATCCACTGCAGAAAGTTGTGTGCTTCAACCACGATA
ATACCTTGCTTGCCACTGGAGGAACAGATGGCTACGTCCGTGTCTGGAAGGTGCCCAGCCTGGAGAAGGTTCTGG
AGTTCAAAGCCCACGAAGGGGAGATTGAAGACCTGGCTTTAGGGCCTGATGGCAAGTTGGTAACCGTGGGCGGG
ACCTTAAGGCCTCTGTGTGGCAGAAGGATCAGCTGGTGACACAGCTGCACTGGCAAGAAAAATGGACCCACCTTTT
CCAGCACACCTTACCGCTACCAGGCCTGCAGGTTTGGGCAGGTTCCAGACCAGCCTGCTGGCCTGCGACTCTTCA
CAGTGCAAATTTCCCAACAAGCGCTGCGCCAGCCCCCTCCCTGCTACCTCACAGCCTGGGATGGCTCCAACCTTCT
TGCCCCCTTCGGACCAAGTCTGTGGCCATGAAGTCGTCTCCTGCCTCGATGTCAGTGAATCCGGCACCTTCCTAG
GCCTGGGCACAGTCACTGGCTCTGTTGCCATCTACATAGCTTTCTCTCTCCAGTGCCTCTACTACGTGAGGGAGG
CCCATGGCATTGTGGTGACGGATGTGGCCTTTCTACCTGAGAAGGGTCGTGGTCCAGAGCTCCTTGGGTCCCATG
AAACTGCCCTGTTCTCTGTGGCTGTGGACAGTCGTTGCCAGCTGCATCTGTTGCCCTCACGGCGGAGTGTTCCCTG
TGTGGCTCCTGCTCCTGCTGTGTGTGCGGGCTTATTATTGTGACCATCCTGCTGCTCCAGAGTGCCTTTCCAGGTT
TCCTTTAGCTTCCCTGCTTCCTGGGAATCAGGAGCCTGGACACTGCCATCTCTAGAGCAGAGTGGAGGCCTGGAC
TCCCTTTGCTCACTCCATTGCGGTCCACAGCTGAGGTTGCCGCTGACAAGATGAATGGGCACTGCCTGCCCTTCT
AGTGAAAAGGCTTGCTATGGCCCTGTGTGACTCCAGGTCCAGGAACCTTGCCCTTCGTCATCTGTGGATCCATC
CAGAACAGCGGTATCTGAAGCCCAGGCCATACTCCCTGCCTCCTTTCTTCTGCCTACCAGAGGCTCCAGAGTTGA
GCTTGTCTTATCTAGAAACATGTGAAGATGCCCCAAGAGCCTGGAGGCACTGCTGTCCTTCCTGCAGAAACAGTT
TCTCCTCCTCCCCTCAGCCTTGTGGCCAGTTCCCTCTTACATGAAGCCCCTGGCATTGCTGGGGGAAGGGACTGG
CCTGGTACTTGCTGTTAGGGCAGGAAGGGGCAAAAGGAAGACTTGGGTAGTAATCTGGGGGTTTCAAGTGGGTAGC
ACTAAGCCAGCTGGCCTAAAGATGCAATAAGTTCCCTAGGTAGTCTACCCTTACCTTGAGGAATGGGAAAATGAAC
CTCAGCCCATTAGGCAGGAAAAGTTGATATTTAATAACAAGGAAAGAGTGAAGTGAAGACCC

751/6881
FIGURE 701

GTAGCCTCATGGGAAGAGAAGCAGATCCTGTGCGTGGGGCTAGTGGTGCTGGACGTCATCAGCCTGGTGGACAAGT
ACCCTAAGGAGGACTCGGAGATAAGGTGTTTGTCCCAGAGATGGCAGCGCGGAGGCAACGCGTCCAACCTCCTGCA
CCGTTCTCTCCCTGCTCGGAGCCCCCTGTGCCTTCATGGGCTCAATGGCTCCTGGCCATGTTGCTGATTTTGTCC
TGGATGACCTCCGCCGCTATTCTGTGGACCTACGCTACACAGTCTTTCAGACCACAGGCTCCGTCCCCATCGCCA
CGGTCATCATCAACGAGGCCAGTGGTAGCCGCACCATCCTATACTATGACAGGAGCCTGCCAGATGTGTCTGCTA
CAGACTTTGAGAAGGTTGATCTGACCCAGTTCAAGTGGATCCACATTGAGGGCCGGAACGCATCGGAGCAGGTGA
AGATGCTGCAGCGGATAGACGCACACAACACCAGGCAGCCTCCAGAGCAGAAGATCCGGGTGTCCGTGGAGGTGG
AGAAGCCACGAGAGGAGCTCTTCCAGCTGTTTGGCTACGGAGACGTGGTGTTTGTGAGCAAAGATGTGGCCAAGC
ACTTGGGGTTCCAGTCAGCAGAGGAAGCCTTGAGGGGCTTGTATGGTCTGTGAGGAAAGGGGCTGTGCTTGTCT
GTGCCTGGGCTGAGGAGGGCGCCGACGCCCTGGGCCCTGATGGCAAATTGCTCCACTCGGATGCTTTCCCGCCAC
CCGCGTGGTGGATACACTGGGAGCTGGAGACACCTTCAATGCCTCCGTCTCTTCAGCCTCTCCCAGGGGAGGA
GCGTGCAGGAAGCACTGAGATTCGGGTGCCAGGTGGCCGGCAAGAAGTGTGGCCTGCAGGGCTTTGATGGCATCG
TGTGAGAGCAGGTGCCGGCTCCTCACACACCATGGAGACTACCATTGCGGCTGCATCGCCTTCTCCCTCCATCC
AGCCTGGCGTCCAGGTTGCCCTGTTCAGGGGACAGATGCAAGCTGTGGGGAGGACTCTGCCTGTGTCTGTGTTT
CCCACAGGGAGAGGCTCTGGGGGGATGGCTGGGGGATGCAGAGCCTCAGAGCAAATAAATCTTCTCAGAGCCAG
CTTCTCCTCTCAATGTCTGAAC TGCTCTGGCTGGGCATTCTGAGGCTCTGACTCTTCGATCCTCCCTCTTTGTG
TCCATTCCCCAAATTAACCTCTCCGCCCAGGCCCAGAGGAGGGGCTGCCTGGGCTAGAGCAGCGAGAAGTGCCCT
GGGCTTGCCACCAGCTCTGCCCTGGCTGGGGAGGACACTCGGTGCCCCACACCCAGTGAACCTGCCAAAGAAACC
GTGAGAGCTCTTCGGGGCCCTGCGTTGTGCAGACTCTATTCCCACAGCTCAGAAGCTGGGAGTCCACACCGCTGA
GCTGAAC TGACAGGCCAGTGGGGGGCAGGGGTGCGCCTCCTCTGCCCTGCCACCAGCCTGTGATTTGATGGGGT
CTTCATTGTCCAGAAATACCTCCTCCCGCTGACTGCCCCAGAGCCTGAAAGTCTCACCCCTGGAGCCCACCTTGG
AATTAAGGGCGTGCCTCAGCCACAAATGTGACCCAGGATACAGAGTGTTGCTGTCCTCAGGGAGGTCCGATCTGG
AACACATATTGGAATTGGGGCCAACTCCAATATAGGGTGGGTAAGGCCTTATAATGTAAAGAGCATATAATGTAA
AGGGCTTTAGAGTGAGACAGACCTGGATTCAAATCTGCCATTTAATTAGCTGCATATCACCTTAGGGTACAGCAC
TTAACGCAATCTGCCTCAATTTCTTCATCTGTCAAATGGAACCAATTCTGCTTGGCTACAGAATTATTGTGAGGA
TAAAAATCATATATAAAAAAAAAA

752/6881
FIGURE 702

MEEKQILCVGLVVLVDVISLVDKYPKEDSEIRCLSQRWQRGGNASNSCTVLSLLGAPCAFMGSMAPGHVADFVLDD
LRRYSVDLRYTVFQTTGSVPIATVIINEASGSRTILYYDRSLPDVSATDFEKVDLTQFKWIIHIEGRNASEQVKML
QRIDAHNTRQPPEQKIRVSVEVEKPREELFQLFGYGDVVFVSKDVAKHLGFQSAEEALRGLYGRVRKGAVLVCW
AEEGADALGPDGKLLHSDAFPPRVVDTLGAGDTFNASVIFSLSQGRSVQEALRFGCQVAGKKCGLQGFDGIV

753/6881
FIGURE 703

GTAGCCTCATGGGAAGAGAAGCAGATCCTGTGCGTGGGGCTAGTGGTGCTGGACGTCATCAGCCTGGTGGACAAGT
ACCCTAAGGAGGACTCGGAGATAAGGTGTTTGTCCCAGAGATGGCAGCGCGGAGGCAACGCGTCCAACTCCTGCA
CCGTTCTCTCCCTGCTCGGAGCCCCCTGTGCCTTCATGGGCTCAATGGCTCCTGGCCATGTTGCTGACTTCCTGG
TGGCCGACTTCAGGCGGGCGGGCGTGGACGTGTCTCAGGTGGCCTGGCAGAGCAAGGGGGACACCCCCAGCTCCT
GCTGCATCATCAACAACCTCCAATGGCAACCGTACCATTTGTGCTCCATGACACGAGCCTGCCAGATGTGTCTGCTA
CAGACTTTGAGAAGGTTGATCTGACCCAGTTCAAGTGGATCCACATTGAGGGCCGGAACGCATCGGAGCAGGTGA
AGATGCTGCAGCGGATAGACGCACACAACACCAGGCAGCCTCCAGAGCAGAAGATCCGGGTGTCCGTGGAGGTGG
AGAAGCCACGAGAGGAGCTCTTCCAGCTGTTTGGCTACGGAGACGTGGTGTGTTGTGTCAGCAAAGATGTGGCCAAGC
ACTTGGGGTTCCAGTCAGCAGAGGAAGCCTTGAGGGGGCTTGATGGTTCGTGTGAGGAAAGGGGCTGTGCTTGTCT
GTGCCTGGGCTGAGGAGGGCGCCGACGCCCTGGGCCCTGATGGCAAATTGCTCCACTCGGATGCTTTCCCGCCAC
CCCGCGTGGTGGATACACTGGGAGCTGGAGACACCTTCAATGCCTCCGTTCATCTTCAGCCTCTCCCAGGGGAGGA
GCGTGCAGGAAGCACTGAGATTGCGGTGCCAGGTGGCCGGCAAGAAGTGTGGCCTGCAGGGCTTTGATGGCATCG
TGTGAGAGCAGGTGCCGGCTCCTCACACACCATGGAGACTACCATTTGCGGCTGCATCGCCTTCTCCCCCTCCATCC
AGCCTGGCGTCCAGGTTGCCCTGTTTCAAGGGACAGATGCAAGCTGTGGGGAGGACTCTGCCTGTGTCTGTGTTT
CCCACAGGGAGAGGCTCTGGGGGGATGGCTGGGGGATGCAGAGCCTCAGAGCAAATAAATCTTCTCAGAGCCAG
CTTCTCCTCTCAATGTCTGAACTGCTCTGGCTGGGCATTCTGAGGCTCTGACTCTTCGATCCTCCCTCTTTGTG
TCCATTCCCCAAATTAACCTCTCCGCCCAGGCCCAGAGGAGGGGCTGCCTGGGCTAGAGCAGCGAGAAGTGGCCT
GGGCTTGCCACCAGCTCTGCCCTGGCTGGGGAGGACACTCGGTGCCCCACACCCAGTGAACCTGCCAAAGAAACC
GTGAGAGCTCTTCGGGGCCCTGCGTTGTGCAGACTCTATTCCCACAGCTCAGAAGCTGGGAGTCCACACCGCTGA
GCTGAACTGACAGGCCAGTGGGGGGCAGGGGTGCGCCTCCTCTGCCCTGCCACCAGCCTGTGATTTGATGGGGT
CTTCATTGTCCAGAAATACCTCCTCCCGCTGACTGCCCCAGAGCCTGAAAGTCTCACCCCTTGAGGCCACCTTGG
AATTAAGGGCGTGCCTCAGCCACAAATGTGACCCAGGATACAGAGTGTTGCTGTCTCAGGGAGGTCCGATCTGG
AACACATATTGGAATTGGGGCCAACTCCAATATAGGGTGGGTAAAGGCCTTATAATGTAAAGAGCATATAATGTAA
AGGGCTTTAGAGTGAGACAGACCTGGATTCAAATCTGCCATTTAATTAGCTGCATATCACCTTAGGGTACAGCAC
TTAACGCAATCTGCCTCAATTTCTTCATCTGTCAAATGGAACCAATTCTGCTTGGCTACAGAATTATTGTGAGGA
TAAAAATCATATATAAAAAAAAAA

754/6881
FIGURE 704

MEEKQILCVGLVVLDVISLVDKYPKEDSEIRCLSQRWQRGGNASNSCTVLSLLGAPCAFMGSMAPGHVADFLVAD
FRRRGVDVSQVAWQSKGDTTPSSCCIINNSNGNRTIVLHDTSLPDVSATDFEKVDLTQFKWIIHIEGRNASEQVKML
QRIDAHNTRQPPEQKIRVSVEVEKPREELFQLFGYGDVVFVSKDVAKHLGFQSAEEALRGLYGRVRKGAVLVCAW
AEEGADALGPDGKLLHSDAFPPRVVDTLGAGDTFNASVIFSLSQGRSVQEALRFGCQVAGKKCGLQGFDGIV

755/6881
FIGURE 705

ATGCCCCCCCCGACCCCTCTGGAGCTGCTACCTCTGCTGCCTGCTGACGGCAGCTGCAGGGGCCGCCAGCTACCCCT
CCTCGAGGTTTTCAGCCTCTACACAGGTTCCAGTGGGGCCCTCAGCCCCGGGGGGCCCCAGGCCAGATTGCCCCC
CGGCCAGCCAGCCGCCACAGGAAC TGGTGTGCCTACGTGGTGACCCGGACAGTGAGCTGTGTCTT GAGGATGGA
GTGGAGACATATGTCAAGTACCAGCCTTGTGCCTGGGGCCAGCCCCAGTGTCCCCAAAGCATCATGTACCGCCGC
TTCTCCGCCCTCGCTACCGTGTGGCTTACAAGACAGTGACCGACATGGAGTGGAGGTGCTGT CAGGGTTATGGG
GGCGATGACTGTGCTGAGAGTCCCGCTCCAGCGCTGGGGCCTGCGTCTTCCACACCACGGCCCCCTGGCCCCGGCT
GCCCCCCCCAACCTCTCTGGCTCCAGTGCAGGCAGCCCCCTCAGTGGACTGGGGGGAGAAGGTCCTGGGGAGTCA
GAGAAGGTGCAGCAGCTGGAGGAACAGGTGCAGAGCCTGACCAAGGAGCTGCAAGGCCTGCGGGGCGTCTTGCAA
GGACTGAGCGGGCGCCTGGCAGAGGATGTGCAGAGGGCTGTGGAGACGGCCTTCAACGGGAGGCAGCAGCCAGCT
GACGCGGCTGCCCCGCCCTGGGGTGCATGAAACCCTCAATGAGATCCAGCACCAGCTGCAGCTCCTGGACACCCGC
GTCTCCACCCACGACCAGGAGCTGGGTACCTCAACAACCATCATGGCGGCAGCAGCAGCAGTGGGGGCAGCAGG
GCCCCAGCCCCAGCCTCAGCCCCCTCCGGGGCCCCAGTGAGGAGCTGCTGCGGCAGCTGGAGCAGCGGTTGCAGGAG
TCCTGCTCCGTGTGCCTGGCCGGGCTAGATGGCTTCCGCCGGCAGCAGCAGGAGGACAGGGAGCGGCTGCGAGCG
ATGGAGAAGCTGCTGGCCTCGGTGGAGGAGCGGCAACGGCACCTCGCAGGGCTGGCGGTGGGGCCG CAGGCCCCCT
CAGGAATGCTGCTCTCCAGAGCTGGGCCGGC GACTGGCAGAGCTGGAGCGCAGGCTGGATGTCTGTGGCCGGCTCA
GTGACAGTGTGAGTGGGCGGCGAGGCACAGAGCTGGGAGGAGCCGCGGGGCAGGGAGGCCACCCCCCAGGCTAC
ACCAGCTTGGCCTCCCGCCTGTCTCGCCTGGAGGACCGCTTCAACTCCACCCTGGGCCCTTCGGAGGAGCAGGAG
GAGAGCTGGCCTGGGGCTCCTGGGGGGCTGAGCCACTGGCTGCCTGCTGCCGGGGCCGACTAGAGCAGTTGGGG
GGGCTGCTGGCCAATGTGAGCGGGGAGCTGGGGGGCGGTTGGATCTGTTGGAGGAGCAGGTGGCAGGGGGCCATG
CAGGCATGCGGGCAGCTCTGCTCTGGGGCCCCCTGGGGAGCAGGACTCTCAAGTCAGCGAGATCCTCAGTGCCTTG
GAGCGCAGGGTGCTGGACAGTGAGGGGCAGCTGCGGCTGGTGGGCTCCGGCCTGCACACGGTGGAAGCAGCGGGG
GAGGCCCCGCAGGCCACGCTGGAGGGATTACAAGAGGTTGTGGGCCGGCTCCAGGATCGTGTGGATGCCAGGAT
GAGACAGCTGCAGAGTTCACTACGGCTGAATCTCACTGCGGCCCGGCTAGGCCAACTGGAGGGGCTGCTGCAG
GCCCATGGGGATGAGGGCTGTGGGGCCTGTGGCGGAGTCCAAGAGGAAC TAGGCCGCTTCGGGATGGTGTGGAG
CGCTGCTCCTGCCCCCTGTTGCCCTCCTCGGGGTCTGGGGCTGGTCCAGGTGTTGGGGGCCCAAGCCGTGGGGCC
CTGGACGGCTTCAGCGTGTTTGGGGGCAGCTCAGGCTCAGCCCTGCAGGCCCTGCAAGGAGAGCTCTCTGAGGTT
ATTCTCAGCTTCAGCTCCCTCAATGACTCACTGAATGAGCTCCAGACCACTGTGGAGGGCCAGGGCGCTGATCTG
GCTGACCTGGGGGCAACCAAGGACCGTATCATTTCTGAGATTAACAGGCTGCAGCAGGAGGCCACAGAGCATGCT
ACAGAGAGTGAAGAGCGCTTCCGAGGCCTAGAGGAGGGACAAGCACAGGCCCGGCCAGTGCCCCAGCTTAGAGGGG
CGATTGGGGCGTCTTGAGGGTGTCTGTGAACGGTTGGACACTGTGGCTGGGGGACTGCAGGGCCTGCGCGAGGGC
CTTTCCAGACACGTGGCTGGGCTCTGGGCTGGGCTCCGGGAAACCAACACCACCAGCCAGATGCAGGCAGCCCTG
CTGGAGAAGCTGGTTCGGGGGACAGGCGGGCCTGGGCAGGCGGCTGGGTGCCCTTAACAGCTCCCTGCAGCTCCTG
GAGGACCGTCTGCACCAGCTCAGCCTGAAGGACCTCACTGGGCCTGCAGGAGAGGCTGGGGCCCCAGGGCCTCCT
GGGCTGCAGGGACCCCCAGGCCCTGCTGGACCTCCAGGATCACCAGGCAAGGACGGGCAAGAGGGCCCCATCGGG
CCACCAGGTCTCAAGGGGAACAGGGAGTGGAGGGGGCACCAGCAGCCCCCTGTGCCCCAAGTGGCATTTCAGCT
GCTCTGAGTTTGCCCCGGTCTGAACCAGGCACGGTCCCCTTCGACAGAGTCCTGCTCAATGATGGAGGCTATTAT
GATCCAGAGACAGGCGTGTTCACAGCGCCACTGGCTGGACGCTACTTGCTGAGCGCGGTGCTGACTGGGCACCGG
CACGAGAAAGTGGAGGCCGTGCTGTCCCGCTCCAACCAGGGCGTGGCCCCGCTAGACTCCGGTGGCTACGAGCCT
GAGGGCCTGGAGAATAAGCCGGTGGCCGAGAGCCAGCCAGCCCCGGGCACCCTGGGCGTCTTCAGCCTCATCCTG
CCGCTGCAGGCCGGGGACACGGTCTGCGTCGACCTGGTTCATGGGGCAGCTGGCGCACTCGGAGGAGCCGCTCACC
ATCTTCAGCGGGGCCCTGCTCTATGGGGACCCAGAGCTTGAACACGCGTAGACTGGGGTCCCGCCCCGACGTGTCT
ACGTCCGGCTGAAGAGACAGCGGGGGCGGCGGGCTCCTGGGGTCTCGCCTGAGACGGGGCACCTAGCCCTGGGCGA
GCGCCGCACCCGGGCCCCGAGCGGCACCGCGCCCAGAGCGGCCTCTCCCCACGCCGGGGCGCGCCGGCTCAGGG
AGGCTCGGGGCGGCCCATGCAGACTTTTGGCCTGGCGCGATCCCCAAGAACCCCTCCAGGGCCGGCCTGCGGAG
GAGCCGATCCTCGCACCCCTCCGCTCCCTCCACTGGCCCTCCAGGTCGATTCCCTGGGCTCCAGGCTCCCCCGCGC
GGGCGCCGCCACCGCCATACTAAACGATCGAGGAATAAAGACACTTGGTTTTTCT

756/6881
FIGURE 706

MAPRTLWSCYLCCLLTAAAGAASYPPRGFSLYTGSSGALSPGGPQAQIAPRPASRHRNWCAYVVTRTVSCVLEDG
VETYVKYQPCAWGQPQCPQSIMYRRFLRPRYRVAYKTVTDMEWRCQGYGGDDCAESPAPALGPASSTPRPLARP
ARPNLSGSSAGSPLSGLGGEGPGESEKVQQLEEQVQSLTKELQGLRGVLQGLSGRLAEDVQRAVETAFNGRQQPA
DAAAREPGVHETLNEIQHQLQLLDTRVSTHDQELGHLNNHHGGSSSSSGSRAPAPASAPPGPSEELLRQLEQRLQE
SCSVCLAGLDGFRQQQEDRERLRAMEKLLASVEERQRHLAGLAVGRPPQECCSPELGRRLAELERRLDVVAGS
VTVLSGRRGTELGAAGQGGHPPGYTSLASRLSRLED RFNSTLGPSEEQEE SWPGAPGGLSHWLPAARGRLEQLG
GLLANVSGELGGRLDLLLEEQVAGAMQACGQLCSGAPGEQDSQVSEILSALERRVLDSEGQLRLVGSGLHTVEAAG
EARQATLEGLQEVVGRQLQDRVDAQDETAAEFTLRLNLTAARLGQLEGLLQAHGDEGCGACGGVQEELGRLRDGVE
RCSCP LLPPRGPGAGPGVGGPSRGPLDGF SVFGSSGSALQALQGELSEVILSFSSLNDSLNELQTTVEGQGADL
ADLGATKDRI ISEINRLQQEATEHATESEERFRGLEEGQAQAGQCPSLEGR LGRLEGVCERLDTVAGGLQGLREG
LSRHVAGLWAGLRETNTTSQMQAALLEKLVGGQAGLGRR LGALNSSLQ LLEDRLHQLSLKDLTG PAGEAGPPGPP
GLQGPPGPAGPPGSPGKDGQEGP IGPPGPQGEQGV EGAPAAPVPQVAFSAALSLPRSEPGTVPFDRVLLNDGGYY
DPETGVFTAPLAGRYLLSAVLTGHRHEKVEAVLSRSNQGVARVDSGGYEPEGLENKPV AESQPSPGTLGVFSLIL
PLQAGDTVCDLVMQLAHSEEPLTIFSGALLYGDPELEHA

757/6881
FIGURE 707

GGCACGAGGGGCACCGCGCGCTCGGGTGTTTTTGGGGGGCCCGGGTGGAGGGCCCCGGGTGCCGGGGCCCAAGGTG
CGGCTCGCTAGCGGGAGAGGGAGCGGGATCACCGGCCCGGAGAGAGCTCTCAGGGCCAGAGCGGGGCAGGAGGA
TGCTTTCCAGCCCCACCATGGAGCTGCGCTGTGGGGGATTGCTGTTCAGTTCTCGCTTTGATTTCAGGGAATCTA
GCCCACGTGGAGAAGGTGGAATCTTTGTCCAGTGATGGGGAAGGGGTAGGAGGTGGGGCGTCAGCCCTGACCAGT
GGCATTGCCTCTTCCCCTGACTATGAATTCAACGTGTGGACCCGACCAGACTGTGCTGAAACGGAATTTGAGAAT
GGGAACAGGTCATGGTTCTACTTCAGCGTCCGGGGAGGAATGCCAGGAAAACATCAAGATCAACATTATGAAC
ATGAACAAGCAGAGCAAGCTGTATTCCCAGGGCATGGCCCCCTTTGTGCGCACACTGCCACCCGGCCACGCTGG
GAACGCATTTCAGACCGGCCCCACCTTTGAGATGACAGAGACGCAGTTTGTGTTATCCTTTGTTTCATCGTTTCGTG
GAGGGCCGTGGGGCCACCACCTTCTTCGCTTCTGCTACCCCTTCTCCTACAGTGACTGCCAGGAACCTGCTAAAC
CAGCTAGACCAGCGCTTTCCGGAGAACCACCTTACCCATAGCAGCCCCCTGGATACCATCTATTACCATCGGGAG
CTCCTTTGCTATTCTCTGGATGGACTTCGTGTAGATCTGCTGACGATCACTTCCTGCCATGGGCTTCGAGAAGAT
CGAGAGCCCCGTCTAGAGCAGCTATTTCTTGATACCAGCACCCCTCGACCATTCCGTTTCGCGAGGCAAGAGGATA
TTCTTCTTAAGCAGTAGAGTACACCCAGGGGAGACTCCATCTAGCTTTGTCTTCAATGGCTTTCTGGACTTCATC
CTCCGACCTGATGATCCCCGGGGCCCAAACCTCCGTGCGCTCTTCGTCTTTAAGCTGATTCCCATGTTGAACCC
GATGGTGTGGTCCGGGGACACTACCGCACAGACTCACGTGGAGTGAATCTGAACCGTCAGTACCTGAAGCCTGAT
GCCGTCTGCACCCGGCCATCTATGGGGCCAAAGCTGTGCTTCTCTACCACCATGTGCACTCTCGTCTGAACCTC
CAGAGTTCTCTGAGCACCAGCCCAGTTCCTGTCTCCCTCCTGATGCTCCTGTTTCTGACCTGGAGAAAGCCAAC
AATCTCCAAAATGAAGCTCAGTGTGGGCACTCAGCTGACAGGCATAACGCTGAAGCCTGGAAACAAACAGAGCCA
GCAGAACAGAAGCTCAACAGTGTGTGATTATGCCACAACAGTCTGCGGGGCTTGAAGAGTCAGCCCTGATACC
ATCCCCCCCCAAAGAGAGTGGCGTTGCTTACTATGTGGACCTGCATGGACATGCTTCCAAAAGGGGCTGCTTCATG
TACGGAAACAGCTTTAGTGATGAGAGCACCCAGGTGGAAAACATGCTATATCCAAAGCTCATCTCCTTGAATTCA
GCCCACTTCGACTTCCAGGGCTGCAATTTCTCAGAGAAGAATATGTATGCCCGAGACCGTAGAGATGGCCAGTCT
AAAGAGGGAAGCGGCCGTGTTGCAATCTACAAAGCCTCAGGGATAATCCACAGCTACACACTTGAATGCAACTAC
AACACTGGACGCTCAGTAAACAGCATCCCTGCTGCCTGCCATGACAATGGGCGTGCCAGCCCCCTCCCCGCGG
GCTTTCCCTCCAGATACACTGTGGAACATTTTGTGAGCAGGTGGGACGAGCTATGGCCATTGCAGCCCTGGACATG
GCGGAATGTAATCCGTGGCCCCGAATTGTACTGTGAGAGCACAGCAGCCTTACTAATCTACGGGCCTGGATGCTG
AAACATGTACGCAACAGCCGAGGCCTAAGCAGCACTCTGAATGTGGGTGTCAACAAGAAGAGGGGCCTTCGAAC
CCACCCAAAAGTCACAATGGGTTGCCTGTCTCCTGCTCCGAAAACACCTTGAGTCGGGCACGAAGTTTTAGCACC
GGCACAAGTGCCGGTGGTAGCAGCAGCAGCCAACAAAATTCTCCACAGATGAAGAATTCCCCCAGCTTTCTTTTT
CATGGCAGTCGGCCTGCAGGGCTGCCAGGCCTGGGCTCTAGTACCCAAAAGGTCACCCACCGGGTGCTGGGCCCC
GTCAGAGAGCCCCGAAGCCAGGACAGGAGACGGCAGCAGCAGCCCTGAACCATCGTCTGCAGGCAGCCTCGCT
CCATCCCCAGCTCCTACTAGTTCTGGCCAGCCTCCTCACACAAGCTGGGCTCCTGTCTACTGCCTGATTCAATC
AACATACCAGGGAGCAGTTGCTCACTCTTGTCTCTGGAGACAAACCAGAGGCTGTGATGGTAATCGGGAAAGGT
CTGCTAGGGACTGGAGCTCGGATGCCCTGCATCAAGACTCGATTGCAGACCTGTCCGAGGAGAGTTTCCGCCAGG
AGGGGTCCCGGATTCCCCAGGCTAGGCCAGGTTGGGGCCGGGGCTCACCGCCGACTCGCAGAGGGATTGAAAGGCT
CTTCAGGCCCCACATCCCCTACCCCCCGGACCAGGGAGAGCAGTGAGCTGGAGCTGGGATCCTGCTCTGCTACAC
CAGGGCTGCCTCAGGCCAGGCCCCACGGCCCCGCTCTGCCCTGCCTTTTCTCCTATATCCTGTAGTCTATCTG
ACTCCCCATCCTGGAATTGTTACAGCAGGGGTCCCTTGGGCCAACCTGAGGTTTGTTTTGTCCCTAAATCTCCCC
CACTGACTGTTTCTCCCCGGGTCTGATAATGCCTTTATGTTCAATCCAGGATATAGCCCCAAGATGGGGTAACA
GTGGGAAATATGCTAGTTCCCTCCAGGCCGCTGATTCCATGTGACAGCCGTTAAGTCCTTGGAATGCCAGCCAC
GCTGTCCAAGGCATTACAGAGTATCACCTTGAGACAGAACAAAACAGGGACCTGCCACCCCTTCCCTCCCTCCGC
AGCACAAAGATTTTGGGACCACAAAAAAGTCTATATTTTATATTGGGGGGAGGGAGTAGAAAAGCAAGCCCT
ATACTGGGCCCTATTTCAGTGGCAGCTTCTTGTTCATAGGATTAAGGAAGACTCTGAGGAAATAAAAGTTGTTTG
GAAAAATCCAAAAA

758/6881
FIGURE 708

MNMNKQSKLYSQGMAPFVRTLPTRPRWERIRDRPTFEMTETQFVLSFVHRFVEGRGATTFFAFICYPPFSYSDCQEL
LNQLDQRFPENHPTHSSPLDTIYYHRELLCYSLDGLRVDLLTITSCHGLREDREPRLEQLFPDTSTPRPFRFAGK
RIFFLSSRVHPGETPSSFFVNGFLDFILRPDDPRAQTLRRLFVFKLIPMLNPDGVVRGHYRTDSRGVNLNRQYLK
PDAVLHPAIYGAKAVLLYHHVHSRLNSQSSSEHQPSCLPPDAPVSDLEKANNLQNEAQCGHSADRHNAEAWKQT
EPAEQKLNSVWIMPQQSAGLEESAPDTIPPKEGVAIYKASGIIHSYTLECNNTGRSVNSIPAACHDNGRASPPP
PPAFPSRYTVELFEQVGRAMAIAALDMAECNPWRIVLSEHSSLTNLRAWMLKHVRNSRGLSSTLNVGVNKKRGL
RTPPKSHNGLPVSCSENTLSRARSFSTGTSAGGSSSSQQNSPQMKNSPSFPFHGSRPAGLPGLGSSTQKVTHRVL
GPVREPRSQDRRRQQQPLNHRPAGSLAPSPAPTSSGPASSHKLGSCLLPDSFNIPGSSCSLLSSGDKPEAVMVG
KGLLGTGARMPCIKTRLQTCPRRVSARRGPGFPRLGPGWAGAHRRLAEG

759/6881
FIGURE 709

CCCCCCCCACTCTGGACTCCCGCGCTGGGCGCGCTGAGGCGGCCCCCGAGCGAGCGCGCGTGCAGCCGCCGCCG
CCCCGAGCACCCGACGCTCCGGCGCCGCGGCGAGACGGAGACGGACCGAGCCACGGGCCCCCGCGGCCGACGCATC
TCGGAGGAGAAACATGCTTGCCAACTCAGCCAGCGTGAGGATCCTCATCAAGGGAGGCAAGGTGGTGAACGATGAC
TGACCCACGAGGCTGACGTCTACATCGAGAATGGCATCATCCAGCAGGTGGGCCGCGAGCTCATGATCCCTGGC
GGGGCCAAGGTGATTGATGCCACAGGAAAACCTGGTGATCCCTGGTGGCATCGACACCAGCACCCACTTCCACCAG
ACCTTCATGAATGCCACGTGCGTGGACGACTTCTACCATGGGACCAAGGCAGCACTCGTCGGAGGCACCACCATG
ATCATCGGCCACGTCCTGCCCGACAAGGAGACCTCCCTTGTGGACGCTTATGAGAAGTGCCGAGGTCTGGCCGAC
CCCAAGGTCTGCTGTGATTACGCCCTCCACGTGGGGATCACCTGGTGGGCACCCAAGGTGAAAGCAGAAATGGAG
ACACTGGTGAGGGAGAAGGTGTCAACTCGTTCAGATGTTTCATGACCTACAAGGACCTGTACATGCTTCGAGAC
AGTGAGCTGTACCAAGTGTTCACGCTTGCAAGGACATTGGGGCAATCGCCCGCGTCCATGCTGAAAATGGGGAG
CTTGTGGCCGAGGTGCTAAGGAGGCACTGGATTGGGGATCACAGGCCAGGAAGGAATCGAGATCAGCCGTCCA
GAGGAGCTGGAAGCTGAAGCCACTCATCGTGTATACCAATTGCAAACAGGACTCACTGTCCAATCTACCTGGTC
AACGTGTCCAGTATCTCGGCTGGTGACGTTATCGCAGCTGCTAAGATGCAAGGGAAGGTTGTGCTGGCGGAGACC
ACCACTGCACATGCCACGCTGACAGGCTTACACTACTACCACCAGGACTGGTCCCACGCGGCTGCCTATGTACG
GTGCTCCCCTGAGACTGGACACCAACACCTCAACCTACCTCATGAGCCTGCTGGCCAATGACACTCTGAACATC
GTGGCATCAGATCACCGGCCCTTTCACCACAAAGCAGAAAGCTATGGGCAAGGAAGACTTCACCAAGATCCACAT
GGAGTGAGTGCGCTGCAGGACCGCATGAGCGTCATCTGGGAGAGAGGAGTGTTGGAGGAAAGATGGATGAGAAC
CGTTTTGTGGCGTTACCAGTTCCAACGCAGCTAAGCTTCTGAACCTGTATCCCCGCAAGGGCCGCATTATTCCC
GGAGCCGATGCTGATGTGGTGGTGTGGGACCCAGAAGCCACAAAGACCATCTCAGCCAGCACGCAGGTCCAGGGA
GGAGACTTCAACCTGTATGAGAATGCGCTGCCACGGCGTGCCACTGGTCACCATCAGCCGGGGGCGCGTCTGT
TATGAGAACGGCGTCTTCATGTGCGCCGAGGGCACCGGCAAGTTCTGTCCCCTGAGGTCCTTCCCAGACACTGTC
TACAAGAAGCTGGTCCAGAGAGAGAAGACTTTAAAGGTTAGAGGAGTGACCGCACTCCCTACCTGGGGGATGTC
GCTGTTGTCTGTCACCCTGGGAAAAAAGAGATGGGAACCCCACTCGCAGACACTCCTACCCGGCCCGTCAACCGG
CATGGGGGCATGAGGGACCTTACGAATCCAGCTTACGCCTCTCTGGCTCTCAGATCGATGACCATGTTCCAAAG
CGAGCTTCAGCTCGGATCCTCGCTCCTCCCGGAGGCAGGTGAGTGGCATTTGGTAAAGGCATTGCCAAGCCCC
CGAGTGAGGACGCACCGCCGCCACCAGCCCGCAACTCTCCAGCCGAAGCTGCAGGGGCAGGAGAGGCTGGGCTGG
GTGGCACACCACCCGAGGGGGGCCCCGGGACCCACGGAGCCCTCCCTATGTCTGCAAAGTGATTCACTGTGCTTC
GAGCCAACTCTAACAGGCACTTTGAGATGTGTTCCCTCCTGCTGTAGTCCTTTCTGCCTTGGCCTCGGCGGGCTTT
TCTGGGGCCCAGGAAGCCACACTATGCACAGAGCCCAATGCATAGAGCCCTGGCCAGCCCTTCCCTCTCACTCCT
GCCTCCGCTGGCTTTGGGAAAGCCAGACTTTAGTGCCCTGCCCCCTGGCTGACTGGCCAGTTGCCAGAGCACT
TTAGCAGATGTGGTTTCAAAGTAAAGGCCTCCTCCCCACCCCTTAGGCCCCGTGGTGACATTTCCCAAGTCAGA
CAGATGTCAGCTTCCAGCCATGCCAGGACGTCCTATCTCCCCCAACCCACCTCTGGCCCTGTGTAGGGGCAGG
GATGGGGGTGGCTGGGACTCCTGGTGCCCCCTCGCCAGCTTCTCCTGCGCCCCGCCACACCCTCGGGGGGGTCAC
AGGCCCAGAAGGGTAGCTGGGCGGGGCTCGAGGCTGGTGCCAGGCGCGTGTAATGGTTTTGTGTTTGCAGTTTG
GTTTGCGCAGTAGTTTGGTTTGACTTGTTGTGTCATCCTGTGAAAAATAACGGTGCTTGTGTCACTAGCATAGAA
TAGCGACAGGAATAGATGTGGTCCTTAGGAGACGCTGCACCTTGACACCAACCAGACAGCACAGGGCAGGGGTGGT
GGAGGGGGCTGGGCTCACAGGCCTCTCTTTCCCCGCCTGCAGTCTTCTGGGCTGCGGGAGGCCCTGGCCCTTTC
CCCTTCCCTTCCCTCTTGTCTAGTTTCCACATTCCAAAAGGGGGCCTGGGATGCTAGCCCCAGAGATGCCAG
CCCTTCAGGAAGCAGGTGTCTTTCCCTCTCTGCCCCCTGATCACTCCCAGCACTCCCTTGCCTTCCCTGTCT
TCACCTGCCACCACACACACACACACACACACACACACACACGCATGGCTTCTATAACTTCTTCTCTGCTG
GACAGAGACTCAGCGCTCCTCCTGTGTGACTGGCAAGAGGCCTCATGCCTGCTGAGAGAGGGTCGACGCGGCCG

760/6881
FIGURE 710

MLANSASVRILIKGGKVVNDCTHEADVYIENGIIQQVGRELMIPGGAKVIDATGKLVIPGGIDTSTHFHQTFMN
ATCVDDFYHGTKAALVGGTTMIIGHVLPDKETSLVDAYEKCRLADPKVCCDYALHVGITWWAPKVKAEMETLVR
EKGVNSFQMFMTYKDLYMLRDSELYQVLHACKDIGAIARVHAENGELVAEGAKEALDLGITGPEGIEISRPEELE
AEATHRVITIANRTHCPIYLVNVSSISAGDVIAAAKMQGKVLAETTTAHATLTGLHYHQDWSHAAAYVTVFPL
RLDTNTSTYLMSELLANDTLNIVASDHRPFTTKQKAMGKEDFTKIPHGVSGVQDRMSVIWERGTVGGKMDENRFVA
VTSSNAAKLLNLYPRKGRIIPGADADVVDPEATKTISASTQVQGGDFNLYENMRCHGVPLVTISRGRVYENG
VFMCAEGTGKFCPLRSFPDTVYKKLVQREKTLKVRGVDRTPYLGDVAVVVHHPGKKEMGTPLADTPTRPVTRHGM
RDLHESSFSLSGSQIDDHVPKRASARILAPPGGRSSGIW

761/6881
FIGURE 711

CTTGCTCCGAGAGGGAGTCCTCGCGGACGTCAGCCAAGATTCCAGAAATGACTATCTTGACTTACCCCTTTAAAAA
TCTTCCCACTGCATCAAAATGGGCCCTCAGATTTTCCATAAGACCTCTGAGCTGTTCTCCAGCTACGAGCTGC
CCCAGCTGTCCAGACCAAAACGAAGAAGACGTTAGCCAAACCAATATAAGGAATGTTGTGGTGGTGGATGGTGT
TCGCACTCCATTTTTGCTGTCTGGCACTTCATATAAAGACCTGATGCCACATGATTTGGCTAGAGCAGCGCTTAC
GGGTTTGTGGCATCGGACCAGTGTCCTAAGGAAGTAGTTGATTATATCATCTTTGGTACAGTTATTCAGGAAGT
GAAAACAAGCAATGTGGCTAGAGAGGCTGCCCTTGGAGCTGGCTTCTCTGACAAGACTCCTGCTCACACTGTAC
CATGGCTTGTATCTCTGCCAACCAAGCCATGACCACAGGTGTTGGCTTGATTGCTTCTGGCCAGTGTGATGTGAT
CGTGGCAGGTGGTGTGAGTTGATGTCCGATGTCCCTATTTCGTCACCTCAAGGAAAATGAGAAAATGATGCTTGA
TCTCAATAAGGCCAAATCTATGGGCCAGCGACTGTCTTTAATCTCTAAATTCGATTTAATTTCTAGCACCTGA
GCTCCCTGCGGTTTCTGAGTTCTCCACCAGTGAGACCATGGGCCACTCTGCAGACCGACTGGCCGCTGCCTTTGC
TGTTTCTCGGCTGGAACAGGATGAATATGCACTGCGCTCTCACAGTCTAGCCAAGAAGGCACAGGATGAAGGACT
CCTTTCTGATGTGGTACCCTTCAAAGTACCAGGAAAAGATACAGTTACCAAAGATAATGGCATCCGTCCTTCCTC
ACTGGAGCAGATGGCCAAACTAAAACCTGCATTTCATCAAGCCCTACGGCACAGTGACAGCTGCAAATTCCTCTTT
CTTGACTGATGGTGCATCTGCAATGTTAATCATGGCGGAGGAAAAGGCTCTGGCCATGGGTTATAAGCCGAAGGC
ATATTTGAGGGATTTTATGTATGTGTCTCAGGATCCAAAAGATCAACTATTACTTGGACCAACATATGCTACTCC
AAAAGTTCTAGAAAAGGCAGGATTGACCATGAATGATATTGATGCTTTTGAATTTTCATGAAGCTTTCTCGGGTCA
GATTTTGGCAAATTTTAAAGCCATGGATTCTGATTGGTTTGCAGAAAACCTACATGGGTAGAAAACCAAGGTTGG
ATTGCCTCCTTTGGAGAAGTTTAATAACTGGGGTGGATCTCTGTCCCTGGGACACCCATTTGGAGCCACTGGCTG
CAGGTTGGTCATGGCTGCTGCCAACAGATTACGGAAAGAAGGAGGCCAGTATGGCTTAGTGGCTGCGTGTGCAGC
TGGAGGGCAGGGCCATGCTATGATAGTGAAGCTTATCCAAAATTAATAGATCCAGAAGAAGTGACCTGAAGTTTC
TGTGCAACACTCACACTAGGCAATGCCATTTCAATGCATTACTAAATGACATTTGTAGTTCTAGCTCCTCTTAG
GAAAACAGTTCTTGTGGCCTTCTATTAAATAGTTTGCACCTTAAGCCTTGCCAGTGTTCTGAGCTTTTCAATAATC
AGTTTACTGCTCTTTAGGGATTCTAAGCCACCAGAATCTCACATGAGATGTGTGGGTGGTTGTTTTTGGTCTC
TGTTGTCACTAAAGACTAAATGAGGGTTTGCAGTTGGGAAAGAGGTCAACTGAGATTGGAAATCATCTTTGTAA
TATTTGCAAATTATACTTGTCTTATCTGTGTCCTAAAGATGTGTTCTCTATAAAATACAAACCAACGTGCCTAA
TTAATTATGAAAAATAATTCAGAATCTAAACACCACTGAAAACTTATAAAAAATGTTTAGATACATAAATATGG
TGGTCAGCGTTAATAAAGTGAGAAATATTGAAAAA

762/6881
FIGURE 712

MTILTYPFKNLPTASKWALRFSIRPLSCSSQLRAAPAVQTKTKKTLAKPNIRNVVVVDGVRTPFLLSGTSYKDLM
PHDLARAALTGLLHRTSVPKEVVDYIIFGTVIQEVKTSNVAREAAALGAGFSDKTPAHTVTMACISANQAMTTGVG
LIASGQCDVIVAGGVELMSDVPIRHSRKMRLMLDLNKAQDEGLLSKVPGKDTVTKDNGIRPSSLEQMAKLKPAFIKPY
SADRLAAFAVSRLEQDEYALRSHSLAKKAQDEGLLSKVPGKDTVTKDNGIRPSSLEQMAKLKPAFIKPY
GTVTAANSSFLTGDASAMLIAMAEKALAMGYKPKAYLRDFMYVSQDPKDQLLLGPTYATPKVLEKAGLTMNDIDA
FEFHEAFSGQILANFKAMDSWFAENYMGRTKVGLPPLKFNWGGSLSLGHPFGATGCRLVMAAANRLRKEGG
QYGLVAACAAGGQGHAMIVEAYPK

763/6881
FIGURE 713

GGCACGAGGCCACTGCTGTCTCTTCAGCTCAAGATGGTGGCCTGCCGGGCGATTGGCATCCTCAGCCGCTTTTC
TGCCITTCAGGATCCTCCGCTCCCGAGGTTATATATGCCGCAATTTTACAGGGTCTTCTGCTTTGCTGACCAGAAC
CCATATTAACATATGGAGTCAAAGGGGATGTGGCAGTTGTTTGAATTAACCTCTCCCAATTCAAAGGTAAATACACT
GAGTAAAGAGCTACATTCAGAGTTCTCAGAAGTTATGAATGAAATCTGGGCTAGTGATCAAATCAGAAGTGCCGT
CCTTATCTCATCAAAGCCAGGCTGCTTTATTGCAGGTGCTGATATCAACATGTTAGCCGCTTGCAAGACCCTTCA
AGAAGTAACACAGCTATCACAAGAAGCACAGAGAATAGTTGAGAACTTGAAAAGTCCACAAAGCCTATTGTGGC
TGCCATCAATGGATCCTGCCCTGGGAGGAGGACTTGAGGTTGCCATTTTCATGCCAATACAGAATAGCAACAAAAGA
CAGAAAAACAGTATTAGGTACCCCTGAAGTTTGTGTTGGGGGCTTACCAGGAGCAGGAGGCACACAAAGGCTGCC
CAAAATGGTGGGTGTGCCCTGCTGCTTTGGACATGATGCTGACTGGTAGAAGCATTTCGTGCAGACAGGGCAAAGAA
AATGGGACTGGTTGACCAACTGGTGGAACCCCTGGGACCAGGACTAAAACCTCCAGAGGAACGGACAATAGAATA
CCTAGAAGAAGTTGCAATTACTTTTGCCAAAGGACTAGCTGATAAGAAGATCTCTCCAAAGAGAGACAAGGGATT
GGTGGAAAAATTGACAGCGTATGCCATGACTATTCCATTTGTGAGGCAACAGGTTTACAAAAAGTGAAGAAAA
AGTGCAGAAAGCAGACTAAAGGCCCTTTATCCTGCACCTCTGAAAAATAATTGATGTGGTAAAGACTGGAATTGAGCA
AGGGAGTGATGCCGGTTATCTCTGTGAATCTCAGAAATTTGGAGAGCTTGTAATGACCAAAGAATCAAAGGCCTT
GATGGGACTCTACCATGGTCAGGTCTGTGCAAGAAGAATAAATTTGGAGCTCCACAGAAGGATGTTAAGCATCT
GGCTATTCTTGGTGAGGGCTGATGGGAGCAGGCATCGCCCAAGTCTCCGTGGATAAGGGGCTAAAGACTATACT
TAAAGATGCCACCCCTCACTGCGCTAGACCGAGGACAGCAACAAGTGTCAAAGGATTGAATGACAAAGTGAAGAA
GAAAGCTCTAACATCATTTGAAAGGGATTCCATCTTCAGCAACTTGACTGGGCAGCTTGATTACCAAGGTTTTGA
AAAGGCCGACATGGTGATTGAAGCTGTGTTTGAGGACCTTAGTCTTAAGCACAGAGTGCTAAAGGAAGTAGAAGC
GGTGATTCCAGATCACTGTATCTTTGCCAGTAACACATCTGCTCTCCCAATCAGTGAAATCGCTGCTGTCAGCAA
AAGACCTGAGAAGGTGATTGGCATGCACTACTTCTCTCCCGTGACAAGATGCAGCTGCTGGAGATTATCACGAC
CGAGAAAACCTTCAAAGACACCAGTGCTTCAGCTGTAGCAGTTGGTCTCAAGCAGGGGAAGGTCATCATTTGTGGT
TAAGGATGGACCTGGCTTCTATACTACCAGGTGTCTTGCGCCCATGATGTCTGAAGTCATCCGAATCTCCAGGA
AGGAGTTGACCCGAAGAAGCTGGATTCCCTGACCACAAGCTTTGGCTTCTCTGTGGGTGCCGCCACACTGGTGGA
TGAAGTTGGTGTGGATGTAGCGAAACATGTGGCGGAAGATCTGGGCAAAGTCTTTGGGGAGCGGTTTGGAGGTGG
AAACCCAGAAGTCTGACACAGATGGTGTCCAAGGGCTTCTAGGTCTGTAATCTGGGAAGGGCTTTTACATCTA
TCAGGAGGGTGTGAAGAGGAAGGATTTGAATTCTGACATGGATAGTATTTTAGCGAGTCTGAAGCTGCCTCCTAA
GTCTGAAGTCTCATCAGACGAAGACATCCAGTTCCGCCTGGTGACAAGATTTGTGAATGAGGCAGTCATGTGCCT
GCAAGAGGGGATCTTGCCACACCTGCAGAGGGAGACATCGGAGCCGTCTTTGGGCTTGGCTTCCCGCCTTGCTCT
GGGAGGGCCTTTCCGCTTTGTGGATCTGTATGGCGCCAGAAAGATAGTGGACCGGCTCAAGAAATATGAAGCTGC
CTATGGAAAACAGTTACCCCATGCCAGCTGCTAGCTGACCATGCTAACAGCCCTAACAAAGATTCTACCAGTG
AGCAGGCCTCATGCCTCGCTCAGTCAGTGCACTAACCCAGCTGCCGGCAGTGCTGGTTCTCCAACAGAGTGGTG
TCTAGATTTATCAGAGTAACGAGAAGACAACTCCGGCACTGGGTTTGTCTCCCTGATTAAAGTGCCCTCAGCCAA
GACCATCTCTCCCTCCTGGTGAAAGTGTGACTTTCGAATTAGTTTGCACCTTCTATTGGAAGGTAGAGCCCACTGCT
CATTTGTATAAGCCCCGAGGCCTAGAGTGGCAGCCAAGAGCCATCTGAAGCCACCTCTCTGCCTGTTCTCCCAAG
AGGCCAGGGTGGCCAGGGGTGGTGAGGGCAGTTCTGCACCCAGCCAAACACATAACAATAAAAACCAAACCTCTGT
GTCAGCATCTTTGCCCTTCTGGTTTAAACGCCTCCTTCAAAAAGCAATCTGGAAGAAAGCCCTGTGCTTTGGGGG
AGTAAGAATGTGTGTGAGAATTCTAGGCAGCACCTTAGGGAGGGACTGGGATGAGAGAAAGTGGGACCTGGTGG
GCTCAACCACACACCTGTCTGTGCAGATGCTTTGCCAGGCTTCTCACCACGGGTGACCGGGATATTAAACCT
CTTTCCCCAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

764/6881
FIGURE 714

MVACRAIGILSRFSAFRILRSRGYICRNFTGSSALLTRTHINYGVKGDVAVVRINSPNSKVNTLSKELHSEFSEV
MNEIWASDQIRSAVLISSKPGCFIAGADINMLAACKTLQEVTLQSQEAQRIVEKLEKSTKPIVAAINGSCLGGL
EVAISCQYRIATKDRKTVLGTPEVLLGALPGAGGTQRLPKMVGVPAAALDMMLTGRSIRADRAKKMGLVDQLVEPL
GPGLKPPEERTIEYLEEVAITFAKGLADKKISPKRDKGLVEKLTAYAMTIPFVRQQVYKKVEEKVRKQTKGLYP
PLKIIDVVKTGIEQGS DAGYLCESQKFGE LVMTKESKALMG LYGQVLCKKNKFGAPQKDVKHLAILGAGLMGAG
IAQVSVDKGLKTI LKDATLTALDRGQQQVFKGLNDKVKKKALTSFERDSIFSNLTGQLDYQGF EKADMVIEAVFE
DLSLKHRLKEVEAVIPDHCIFASNTSALPISEIAAVSKRPEKVI GMHYFSPVDKMQ LLEIITTEKTSKDTSASA
VAVGLKQGVIIIVVKDGP GFYTTRCLAPMMSEVIRILQEGVDPKKLDSLTSFGFPVGAATLVDEVGVDAKHVA
EDLGKVFGERF GGNPELLTQMVSKGFLGRKSGKGFYIYQEGVKRKDLNSDMSILASLKLPPKSEVSSDEDIQF
RLVTRFVNEAVMCLQEGILATPAEGDIGAVFGLGFPPCLGGPFRFVDLYGAQKIVDRLKKYEAA YGKQFTPCQLL
ADHANSPNKKFYQ

765/6881
FIGURE 715

TTCTGTTTTTCTCTCTCATTCTCCAGTGGCGGCGGCGGGGAAGGCGGAGGCAGAGGCAGCAGCAGCCGCGCTGGC
TGCAATGAATGATCCCCAGCTTGGGGGGAGGACTCCAGGTGAGCCTCTGCCCTCGGGAGGCCCGGGACCCCCGG
CCGCCCACGACCGGCAGCCCACGCTATGGATCCCTAGAGGAAGGAGGAGAAGACAGCTCGCCGCCCCACCCCCATC
CCATTTTCTCTTCTTTATCTCATTGTTGCCGAAGCTGTTTACGGCAGCGCTCCCTCTGCTCCAGGACTCCCTG
GGGGGAATGCCAAGACCATCATGGTAGCCACACTGGGGCCAGCTTCTCACAGCTACGATGAGAGCCTCTCCACC
TTGCGCTTTGCCAACCGAGCCAAGAACATCAAGAACAAGCCCCAGGTGAACGAGGACCCAAGGACACACTGCTG
CGGGAATTCCAAGAGGAGATTGCCCGCCTGAAGGCCCAGCTGGAGAAGAGGGGGATGCTGGGGAAGCGGCCCCGG
AGGAAGAGCAGCCGCAGGAAGAAGGCCGTGTCCGCCCCGCTGGGTACCCTGAGGGCCCAGTGATTGAGGCCTGG
GTGGCAGAAGAGGAGGATGACAACAACAACCACCGCCCCGCCCCAGCCATCCTGGAGTCAGCCTTGAGAGAAG
AACATGGAGAATTACCTGCAGGAACAGAAGGAGCGGCTGGAGGAGGAGAAGGCAGCCATCCAGGATGACCGCA

766/6881
FIGURE 716A

GCTGGAGGTGGCCTCCCCTCCGCCCCAGACAAGAAGAGGCCCTCAGCCCTCCCCGGTCTCAGAGAGCCCTGAGA
GGAGGCCAGTCCAGAGCTCTTCTCCGTTCCCAGTCCACTTCTCTAGGGCCAGTAGCAGACACCAGCCAGTATG
CCGAGGAACCAGGGCTTCTCCGAGCCCGAATACTCGGCCGAGTACTCAGCCGAGTACTCCGTGAGCCTGCCCTCC
GACCCTGACCGCGGGGTGGGCCGGACCCATGAAATCTCGGTCCGGAACCTCGGGCTCCTGCCTGTGCCTGCCTCGC
TTCATGCGGTGACTTTTCGTGCCGGAGTCCTTGAGAACCTCTACCAGACCTACTTCAAAGGCAGCGCCACGAG
ACCCTGCTGGTGCTGGTGGTCTTTGCAGCCCTCTTTGACTGCTACGTGGTGGTTCATGTGTGCTGTGGTCTTCTCC
AGCGACAAGCTGGCTTCCCTCGCCGTGGCTGGAATTGGACTGGTGTGGACATCATCCTCTTCGTGCTCTGCAAA
AAGGGGCTGCTCCCGGACCGGGTCACCCGAGAGTGTGCCCTACGTGCTGTGGCTGCTCATAACCGCCCAGATC
TTCTCCTACCTGGGCCTGAACTTCGCGCGTGGCCACGCGGCTAGTGACACGGTGGGCTGGCAGGTCTTCTTTGTCT
TTCTCCTTCTTCATCACGCTGCCCCCTCAGCCTCAGCCCCATCGTGATCATCTCCGTGGTCTCCTGTGTGGTGCAC
ACGTTGGTCTCCTGGGGGTACCGTGGCCAGCAGCAGCAGGAGGAGCTCAAGGGGATGCAGCTGCTGCGGGAGATC
CTGGCCAACGTCTTCTCTACCTGTGCGCCATCGCTGTGGGCATCATGTCTACTACATGGCTGACCGCAAGCAC
CGCAAGGCCTTCCCTGGAGGCCCGCCAGTGCCTGGAGGTGAAGATGAACCTGGAAGAGCAGAGCCAGCAGCAGGAG
AACCTCATGCTTTCCATCCTGCCAAGCAGTGGCTGACGAGATGCTGAAAGACATGAAGAAAGACGAGAGCCAG
AAGGACCAGCAGCAGTTCAACACCATGTACATGTACCGTACGAGAACGTGAGCATCCTCTTTGCCGACATCGTG
GGCTTTACCCAGCTGTCTTCTGCCTGCAGTGGCCAGGAGCTTGTGAAGCTGCTCAACGAGCTCTTTGCCCGCTTT
GACAAGCTGGCAGCTAAATACCACCAGCTGCGGATTAAGATCCTGGGCGACTGCTACTACTGCATCTGCGGCTTG
CCCGACTACCGGGAGGACCACGCCGTCTGCTCCATCCTCATGGGGCTGGCCATGGTGGAGGCCATCTCGTATGTG
CGGGAGAAGACCAAGACTGGGGTGGACATGCGTGTGGGGGTGCACACGGGCACCGTGTGGGGGGCGTCTGGGC
CAGAAGCGCTGGCAGTACGACGTGTGGTGCAGTGTGCTACTGTAGCCAACAAGATGGAGGCCGGCGGCATCCCT
GGGCGCGTGCACATCTCCCAGAGCACCATGGACTGCCTGAAAGGGGAGTTTGATGTGGAGCCAGGCGATGGGGGC
AGCCGCTGTGATTACCTAGAAGAGAAGGGTATTGAAACCTACCTCATCATTGCCTCCAAGCCAGAGGTGAAGAAA
ACAGCCACCCAGAATGGCCTCAATGGCTCGGCCCTGCCAATGGAGCACCAGCTTCTCAAAGTCCAGCTCCCCT
GCCCTCATTGAGACCAAGGAGCCCAACGGGAGTGCCACAGCAGTGGGTCCACGTGCGAGAAGCCCCGAGGAGCAG
GATGCCCAGGCCGACAACCCCTCATTCCCCAACCCACGCCGGAGGCTGCGCCTGCAGGACCTGGCTGACCGAGTG
GTGGATGCCTCTGAAGATGAGCACGAGCTCAACCAGCTGCTCAACGAGGCCCTGCTTGAGCGAGAGTCCGCCCAA
GTGTAAAGAAGAGAAAACACCTTCTTGTCCATGCGGTTTCATGGACCCCGAGATGGAACCCGCTACTCGGTGG
AGAAGGAGAAGCAGAGTGGGGTGCCTTACGCTGCTCCTGCGTCGTCCTGCTCTGCACGGCCCTGGTGCAGATAC
TCATCGACCCCTGGCTAATGACAACTATGTGACCTTCATGGTGGGGGAGATTCTGCTCCTCATCTGACCATCT
GCTCCCTGGCTGCCATCTTTCCCCGGGCCTTTTCTAAGAAGCTTGTGGCCTTCTCAACTTGGATTGACCGGACCC
GCTGGGCCAGGAACACCTGGGCCATGCTCGCCATCTTCATCCTGGTGATGGCAAATGTCGTGGACATGCTCAGCT
GTCTCCAGTACTACACGGGACCCAGCAATGCAACGGCAGGGATGGAAACGGAGGGCAGCTGCCTGGAGAACCCCA
AGTATTACAACATATGTGGCCGTGCTGTCCCTCATCGCCACCATCATGTGTTGTCAGGTGAGCCACATGGTGAAGC
TCACGCTCATGCTGCTCGTCGAGGCGCCGTGGCCACCATCAACCTCTATGCCTGGCGTCCCGTCTTTGATGAAT
ACGACCACAAGCGTTTTTCGGGAGCAGACTTACCTATGGTGGCCTTAGAGCAGATGCAAGGATTCAACCCCTGGGC
TCAATGGCACTGACAGGCTGCCCCTGGTGCCTTCCAAGTACTCTATGACGGTGTGTTTCTCATGATGCTCA
GCTTCTACTACTTCTCCCCGCCAGTAGAAAACTGGCACGGACACTTTTCTTGTGGAAGATTGAGGTCCACGACC
AGAAGGAACGTGTCTATGAGATGCGACGCTGGAACGAGGCCTTGGTCACCAACATGTTGCCTGAGCACGTGGCAC
GCCATTTCTGGGGTCCAAGAAGAGAGATGAGGAGCTGTATAGCCAGACGTATGATGAGATTGGAGTCATGTTTG
CCTCCCTGCCCAACTTTGCTGACTTCTACACAGAGGAGAGCATCAACAATGGTGGTATTGAGTGTCTGCGTTTCC
TCAATGAAATCATCTCAGATTTTGACTCTCTCCTGGACAATCCCAAGTTCCGGGTGATCACCAAGATCAAAACCA
TTGGCAGCACGTATATGGCGGCTTACAGAGTCACCCCCGATGTCAACACCAATGGCTTTGCCAGCTCCAACAAGG
AAGACAAGTCCGAGAGAGAGCGCTGGCAGCACCTGGCTGACCTGGCCGACTTCGCGCTGGCCATGAAGGATACGC
TCACCAACATCAACAACCAGTCCTTCAATAACTTCATGTGCGCATAGGCATGAACAAAGGCGGGGTTCTGGCTG
GGGTCATCGGAGCCCGGAAACCACACTACGACATCTGGGGCAATACAGTCAATGTAGCCAGCAGGATGGAGTCCA
CGGGGGTTCATGGGCAACATTCAGGTATGTCCAGTGGCACAGCTGGCACGTGCTCAGACTCGGCATGAGAACAAAA
CCGGAACAGTGCTTTCCACGTGCCCTGCCTCCCACCTGGCCCTGAACAGTAAGTCCAGAGGCAGAGACGTGG
GGCAAGTGGAAAAGAATCTCTGCAATAGCTAGCCTCAGCACAGGAAGAAACACTTCCACCCATCCACAAAATCTG

767/6881
FIGURE 716B

GGCTGAAGTTCTAGATGCATATGGCCTACCTTTGGGTATGAACCTTCTAATACCTTGTGATCTGTCTCAGTGGCG
TCTGGCAGAAAAGCTCCACGAAAGGGGCAAAGGGACAGAAGAGCAGGCAGTGGCAGTTTCCAGGTAACAGTGCTG
CCACCCAGGTGACCATGGCCATCCTAGGAGAGAAGTCTCTGGATGAGAGGAGGCCCCCAGCCAGTCACTCCAGGG
TTCTCCTTCCCACCCGCTGCTCGCCACGGGTGGAAGGGCTTGGCCC

768/6881
FIGURE 717

GCCGCGGCACACAGGGCGCGCAGCCGGGCCGGCCGACCCACCGGCCATACGGTGGAGCCATCGAAGCCCCACC
CACAGGCTGACAGAGGCACCGTTACACAGAGGGCTCAACACCGGGATCTATGTTTAAAGTTTAACTCTCGCTCC
AAAGACCACGATAATTCTTCCCCAAAGCCAGCAGCCCCCAGCCCCGCGCAGCCCCAGCCTGCCTCCCGGCGC
CCAGATGCCCCGCCATGCCCTCCAGCGGCCCGGGGACACCAGCAGCTCTGCTGCGGAGCGGGAGGAGGACCGAAA
GGACGGAGAGGAGCAGGAGGAGCCGCGTGGCAAGGAGGAGCGCCAAGAGCCCAGCACACGGCACGGAAGGTGGG
GCGGCCTGGGAGGAAGCGCAAGCACCCCCCGGTGGAAAGCGGTGACACGCCAAAGGACCCTGCGGTGATCTCCAA
GTCCCCATCCATGGCCCAGGACTCAGGCGCCTCAGAGCTATTACCCAATGGGGACTTGGAGAAGCGGAGTGAGCC
CCAGCCAGAGGAGGGGAGCCCTGCTGGGGGGCAGAAGGGCGGGGCCCCAGCAGAGGGAGAGGGTGCAGCTGAGAC
CCTGCTGAAGCCTCAAGAGCAGTGGAAAATGGCTGCTGCACCCCCAAGGAGGGCCGAGGAGCCCTGCAGAAGC
GGGCAAAGAACAGAAGGAGACCAACATCGAATCCATGAAAATGGAGGGCTCCCGGGGCGCGGTGCGGGGTGGCTT
GGGCTGGGAGTCCAGCCTCCGTCAGCGGCCCATGCCGAGGCTCACCTTCCAGGCGGGGGACCCCTACTACATCAG
CAAGCGCAAGCGGGACGAGTGGCTGGCACGCTGGAAAAGGGAGGCTGAGAAGAAAAGCCAAGGTCAATGTCAGGAAT
GAATGCTGTGGAAGAAAACAGGGGCCCGGGGAGTCTCAGAAGGTGGAGGAGGCCAGCCCTCCTGCTGTGCAGCA
GCCACTGACCCCGCATCCCCACTGTGGCTACCACGCCTGAGCCCGTGGGGTCCGATGCTGGGGACAAGAATGC
CACCAAAGCAGGCGATGACGAGCCAGAGTACGAGGACGGCCGGGGCTTTGGCATTGGGGAGCTGGTGTGGGGGAA
ACTGCGGGGCTTCTCCTGGTGGCCAGGCCGCATTGTGTCTTGGTGGATGACGGGCGGGAGCCGAGCAGCTGAAGG
CACCCGCTGGGTTCATGTGGTTTCGAGACGGCAAATTCTCAGTGGTGTGTGTTGAGAAGCTGATGCCGCTGAGCTC
GTTTTGCAGTGCCTTCCACCAGGCCACGTACAACAAGCAGCCCATGTACCGCAAAGCCATCTACGAGGTCTTGCA
GGTGGCCAGCAGCCGCGCGGGGAAGCTGTTCCCGGTGTGCCACGACAGCGATGAGAGTGACACTGCCAAGGCCGT
GGAGGTGCAGAACAAGCCCATGATTGAATGGGCCCTGGGGGGCTTCCAGCCTTCTGGCCCTAAGGGCCTGGAGCC
ACCAGAAGAAGAGAAGAATCCCTACAAAGAAGTGTACACGGACATGTGGGTGGAACCTGAGGCAGCTGCCTACGC
ACCACCTCCACCAGCCAAAAAGCCCGGAAGAGCACAGCGGAGAAGCCCAAGGTCAAGGAGATTATTGATGAGCG
CACAAGAGAGCGGCTGGTGTACGAGGTGCGGCAGAAGTGCCGGAACATTGAGGACATCTGCATCTCCTGTGGGAG
CCTCAATGTTACCCTGGAACACCCCTCTTCGTTGGAGGAATGTGCCAAACTGCAAGAAGTCTTTCTGGAGTG
TGCCTACAGTACGACGACGACGGCTACCAGTCTACTGCACCATCTGCTGTGGGGGCCGTGAGGTGCTCATGTG
CGGAAACAACAAGTGTGTCAGGTGCTTTTGCCTGGAGTGTGTGGACCTCTTGGTGGGGCCGGGGGCTGCCCAGGC
AGCCATTAAGGAAGACCCCTGGAAGTGTACATGTGCGGGCACAAGGGTACCTACGGGCTGCTGCGGCGGCGAGA
GGACTGGCCCTCCCGGCTCCAGATGTTCTTCGCTAATAACCACGACCAGGAATTTGACCCTCCAAAGGTTTACCC
ACCTGTCCCAGCTGAGAAGAGGAAGCCCATCCGGGTGCTGTCTCTCTTTGATGGAATCGCTACAGGGCTCCTGGT
GCTGAAGGACTTGGGCATTGAGGTGGACCGCTACATTGCCTCGGAGGTGTGTGAGGACTCCATCACGGTGGGCAT
GGTGCGGCACCAGGGGAAGATCATGTACGTGCGGGACGTCCGACGCTCACACAGAAGCATATCCAGGAGTGGGG
CCCATTGATCTGGTGATTGGGGGCAGTCCCTGCAATGACCTCTCCATCGTCAACCCCTGCTCGCAAGGGCCTCTA
CGAGGGCACTGGCCGGCTCTTCTTTGAGTTCTACCGCCTCCTGCATGATGCGCGGCCCAAGGAGGGAGATGATCG
CCCCTTCTTCTGGCTCTTTGAGAAATGTGGTGGCCATGGGCGTTAGTGACAAGAGGGACATCTCGCGATTTCTCGA
GTCCAACCCCTGTGATGATTGATGCCAAAGAAGTGTGAGCTGCACACAGGGCCCCGCTACTTCTGGGGTAACCTTCC
CGGTATGAACAGGCCGTTGGCATCCACTGTGAATGATAAGCTGGAGCTGCAGGAGTGTCTGGAGCATGGCAGGAT
AGCCAAGTTTCAGCAAAGTGAGGACCATTACTACGAGGTCAAACCTCCATAAAGCAGGGCAAAGACCAGCATTTTCC
TGTCTTCATGAATGAGAAAGAGGACATCTTATGGTGCAGTGAATGGAAAGGGTATTTGGTTTCCCAGTCCACTA
TACTGACGTCTCCAACATGAGCCGCTTGGCGAGGCAGAGACTGCTGGGCCGGTCATGGAGCGTGCCAGTCATCCG
CCACCTCTTCGCTCCGCTGAAGGAGTATTTTGCCTGTGTGTAAAGGACATGGGGGCAAAGTGAAGGTAGCGACACA
AAGTT

769/6881
FIGURE 718

MPAMPSSGPGDTSSSAAEREEDRKDGEEQEEPRGKEERQEPSTTARKVGRPGRKRKHPPVESGDTPKDPAVISKS
PSMAQDSGASELLPNGDLEKRSEPQPEEGSPAGGQKGGAPAE GEGAAETLPEASRAVENGCCTPKEGRGAPAEAG
KEQKETNIESMKMEGSRGRLRGGLGWESSLRQRPMPRLTFQAGDPYYISKRRDEWLARWKREAEKKAKVIAGMN
AVEENQGPGESQKVEEASPPAVQQPTDPASPTVATTPEFVGSDAGDKNATKAGDDEPEYEDGRGFGIGELVWGKL
RGFSWWPGRIVSWWMTGRSRAAEGTRWVMWFGDGKFSVVCVEKLMPLSSFCSAFHQATYNKQPMYRKAIYEVLQV
ASSRAGKLFVCHDSDESDTAKAVEVQNKPMIEWALGGFQPSGPKGLEPPEEEKNPYKEVYTDMMWVEPEAAAYAP
PPPAKKPRKSTAEKPKVKEIIDERTRERLVYEVQKCRNIEDICISCGSLNVTLEHPLFVGGMCQNCKNCFLECA
YQYDDDDGYQSYCTICCGGREVL MCGNNNCCRCFCVECDLLVGPAAQAAIKEDPWNCYMCGHKGTYGLLRRED
WPSRLQMFFANNHDQEFDPKVPVPPVPAEKRP IRVLSLFDGIATGLLVLKDLGIQVDRIYASEVCEDSITVGMV
RHQ GKIMYVG DVRSVTQKHIQEWGPFDLVIGGSPCNDLSIVNPARKGLYEGTGRLFFEFYRLLHDARPKEGDDRP
FFWLFENVVAMGVSDKRDISRFLSNPVMIDAKEVSAHRARYFWGNLPGMNRPLASTVNDKLELQECLEHGRIA
KFSKVRTITTRSNSIKQGKDQHFPVFMNEKEDILWCTEMERVFGFPVHYTDVSNMSRLARQRLGRSWSVPVIRH
LFAPLKEYFACV

770/6881
FIGURE 719

CTGACCGCCGGGGGGTGTCCCCGGGACGTAGCGCCGCGGAGAGGAAGCGGCAAAGGGGACC**ATG**CGGCGCCTGAC
TCGTGGGCTGGTTCTGCCAGTCTTCGGGGTGCTCTGGATCACGGTGCTGCTGTTCTTCTGGGTAACCAAGAGGAA
GTTGGAGGTGCCGACGGGACCTGAAGTGCAGACCCCTAAGGTTTGGTCCTTGTTTTTCAAGGTGGCTGGGATGAG
CCCTTGGGCGCCTCAGGTGCCTGTATCACCCACTCCTCCCTACCAAAGAGGGCATCTTCTACAGGAGGACACCT
TGCTGTATGTCAATTTCCCATGTCTCTTGCAAGAAGCTCAGTTCCATTGTCAGACTCAGGTCTTTCTTCAAGTCAG
ATGCACACTGCTGGTGTATTGCACGGACCTTCCACCCACTAGCATCATCATCACCTTCCACAACGAGGCCCCGCTC
CACGCTGCTCAGGACCATCCGCAGTGTATTAAACCGCACCCCTACGCATCTGATCCGGGAAATCATATTAGTGGA
TGACTTCAGCAATGACCCTGATGACTGTAAACAGCTCATCAAATTGCCCAAGGTGAAATGCTTGCGCAATAATGA
ACGGCAAGGTCTGGTCCGGTCCCGGATTCCGGGGCGCTGACATCGCCCAGGGCACCCTCTGACTTTCTCGACAG
CCACTGTGAGGTGAACAGGGACTGGCTCCAGCCTCTGTTGCACAGGGTCAAAGAGGACTACACGCGGGTGGTGTG
CCCTGTGATCGATATCATTAACCTGGACACCTTACCTACATCGAGTCTGCCTCGGAGCTCAGAGGGGGGTTTGA
CTGGAGCCTCCACTTCCAGTGGGAGCAGCTCTCCCCAGAGCAGAAGGCTCGGCGCCTGGACCCACGAGCCCAT
CAGGACTCCTATCATAGCTGGAGGGCTCTTCGTGATCGACAAAGCTTGTTTGATTACCTGGGGAAATATGATAT
GGACATGGACATCTGGGGTGGGGAGAACTTTGAAATCTCCTTCCGAGTGTGGATGTGCGGGGGCAGCCTAGAGAT
CGTCCCCTGCAGCCGAGTGGGGCACGTCTTCCGGAAGAAGCACCCCTACGTTTTCCCTGATGGAAATGCCAACAC
GTATATAAAGAACACCAAGCGGACAGCTGAAGTGTGGATGGATGAATACAAGCAATACTATTACGCTGCCCGGCC
ATTGCCCTGGAGAGGCCCTTCGGGAATGTTGAGAGCAGATTGGACCTGAGGAAGAATCTGCGCTGCCAGAGCTT
CAAGTGGTACCTGGAGAATATCTACCCTGAACTCAGCATCCCCAAGGAGTCTCCATCCAGAAAGGGCAATATCCG
ACAGAGACAGAAGTGCCTGGAATCTCAAAGGCAGAACAACCAAGAAACCCCAAACCTAAAGTTGAGCCCCTGTGC
CAAGGTCAAAGGCGAAGATGCAAAGTCCCAGGTATGGGCCTTACATACACCCAGCAGATCCTCCAGGAGGAGCT
GTGCCTGTCTAGTCATCACCTTGTTCCTGGCGCCCCAGTGGTTCTTGTCTTTGCAAGAATGGAGATGACCGACA
GCAATGGACCAAACTGGTTCCACATCGAGCACATAGCATCCACCTCTGCCTCGATACAGATATGTTGGGTGA
TGGCACCAGAAACGGCAAGGAAATCGTCGTCAACCCATGTGAGTCCTCACTCATGAGCCAGCACTGGGACATGGT
GAGCTCT**TGAGG**ACCCCTGCCAGAAGCAGCAAGGGCCATGGGGTGGTGCTTCCCTGGACCAGAACAGACTGGAAA
CTGGGCAGCAAGCAGCCTGCAACCACCTCAGACATCCTGGACTGGGAGGTGGAGGCAGAGCCCCCAGGACAGGA
GCAACTGTCTCAGGGAGGACAGAGGAAAACATCACAAGCCAATGGGGCTCAAAGACAAATCCACATGTTCTCAA
GGCCGTTAAGTTCCAGTCCTGGCCAGTCATTCCCTGATTGGTATCTGGAGACAGAAACCTAATGGGAAGTGTTTA
TTGTTCTTTTTCTACAAAGGAAGCAGTCTCTGGAGGCCAGAAAGAAAAGCCTTCTTTTTTCACTAGGCCAGGACT
ACATTGAGAGATGAAGAATGGAGGTTGTTTCCAAAAGAAATAAAGAGAAACTTAGAAGTTGTCTCTGG

771/6881
FIGURE 720

MRRLTRRLVLPVFGVLWITVLLFFWVTKRKLEVPTGPEVQTPKVWSLFFKVAGMSPWAPQVPVSPTPPYQRGHLPTGGHLAVCHFPCLLQEAQFHLQTQVFLQVRCTLLVYCTDLPPTSIIITFHNEARSTLLRTIRSVLNRTPTHIREIILVDDFSNDPDDCKQLIKLPKVKCLRNNERQGLVRSRIRGADIAQGTTLTFLDSHCEVNRDWLQPLLHRVKEDYTRVVCPVIDIINLDTFTYIESASELRGGFDWSLHFQWEQLSPEQKARRLDPTPIRTPIIAGGLFVIDKAWFDYLGKYDMDMDIWGGENFEISFRVWMC GGSL EIVPCSRVGHVFRKKHPYVFPDGNANTYIKNTKRTAEVWMDEYKQYYYAARPFALERPF GNVESRLDLRKNLRCQSFKWYLENIYPELSIPKESSIQKGNIRQRQKCLESQRQNNQETPNLKLSPCAKVKGEDAKSQVWAFTYTQQILQEELCLSVITLFFPGAPVVLVLCKNGDDRQQWTKTGSHIEHIASHLCCLDTDMFGDGTENGKEIVVNPCESLMSQHWD MVSS

772/6881
FIGURE 721

GGTGTTCACTCAACTTGGATCTGTGCTGAAAAATTGTGACATTTTCAGTACATCTGGTAGAGGGTACAGCTTTTAT
CTTGACATGAATTTTTTGTATGTTCTTCCTGTGCATAAATTTTCAGAAAACACCACAGGGATGGCGAGAAGTATTT
GTTGACATTGATCCACAGGTTTCTGATAAACTGAGGTTTGTTTTGGCACCTTCTGCCACCCCAGCAGAAGCCTTC
ATACAACATGACGAAACAAGGGATCATGTTGAAGTGTGTCCTGATGCTGGTGTTATCATCGAGGAACCTTCTCAA
CGCATTGCATTAACTGGAGGTGCTGCACTGGTTGCTGATTATGGTCATGATGGAACAAAGACAGATACCTTCAGA
GGGTTTTTGGCACCACAAGCTTCATGATGTCTTAATTGCCCCAGGAACAGCAGATCTAACAGCTGATGTGGACTTC
AGTTATTTGCGAAGAATGGCACAGGGAAAAAGTAGCCTCTCTGGGCCCAATAAAACAACACACATTTTTAAAAAAT
ATGGGTATTGATGTCCGGCTGAAGGTTCTTTTAGATAAATCAAATGAGCCATCAGTGAGGCAGCAGTTACTTCAA
GGATATGATATGTTAATGAATCCAAAGAAGATGGGAGAGAGATTTAACTTTTTTGCCCTTGCTACCTCATCAGAGA
CTTCAAGGTGGAAGATATCAGAGGAATGCACGTCAGTCAAACCCTTTGCATCCGTTGTAGCTGGGTTTAGTGAA
CTTGCTTGGCAGTGAATATTTTCAGCTTGGACATTTTACCCTTCAGTCGGGCCCAAGAAATCAAAATAAAGGAAACAC
ATTTTCATATACTGCAGGTAACAAAAGTCAAAGTATTTTATCTTTTCACAGCAAGAACAGTCCATGTTGTATATAA
TACAACCAACATTATAGAACTTTTAGGGTTGTGACTGGCTTTGGTGCAAATGTGTGCTCAAGCTAATAAGTTATT
GTGAAACTGAGTTTCTTTAACTTACAAAGCTAGTTGCCATATTTCTATTTTATTTTAAAAAGTAAACATGCGGC
TGGGCGTGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGGCATATCACCTGAGGTCAGCAGT
TAAAGACCAGCCTGACCAAAATGGAGAAACCCCATCTCTACTAAAAATACAAAACCTAGCCGGGTATGGTGGTACA
TGCTGTAAATCCCAGC

773/6881
FIGURE 722

MAQGKVASLGPIKQHTFLKNMGIDVRLKVLLDKSNEPSVRQQLQGYDMLMNPKKMGERFNFFALLPHQRLQGGR
YQRNARQSKPFASVVAGFSELAWQ

774/6881
FIGURE 723

CTTCTCTCGCCAGGCATCCTCGTGGAAGTGACATCGTCTTTAAACCCTGCGTGGCAATCCCTGACGCACCGCCGT
GATGCCCAGGGAAGACAGGGCGACCTGGAAGTCCAACACTTCTTAAGATCATCCAACACTATTGGATGATTATCC
AAAATGTTTCATCGTGGGAGCAGACAATGTGGGCTCCAAGCAGATGCAGCAGATCCGCATGTCCCTTCGCGGGAA
GGTCGTGGTGCTGATGGGCAAGAACACCATGATGCGCAAGGCCATCCGAGGGCACCTGGAAAACAACCCAGCTCT
GGAGAAACTGCTGCCTCATATCTGGGGGAATGTGGGCTTTGTGTTCACCAAGGAGGACCTCACTGAGATCAGGGA
CATGTTGCTGGCCAATAAGGTGCCAGCTGCTGCCCCTGCTGGTGCCATTGCCCCATGTGAAGTCACTGTGCCAGC
CCAGAACACTGGTCTCGGGCCCCGAGAAGACCTCCTTTTTTCCAGGCTTTAGGTATCACCCTAAAATCTCCAGGGG
CACCATTGAAATCCTGAGTGATGTGCAGCTGATCAAGACTGGAGACAAAAGTGGGAGCCAGCGAAGCCACGCTGCT
GAACATGCTCAACATCTCCCCCTTCTCCTTTGGGCTGGTCAATCCAGCAGGTATTTCGACAATGGCAGCATCTACAA
CCCTGAAGTGCTTGATAAAACAGAGGAAACTCTGCATTCTCGCTTCCTGGAGGTGTCCGCAATGTTGCCAGTGT
CTGTCTGCAGACTGGCTACCCAACTGTTGCATCAGTACCCCATCTATCATCAACGGGTACAAACGAGTCCTGGC
CTTGCTGTGGAGACGGATTACACCTTCCCACTTGCTGAAAATGTCAAGGCCTTCTTGCTGATCCATCTGCCTT
TGTGGCTGCTGCCCCTGTGGCTGCTGACACCACAGCTGCTCCTGCTGCTGCTGCAGCCCCAGCTAAGGTTGAAGC
CAAGGAAGAGTCGGAGGAGTCGGACGAGGATATGGGATTTGGTCTCTTTGACTAATACCAAAAAGCAACCAACT
TAGCCAGCTTTATTTGCAAAACAAGGAAATAAAGGCTTACTTCTTT

775/6881
FIGURE 724

MPREDRATWKSNYFLKIIQLDDYPKCFIVGADNVGSKQMQQIRMSLRGKVVVL MGKNTMMRKAIRGHLENNPAL
EKLLPHIWGNVGFVFTKEDLTEIRDMLLANKVPAAARAGAIAPCEVTVPAQNTGLGPEKTSFFQALGITTKISRG
TIEILSDVQLIKTGDKVGASEATLLNMLNISPFSGGLVIQQVFDNGSIYNPEVLDKTEETLHSRFLEGVRNVASV
CLQTYPTVASVPHSIINGYKRVLALSVETDYTFPLAENVKAFLADPSAFVAAAPVAADTTAAPAAAAAPAKVEA
KEESEESDEDMGFGLFD

776/6881
FIGURE 725

GTCTTTAAACCCTGCGTGGCAATCCCTGACGCACCGCCGTGATGCCAGGGAAGACAGGGCGACCTGGAAGTCCA
ACTACTTCCTTAAGATCATCCAACCTATTGGATGATTATCCAAAATGTTTCATCGTGGGAGCAGACAATGTGGGCT
CCAAGCAGATGCAGCAGATCCGCATGTCCCTTCGCGGGAAGGTCGTGGTGCTGATGGGCAAGAACACCATGATGC
GCAAGGCCATCCGAGGGCACCTGGAAAACAACCCAGCTCTGGAGAAACTGCTGCCTCATATCTGGGGGAATGTGG
GCTTTGTGTTACCAAGGAGGACCTCACTGAGATCAGGGACATGTTGCTGGCCAATAAGGTGCCAGCTGCTGCCC
GTGCTGGTGCCATTGCCCCATGTGAAGTCACTGTGCCAGCCCAGAACACTGGTCTCGGGCCCGAGAAGACCTCCT
TTTTCCAGGCTTTAGAGTGATGTGCAGCTGATCAAGACTGGAGACAAAGTGGGAGCCAGCGAAGCCACGCTGCTG
AACATGCTCAACATCTCCCCCTTCTCCTTTGGGCTGGTCATCCAGCAGGTATTGACAATGGCAGCATCTACAAC
CCTGAAGTGCTTGATAAAACAGAGGAAACTCTGCATTCTCGCTTCCTGGAGGGTGTCCGCAATGTTGCCAGTGTC
TGTCTGCAGACTGGCTACCCAACCTGTTGCATCAGTACCC

777/6881
FIGURE 726

CTGCGTGGCAATCCCTGACGCACCGCCGTGATGCCCAGGGAAGACAGGGCGACCTGGAAGTCCAAC TACTTCCTT
AAGATCATCCAAC TATTGGATGATTATCCAAAATGTTTCATCGTGGGAGCAGACAATGTGGGCTCCAAGCAGATG
CAGCAGATCCGCATGTCCCTTCGCGGGAAGGTCGTGGTGCTGATGGGCAAGAACACCATGATGCGCAAGGCCATC
CGAGGGCACCTGGAAAAACAACCCAGCTCTGGAGAAACTGCTGCCTCATATCTGGGGGAATGTGGGCTTTGTGTTC
ACCAAGGAGGACCTCACTGAGATCAGGGACATGTTGCTGGCCAATAAGGTGCCAGCTGCTGCCC GTGCTGGTGCC
ATTGCCCCATGTGAAGTCACTGTGCCAGCCCAGAACACTGGTCTCGGGCCCGAGAAGACCTCCTTTTTTCCAGGCT
TTAGGTATCACC ACTAAAATCTCCAGGGGCACCATTGAAATCCTGACAGGTATTCGACAATGGCAGCATCTACAA
CCCTGAAGTGCTTGATAAAACAGAGGAAACTCTGCATTCTCGCTTCCTGGAGGGTGTCCGCAATGTTGCCAGTGT
CTGTCTGCAGACTGGCTACCCAACTGTTGCATCAGTACCCCATTCATCATCAACGGGTACAAACGAGTCCTGGC

778/6881
FIGURE 727

CCTCTAGCTTAGCGAGCGCTGGAGTTTGAAGAGCGGGCAGTGGCTGCACACGCCAACTTTCCCT**ATG**GCTTCGG
TGACCAGGGCCGTGTTTGGAGAGCTGCCCTCGGGAGGAGGGACAGTGGAGAAGTTCCAGCTGCAGTCAGACCTCT
TGAGAGTGGACATCATCTCTGGGGCTGCACGATCACAGCCCTAGAGGTCAAAGACAGGCAGGGGAGAGCCTCGG
ACGTGGTGCTTGGCTTCGCCGAGTTGGAAGGATACCTCCAAAAGCAGCCATACTTTGGAGCAGTTATTGGGAGGG
TGGCCAACCGAATCGCCAAAGGAACCTTCAAGGTGGATGGGAAGGAGTATCACCTGGCCATTAAACAAGGAACCCA
ACAGTCTGCATGGAGGAGTCAGAGGGTTTGATAAAGTGCTCTGGACCCCTCGGGTGCTGTCAAATGGCGTCCAGT
TCTCGCGCATCAGTCCAGATGGTGAAGAAGGCTACCCCGGAGAGTTAAAAGTCTGGGTGACATACACCCTGGATG
GCGGAGAGCTCATAGTCAACTACAGAGCACAAGCCAGTCAGGCCACACCAGTCAACCTGACCAACCATTCTTACT
TCAACCTGGCAGGCCAGGCTTCCCCAAATATAAATGACCATGAAGTCACCATAGAAGCGGATACTTATTTGCCTG
TGGATGAAACCCTGATTCTTACAGGAGAAGTTGCCCCAGTGAAGGCACTGCATTGACCTGAGAAAGCCAGTGG
AGCTTGGAAAACACCTGCAGGACTTCCATCTCAATGGTTTTTGACCACAATTTCTGTCTGAAGGGATCTAAAGAAA
AGCATTTTTTGTGCAAGGGTGCATCATGCTGCAAGCGGGCGGGTACTAGAAGTATACACCACCCAGCCCCGGGTCC
AGTTTTTACACGGGCAACTTCTTGATGGCACATTAAAGGGCAAGAATGGAGCTGTCTATCCCAAGCACTCCGGTT
TCTGCCTGGAGACTCAGAACTGGCCTGATGCAGTCAATCAGCCCCGCTTCCCTCCTGTGCTGCTGAGGCCTGGTG
AGGAGTATGACCACACCACCTGGTTCAAGTTTTCTGTGGCT**TAA**GGAAGTGTGAAGATATGATCCAGTCCAGGGC
TAGGCTCAGCCACCTGTCTCCTGTCCAGAAAAAGGTGAAGATTAAGAAGCTTTCAGAATGATTCTATGGATTAA
AATCATACAAATGGTGGCTGTTCTGAGAATCAGTCTGGGTATTGATTTCTTTTCCAGTGAAGTCCAGGCCA
TGTCTAATGACCAGCTCGATTCCCTGTGCAGTTCAGAGAGCAAGTGAACCCAACCAACAATGTCGTCTATCTAAGC
CCTGACCCTAGCCAGGGACTCCCATGCTGCTGTTGGCTCCATCTCTCCACACTGCCTCTTTCTTTTCAACTTTTT
GCCCTTCCTTTCTTTAAAGCTATTCTCACATTGCTTTTATTTCTCTCCTTCACCTCCAACCACTGTGAGCAGC
ACTCTGGAGTTTTCAAATGTCACATTAGCCTCACCTGCATGCTAGGAGATGGACCTGTCTCTATACAGCAGTAG
ATGATTGATAAGTGAGGAACTGAGGCTTACAGAGGTTGAAGACCAACAAGCTAATAAATAAAAAGTTGAGGCCG
GGCACGGTGGCTCAGCCTGTAATCCCAGCACTTTGGAAGGCCGAGGCAGGCGGATCACGAGGTGAGGAGATCGA
GACCATCCTGGCTAACACGGTGAAACCCCGTCTCTACATAAAAAATTAGCTGGGTGTGGTAGCACGCACCCGTAG
TTCCAGCTACTTGGGAGGCTGAAGCAGGAGAATCGCTTGAACCTGGGAGGTGGAGGTTGCAGTGAGCCGAGATCA
TGCCACTGCACTGGGCAACAGAGCAAACTCGATCTCAAAAAAAAAAAAAAAAAAAAAA

779/6881
FIGURE 728

MASVTRAVFGELPSGGGTVEKFQLQSDLLRVDIISWGCTITALEVKDRQGRASDVVLGFAELEGYLQKQPYFGAV
IGRVANRIAKGTFKVDGKEYHLAINKEPNSLHGGVVRGFDKVLWTPRVLSNGVQFSRISPDGEEGYPGELKVWVTY
TLDGGELIVNYRAQASQATPVNLTNHSYFNLAGQASPNINDHEVTIEADTYLPVDETLIPTGEVAPVQGTAFDLR
KPVELGKHLQDFHLNGFDHNFCLKGSKEKHFCARVHHAASGRVLEVYTTQPGVQFYTGNFLDGTLKGKNGAVYPK
HSGFCLETQNWPDVNQPRFPPVLLRPGEEDHTTWKFSVA

780/6881
FIGURE 729

GACTTCAGGAAAAATCAACCCAGCACCAGCAGCTACCAACCACCATTCCATCTCTTCACTTGAACAGCATTAGTT
AAGTCCAGATGTGGGAACCCTTCTCTTGAAGAAGTTCCTAATTGTGTCTCAGACCGGTGTAAACAAACCAGCCA
GCCGCCACCTTGCTAAACCTATAAGCTTTTTAAATCCAATATATTCTGCCAAGAATATGCCTTGATAGTTAGCC
CTCAGCCCATAGGTGTTTTTTGTTTTTAAACAGAATTATATATGTCTGGGGGTGAAAAAACCTTGCATTCCAAA
GGTCCATACTGGTTACTTGGTTTCATTGCCACCACTTAGTGGATGTTTCAGTTTAGAACCATTTTGTCTGCTCCCT
CTGGAAGCCTTGCGCAGAGCTTACTTTGTAATTGTTGGAGAATAACTGCTGAATTTTGTAGCTGTTTGTAGTTGAT
TCGCACCACTGCACCACAACCTCAATATGAAAACTATTTAACTTATTTATTATCTTGTGAAAAGTATACAATGAAA
ATTTTGTTCATACTGTATTTATCAAGTATGATGAAAAGCAATAGATATATATTCTTTTATTATGTTAAATTATGA
TTGCCATTATTAATCGGCAAAATGTGGAGTGTATGTTCTTTTACAGTAATATATGCCTTTTGTAACTTCACTTG
GTTATTTTATTGTAAATGAGTACAAAATTCTTAATTTAAGAGATTGTATGTAATATTTATTTTCAATTAATTTCTTT
CCTTGTTTACGTAAATTTTGAAAGATTGCATGATTTCTTGACAGAAATCGATCTTGATGCTGTGGAAGTAGTTTG
AGGAACATCCTATGAGTTTTCTTAGAATGTATAAAGGTTGTAGCCCATCCAACCTTCAAAGAAAAAATGACCACA
TACTTTGCAATCAGGCTGAAATGTGGCATGCTTTTCTAATTCCAACCTTTATAAACTAGCAAAAAAGTGTGCTT
ATTCCACCAGTTCTACTGTGACATACTCGAGTATAAAGACATGTAGCAATAACGGGGAGTGGGGGGGAGTCTCA
CAGTGCCTTTGGAAGGGCCCCGAACCTGCCTTAAATCTTCCTCAACCAATAAGTATTTTATTAGTGCTTGAGAGA
ATCTGAATGTAGGATGGGTTCAACTGCACAAAAGGAAAAGATTTTTTACCCTTTTTTTATATAGATATAAAGTGA
AGCAACCGCCTTAGTGCTGAAATATGTAGTACATGAATATGCCTTGTTTAAATTACAGAAAATTCCTTCCTGGACA
GCAGATGAATGAGCGGTAGCTTTAGTTTGTACGTAGGTACAGTTGGAGCACTATATGTACTCTCTGGACTACTTT
GGACAGAAGTAGGTTTTTGAATGTAACAAGATAAGTCAACTTGAGTTGTAATATATTTTGGGGAATCAGCTCACT
ACAAATTGTGACTGTAAACATTGTACTGTAAATGTTTTGTAGTT

781/6881
FIGURE 730

MWEPFSWKKFLIVSQTGVNKPASRHLAKPISFLKSNIFCQEYALIVSPQPIGVFCFLTELYMSGGEKTLAFQRSI
LVTWFHCHHLVDVQFRITLSAPSGSLAQSLCNCWRITAEFLAVLS

782/6881
FIGURE 731

CCTGATTCTAGGCTGGTCACTACTCCGAGCCTGTGACGTTTGCGGCAGCCAGGCCGTGACGATGCCCAGTGAAA
CTCTCTGGGAAATTGCAAAAGCTGAAGTGGAAAAAAGGGGAATTAATGGAAGTGAAGGTGATGGAGCTGAAATTG
CAGAAAAATTTGTTTTCTTCATTGGCAGTAAAAATGGGGGAAAGACTACTATTATTCTAAGGTGTCTTGACAGAG
ATGAACCACCAAAACCAACCTTAGCTTTGGAATATACATATGGAAGAAGAGCAAAAGGGCACAACACACCAAAAG
ATATCGCTCACTTTTGGGAACTCGGTGGAGGAACCTCTTTATTGGACTTAATCAGCATACCCATCACAGGTGACA
CCTTACGGACGTTTTCTCTTGTTCTCGTTCTGGATCTTTCAAAACCTAATGATCTCTGGCCCACCATGGAAAATC
TCTTGCAAGCCACAAAAAGCCATGTAGACAAAGTGATAATGAACTGGGAAAGACAAATGCTAAAGCAGTTTCTG
AAATGAGACAGAAGATCTGGAATAATATGCCGAAGGATCATCCTGATCATGAATTAATTGACCCATTTCCGGTAC
CTCTGGTCATAATTGGAAGTAAATATGATGTTTTTCAGGATTTTGAGTCTGAGAAGAGAAAGGTAATATGCAAGA
CACTTCGATTTGTTGCACATTATTATGGAGCATCATTAAATGTTTACCAGTAAATCAGAAGCTCTATTACTAAAAA
TACGTGGAGTTATCAACCAGTTGGCATTTGGCATTGACAAAAGCAAATCAATATGTGTGGATCAGAATAAACCGC
TGTTTATCACAGCAGGATTGGATTCTTTCCGGTCAAATAGGATCTCCTCCTGTTCTGAAAAATGACATTGGAAAGC
TTCATGCCCACTCACCTATGGAGTTGTGAAAAAAGTGTATGAAAAGCTCTTTCCACCAAAGAGTATTAACACGC
TGAAAGATATCAAGGACCCTGCGAGAGATCCTCAGTATGCTGAAAATGAAGTCGATGAGATGAGAATTCAGAAGG
ATCTGGAACCTGGAACAGTACAAAAGAAGTTCTTCCAAGTCTTGAAACAAATCGAGCTTGATTCTTTGAACCTATT
TCAATTATTGTATATTTATTTCTTCTTTTCCAAATACAAATAAGATTATACTGTGAATTAATTATTGTGGCAATA
TGTGAAGAAAGTTAAACTGTATAATTTGTTAAAGGACAAGCTGGATTTCTTGGAAGTAGTGCATCTCCCTGTATAT
CTTGAAGCTTTTTTAAAAGGAAAAATTATTGTAGAACCACGTGTAATTTTTTTTTTAAATAAAAGAATCTTCTACTA
CCTACCTCT

783/6881
FIGURE 732

MPSETLWEIAKAEVEKRGINGSEGDGAEIAEKFVFFIGSKNGGKTTIILRCLDRDEPPKPTLALEYTYGRRAKGH
NTPKDIAHFWELGGGTSLLDLISIPITGDTLRTFSLVLVLDLSKPNDLWPTMENLLQATKSHVDKVIMKLGKTNA
KAVSEMRQKIWNMFKDHPDHELIDPFVPLVIIGSKYDVFDQFESEKRRKVICKTLRFVAHYYGASLMFTSKSEA
LLLKIRGVINQLAFGIDKSKSICVDQNKPLFITAGLDSFGQIGSPFPENDIGKLHAHSPMELWKKVYEKLFPPK
SINTLKDIKDPARDPQYAENEVDEMRIQKDLELEQYKRSSSKSWKQIELDS

784/6881
FIGURE 733A

ACATGCTCCTCCTGTCTTCTGGCGGAGCGTGCTTCCCGCTGCGGGGACGTTTCGAGCAATGGCAGCCCTGCTGAG
ATCCGCGCGTTGGTTGCTGCGTGCCGGGGCGGCCCCGCGCCTCCCGCTCTCCCTGCGCCTCCTCCCTGGCGGGCC
GGGCGGCTGCGATGCCGCTCCTATCTGCCCCGCGCTCGCGCCGGGCGCGTGGCCGGAGGACTACTGAGCCCAGC
CAGGCTGTATGCCATTGCTGCCAAAGAAAAAGATATTCAAGAGGAGTCCACTTTTTCTTCTAGGAAGATTTCCAA
TCAGTTTGATTGGGCTCTAATGAGACTAGATCTTTCTGTTTGAAGAACTGGCCGCATTCCAAAGAAGCTTCTACA
AAAAGTTTTTAATGATACCTGCCGCTCAGGTGGCCTAGGTGGTAGTCATGCCTTGCTTCTACTACGTAGTTGTGG
TTCTCTCTTGCCCTGAACTAAAGCTTGAAGAGAGAACAGAATTTGCTCATAGGATATGGGACACACTTCAGAAATT
AGGTGCTGTGTATGATGTGAGTCACTATAATGCTTTACTTAAAGTCTATCTTCAAAATGAATATAAATTCTCACC
AACTGATTTTCTGGCAAAAATGGAGGAAGCAAACATTCAACCAAATCGAGTGACATACCAGAGATTGATTGCTTC
TTATTGTAATGTAGGAGATATTGAAGGTGCCAGCAAGATTCTTGGATTATGAAAATAAGGATCTCCAGTTAC
AGAGGCAGTATTGAGTGCCCTTGTGACAGGGCATGCCAGAGCTGGTGATATGGAGAATGCAGAAAACATTCTCAC
AGTGATGAGAGATGCCGGAATTGAGCCTGGTCCAGACACATACCTCGCATATTGTAATGCATATGCTGAGAAGGG
CGACATTGACCATGTTAAGCAGACTCTGGAGAAGGTGGAGAAGTCCGAGCTTCACCTTATGGACCGTGATTTACT
GCAAATTATTTTTAGCTTCAGTAAAGCTGGGTATCCTCAGTATGTCTCAGAAATTTTGGAAAAAGTTACATGTGA
AAGAAGATATATTCCAGATGCAATGAACCTCATTTTACTTTTACTGACTGAAAAATTGGAAGATGTAGCGTTGCA
AATTTTACTAGCATGCCCCGTATCAAAGGAAGATGGCCCAAGTGTCTTGGCAGTTTCTTTTTACAACACTGTGT
GACTATGAATACGCCTGTGGAGAAGCTAACAGACTACTGTAAGAAGTTAAAGGAAGTCCAGATGCACTCCTTTCC
TCTGCAGTTACCCCTCCATTGTGCTTTACTCGCCAATAAAACTGATTTGGCAAAAGCCTTAATGAAGGCTGTGAA
GGAGGAAGGTTTTCTATCAGACCTCACTATTTCTGGCCATTGCTAGTTGGACGTCGGAAGGAAAAAATGTTCA
AGGTATAATTGAAATCCTCAAAGGAATGCAAGAATTGGGAGTACATCCTGATCAGGAAACATATACAGATTATGT
GATTCCATGCTTTGATAGTGTAACCTCAGCACGAGCCATTTTGAGGAAAATGGATGTCTGTCTGATAGTGATAT
GTTTTCTCAAGCTGGATTGAGAAGTGAAGCAGCAAATGGGAACCTAGACTTTGTATTATCATTTTTTGAAATCAAA
TACATTGCCCATCTCGCTGCAGTCTATAAGAAGTAGCCTACTGCTAGGCTTCAGGAGGTCTATGAATATAAATCT
TTGGAGCGAGATAACAGAATTGTTGTACAAGGATGGACGTTATTGCCAGGAGCCTCGAGGACCGACGGAAGCTGT
TGGCTATTTTTCTTTATAACTTGATTGACAGCATGAGTGACTCAGAGGTACAGGCCAAGGAGGAGCATTGAGACA
ATACTTCCATCAGCTGGAGAAGATGAATGTAAAAATTCCTGAAAATATCTACAGAGGCATTGCTAATCTCCTGGA
AAGCTACCATGTTTCTGAATTGATTAAAGGATGCTCACTTGTTGGTTGAGAGTAAGAATTTAGACTTTCAAAAAAC
TGTGCAACTTACATCATCTGAATTGGAGTCCACACTTGAAACACTAAAAAGCTGAAAATCAACCTATAAGAGATGT
CCTAAAGCAACTCATATTAGTGCTTTGTTTCAAGAGAATATGCAAAAAAGCCCTTGAATTGAAAGCAAAATATGA
ATCCGACATGGTTACTGGTGGCTATGCAGCTTTAATAAATTTATGCTGTGACATGATAAAGTAGAAGATGCCTT
GAACTTGAAAGAAGAATTTGACCGCTTAGATTTCATCTGCTGTCTTGGACACCGGCAAGTATGTAGGCCTTGTAAG
AGTATTGGCAAAGCATGGCAAAGCTCCAAGATGCTATTAAACATTCTGAAGGAGATGAAAGAGAAGGATGTTCTTAT
CAAAGATACAACAGCCTTGCTCTTTTTCCACATGCTAAATGGCGCAGCTTTAAGAGGTGAAATTGAAACAGTAAA
ACAGTTGCATGAAGCCATCGTGACTCTAGGGTTAGCAGAACCATCCACCAACATAAGTTTTCCATTGGTCACTGT
ACACTTGGAAGAGGGCGACCTATCTACTGCTCTTGAGGTGCGCATTGACTGCTATGAAAAGTATAAAGTATTACC
AAGGATTCATGATGTCTTGTGTAACTGGTAGAGAAAGGCGAGACTGATCTAATTCAGAAAGCAATGGACTTTGT
GAGCCAAGAACAAGGTGAAATGGTGATGCTCTATGATCTCTTCTTTGCCTTCCTACAAACAGGAAATTACAAAGA
GGCCAAGAAGATCATTGAGACTCCAGGGATTAGAGCTCGATCTGCAAGGCTTCAGTGTTTGTGACAGATGTGT
TGCAAATAATCAGGTTGAAACTCTGGAAAAATTAGTGAGCTGACACAGAAGCTATTTGAATGTGATAGAGACCA
GATGTACTACAATCTGCTAAACTGTATAAAATAAACGGTGACTGGCAAAGAGCTGATGCAGTCTGGAATAAAAT
CCAAGAAGAAAATGTTATTCTCGTGAAAAGACATTAAGATTATTAGCAGAAATCCTTAGAGAGGGTAACCAGGA
AGTTCCGTTTGACGTACCTGAGTTGTGGTATGAAGATGAAAAACATTCCCTGAATTCTTCGTACGCCTCAACCAC
AGAACCTGATTTCCAGAAAGATATATTGATTGCCTGCCGATTGAACCAAAAAAAGGGGCATATGATATTTTCT
GAATGCAAAAGAGCAAAACATTGTGTTTTAATGCTGAAACCTACAGCAATCTCATTAAATTACTGATGTGAGAAGA
TTATTTTACACAAGCAATGGAAGTGAAAGCATTGCGGAGACCCACATCAAGGGCTTCACACTGAACGATGCTGC
CAACAGCCGCTCATCATAACGCAAGTTAGGCGGGATTATTTGAAAGAGGCTGTGACAACACTGAAAAACAGTATT
GGATCAGCAGCAGACCCCTTCTAGGTTAGCAGTGACCCGTGTATCCAGGCATTGGCCATGAAGGGTGATGTTGA
AAACATAGAAGTAGTTTCAAGAAGATGTTAAATGGACTCGAAGACTCCATTGGACTTTCAAAAATGGTTTTTCATCAA

785/6881
FIGURE 733B

TAACATTGCTTTGGCTCAAATAAAGAATAATAACATAGATGCCGCAATAGAAAACATTGAAAATATGCTTACTTC
AGAGAATAAAGTCATTGAACCCCAATACTTCGGCTTGGCATACTTATTCAGAAAAGTAATAGAGGAGCAGTTGGA
ACCAGCAGTTGAAAAGAGTAACATCATGGCGGAGAGATTGGCCAATCAGTTTGCAATTTATAAACCTGTCACTGA
TTTTTTCCTTCAACTTGTGGATGCAGGCAAGGTGGATGATGCCAGAGCTCTCCTACAGAGATGTGGTGCAATTGC
TGAACAAACCCCGATTTTGTGTTGTTTCCTCCTTAGGAATTCTAGGAAACAAGGAAAGGCATCAACTGTGAAATC
TGTGTTAGAATTGATTCTGAATTAAATGAAAAGGAAGAAGCATACAATTCCCTCATGAAAAGCTATGTCTCAGA
GAAAGATGTCACATCTGCTAAAGCACTGTATGAACATTTGACTGCAAAGAATACAAAATTGGATGATCTGTTTCT
AAAGCGTTACGCATCTTTGCTGAAGTATGCTGGAGAGCCTGTCCCTTTCATTGAACCCCTGAAAGCTTTGAATT
TTATGCACAGCAGCTAAGAAAATTGAGGGAAAACCTCTTCTTGAAATAACCAGGCGATACTTTGTTTTGTATATAT
TTGTGATTCTGTGTCTACATGTTATTTTGAAGTATATCTGAGGGAAAAATAAATGAAAATTTTCTTTATGTACTT
ATGTATGTGTGATGCATGTTCAAAGTCTTATTGACCATAACTCTGTGCACTTGGTTATTGGACATTTTTTGGAGTT
TTTTTCTCTGGGAAAAATCGATAGTGTTTTCTTCAATGCTGCTGCTGTGTGAAGCCATACTTTTTTCAAGATTCTT
CCCCTAATTGGCTCTTTGGTTTCCCTGCTCTGTTTCATTTATTTTCAATTAATAATGTTATTCCTTTATTTAAGATTCT
ACTTATTAGTCTGCTGTTTCTCTGAAAAATTTTAGAGCTAGGTATAGTGACCGTGAACCTTTCTAACGCATAATAT
TCTGTGATACAGCCATTCCGTACATGTGTGAAGTCCTGCATAACTTTCGAACCTTGTAAATGTTGGCACTAGGA
GTCATCAGATCTAGGCTTCATCATTTTCCAGTGAGAAGCAGAGACCCAAAGGGCCTGTTACTTGTGCTTGGTCAG
GGGACTGTCTGTGATGCCTGGAGGCTCTTCGGCACACTTCCCCATCTTCCCTTCTGCCACTGTGGCTTCAAGCA
CCTCTGTTCATAGAGCGTCTCTGAAATTGAGTCTCGGTGATGACTTATCCCGAAGTAGAGCAATGTGTTTCTCT
CATTGTAGTTTCAAGACTTTGTCAGTACAAGCTCTGCCCTAGGCTTGTTACTTTATACTCATATCTTGAAAAGAT
GTGATTTTATCTATGAAGGGGTAAAATATTGGTTTGTATTTAATTGTTTGAATAAAAGTGATCCCTATATTG

786/6881
FIGURE 734

ATGGGCTCAGGCTACACCAAGGCCGTGTACCGGGTCCGCCTGCCCGGCCGGTGCCGCGGTGGCGCTCAAGGCGGTG
GACTTTAGCGGCCACGATCTGGGCAGCTGCGTGCGGAGTTCGGGGTACGGAGGGGCTGCTATCGGCTGGCGGCC
CACAAGCTGCTTAAGGAGATGGTGCTGCTGGAGCGGCTGCGGCACCCCAACGTGCTGCAGCTCTATGGCTACTGC
TACCAGGACAGCGAGGACATCCAGACACCCTGACCACCATCACGGAGCTGGGCGCCCCTGTAGAAATGATCCAG
CTGCTGCAAACTTCCTGGGAGGATCGATTCCGAATCTGCCTGAGCCTGGGCGCCTCCTCCACCACCTGGCCAC
TCCCCACTGGGCTCCGTCACTCTGCTGGACTTCCGCCCTCGGCAGTTTGTGCTGGTGGATGGGGAGCTCAAAGTG
ACGGACCTGGATGACGCACGTGTGGAGGAGACGCCGTGTGCAGGCAGCACCGACTGCATACTCGAGTTTCCGGCC
AGGAACTTCACCCTGCCCTGCTCAGCCCAGGGCTGGTGCGAGGGCATGAACGAGAAGCGGAACCTCTATAATGCC
TACAGGTTTTTCTTCACATACCTCCTGCCTCACAGTGCCCCGCCTTCACTGCGTCCTCTGCTGGACAGCATCGTC
AACGCCACAGGAGAGCTCGCCTGGGGGGTGGACGAGACCCTGGCCCAGCTGGAGAAGGTGCTGCACCTGTACCGG
AGCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTACCGAGTACCAAGTGTATCCCAGACAGCACCATCCCC
CAGGAAGACTACCGCTGCTGGCCATCCTACCACCACGGGAGCTGCCTCCTTTTCAGTGTTCAACCTGGCTGAGGCT
GTGGATGTCTGTGAGAGCCATGCCCAGTGTCGGGGCCTTTGTGGTCACCAACCAGACCACCTGGACAGGTCGGCAG
CTGGTCTTTTTCAAGACTGGATGGAGCCAAGTGGTCCCTGATCCCAACAAGACCACATATGTGAAGGCCTCTGGC
TGA

787/6881
FIGURE 735

MSGYTKAVYRVRLPGGAVALKAVDFSGHDLGSCVREFGVRRGCYRLAAHKLLKEMVLLERLRHPNVLQLYGYC
YQDSEDIPDTLTTITELGAPVEMIQLLQTSWEDRFRICLSLGRLLHHLAHSP LGSVTLDDFRPRQFVLVDGELKV
TDLDDARVEETPCAGSTDCILEFPARNFTLPCSAQGWCEGMNEKRNLNAYRFFFTYLLPHSAPPSLRPLLDIV
NATGELAWGVDETLAQLEKVLHLYRSGQYLQNSTASSSTEYQCIPDSTIPQEDYRCWPSYHHGSCLLSVFNLAEA
VDVCESHAQCRAFVVTNQTWTGRQLVFFKTGWSQVVPDPNKTTYVKASG

788/6881
FIGURE 736

GCTAACATCCCAGACAGACAGATGTGACCAGGACAAACGTGCAATAATGCCAAATGTTAAAATGTGAGTTTACCA
GCCTAGCTATGGGACTGCTGGCTCCTAGTCCAGGAATCATGGGGGTATGACTGCCTCTCCAACCCTGTGGGCTGT
AAGCAAGCTCAGGCTAGTCTCCCCACTGGGGGCTGTGCCCTCCCTGGGACGGTTCGGTGGGCAGCCCCATCACT
GTGTTCAATAGTGTGAGAATGTAGCTGCGTGGGGACAATCCATCGTGGAGTGTTCTCTCAGCTTAGGTCTGGACA
GGAGACTTGGCGGGAGATGCTCCAGGATGTGGGTGATTCTGTACCTGGGGAGGCTATCTCTGACCTCCCGACAGG
GGACACTCCCAGGCCAGCCCAGGGGTCAGGGGCAGAGGTGCACACCTCAGCATGAGCCAAGACTGGGGTCAGGGA
GCAGGTGTGGTTTGAGCCAGGACCTGGGGCGGGGGTGGGGCCGGGGCCTTTCTGCCTCATTGCTTTCAATGAAA
GCCTCAAAGCAGCCAAAACCAGGCTTTCCCCCTTCCTCGAGTTTGAATATCCAGAATCTTTGTACTTCTTGTTG
GTTAAATTGTTTATTTTGTAAAAATAAAATAAAATTAGTTAATAA

789/6881
FIGURE 737

MWVILYLGRLSLTSRQGTLPGQPRGQGQRCTPQHEPRLGSGSRCGLSQDLGRGWGRGLSASFANESLKAAKTRL
SPFLEFEYPESFVLLVG

790/6881
FIGURE 738A

AGATGACTTTGGGAAATTGCTGCTGGCTGAGGCCCTCCTGGAGCAGTGTTTGAAGGAGAACCATGCCAAAAATAAA
AGACTCCATGCCTTTGCTGGAGAAGAATGAGCCGAAGATGAGCGAAGCCAAAAATTATCTAAGCAGTATCCTTAA
CCATGGGAGGCTCTCGCCACAGTACATGTGTGAGGCCATGCTGATCCTGGGCAAACCTGCATTACGTGGAGGGCTC
ATACCGAGATGCCATCAGCATGTACGCACGGGCGGGATTGATGACATGTCCATGGAGAACAAGCCCCCTGTATCA
GATGCGGCTGCTGTCGGAGGCTTTTGTATCAAAGGCCTCTCTCTGGAACGCCTACCCAACCTCCATCGCCTCCCG
CTTCCGCCTGACAGAGAGGGAGGAGGAAGTGATCACCTGTTTTGAGAGGGCCTCCTGGATCGCTCAGGTGTTCT
GCAGGAATTGGAGAAGACCACAAATAACAGCACGTCGAGGCATCTGAAAGGCTGTCACCCGCTTGACTATGAGCT
CACCTACTTCTGGAAGCTGCCCTCCAGAGCGCCTATGTGAAAAACCTGAAGAAGGGGAACATCGTGAAGGGCAT
GAGAGAGCTCCGGGAGGTGCTGCGGACTGTGGAGACCAAAGCAACTCAGAACTTCAAAGTGATGGCGGCCAAGCA
CCTGGCGGGGGTCTGCTGCACTCCCTGAGTGAGGAGTGCTACTGGAGCCCCCTGTCCCACCCTCTGCCTGAGTT
CATGGGCAAGGAGGAGAGTTCTTTCGCCACTCAGGCCCTGCGGAAACCTCACCTCTATGAAGGAGACAACCTCTA
CTGCCCCAAGGACAACATCGAGGAAGCCCTCCTGCTCCTCCTCATCAGCGAATCCATGGCAACTCGAGATGTGGT
GCTGAGCCGGGTGCCGAGCAGGAGGAGGACCGGACAGTGAGCTTGCAGAAATGCCGAGCCATCTATGACCTCCT
GAGCATCACGTTGGGCAGAAAGGGGACAGTACGTATGCTCTCGGAGTGCTTGGAGCGAGCCATGAAGTTTGCCTT
TGGAGAATTTACCTTTGGTACCAGGTGGCCCTCTCCATGGTGGCTTGTGGGAAGTCAGCCTACGCTGTGTCCCT
GCTGCGGGAGTGCTGTGAAGTTGCGGCCCTCGGACCCACCGTGCCCTGATGGCCGCGAAGGTCTGCATCGGGTC
CCTTTCGCTGGCTAGAGGAAGCAGAGCACTTTGCCATGATGGTGATCAGCCTCGGAGAGGAAGCCGGGGAGTTCT
CCCCAAGGGCTACCTGGCTCTGGGTCTCACCTATAGCCTGCAGGCCACCGACGCCACCCTGAAGTCCAAGCAAGA
TGAATTGCACCCGAAGGCACTGCAGACGCTGGAGAGGGCTCAGCAGCTGGCGCCCAGTGACCCCCAGGTATCCT
CTATGTCTCGCTGCAGCTGGCCCTCGTCCGACAGATCTCCAGTGCCATGGAGCAGCTGCAGGAGGCCCTGAAGGT
ACGCAAGGATGATGCCACGCCCTCCACCTGCTGGCACTGCTCTTCTCTGCCCAGAAGCACCACCAGCATGCCCT
GGATGTTGTCAACATGGCCATCACCGAGCACCTTGAGAACTTCAACCTGATGTTTACCAAGGTGAAGCTGGAGCA
GGTGCTGAAAGGCCCAGAGGAAGCCCTCGTGACCTGCAGACAAGTGCTGAGGCTGTGGCAGACCCTGTACAGCTT
CTCCCAGCTGGGAGGCCTAGAAAAGGATGGCAGCTTCGGTGAGGGCCTCACCATGAAGAAGCAGAGTGGCATGCA
CCTGACTTTGCCTGATGCCATGATGCAGACTCTGGCTCCCGCGGGCTTCGTCCATCGCCGCCTCCCGGCTGGA
GGAGGCCATGTCAGAGCTGACTATGCCCTCTTCGGTCTGAAGCAGGGCCCCATGCAGCTGTGGACCACGCTGGA
ACAGATCTGGCTGCAGGCTGCTGAGCTGTTTATGGAGCAGCAGCACCTCAAGGAAGCAGGTTTCTGCATCCAGGA
GGCGGCGGGCTCTTCCCCACTTCTACTCAGTACTCTATATGCGGGCGGCTGGCTGAGGTGAAGGGCAACCT
GGAGGAGGCCAAGCAGCTGTACAAGGAGGCGCTCACGGTGAACCCAGATGGCGTGCGCATCATGCATAGCCTGGG
TCTGATGCTGAGTCGGCTGGGCCACAAGAGCTTGCCCCAGAAGGTGCTTCGTGATGCCGTGGAGAGGCAGAGTAC
GTGCCACGAGGCGTGGCAGGGCCTGGGCGAGGTGCTGCAGGCCCAGGGCCAGAACGAGGCTGCCGTTGACTGCTT
CCTCACCGCCCTTGAGCTGGAGGCCAGCAGCCCTGTACTGCCCTTCTCCATCATCCCCAGAGAGCTCTGACGACG
CTGCAGCCGCAGGGAGGGAGGGGCTGGCCAGAGGGAGAGGCAGCAGGGAACGTGGGTGAGGGTGGGGCAACAGTG
GCATCAGGTGCGGGGCCTCAGGGAAATACATCTTTAGTGAAACGCCTCTGCAGCTGCAGCCCTCGTTCTCTTGGCT
GGGCCAAGAGGGCCTTCTGGATTCTTTGTTGGTGCTTGGGAAACAGTCTGACTTGAACCCCTAAGTGCCTTTG
GAGAGTTTTGTGGTGACCAGACTTGCTCCCCAAGAGCTGGGCAGCGGGGAGCCTCACAGCTGTCTTACCCTCA
CCCATGCCTCTGGCTTGGAGTCTGGGTGGGGGTTCTCACTCCCCACTCTCAGCACAGTACAGACTTCTGGATCT
CTCTCAGGTCTTGCCAGGGCGGTACAAATGTGAAGAACTGCGGGCAAGTGGGAAGACTATGAGATTTCTGGGT
TCCCTTCTCAGACTTGGAGTTAGTAGATGATTCCTGCATTGCCCTGCTTGCCCTCTGAGACCAGCTGGGCCCCA
CCTTGCTCTTTCCCCCTGCTACCAAGTGCTTTGGGGTCTGACCAGGGGTACTGAGCACCGGCCCTAACACTTCC
ATCTCCACCCACCCCATCTCCCTGGCGATGTGCTCCAGCCCAAGCAGCCTCCGTAGGCTTTAGATCCTGTGGTTG
CTAGATCCAGTCTTTCTAATACCCTGAGTCAACACATTACTCCTGCAGGTCTTAGGCTACAATGCAGGTCCCTT
GAGGGCCACCAACATGGAGGTAGGCAGTTTCTAGGACTGTCCCCAGTACATCTCACCACCCACAGCCCTTTTTTT
GCCTTGATTGAGCCTCACCTGGCCTTTTGGCTTCCCTGCCTGAGAGAGACCTGAGGAGGGGACAGAGCCAG
CCCCTCTCCTGTGGCTGAGCAGGCCTCTGTGTCCATGACACCTGTCTTCCGGGCCTGGGGGCTGTGGGTGTATGT
CCTCCCTACTGGCTTCCCCGGCCCCCTGCTGCATGATGCTCTTGGAACCTCTTCTCAAGGAGTCAGTCCCCCAGGC
CTATCAGGGGATCCTTTTGTATCTGCACTTTGGGTTTTAGTTTCAAAGCTCCATCAGGTACAGCTTGCAATTCAG
GATGTGTGGAAGCTCGGGTGAGGGCTGCCCTGGTTCATCATAGCTCCACCTTCTCGGAAGGAGTGGGCTGTTG

791/6881
FIGURE 738B

GAGACCCCCCATCCATGGCACACTAGCTCAGCACTGCATTTCCCGAGATGATTCCCAAGACAGCTGGTGCCTCCT
GGCTTTCCTGTGCCAGGCCAAGGGGCACCACAGAGGACCCTGGATCCTTTGCCTCTTCTTGGTTGAAGGATCTCT
ATGTATGTGTGTATATAAATATAGTTTTTATCTATATATATAAATAGAGATCTATTTTTTTCTGGAATTCTG
TTAGAAAAGTAAAGAAAAAGCAAATGCTGTTGGTTTATCTCAGGGTGCCCAAAGTGTTATAGTCAATTTTTGGT
ACTAGGAAAGGCACCCAATGCATTTCCCTGACTTTTAAGCATTTCCCTTGTTGGAAGCAGCAGAGGGCCAGGCCAAG
TTGCTGACAGTGACTTTGCAGGTTGAATAAAGAAACCCTTGGAGGGGAAGCAGGCTTGCTCTGAAGCAGCATGTAT
ATTCAGTGGGCATGTAGCTCCACACCAGCCTTGAGCCAGGCCCTGGACAGGAGGGGCTGTTGCAGGATGAGGGA
GGCCAGAGAAGGCATCGAAGCCAAGACCTGGGCCCACCTGGGGAGGGATGTGGGAAAGGAAGGATGGGAGGGAGG
ACCTCTGGGAAAATGTGGATTTGAGCTGGTGAGAGTGTTGCTAAGGCTGGGCTAAAGCCTGGAGAGGGTAGGAG
GAGGCAAGAGGGGTCCAGGCAGGGCTGATCCTGGCCTCTGACCTGTCCAGGGCGACCCCTGAAGCCCCTGCTGCC
TCTGGGCATTGCTGGGAGAGGCCAAGGCAGGACTCACGTCTGAACAGAGATCCCCCTCGGGCATTGCTGATGGGCC
ACCTTCAGCTGCAGGGAAGAAGCCTAGGAGAGGAGGCATGGGAGGGACCTGGGCCTTGTTTCAGATTGGCCACCTC
TGCTGAGAAGTCCATACCAGTACACCCCTAATAAGTTATGCCACATACCAACGTACTGTGGATATTATAACCTGC
ATTAAAACAACCTCTAAAGAACGCTGCTCATT

792/6881
FIGURE 739

MAAKGAHGSYKVESELERCRAEGHWDRMPELVRQLQTLSPGGGGNRRGSPSAAFTFPDITDDFGKLLLAEEALLE
QCLKENHAKIKDSMPLEKNEPKMSEAKNYLSSILNHGRLSPQYMCEAMLILGKLHYVEGSYRDAISMYARAGID
DMSMENKPLYQMRLLEAFVIKGLSLERLPNSIASRFRITEREEEVITCFERASWIAQVFLQEELEKTNNSTSRH
LKGCHPLDYELTYFLEAALQSAYVKNLKKGNIVKGMRELREVLRTVETKATQNFKVMAAKHLAGVLLHSLSEECY
WSPLSHPLPEFMGKEESSFATQALRKPHLYEGDNLYCPKDNIEEALLLLISESMATRDRVLSRVPEQEEDRTVS
LQNAAAIYDLLSITLGRRGQYVMLSECLERAMKFAFGFHLWYQVALSMVACGKSAYAVSLLRECVKLRPDPTV
PLMAAKVCIGSLRWLEEAHFAMMVISLGEEAGEFLPKGYLALGLTYSLOATDATLKSQDELHRKALQTLERAQ
QLAPSDPQVILYVSLQALVRQISSAMEQLQEALKVRKDDAHALHLLALLFSAQKHHQHALDVVNMAITEHPENF
NLMFTKVKLEQVLKGPEEALVTCRQVLRWLWQTLYSFSQLGGLKDGSGFGEGLTMKKQSGMHLTLPAHDADSGSR
RASSIAASRLLEEAMSELTMPSSVLKQGPMQLWTTLEQIWLQAAELFMEQQHLKEAGFCIQEAAGLFPTSHSVLYM
RGRLAEVKGNLEEAKQLYKEALTVNPDGVRIMHSLGLMLSLRLGHKSLAQKVLRDAVERQSTCHEAWQGLGEVLQA
QGQNEAAVDCFLTALALEASSPVLFPFSIIPREL

793/6881
FIGURE 740

AGTCCGAGTGGAGAGAGCGAGCTGAGTGGTTGTGTGGTCGCGTCTCGGAAACCGGTAGCGCTTGCAGCATGGCTG
ACCAACTGACTGAAGAGCAGATTGCAGAATTCAAAGAAGCTTTTTCCTACTATTTGACAAAGATGGTGATGGAACCTA
TAACAACAAAGGAATTGGGAAGTGAATGAGATCTCTTGGGCAGAATCCACAGAAGCAGAGTTACAGGACATGA
TTAATGAAGTAGATGCTGATGGTAATGGCACAATTGACTTCCCTGAATTTCTGACAATGATGGCAAGAAAAATGA
AAGACACAGACAGTGAAGAAGAAATTAGAGAAGCATTCCGTGTGTTTGATAAGGATGGCAATGGCTATATTAGTG
CTGCAGAACTTCGCCATGTGATGACAAACCTTGGAGAGAAGTTAACAGATGAAGAAGTTGATGAAATGATCAGGG
AAGCAGATATTGATGGTGATGGTCAAGTAACTATGAAGAGTTTGTACAAATGATGACAGCAAAGTGAAGACCTT
GTACAGAATGTGTTAAATTTCTTGTACAAAATTGTTTATTTGCCCTTTTCTTTGTTTGTAACCTATCTGTAAAAGG
TTTCTCCCTACTGTCAAAAAAATATGCATGTATAGTAATTAGGACTTCATTCCCTCCATGTTTTCTTCCCTTATCT
TACTGTCATTGTCCTAAAACCTTATTTTAGAAAATTGATCAAGTAACATGTTGCATGTGGCTTACTCTGGATATA
TCTAAGCCCTTCTGCACATCTAACTTAGATGGAGTTGGTCAAATGAGGGAACATCTGGGTTATGCCTTTTTTAA
AGTAGTTTTCTTTAGGAAGTGTGAGCATGTTGTTGTTGAAGTGTGGAGTTGTAACCTCTGCGTGGACTATGGACAG
TCAACAATATGTACTTAAAAGTTGCACTATTGCAAAACGGGTGTATTATCCAGGTACTCGTACACTATTTTTTTG
TACTGCTGGTCCTGTACCAGAAACATTTTCTTTTATTGTTACTTGCTTTTTTAACTTTGTTTAGCCACTTAAAT
CTGCTTATGGCACAATTTGCCTCAAAATCCATTCCAAGTTGTATATTTGTTTTCCAATAAAAAAATTACAATTT

794/6881
FIGURE 741

GGCGGGAAACAGCTTAGTGGGTGTGGGGTCGCGCATTTTCTTCAACCAGGAGGTGAGGAGGTTTCGACATGGCGG
TGCAGCCGAAGGAGACGCTGCAGTTGGAGAGCGCGGCCGAGGTCGGCTTCGTGCGCTTCTTTCAGGGCATGCCGG
AGAAGCCGACCACCACAGTGCGCCCTTTTCGACCGGGGCGACTTCTATACGGCGCACGGCGAGGACGCGCTGCTGG
CCGCCCCGGGAGGTGTTCAAGACCCAGGGGGTGATCAAGTACATGGGGCCGGCAGGAGCAAAGAATCTGCAGAGTG
TTGTGCTTAGTAAAATGAATTTTGAATCTTTTGTAAAAGATCTTCTTCTGGTTCGTCAGTATAGAGTTGAAGTTT
ATAAGAATAGAGCTGGAAATAAGGCATCCAAGGAGAATGATTGGTATTTGGCATATAAGGCTTCTCCTGGCAATC
TCTCTCAGTTTGAAGACATTCTCTTTGGTAACAATGATATGTCAGCTTCCATTGGTGTGTGGGTGTTAAAATGT
CCGCAGTTGATGGCCAGAGACAGGTTGGAGTTGGGTATGTGGATTCCATACAGAGGAAACTAGGACTGTGTGAAT
TCCCTGATAATGATCAGTTCTCCAATCTTGAGGCTCTCCTCATCCAGATTGGACCAAAGGAATGTGTTTTACCCG
GAGGAGAGACTGCTGGAGACATGGGGAAACTGAGACAGATAATTCAAAGAGGAGGAATTCTGATCACAGAAAGAA
AAAAAGCTGACTTTTCCACAAAAGACATTTATCAGGACCTCAACCGGTTGTTGAAAGGCAAAAAGGGAGAGCAGA
TGAATAGTGCTGTATTGCCAGAAATGGAGAATCAGGTTGCAGTTTCATCACTGTCTGCGGTAATCAAGTTTTTAG
AACTCTTATCAGATGATTCCAACCTTTGGACAGTTTGAAGTACTACTTTTGAAGTTCAGCCAGTATATGAAATTGG
ATATTGCAGCAGTCAGAGCCCTTAACCTTTTTTCAGGGTCTGTTGAAGATAACCACTGGCTCTCAGTCTCTGGCTG
CCTTGCTGAATAAGTGTAACCCCTCAAGGACAAAGACTTGTTAACCAGTGGATTAAGCAGCCTCTCATGGATA
AGAACAGAATAGAGGAGAGATTGAATTTAGTGGAAGCTTTTGTAGAAGATGCAGAATTGAGGCAGACTTTACAAG
AAGATTTACTTCGTCGATTCCCAGATCTTAACCGACTTGCCAAGAAGTTTCAAAGACAAGCAGCAAACCTTACAAG
ATTGTTACCGACTCTATCAGGGTATAAATCAACTACCTAATGTTATACAGGCTCTGGAAAAACATGAAGGAAAAC
ACCAGAAATTATTGTTGGCAGTTTTTGTGACTCCTCTTACTGATCTTCGTTCTGACTTCTCCAAGTTTCAGGAAA
TGATAGAAACAACCTTTAGATATGGATCAGGTGGAAAACCATGAATTCCTTGTAACCTTCATTTGATCCTAATC
TCAGTGAATTAAGAGAAATAATGAATGACTTGGAAGAAGATGCAGTCAACATTAATAAGTGCAGCCAGAGATC
TTGGCTTGACCCCTGGCAAACAGATTAACTGGATTCCAGTGCACAGTTTGATATTACTTTTCGTGTAACCTGTA
AGGAAGAAAAAGTCCTTCGTAACAATAAAAACCTTAGTACTGTAGATATCCAGAAGAATGGTGTTAAATTTACCA
ACAGCAAATTGACTTCTTTAAATGAAGAGTATACCAAAAATAAAACAGAATATGAAGAAGCCCAGGATGCCATTG
TTAAAGAAATTGTCAATATTTCTTCAGGCTATGTAGAACCAATGCAGACACTCAATGATGTGTTAGCTCAGCTAG
ATGCTGTTGTGTCAGCTTTGCTCACGTGTCAAATGGAGCACCTGTTCCATATGTACGACCAGCCATTTTGGAGAAAG
GACAAGGAAGAATTATATTAAGCATCCAGGCATGCTTGTGTTGAAGTTCAAGATGAAATTGCATTTATTCTTA
ATGACGTATACTTTGAAAAAGATAAACAGATGTTCCACATCATTACTGGCCCCAATATGGGAGGTAAATCAACAT
ATATTCGACAAACTGGGGTGATAGTACTCATGGCCCCAATTGGGTGTTTTGTGCCATGTGAGTCAGCAGAAGTGT
CCATTGTGGACTGCATCTTAGCCCGAGTAGGGGCTGGTGACAGTCAATTGAAAGGAGTCTCCACGTTTCATGGCTG
AAATGTTGGAAACTGCTTCTATCCTCAGGTCTGCAACCAAAGATTCATTAATAATCATAGATGAATTGGGAAGAG
GAACTTCTACCTACGATGGATTGGGGTAGCATGGGCTATATCAGAATACATTGCAACAAAGATTGGTGCTTTTT
GCATGTTTGCAACCCATTTTCATGAACCTTACTGCCTTGCCCAATCAGATACCAACTGTTAATAATCTACATGTCA
CAGCACTCACCCTGAAGAGACCTTAACTATGCTTTATCAGGTGAAGAAAGGTGTCTGTGATCAAAGTTTTGGGA
TTCATGTTGCAGAGCTTGCTAATTTCCCTAAGCATGTAATAGAGTGTGCTAAACAGAAAAGCCCTGGAACCTGAGG
AGTTTCAGTATATTGGAGAATCGCAAGGATATGATATCATGGAACCAGCAGCAAAGAAGTGCTATCTGGAAAGAG
AGCAAGGTGAAAAAATTATTCAGGAGTTCCGTGCCAAGGTGAAACAAATGCCCTTTACTGAAATGTCAGAAGAAA
ACATCACAATAAAGTTAAACAGCTAAAAGCTGAAGTAATAGCAAAGAATAATAGCTTTGTAAATGAAATCATTT
CACGAATAAAAGTTACTACGTGAATAATCCAGTAATGGAATGAAGGTAATATTGATAAGCTATTGTCTGTAATA
GTTTTATATTGTTTTATATTAACCCCTTTTCCATAGTGTTAACTGTCAGTGCCCATGGGCTATCAACTTAATAAG
ATATTTAGTAATATTTTACTTTGAGGACATTTTCAAAGATTTTTATTTTGAAGAAATGAGAGCTGTAAGTGGAC
TGTTTGCAATTGACATAGGCAATAATAAGTGATGTGCTGAATTTTATAAATAAAATCATGTAGTTTGTGG

795/6881
FIGURE 742

MAVQPKETLQLESAAEVGFVRFFQGMPEKPTTTVRLFDRGDFYTAHGEDALLAAREVFKTQGVIKYMGPAKAKNL
QSVVLSKMNFESEFVKDLLLVQRVEVYKNRAGNKASKENDWYLAYKASPGNLSQFEDILFGNNDMSASIGVVG
KMSAVDGGRRQVGVGVDISIQRKLGLCEFPDNDQFSNLEALLIQIGPKECVLPGETAGDMGKLRQIIQRGGILIT
ERKKADFSTKDIYQDLNRLKGGKGEQMNSAVLPEMENQVAVSSLSAVIKFLELLSDDSNFGQFELTTDFDSQYM
KLDIAAVRALNLFQGSVEDTTGSQSLAALLNKCKTPQGQRLVNQWIKQPLMDKNRIEERLNLVEAFVEDAELRQT
LQEDLLRRFPDLNRLAKKFQRQAANLQDCYRLYQGINQLPNVIALEKHEGKHQKLLAVFVTPPLTDLRSDFS
QEMIETTLMDQVENHEFLVKPSFDPNLSELREIMNDLEKKMQSTLISAARDLGLDPGKQIKLDSSAQFGYYFRV
TCKEEKVLRNNKNFSTVDIQKNGVKFTNSKLTSLNEEYTKNKTEYEEAQDAIVKEIVNISSGYVEPMQTLNDVLA
QLDAVVSFAHVSNGAPVPYVRPAILEKGQGRIILKASRHACVEVQDEIAFIPNDVYFEKDKQMFHIIITGPNMGGK
STYIRQTGVIVLMAQIGCFVPCESAESIVDCILARVGAGDSQLKGVSTFMAEMLETASILRSATKDSLIIIDEL
GRGTSTYDGFGLAWAISEYIATKIGAFCMFATHFHETALANQIPTVNNLHVTALTTEETLTMLYQVKKGVCDQS
FGIHVAELANFPKHVIECAKQKALELEEFQYIGESQGYDIMEPAAKKCYLEREQGEKIIQEFLSKVKQMPFTEMS
EENITIKLKQLKAEVIAKNNSFVNEIISRIKVT

796/6881
FIGURE 743

CTTTTGCGGGTGGCGGCGAACGCGGAGAGCACGCCATGAAGGCCTCGGGCACACTACGAGAGTACAAAGTAGTGG
GTCGCTGCCTGCCCACCCCAAATGCCACACACCACCCCTCTACCGCATGCGAATCTTTGCGCCTAATCATGTCG
TCGCCAAGTCCCGCTTCTGGTACTTCGTATCTCAGTTAAAGAAGATGAAGAAGTCTTCAGGGGAGATTGTCTACT
GTGGGCAGGTGTTTGAGAAGTTCCCCTTGCGGGTGAAGAACTTCGGGATCTGGCTGCGCTATGACTCCCGGAGCG
GCACCCACAACATGTACCGGGAATACCGGGACCTGACCACCGCAGGCGCTGTCACCCGGTGCTACCGAGACATGA
GCGCCCGGCACGGCGGCCGGGCCCCTCCATTCAGATCATGAAGGTGGAGGAGATCGCGGCCAGCAAGTGCCGCC
GGCCGGCTGTCÀAGCAGTTCCACGACTCCAAGATCAAGTTCCCGCTGCCCCACCGGGTCCTGCGCCGTGAGCACA
AGCCACGCTTCACCACCAAGAGGCCCAACACCTTCTTCTAGGTGCAGGGCCCTCGCCCGGGTGTGCCCCAAATAA
ACTCAGGAACGCCCC

797/6881
FIGURE 744A

ATTTCCCGCCAGCAGGAGCCGCGCGGTAGATGCGGTGCTTTTAGGAGCTCCGTCCGACAGAACGTTGGGCCTTG
CCGGCTGTGCGTATGTCGCGACAGAGCACCCCTGTACAGCTTCTTCCCCAAGTCTCCGGCGCTGAGTGATGCCAAC
AAGGCCTCGGCCAGGGCCTCACGCGAAGGCGGCCGTGCCGCGCTGCCCCGGGGCCTCTCCTTCCCCAGGCGGG
GATGCGGCCTGGAGCGAGGCTGGGCCTGGGCCAGGCCCTTGGCGCGATCCGCGTCACCGCCCCAAGGCGAAGAAC
CTCAACGGAGGGCTGCGGAGATCGGTAGCGCCTGCTGCCCCACCAGTTGTGACTTCTCACCAGGAGATTGGTT
TGGGCCAAGATGGAGGGTTACCCCTGGTGGCCTTGTCTGGTTTACAACCACCCCTTTGATGGAACATTTCATCCGC
GAGAAAGGGAAATCAGTCCGTGTTTCATGTACAGTTTTTTGATGACAGCCCAACAAGGGGCTGGGTTAGCAAAAGG
CTTTTAAAGCCATATACAGGTTCAAAATCAAAGGAAGCCAGAAAGGGAGGTCATTTTTACAGTGCAAAGCCTGAA
ATACTGAGAGCAATGCAACGTGCAGATGAAGCCTTAAATAAAGACAAGATTAAGAGGCTTGAATTGGCAGTTTGT
GATGAGCCCTCAGAGCCAGAAGAGGAAGAAGAGATGGAGGTAGGCACAACCTTACGTAAACAGATAAGAGTGAAGAA
GATAATGAAATTGAGAGTGAAGAGGAAGTACAGCCTAAGACACAAGGATCTAGGCGAAGTAGCCGCCAAATAAAA
AAACGAAGGGTTCATATCAGATTCTGAGAGTGACATTGGTGGCTCTGATGTGGAATTTAAGCCAGACACTAAGGAG
GAAGGAAGCAGTGATGAAATAAGCAGTGGAGTGGGGGATAGTGAGAGTGAAGGCCTGAACAGCCCTGTCAAAGTT
GCTCGAAAGCGGAAGAGAATGGTGACTGGAAATGGCTCTCTTAAAGGAAAAGCTCTAGGAAGGAAACGCCCTCA
GCCACCAACAAGCAACTAGCATTTTCATCAGAAACCAAGAATACTTTGAGAGCTTTCTCTGCCCCCTCAAATTTCT
GAATCCCAAGCCCACGTTAGTGAGGTTGGTGATGACAGTAGTCGCCCTACTGTTTGGTATCATGAACTTTAGAA
TGGCTTAAGGAGGAAAAGAGAAGAGATGAGCACAGGAGGAGGCCTGATCACCCGATTTTGATGCATCTACACTC
TATGTGCCTGAGGATTTCTCAATTCTTGTACTCTGGGATGAGGAAGTGGTGGCAGATTAAGTCTCAGAACTTT
GATCTTGTCTATCTGTTACAAGGTGGGGAAATTTTATGAGCTGTACCACATGGATGCTCTTATTGGAGTCAGTGAA
CTGGGGCTGGTATTTCATGAAAGGCAACTGGGCCATTCTGGCTTTCTGAAATTGCATTTGGCCGTTATTTCAGAT
TCCCTGGTGCAGAAGGGCTATAAAGTAGCAGAGTGAACAGACTGAGACTCCAGAAATGATGGAGGCACGATGT
AGAAAGATGGCACATATATCCAAGTATGATAGAGTGGTGAGGAGGGAGATCTGTAGGATCATTACCAAGGGTACA
CAGACTTACAGTGTGCTGGAAGGTGATCCCTCTGAGAACTACAGTAAGTATCTTCTTAGCCTCAAAGAAAAAGAG
GAAGATTCTTCTGGCCATACTCGTGCATATGGTGTGTGCTTTGTTGATACTTCACTGGGAAAGTTTTTCATAGGT
CAGTTTTCAGATGATCGCCATTGTTTCGAGATTTAGGACTCTAGTGGCACACTATCCCCAGTACAAGTTTTTATT
GAAAAAGGAAATCTCTCAAAGGAACTAAAACAATTCTAAAGAGTTTCATTGTCCTGTTCTCTTCAGGAAGGTCTG
ATACCCGGCTCCAGTTTTTGGGATGCATCCAAACTTTGAGAACTCTCCTTGAGGAAGAATATTTTAGGGAAAAG
CTAAGTGATGGCATTGGGGTGATGTTACCCAGGTGCTTAAAGGTATGACTTCAGAGTCTGATTCCATTGGGTTG
ACACCAGGAGAGAAAAGTGAATTGGCCCTCTCTGCTCTAGGTGGTTGTGTCTTCTACCTCAAAAAATGCCTTATT
GATCAGGAGCTTTTATCAATGGCTAATTTTGAAGAATATATTCCTTGGATTCTGACACAGTCAGCACTACAAGA
TCTGGTGCTATCTTACCAAAGCCTATCAACGAATGGTGCTAGATGCAGTGACATTAAACAACCTGGAGATTTTT
CTGAATGGAACAAATGGTTCTACTGAAGGAACCCTACTAGAGAGGGTTGATACTTGGCATACTCCTTTTGTAAG
CGGCTCCTAAAGCAATGGCTTTGTGCCCCACTCTGTAACCATTATGCTATTAATGATCGTCTAGATGCCATAGAA
GACCTCATGGTTGTGCCTGACAAAATCTCCGAAGTTGTAGAGCTTCTAAAGAAGCTTCCAGATCTTGAGAGGCTA
CTCAGTAAATTCATAATGTTGGGTCTCCCCCTGAAGAGTCAGAACCACCCAGACAGCGGGCTATAATGTATGAA
GAACTACATACAGCAAGAAGAAGATTATTGATTTTCTTTCTGCTCTGGAAGGATTCAAAGTAATGTGTAAAATT
ATAGGGATCATGGAAGAAGTTGCTGATGGTTTTAAGTCTAAAATCCTTAAGCAGGTCTCTCTCTGCAGACAAAA
AATCCTGAAGGTCGTTTTCTGATTTGACTGTAGAATTGAACCGATGGGATACAGCCTTTGACCATGAAAAGGCT
CGAAAGACTGGACTTATTACTCCCAAAGCAGGCTTTGACTCTGATTATGACCAAGCTCTTGCTGACATAAGAGAA
AATGAACAGAGCCTCCTGGAATACCTAGAGAAACAGCGCAACAGAATTGGCTGTAGGACCATAGTCTATTGGGGG
ATTGGTAGGAACCGTTACCAGCTGGAATTCCTGAGAATTTCACTACTCGCAATTTGCCAGAAGAATACGAGTTG
AAATCTACCAAGAAGGGCTGTAAACGATACTGGACCAAACTATTGAAAAGAAGTTGGCTAATCTCATAAATGCT
GAAGAACGGAGGGATGTATCATTGAAGGACTGCATGCGGCGACTGTTCTATAACTTTGATAAAAATTACAAGGAC
TGGCAGTCTGCTGTAGAGTGTATCGCAGTGTGGATGTTTTACTGTGCCTGGCTAACTATAGTCGAGGGGGTGAT
GGTCTATGTGTGCGCCAGTAATTCTGTTGCCGGAAGATACCCCCCTTCTTAGAGCTTAAAGGATCACGCCAT
CCTTGCATTACGAAGACTTTTTTTTGGAGATGATTTTATTCCTAATGACATTCTAATAGGCTGTGAGGAAGAGGAG
CAGGAAAATGGCAAAGCCTATTGTGTGCTTGTACTGGACCAAAATATGGGGGGCAAGTCTACGCTTATGAGACAG
GCTGGCTTATTAGCTGTAATGGCCAGATGGGTTGTTACGTCCCTGCTGAAGTGTGCAGGCTCACACCAATTGAT

798/6881

FIGURE 744B

AGAGTGTTTACTAGACTTGGTGCCCTCAGACAGAATAATGTCAGGTGAAAGTACATTTTTTGTGTAATTAAGTGAA
ACTGCCAGCATACTCATGCGATGCAACAGCACATTCTCTGGTGCTTGTGGATGAATTAGGAAGAGGTACTGCAACA
TTTGATGGGACGGCAATAGCAAATGCAGTTGTTAAAGAAGCTTGCTGAGACTATAAAATGTCGTACATTATTTTCA
ACTCACTACCATTTCATTAGTAGAAGATTATTCTCAAAATGTTGCTGTGCGCCTAGGACATATGGCATGCGATGGTA
GAAAATGAATGTGAAGACCCAGCCAGGAGACTATTACGTTCCCTCTATAAATTCATTAAGGGAGCTTGTCTCTAAA
AGCTATGGCTTTAATGCAGCAAGGCTTGCTAATCTCCAGAGGAAGTTATTCAAAAGGGACATAGAAAAGCAAGA
GAATTTGAGAAGATGAATCAGTCACTACGATTATTTTCGGGAAGTTTGCCTGGCTAGTGAAAGGTCAACTGTAGAT
GCTGAAGCTGTCCATAAATTGCTGACTTTGATTAAAGGAATTATAGACTGACTACATTGGAAGCTTTGAGTTGACT
TCTGACCAAAGGTGGTAAATTCAGACAACATTATGATCTAATAAACTTTATTTTTTAAAAATGA

799/6881
FIGURE 745

MSRQSTLYSFFPKSPALSDANKASARASREGGRAAAAPGASPSPGGDAWSEAGPGRPLARSASPPKAKNLNGG
LRRSVAPAAPTSCDFSPGDLVWAKMEGYPPWWPCLVYNHPFDGTFIREKGKSVRVHVQFFDDSPTRGWVSKRLLKP
YTGSKSKEAQKGGHFYSAPKPEILRAMQRADEALNKDKIKRLELAVCDEPSEPEEEEEEMEVEGTTYVTDKSEEDNEI
ESEEEVQPKTQGSRRSSRQIKKRRVISDSESDIGGSDVEFKPDTKEEGSSDEISSGVGDSESEGLNSPVKVARKR
KRMVTGNGLKRRKSSRKETPSATKQATSISSETKNTLRAFSAPOQNSSEQAHVSGGGDDSSRPTVWYHETLEWLKE
EKRRDEHRRRPDHPDFDASTLYVPEDFLNSCTPGMRKWWQIKSQNFDLVICYKVGKFYELYHMDALIGVSELGLV
FMKGNWAHSGFPEIAFGRYSDSLVQKGYKVARVEQTETPEMMEARCRKMAHISKYDRVVRREICRIITKGTQTY
VLEGDPSENYSKYLLSLKEKEEDSSGHTRAYGVCVFDTSLGKFFIGQFSDDRHC SRFRTLVAHYPPVQVLFKGN
LSKETKTILKSSLSLCSLQEG LIPGSQFWDASKTLRLTLEEEYFREKLSDGIGVMLPQVLKGMTSESDSIGLTPGE
KSELALSALGGCVFYLKKCLIDQELLSMANFEEYIPLDSDTVSTTRSGAIFTKAYQRMVLDVAVTLNNLEIFLNGT
NGSTEGTILLERVDTCHTPFGKRLKQWLCAPLCNHYAINDRLDAIEDLMVVPDKISEVVELLKKLPDLERLLSKI
HNVGSPLKSQNHPSRAIMYEETTYSKKKIIDFLSALEGFKVMCKIIGIMEEVADGFKSKILKQVISLQTKNPEG
RFPDLTVELNRWDATFDHEKARKTGLITPKAGFDSYDQALADIRENEQSLLEYLEKQQRNIGCRTIVYWGIGRN
RYQLEIPENFTTRNLPEEYELKSTKKGCKRYWTKTIEKKLANLINAEERRDVSLKDCMRRLFYNFKNYKDWQSA
VECIAVLVDLLCLANYSRGGDGPMCRPVILLPEDTPPFLELKGSRHPCITKTFFGDDFIPNDILIGCEEEQENG
KAYCVLVTGPNMGGKSTLMRQAGLLAVMAQMGCVPAEVCRLTPIDRVFTRLGASDRIMSGESTFFVELSETASI
LMHATAHSLVLVDELGRGTATFDGTAIANAVVKELAETIKRCLTFSTHYHSLVEDYSQNVAVRLGHMACMVENEC
EDPSQETITFLYKFIKACPKSYGFNAARLANLPEEVIQKGRKAREFEKMNQSLRLFREVCCLASERSTVDAEAV
HKLLTLIKEL

800/6881
FIGURE 746A

GTGAGCTGAAGCAGGGCAGGGCATCAACTCACCCAGGAAGTGCAAGGGGTTTGGGGATTTTCCTTTCTAGCCAA
GGGAAGGCATGACAGACTGTACCTGGAAAAACAGGACACTCTTGCCCAAATACTGCACTTTTTGCACAGTCTTAG
CAACTGGCAGACCAGGAGATTCTCTCCTGTGCCTGATTCAATTGGGTCCCACACCCATAGGGCCTTGCTTACTGCC
AGTGACAGCAGTCTGAGATTAACACCCCATCCCCGGGAGAACTCTAAGAAGGAGCTGATGTGGAGGAGCAGCTGAG
ACAGTTCAAG**ATG**ACGACCACAGTAGCCACAGACTATGACAACATTGAGATCCAGCAGCAGTACAGTGATGTCAA
CAACCGCTGGGATGTGACGACTGGGACAATGAGAACAGCTCTGCGCGGCTTTTTGAGCGGTCCCGCATCAAGGC
TCTGGCAGATGAGCGTGAAAGCCGTGCAGAAGAAGACCTTCACCAAGTGGGTCAATTCCCACCTTGCCCGTGTGTC
CTGCCGGATCACAGACCTGTACACTGACCTTCGAGATGGACGGATGCTCATCAAGCTGCTGGAGGTCTCTCTGG
AGAGAGGCTGCCTAAACCCACCAAGGGACGAATGCGCATCCACTGCTTAGAGAATGTGGACAAGGCCCTTCAGTT
CCTGAAGGAGCAGAGAGTCCATCTTGAGAACATGGGGTCCCATGACATCGTGGATGGAAACCACCGGCTGACCCCT
TGGCCTCATCTGGACCATCATCTGCGCTTCAGATCCAGGATATCAGTGTGGAAACTGAAGACAACAAAGAGAA
GAAATCTGCCAAGGATGCATTGCTGTTGTGGTGCCAGATGAAGACAGCTGGGTACCCCAATGTCAACATTACAA
TTTCACCACTAGCTGGAGGGACGGCATGGCCTTCAATGCACTGATACACAAACACCGGCCTGACCTGATAGATTT
TGACAAACTAAAGAAATCTAACGCACACTACAACCTGCAGAATGCATTTAATCTGGCAGAACAGCACCTCGGCCT
CACTAAACTGTTGGACCCCGAAGACATCAGCGTGGACCATCCTGATGAGAAGTCCATAATCACTTATGTGGTGAC
TTATTACCACTACTTCTCTAAGATGAAGGCCTTAGCTGTTGAAGGAAAACGAATTGGAAAGGTGCTTGACAATGC
TATTGAAACAGAAAAAATGATTGAAAAGTATGAATCACTTGCCCTCTGACCTTCTGGAATGGATTGAACAAACCAT
CATCATTCTGAACAATCGCAAATTTGCCAATTCCTGGTTCGGGGTTCAACAGCAGCTTCAGGCATTCAACACTTA
CCGCACTGTGGAGAAACCACCCAAATTTACTGAGAAGGGGAAGTGGAAAGTGCTGCTCTTACCATTACAGAGCAA
GATGAGGGCCAACAACCAGAAGGTCTACATGCCCGGGAGGGGAAGTCTCATCTCTGACATCAACAAGGCCTGGGA
AAGACTGGAAAAAGCGGAACACGAAAGAGAAGTGGCTTTGCGGAATGAGCTCATAAGACAGGAGAAACTGGAACA
GCTCGCCCGCAGATTTGATCGCAAGGCAGCTATGAGGGAGACTTGGTGAGCGAAAACCAGCGTCTGGTGTCTCA
GGACAACCTTTGGGTTTGACCTTCTGCAAGTTGAGGCCGCCACAAAAAGCACGAGGCCATTGAGACAGACATTGC
CGCATACGAGGAGCGTGTGACGGCTGTGGTAGCCGTGGCCAGGGAGCTCGAGGCCGAGAATTACCACGACATCAA
GCGCATCACAGCGAGGAAGGACAATGTATCCGGCTCTGGGAATACCTACTGGAAGTCTCAGGGCCCCGGAGACA
GCGGCTCGAGATGAACCTGGGGCTGCAGAAGATATTCCAGGAAATGCTCTACATTATGGACTGGATGGATGAAAT
GAAGGTGCTAGTATTGTCTCAAGACTATGGCAAACACTTACTTGGTGTGGAAGACCTGTTACAGAAGCACACCCCT
GGTTGAAGCAGACATTGGCATCCAGGCAGAGCGGGTGAGAGGTGTCAATGCCTCCGCCCAGAAGTTCGCAACAGA
CGGGGAAGGTTACAAGCCCTGTGACCCCAAGGTGATCCGAGACCGCGTGGCCACATGGAGTTCTGTTATCAAGA
GCTTTGCCAGCTGGCGGCTGAGCGCAGGGCCCGTCTGGAAGAGTCCCGCCGCTCTGGAAGTTCTTCTGGGAGAT
GGCAGAAGAGGAAGGCTGGATACGGGAGAAGGAGAAGATCCTGTCTCGGACGATTACGGGAAAGACCTGACCAG
CGTCATGCGCCTGCTCAGCAAGCACCGGGCGTTTCGAGGACGAGATGAGCGGCCGAGTGGCCACTTTGAGCAGGC
CATCAAGGAAGGCGAAGACATGATCGCGGAGGAGCACTTCGGGTTCGGAGAAGATCCGTGAGAGGATCATTTACAT
CCGGGAGCAGTGGGCCAACCTAGAGCAGCTCTCGGCCATTTCGGAAGAAGCGCCTGGAGGAGGCCTCCCTGCTGCA
CCAGTTCCAGGCAGATGCTGATGACATTGATGCCTGGATGCTGGACATCCTCAAGATTGTCTCCAGCAGCGACGT
GGGCCACGATGAGTATTCCACACAGTCTCTGGTCAAGAAACACAAGGACGTGGCGGAAGAGATCGCCAATTACAG
GCCACCCCTTGACACGCTGCACGAACAAGCCAGCGCCCTCCCCAGGAGCATGCCGAGTCTCCAGACGTGAGGGG
CAGGCTGTTCGGGCATCGAGGAGCGGTATAAGGAGGTGGCAGAGCTGACGCGGCTGCGGAAGCAGGCACTCCAGGA
CACTCTGGCCCTGTACAAGATGTTTCAGCGAGGCTGATGCCTGTGAGCTCTGGATCGACGAGAAGGAGCAGTGCT
CAACAACATGCAGATCCCAGAGAAGCTGGAGGATCTGGAGGTTCATCCAGCACAGATTTGAGAGCCTAGAACCAGA
AATGAACAACCAGGCTTCCCGGTTGCAAGTGGTGAACCAGATTGCACGCCAGCTGATGCACAGCGGCCACCCAAG
TGAGAAGGAAATCAAAGCCCAGCAGGACAACTCAACACAAGGTGGAGCCAGTTCAGAGAAGTGGTTGACAGGAA
GAAGGATGCCCTCCTGTCTGCCCTGAGCATCCAGAAGTACCACCTCGAGTGCAATGAAACCAAATCCTGGATTCTG
GGAAAAGACCAAGGTTCATCGAGTCCACCCAGGACCTGGGCAATGACCTGGCTGGCGTCATGGCCCTGCAGCGCAA
GCTGACCGGCATGGAGCGGGACTTGGTGGCCATTGAGGCAAAGCTGAGTGACCTGCAGAAGGAGGCGGAGAAAGCT
GGAGTCCGAGCACCCCGACCAGGCCAGGCCATCCTGTCTCGGCTGGCCGAGATCAGCGACGTGTGGGAGGAGAT
GAAGACCACCCCTGAAAAACCGAGAGGCCTCCCTGGGAGAGGCCAGCAAGCTGCAGCAGTTCTTACGGGACTTGG
CGACTTCCAGTCTCTGGCTCTCTAGGACCCAGACAGCGATCGCCTCGGAGGACATGCCAAACACCCCTGACCGAGGC

801/6881
FIGURE 746B

TGAGAAGCTGCTCACGCAGCACGAGAACATCAAGAATGAGATCGACAACACTACGAGGAGGACTACCAGAAGATGAG
GGACATGGGCGAGATGGTCACCCAGGGGCAGACCGATGCCCAGTACATGTTTCTGCGGCAGCGGCTGCAGGCCCT
GGACACTGGATGGAACGAGCTCCACAAGATGTGGGAGAACAGACAAAATCTCCTATCCCAGTCACATGCCTACCA
GCAGTTCTCTCAGAGACACGAAGCAAGCCGAAGCCTTTCTTAACAACCAGGAGTATGTTCTGGCTCACACTGAAAT
GCCTACCACCTTGGAAAGGAGCTGAAGCAGCAATTAAAAAGCAAGAGGACTTCATGACCACCATGGACGCCAATGA
GGAGAAGATCAATGCTGTGGTGGAGACTGGCCGGAGGCTGGTGAGCGATGGGAACATCAACTCAGATCGCATCCA
GGAGAAGGTGGACTCTATTGATGACAGACATAGGAAGAATCGTGAGACAGCCAGTGAACCTTTTGATGAGGTTGAA
GGACAACAGGGATCTACAGAAATTCCTGCAAGATTGTCAAGAGCTGTCTCTCTGGATCAATGAGAAGATGCTCAC
AGCCCAGGACATGTCTTACGATGAAGCCAGAAATCTGCACAGTAAATGGTTGAAGCATCAAGCATTTATGGCAGA
ACTTGCATCCAACAAAAGAAATGGCTTGACAAAATCGAGAAGGAAGGAATGCAGCTCATTTTCAGAAAAGCCTTGAGAC
GGAAGCTGTGGTGAAGGAGAAAATCACTGGTTTTACATAAAAATGTGGGAAGTTCCTTGAATCCACTACCCAGACAAA
GGCCCAGCGGCTCTTTGATGCAAACAAGGCCGAACCTTTTCACCCAGAGCTGTGCAGATCTAGACAAAATGGCTGCA
CGGCCTGGAGAGTCAGATTCACTGTGATGACTATGGCAAACACCTGACCAGTGTCAATATCCTGCTGAAAAAGCA
ACAGATGCTGGAGAATCAGATGGAAGTGCAGGAAGAAGGAGATCGAAGAGCTCCAAAGCCAAGCCCAGGCCCTGAG
TCAGGAAGGGAAGAGCACCGACGAGGTAGACAGCAAGCGCCTCACCGTGCAGACCAAGTTTCATGGAGTTGCTGGA
GCCCTTGAACGAGAGGAAGCATAACCTGCTGGCCTCCAAAGAGATCCATCAGTTCAACAGGGATGTGGAGGACGA
GATC1TGTGGGTTGGAGAGAGGATGCCTTTGGCAACTTCACGGATCATGGCCACAACCTCCAGACTGTGCAGCT
GTTAATAAAGAAAAATCAGACCCTCCAGAAAGAAATCCAGGGGCACCAGCCTCGCATTGACGACATCTTTGAGAG
GAGCCAAAACATCGTCACTGACAGCAGCAGCCTCAGCGCTGAGGCCATCAGACAGAGGCTTGCCGACCTGAAGCA
GCTGTGGGGTCTCCTCATTGAGGAGACAGAGAAACGCCACAGGCGGCTGGAGGAGGCGCACAGGGCCCCAGCAGTA
CTACTTTGACGCTGCTGAGGCCGAAGCCTGGATGAGCGAGCAGGAGCTGTACATGATGTCAGAGGAGAAGGCCAA
GGATGAGCAGAGTGCTGTCTCCATGTTGAAGAAGCACCAGATCTTAGAACAAGCTGTGGAGGACTATGCAGAGAC
CGTGATCAGCTCTCCAAGACCAGCCGGGCCCTGGTGGCCGACAGCCATCCTGAAAGTGAGCGCATTAGCATGCG
GCAGTCCAAAGTGGAATAAATGTACGCTGGTCTGAAAGACCTTGCTGAAGAGAGAAGAGGCAAGCTGGATGAGAG
ACACAGGTTATTCCAGCTCAACCGGGAGGTGGACGACCTGGAGCAGTGATCGCTGAGAGGGAGGTGGTGCAGG
GTCCCATGAACTGGGACAGGACTATGAGCATGTACGATGTTACAAGAAGCATTCCGGGAGTTTGCCCCGAGACAC
CGGGAACATTGGGCAGGAGCGCGTGGACACGGTCAATCACCTGGCAGATGAGCTCATCAACTCTGGACATTGAGA
TGCCGCCACCATCGCTGAATGGAAGGATGGCCTCAATGAAGCCTGGGCCGACCTCCTGGAGCTCATTGACACAAG
AACACAGATTCTTGCCGCTTCCTATGAACTGCACAAGTTTTACCACGATGCCAAGGAGATCTTTGGGCGTATACA
GGACAAACACAAGAAAATCCCTGAGGAGCTTGGGAGAGATCAGAACACAGTGGAGACCTTACAGAGAATGCACAC
TACATTTGAGCATGACATCCAGGCTCTGGGCACACAGGTGAGGCAGCTGCAGGAGGATGCAGCCCGCTCCAGGC
GGCCTATGCGGGTGACAAGGCCGACGATATCCAGAAGCGCGAGAACGAGGTCCTGGAAGCCTGGAAGTCCCTCCT
GGACGCCTGTGAGAGCCGACAGGTGCGGCTGGTGGACACAGGGGACAAGTTCCGCTTCTTCAGCATGGTGCGCCGA
CCTCATGCTCTGGATGGAGGATGTCATCCGGCAGATCGAGGCCCAGGAGAAGCCAAGGGATGTATCATCTGTTGA
ACTCTTAATGAATAATCATCAAGGCATCAAAGCTGAAATTGATGCACGTAATGACAGTTTCACAACCTGCATTGA
ACTTGGGAAATCCCTGTTGGCGAGAAAACACTATGCATCTGAGGAGATCAAGGAAAAATTACTGCAGTTGACGGA
AAAGAGGAAAGAAATGATCGACAAGTGGGAAGACCGATGGGAATGGTTAAGACTGATTCTGGAGGTCCATCAGTT
CTCAAGAGACGCCAGTGTGGCCGAGGCTGGCTGCTTGACAGGAGCCGTACCTATCCAGCCGAGAGATAGGCCA
GAGCGTGGACGAGGTGGAGAAGCTCATCAAGCGCCACGAGGCATTTGAAAAGTCTGCAGCAACCTGGGATGAGAG
GTTCTCTGCCCTGGAAAGGCTGACTACATTGGAGTTACTGGAAGTGCGCAGACAGCAAGAGGAAGAGGAGAGGAA
GAGGCGGCCGCTTCTCCCGAGCCGAGCACGAAGGTTTCAGAGGAAGCCGAGTCCAGCAGCAGTGGGATACTTC
AAAAGGAGAACAAGTTTCCCAAACGGTTTGCCAGCTGAACAGGGATCTCCACGGATGGCAGAAACGGTGGACAC
AAGCGAAATGGTCAACGGCGCTACAGAACAAGGACGAGCTCTAAAGAGTCCAGCCCCATCCCTCCCCGACCTC
TGATCGTAAAGCCAAGACTGCCCTCCCAGCCCAGAGTGCCGCCACCTTACCAGCCAGAACCCAGGAGACACCTTC
GGCCCAGATGGAAGGCTTCCTCAATCGAAACACGAGTGGGAGGCCCAATAAGAAAGCCTCAAGCAGGTCTTG
GCACAATGTTTATTGTGTCATAAATAACCAAGAAATGGGTTTCTACAAAGATGCAAAGACTGCTGCTTCTGGAAT
TCCCTACCACAGCGAGGTCCCTGTGAGTTTGAAAGAAGCTGTCTGCGAAGTGGCCCTTGATTACAAAAAGAAAGAA
ACACGTATTCAAGCTAAGACTAAATGATGGCAATGAGTACCTCTTCCAAGCCAAAGACGATGAGGAAATGAACAC

802/6881
FIGURE 746C

ATGGATCCAGGCTATCTCTTCCGCCATCTCCTCTGATAAACACGAGGTGTCTGCCAGCACCCAGAGCACGCCAGC
ATCCAGCCGCGCGCAGACCCTCCCCACCAGCGTCGTCACCATCACCAGCGAGTCCAGTCCCGGCAAGCGGGAAAA
GGACAAAGAGAAAGACAAAGAGAAGCGGTTTCAGCCTTTTTGGCAAAAAGAAATGAACCTCCTTTCCTTCACCTCCT
GCCCTTCTCTTACCTTTTTCAGTGAAATTCCAGCATGCAAGCTCAGAACCAACACATTACTCTCTGTGCCTAATGT
TCCTCAATGTGGTTGATTTATTTTTTTTTTTTAATTTATAGAGCATTTCTGGGGGGGGTGGGG

803/6881
FIGURE 747

MTTIVATDYDNIEIQQQYSDVNNRWDVDDWDNENSSARLFERSRIKALADEREAVQKKTF TKWVNSHLARVSCRI
TDLYTDLRDGRMLIKLLEVLSGERLPKPTKGRMRIHCLENVDKALQFLKEQRVHLENMGSHDIVDGNHRLTLGLI
WTIILRFQIQDISVETEDNKEKKSADALLWCQMKTAGYPNVNIHNFTTSWRDGMAFNALIHKHRPDLIDFDKL
KKSNAHYNLQNAFNLAEQHLGLTKLLDPEDISVDHPDEKSIITYVVTYYHYFSKMKALAVEGKRIGKVLDNAIET
EKMIKEYESLASDLEWIEQTIIILNNRKFANSLVGVOQQLOAFNTYRTVEKPPKFTEKGNLEVLLFTIQSKMRA
NNQKVYMPREGKLISDINKAWERLEKAEHERELALRNELIRQEKLEQLARRFDRKAAMRETWLSNQRLVSQDNF
GFDLPAVEAATKKHEAIETDIAAYEERVQAVVAVARELEAENYHDIKRITARKDNVIRLWEYILLELLRARRQRLE
MNLGLQKIFQEMLYIMDWMDEMKVVLVSQDYGKHLGVEDLLQKHTLVEADIGIQAERVRGVNASAQKFATDGE
YKPCDPQVIRDRVAHMEFCYQELCQLAAERRARLEESRRLWKFFWEMAE EEGWIREKEKILSSDDYGKDLTSVMR
LLSKHRAFEDEMSGRSGHFEQAIKEGEDMIAEEHFGSEKIRERIIYIREQWANLEQLSAIRKKRLEEASLLHQFQ
ADADDIDAWMLDILKIVSSSDVGHDEYSTQSLVKKHKDVAAEIANRPTLDTLHEQASALPQEHAESP DVGRLS
GIEERYKEVAELTRLRKQALQD TLALYKMFSEADACELWIDEKEQWLNMMQIPEKLEDLEVIQHRFESLEPEMNN
QASRVAVVNQIARQLMHSGHPSEKEIKAQQDKLNTRWSQFRELVD RKKDALLSALS IQNYHLECNETKSWIREKT
KVIESTQDLGNDLAGVMALQRKLTGMERDLVAIEAKLSDLQKEAEKLESEHPDQAQAILSR LAEISDVWEEMKTT
LKNREASLGEASKLQQFLRDLDDFQSWLSRTQTAIASEDMPNTLTAEKLLTQHENIKNEIDNYEEDYQKMRDMG
EMVTQGQTD AQYMLRQRLQALDTGWNELHKMWENRQNLQS SHAYQQFLRDTKQAEAF LNNQEYVLAHTEMP TT
LEGAEAAIKKQEDFMTTMDANEKINAVVETGRRLVSDGNINS DRIQEKVDSIDDRHRKNRETASELLMRLKDNR
DLQKFLQDCQELSLWINEKMLTAQDMSYDEARNLH SKWLKHQAFMAELASNKEWLDKIEKEGMQLISEKPETEAV
VKEKLTGLHKMWEVLESTTQTKAQLRFDANKAELFTQSCADLDKWLHGLESQIQSDDYGKHLTSVNILLKKQQML
ENQMEVRKKEIEELQSQAQALSQEGKSTDEVD SKRLTVQTKFMELLEPLNERKHNLLASKEIHQFN RDVEDEILW
VGERMPLATSTDHGHNLQTVQLLIKKNQTLQKEIQGHQPRIDDIFERSQNI VTDSSSLSAEAI RQLADLKQLWG
LLIETEKRHRRLLEEAHRAQQYYFDAAEAEAWMSEQEL YMMSEEKAKDEQSAVSM LKKHQILEQAVEDYAETVHQ
LSKTSRALVADSHPE SERISMRQSKVDKLYAGLKDLAEERRGK LDERHRLFQLNREVDDLEQWIAEREVVAGSHE
LGQDYEHVTMLQERFREFARDTGNIGQERVDTVNHLADEL INSGHSDAATIAEWK DGLNEAWADLLELIDTRTQI
LAASYELHKFYHDAKEIFGRIQDKHKKLP EELGRDQNTVETLQRMHTT FEHDIQALGTQVRQLQEDAARLQAAYA
GDKADDIQKRENEVLEAWKSLLDACESRRVRLVDTGDKFRFFSMVRDLMLWMEDVIRQIEAQEKPRDVSSVELLM
NNHQGIKAEIDARNDSTFTTCIELGKSL LARKHYASEEIKEKLLQLTEKRKEMIDKWEDRW EWLRLILEVHQFSRD
ASVAEAWLLGQEPYLSREIGQSVDEVEKLIK RHEAFEKSAATWDERFSALERLT TLELLEVR RQQEEEEERKRRP
PSEPESTKVSEEAESQQQWDTSKGEQVSQNGLP AEQGSPRMAETVDTSEMVNGATEQRTSSKESSPIPSPTSDRK
AKTALPAQSAATLPARTQETPSAQMEGFLNRKHEWEAHNKKASSRSWHNVYCVINNQEMGFYKDAKTAASGIPYH
SEVPVSLKEAVCEVALDYKKKKHVFKLRLNDGNEYLFQAKDDEEMNTW IQAISSAISSDKHEVSASTQSTPASSR
AQTLPTS VVTITSESSPGKREKDKEKDKEKRFSLFGKKK

804/6881
FIGURE 748

CACAACCGCCCGCGGCTCTGAGACGCGGCCCCGGCGGCGGCGGCAGCAGCTGCAGCATCATCTCCACCCTCCAGC
CATGGAAGACGAGGAGGAAGAAGAGGAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCT
GGAGAGGAAGCCCGCCGCGGGGCTGTCCGCGGCCCCAGTGCCCAACGCCCCCTGCCGCCGGCGCGCCCCCTGATGGA
CTTCGGAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCCCCGTCGCCCCGGAGCGGCA
GCCGTCTTGGGACCCGAGCCCGGTGTCGTCGACCGTGCCCGCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCC
CTCCAAGCTCCCTGAGGACGACGAGCCTCCGGCCCGG

805/6881
FIGURE 749

TTCTTCCTTTTCGATCCGCCATCTGCGGTGGAGCCGCCACCAAAATGCAGATTTTCGTGAAAACCCTTACGGGGA
AGACCATCACCTCGAGGTTGAACCCTCGGATACGATAGAAAATGTAAAGGCCAAGATCCAGGATAAGGAAGGAA
TTCCTCCTGATCAGCAGAGACTGATCTTTGCTGGCAAGCAGCTGGAAGATGGACGTACTTTGTCTGACTACAATA
TTCAAAAGGAGTCTACTCTTCATCTTGTTGTTGAGACTTCGTGGTGGTGCTAAGAAAAGGAAGAAGAAGTCTTACA
CCACTCCCAAGAAGAATAAGCACAAAGAGAAAGAAGGTTAAGCTGGCTGTCCTGAAATATTATAAGGTGGATGAGA
ATGGCAAAATTAGTCGCCTTCGTGAGAGTGCCCTTCTGATGAATGTGGTGCTGGGGTGTTTATGGCAAGTCACT
TTGACAGACATTATTGTGGCAAAATGTTGCTGACTTACTGTTTCAACAAACCAGAAGACAAGTAACTGTATGAGT
TAATAAAAGACATGAACTAACAAAAA

806/6881
FIGURE 750

MQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQORLIFAGKQLEDGRTLSDYNIQKESTLHLVLRRLRG
GAKKRKKKSYTTPKKNKHKRKKVKLAVLKYYKVDENGKISRLRRECPSDECGAGVFMASHFDRHYCGKCCLTYCF
NKPEDK

807/6881
FIGURE 751

GGCACGAGCAGAATCCAGGGGCCCCGGGGCTGTAGATTCCCTTGACAAGGATATCCTAGCGGCGAAACAACACCGTA
CTGGGAGTCAGAACGTCTGGGTTCTAGTCTTGACTGCCATTAAGTACGGTATGACATTGGAGAAGCTTTTTTGA
CCCTTCTGGATTTCCGTTTCCTTTTCTGTAAAATGAGGAGCTTGGAAGATCCGGAAAATGAGGCCCATAGGAAAC
AAGTGACTTGCTGAGTCCAGATAACACTGACTGTCAGAGAGAAAACATGAACCAGAAGCTACTGAAGTTGGAGAAC
TTGCTACGATTTACACTATTTATAGGCAACTGCACAGTCTGTGTCAAAGAAGAGCATTAAAGACAGTGGAGGCAT
GGGTTTTTCATCTGCTTACCCGTGTGTGGACAGCTCAACTGTGTGCCTGGCCCTGGCCAACAGATGTGCTCAATGGG
GCTGCTTTATCTCAGTATAGGCTTCTAGTAACAAAAAAGGAAGAAGGACCATGGAAATCTCAGTTATCTTCAACA
AAATCTAAAAAGGTGGTAGAAGTATGGATTGGAATGACTATTGAGGAACTGGCCAGGGCAATGGAAAAAACACA
GATTATGTATATGAAGCTTTATTGAACACTGATATTGACATAGATTCACTGGAAGCAGACTCACATTTAGATGAA
GTCTGGATCAAAGAAGTGATAACGAAGGCAGGGATGAAGTTAAAGTGGAGTAAATTAAGACAGGACAAAGTCAGA
AAAAATAAAGATGCTGTAAGAAGCCCCAGGCAGATCCAGCTTTATTAAACCCCAAGGTCCCAGTTGTTACTATA
ATGGGCCATGTTGATCACGGGAAAACGACATTACTTGACAAATTTGAAAACTCAAGTGGCAGCAGTGGAACT
GGAGGCATCACTCAGCACATTGGTGCCTTTCTTGCTCTCTGCCTTCTGGGGAAAAGATAACTTTTCTTGATACT
CCAGGACATGCTGCTTTCTCAGCAATGAGAGCCAGAGGTGCTCAGGTCACTGACATTGTCGTATTGGTTGTAGCT
GCAGATGATGGAGTGATGAAACAACTGTAGAATCTATTGAGCATGCCAAAGATGCACAGGTTCCCTATTATCCTT
GCCGTAAATAAATGTGACAAAGCTGAGGCTGATCCTGAGAAAGTGAAAAAGAGCTGCTGGCTTACGATGTGCTA
TGTGAAGATTATGGAGGTGATGTTCAAGCAGTGCCTGTCTCCGCACTTACGGGCGATAATCTGATGGCTTTGGCA
GAAGCAACAGTTGCTCTTGCAGAAATGTTAGAATTGAAAGCAGATCCCAATGGTCCAGTGAAGGAACAGTAATA
GAGTCTTTACAGACAAAGGAAGAGGTCTTGTTACTACAGCTATAATTCAAAGAGGAACTTTAAGAAAAGGCTCT
GTTCTGGTTGCTGGAAAAATGTTGGGCAAAAGTACGCTTAATGTTTGATGAAAATGGAAAAACAATTGATGAGGCC
TATCCCAGCATGCCAGTGGGAATTACAGGCTGGAGAGACCTTCCTTCTGCAGGAGAAGAAATTCCTGAAGTAGAA
TCTGAGCCAAGGGCACGTGAAGTTGTTGACTGGAGGAAATATGAACAAGAACAGGAGAAAGGTCAGGAGGATCTG
AAAATAATAGAAGAAAAGCGAAAGGAACACAAAGAAGCACATCAGAAAGCCCGTGAGAAGTATGGCCATCTACTG
TGGAAGAAGAGATCAATTCTACGGTTTTTGTAAAGAAAAGAACAAATACCCCTAAAGCCAAAAGAGAAAAGGGAA
AGAGATTCAAATGTACTTTCTGTGATTATTAAGGTGATGTTGATGGTTCTGTTGAGGCCATTTTGAACATTATA
GATACCTATGATGCTTCACACGAGTGTGAAGTAGAATTAGTACATTTTGGAGTGGGTGATATAAGTGCAAATGAT
GTTAACCTTGCTGAAACATTTGATGGTGTATATATGGCTTTAATGTGAATGCAGGCAATGTTATCCAACAGTCA
GCTGCAAAAAAAGGAGTAAAAATTAACTTCACAAAATAATTTACCGTCTTGTTGAAGATTTGCAAGAGGAACTG
AGCAGCAGATTACCTGTGCTGTGGAAGAGCACCCAGTAGGTGAGGCATCTATACTAGCTACCTTCTGTAAACA
GAAGGGAAGAAAAAAGTTCTGTGGCTGGCTGCAGAGTCCAAAAGGGACAGTTAGAAAAACAAAAAAATTTAAA
CTAACCCGTAATGGACATGTAATTTGGAAGGGCTCATTAACCTCATTGAAACACCATAAAGATGACATTTCAATT
GTCAAAACGGGAATGGATTGTGGTCTCAGTTTAGATGAAGACAATATGGAATTTCAAGTGGGAGACAGAATTGTT
TGTTATGAAGAAAAGCAAATTCAGCCAAGACTTCTTGGGATCCAGGATTTTAAATTTACATTAAAAATGTAAAT
AACTCA

808/6881
FIGURE 752

MNQKLLKLENLLRFHTIYRQLHSLCQRRALRQWRHGFSSAYPVWTAQLCAWPWPTDVLNGAALSQYRLLVTKKEE
GPWKSQLSSTKSKKVVEVWIGMTIEELARAMEKNTDYVYEALLNTDIDIDSLEADSHLDEVWIKVITKAGMKLK
WSKLGQDKVRKNKDAVRRPQADPALLTPRSPVVTIMGHVDHGKTTLLDKFRKTQVAAVETGGITQHIGAFVLSLP
SGEKITFLDTPGHAAFSAMRARGAQVTDIVVLVVAADDGVMKQTVESIQHAKDAQVP IILAVNKCDKAEADPEKV
KKELLAYDVVCEDYGGDVQAVPVSAITGDNLMALAEATVALAEMLELKADPNPVEGTVIESFTDKGRGLVTTAI
IQRGTLRKGSVLVAGKCWAKVRLMFDENGKTIDEAYPSMPVGITGWRDLPSAGEEILEVESEPRAREVVDWRKYE
QEKEKGQEDLKIIEEKRKEHKEAHQKAREKYGHLLWKKRSILRFLERKEQIPLKPKEKRERDSNVLSV IIKGDVD
GSVEAILNIIDTYDASHECELELVHFGVGDISANDVNLAETFDGVIYGFNVNAGNVIQQSAAKKGVKIKLHKI IY
RLVEDLQEELSSRLPCAVEEHPVGEASILATFSVTEGKKKVPVAGCRVQKGQLEKQKKFKLTRNGHVIWKGSITS
LKHHKDDISIVKTGMDCGLSLDEDNMEFQVGDRIVCYEEKQIQAKTSWDPGF

809/6881
FIGURE 753

GCGTGCCGGGTGTCATGGCGGCCTGCAGGTA CTGCTGCTCGTGCCCTCCGGCTCCGGCCCCCTGAGCGATGGTCCTT
TCCTTCTGCCACGGCGGGATCGGGCACTCAGGAGTTGCAAGTGCGAGCACTATGGAGTAGCGCAGGGTCTCGAG
CTGTGGCCGTGGACTTAGGCAACAGGAAATTAGAAATATCTTCTGGAAAGCTGGCCAGATTTGCAGATGGCTCTG
CTGTAGTACAGTCAGGTGACACTGCAGTAATGGTCACAGCGGTGAGTAAACAAAACCTTCCCCTTCCCAGTTTA
TGCCTTTGGTGGTTGACTACAGACAAAAGCTGCTGCAGCAGGTAGAATTCCCACAACTATCTGAGAAGAGAGA
TTGGTACTTCTGATAAAAGAAATTCTAACAAGTCGAATAATAGATCGTTCAATTAGACCGCTCTTTCCAGCTGGCT
ACTTCTATGATACACAGGTTCTGTGTAATCTGTTAGCAGTAGATGGTGTAATGAGCCTGATGTCCTAGCAATTA
ATGGCGCTTCCGTAGCCCTCTCATTATCAGATATTCTTTGGAATGGACCTGTTGGGGCAGTACGAATAGGAATAA
TTGATGGAGAATATGTTGTTAACCCAACAAGAAAAGAAATGTCTTCTAGTACTTTAAATTTAGTGGTTGCTGGAG
CACCTAAAAGTCAGATTGTGATGTTGGAAGCCTCTGCAGAGAACATTTTACAGCAGGACTTTTGCCATGCTATCA
AAGTGGGAGTGAAATATACCCAACAATAATTTCAGGGCATTTCAGCAGTTGGTAAAAGAACTGGTGTTACCAAGA
GGACACCTCAGAAGTTATTTACCCCTTCGCCAGAGATTGTGAAATATACTCATAAACTTGCTATGGAGAGACTCT
ATGCAGTTTTTACAGATTACGAGCATGACAAAGTTTCAGAGATGAAGCTGTTAACAAAATAAGATTAGATACGG
AGGAACAATAAAAAGAAAAATTTCCAGAAGCCGATCCATATGAAATAATAGAATCCTTCAATGTTGTTGCAAAGG
AAGTTTTTAGAAGTATTGTTTTGAATGAATACAAAAGGTGCGATGGTCGGGATTTGACTTCACTTAGGAATGTAA
GTTGTGAGGTAGATATGTTTAAAACCTTCATGGATCAGCATTATTTCAAAGAGGACAAACACAGGTGCTTTGTA
CCGTTACATTTGATTCAATAGAACTGTTGTTAAGTCAGATCAAGTTATAACAGCTATAAATGGGATAAAAGATA
AAAATTTTCATGCTGCACTACGAGTTTCTCTCTTATGCAACTAATGAAATGGCAAAGTCACTGGTTTAAATAGAA
GAGAACTTGGGCATGGTGCTCTTGCTGAGAAAGCTTTGTATCTGTTATTCCCCGAGATTTTCTTTTACCATAA
GAGTTACATCTGAAGTCCTAGAGTCAAATGGGTCATCTTCTATGGCATCTGCATGTGGCGGAAGTTTAGCATTAA
TGGATTGAGGGGTTCCAATTTTCATCTGCTGTTGTCAGGCGTAGCAATAGGATTGGTCAACAAAACCGATCCTGAGA
AGGGTGAAATAGAAGATTATCGTTTGCTGACAGATATTTTGGGAATTGAAGATTACAATGGTGACATGGACTTCA
AAATAGCTGGCACTAATAAAGGAATAACTGCATTACAGGCTGATATTAAATTACCTGGAATACCAATAAAAAATTG
TGATGGAGGCTATTCAACAAGCTTCAGTGGCAAAAAAGGAGATATTACAGATCATGAACAAAACCTATTTCAAAC
CTCGAGCATCTAGAAAAGAAAAATGGACCTGTTGTAGAACTGTTTCAAGGTTCCATTATCAAACGAGCAAAATTTG
TTGGACCTGGTGGCTATAACTTAAAAAACTTCAGGCTGAAACAGGTGTAATATTAGTCAGGTGGATGAAGAAA
CGTTTTCTGTATTTGCACCAACACCCAGTGCTATGCATGAGGCAAGAGACTTCATTACTGAAATCTGCAAGGATG
ATCAGGAGCAGCAATTAGAATTTGGAGCAGTATATACCGCCACAATAACTGAAATCAGAGATACTGGTGTAATGG
TAAAATTATATCCAAATATGACTGCGGTACTGCTTCATAACACACAACCTTGATCAACGAAAGATTAAACATCCTA
CTGCCCTAGGATTAGAAGTTGGCCAAGAAATTCAGGTGAAATACTTTGGACGTGACCCAGCCGATGGAAGAATGA
GGCTTTCTCGAAAAGTGCTTCAGTCGCCAGCTACAACCGTGGTCAGAACCTTGAATGACAGAAGTAGTATTGTAA
TGGGAGAACCTATTTACAGTCATCATCTAATTCTCAGTGATTTTTTTTTTTTAAAGAGAATTCTAGAATTCTATT
TTGTCTAGGGTGATGTGCTGTAGAGCAACATTTTAGTAGTATCTTCCATTGTGTAGATTTCTATATAATATAAAT
ACATTTTAATTATTTGTACTAAAATGCTCATTACATGTGCCATTTTTTAATTCGAGTAACCCATATTTGTTTA
ATTGTATTTACATTATAAATCAAGAAATATTTATTATTAAGTAAGTCATTATACATCTTAGAAAAAATTACA
TAGTTTTGTTTTTACAATTTCTGAAATATATGAAAACTTAGATAGAATATGTCATATGTTATTATAACAGATCTC
TTCTACATCTTATTTTCTTCTTTGTATACAGTAGTGACAGTTTACCTTCAGTCATCCTACAGGTCACCTCTGT
GCCAACAACCTTTACTTGCTTACAACGGTTCACAACTGGAACAGGCCATATTCAAAGCCAGTGCCTATTTCTTC
AGAACTGTTAACAGATATAGTGAGTTGAGGGAGCTAATCTGATACACTTTTGATAATATAATGCCTTTCAAATTA
GTTACCAAATCATAAACAGAGTGGAATAAATATAAATGAGATTCTAACTAGGATGAATGTGGTAGTAATGATGTA
TATTTTTCAAATTTACCTAAACAGAAAGATTATTGGCTAAGGCAGGCGGATCATGAGATCAGGAGATCGAGACCA
TCCTGGCTAACACGGTGAAACCCCGTCTCTACTAAAAGTGCAAAAATTAGCCGGGCGTGGTGGCGCATGCCTGTA
ATCCTAGCTACTCAGGAGGCTGAGGCAGAAGAATCACTTCAACCCAGGAGGTGGAGGTTGTAGTGAGCCGAGATT
GCGCCATTGCACTCCAGCTCAGGCAACAAGAGCAAACTCCGTCTC

810/6881
FIGURE 754

MAACRYCCSCLRLRPLSDGPFLLPRRDRAITQLQVRALWSSAGSRAVAVDLGNRKLEISSGKLARFADGSAVVQS
GDTAVMVTAVSKTKPSPSQFMPLVVDYRQAAAAGRIPTNYLRREIGTSDKEILTSRIIDRSIRPLFPAGYFYDT
QVLCNLLAVDGVNEPDVLAINGASVALSLSDIPWNGPVGAVRIGIIDGEYVVPTRKEMSSSTLNLVVAGAPKSQ
IVMLEASAENILQQDFCHAIKVGVKYTQQIIQGIQQLVKETGVTKRTPQKLETPSPEIVKYTHKLAMERLYAVFT
DYEHDKVSREAVNKRDLDEEQLKEKFPEADPYEIIIESFNVAKEVFERSIVLNEYKRCDDRDLTSLRNVSCVD
MFKTLHGSALFQRGQTQVLCTVTFDLSLESGIKSDQVITAINGIKDNFMLHYEFPPYATNEIGKVTGLNRRELGH
GALAEKALYPVIPRDFPFTIRVTSEVLESNGSSSMASACGSLALMDSGVPISSAVAGVAIGLVTKTDPEKGEIE
DYRLTDLILGIEDYNGDMDFKIAGTNKGITALQADIKLPGIPIKIVMEAIQQASVAKKEILQIMNKTISKPRASR
KENGPPVETVQVPLSKRAKRVGPGGYNLKKLQAETGVTISQVDEETFSVFAPTPSAMHEARDFITEICKDDQEQQ
LEFGAVYTATITEIRDTGVMVKLYPNMTAVLLHNTQLDQRKIKHPTALGLEVGQEIQVKYFGRDPADGRMRLSRK
VLQSPATTVVRTLNDRSSIVMGEPISQSSSNSQ

811/6881
FIGURE 755

GACAAGATGGCCACACCGGCGGTACCAGCAAGTGCTCCTCCGGCCACGCCAGCCCCAGTCCCGGCGGCGGTCCCA
GCCTCTGCCCCAGCCTCAGTTCAGCGCCAACGCCAGCACCGGCTGCGGCTCCGGTTCCCGCTGCGGCTCCAGCC
TCATCCTCAGACCCTGCGGCAGCATCGGCTACAAC TGCGGCTCCTGGCCAGACCCCGGCCTCAGCGCAAGCTCCA
GCGCAGACCCAGCGCCCGCTCTGCCTGGTCCTGCTCTTCCAGGGCCCTTCCCCGGCGGCGCGTGGTCAGGCTG
CACCCAGTCATTTTGGCCTCCATTGTGGACAGCTACGAGAGACGCAACGAGGGTGCTGCCCCGAGTTATCGGGACC
CTGTTGGGAAC TGTCGACAAACACTCAGTGGAGGTACCAATTGCTTTTCAGTGCCGCACAATGAGTCAGAAGAT
GAAGTGGCTGTTGACATGGAATTTGCTAAGAATATGTATGAACTGCATAAAAAAGTTTCTCCAAATGAGCTCATC
CTGGGCTGGTACGCTACAGGCCATGACATCACAGAGCACTCTGTGCTGATCCATGAGTACTACAGCCGAGAGGCC
CCCAACCCCATCCACCTCACTGTGGACACAAGTCTCCAGAACGGCCGCATGAGCATCAAAGCCTATGTCAGCACT
TTAATGGGTGTCCCTGGGAGGACCATGGGAGTGATGTTTACACCTCTGACAGTGAAATACGCATACTATGACACT
GAACGCATCGGAGTTGAGCTGATCATGAAGACCTGCTTTAGCCCCAACAGAGTGATTGGACTCTTAAGTGACTTG
CAGCAAGTAGGAGGGGCATCAGCTCGCATCCAGGATGCCCTGAGTACAGTGTTGCAATATGCAGAGGATGTACTG
TCTGGAAAGGTGTGAGCTGACAATACTGTGGGCCGCTTCCTGATGAGCCTGGTTAACCGAGTACCGAAAATAGTT
CCCGATGACTTTTGAGACCATGCTCAACAGCAACATCAATGACCTTTTGATGGTGACCTACCTGGCCAAACCTCACA
CAGTCACAGATTGCCCTCAATGAAAACTTGTAACCTGTGAATGGACCCCAAGCAGTACACTTGCTGGTCTAGG
TATTAACCCAGGACTCAGAAGTGAAGGAGAAATGGGTTTTTTGTGGTCTTGAGTCACACTGAGATAGTCAGTTG
TGTGTGACTCTAATAAACGGAGCCTACCTTTTGT

812/6881
FIGURE 756

MATPAVPASAPPATPAPVPAAVPASAPASVPAPTPAPAAAPVPAAAPASSSDPAAASATTAAPGQTPASAQAPAQ
TPAPALPGPALPGPFPGGRVVRLHPVILASIVDSYERRNEGAARVIGTLLGTVDKHSVEVTNCFSVPHNESEDEV
AVDMEFAKNMYELHKKVSPNELILGWYATGHDITEHSVLIHEYYSREAPNPIHLTVDTSLQNGRMSIKAYVSTLM
GVPGRTMGVMFTPLTVKYAYYDTERIGVELIMKTCFSPNRVIGLLSDLQQVGGASARIQDALSTVLQYAEDVLSG
KVSADNTVGRFLMSLVNRVPKIVPDDFETMLNSNINDLLMVTYLANLTQSQIALNEKLVNL

813/6881
FIGURE 757

GTTGGAGACTCGATTGTTGATGACAGCGGAAGAATGATAACAAAATGCCGGAGCGAGATAGTGAGCCGTTCTCCA
ACCCTTTGGCCCCCTGATGGCCACGATGTGGATGATCCTCACTCCTTCCACCAATCAAACTCACCAATGAAGACT
TCAGGAAACTTCTCATGACCCCCAGGGCTGCACCTACCTCTGCACCACCTTCTAAGTCACGTCACCATGAGATGC
CAAGGGAGTACAATGAGGATGAAGACCCAGCTGCACGAAGGAGGAAAAAGAAAAGTTATTATGCTAAGCTACGCC
AACAAGAAATTGAGAGAGAGAGAGAGCTAGCAGAGAAGTACCGGGGTCGTGCCAAGGAACGGAGAGATGGAGTGA
ACAAAGATTATGAAGAAACCGAGCTTATCAACACCACAGCTAACTACAGGGCTGTTGGCCCCACTACTAAGGCGG
ACAAATCAGCTGCAGAGAAGAGAAGACAGTTGATCCAGGAGTCCAAATTCTTGGGTGGTGACATGGAACACACCC
ATTTGGTGAAAGGCTTGGATTTTGCTCTGCTTCAAAGGTACGAGCTGAGATTGCCAGCAAAGAGAAAGAGGAAG
AGGAACTGATGGAAGACCCAGAAAGAAACCAAGAAAGATGAGGATCCTGAAAATAAAATTGAATTTAAACAC
GTCTGGGCCGCAATGTTTACCGAGTGCTTTTTAAGAACAAGCATATAAGCGGAATGAGTTGTTCTGCCGGGCGG
CATGGCCTATGTGGTAGGCCCTGGATGATGAGTAAGCTGACACAGATATCCCCACCACCTCTTATCCGCAGCAAGGT
TGACTGCCCCACCATGGAGGCCCAGACCATACTGACCACAAATGATATTGTCATTAGCAAGCTTACCCAGTTGCT
TTCATACCTGAGGCAGGGAACCCGTAACAAGAAGCTTAAGAAGAAGGATAAAGGGAAGCTGGAAGAGAAGAAACC
TGCTGAGGCTGACAGGAGTATTTTCGAAGACATTGGGGATTATACACCCTCCACAATCAAGACACCTTGGGACAA
GGAGCGGGAGAGATATCGGGAACGGGAGCGTGATCAGGAGACAGAGACCGTGACCGAGAGCGAGAGCGAGAACGA
GATCAGGAGCGAGAACGAGATCGGGAACGAGAGAGAGAAGAGGAAAAGAAGAGACACAGCTACTTTGAGAAGCCA
AAAGTACATGATGAGTCCGTGGACGTTGACAAAGGACCTGGGTGCGCCAAGGAGTTGATCAAGTCCATCAATGAA
AAGTTTGCTGGGTCTGCTGGCTGGGAAGGCACAGAATCGCTGAAAATTGCAGAAGACAAAAGCAGCTGAGAGAT
TTCTTTGGCATGTCCAACAGTTATGCAGAGTGCTATCCAGCCACGATGGATGACATGGCTGTGGATAGTGATGAG
GAGGTGGATTATAGCAAAATGGACCAGGGTAACAAGAAGAGAACCTTAAGCCGTTGGGACTTTGATACCCAGGAA
GACTACAGCGAGTATATGAACAACAAGAGGCTTTGCCCAAGGCTGCATTCCAGTATGGTATCAAAATGTCTGAA
GGGCGGAAAACCAGACGCTTCAAGGAAACCAATGACAAAGCAGCGCTCGATTGCCAGTGGAAGATTAGTGCAATC
ATTGAGAAGAGGAAGAAGATGGAAGCTGATGGGGTTGAAGTCAAAGACCAAATACTAA

814/6881
FIGURE 758

MPERDSEPF SNPLAPDGHVDVDPHSFHQSKLTNEDFRKLLMTPRAAPTSAPPSKSRHHEMPREYNEDEDPAARRR
KKKSYYAKLRQQEIERERELAEKYRGRAKERRDGVNKDYEETELINTTANYRAVGPTTKADKSAAEKRRQLIQES
KFLGGDMEHTHLVKGLDFALLQKVRAEIASKEKEEEEELMEKPQKETKKDEDPENKIEFKTRLGRNVYRVLFKNKH
ISGMSCSCRAAWPMW

815/6881
FIGURE 759

ATGCCCGAGAATGTGGCACCCCGGAGCGGGGCGACTGCCGGGGCTGCCGGCGGCCGCGGGAAAGGCGCCTATCAG
GACCGCGACAAGCCAGCCAGATCCGCTTCAGCAACATTTCCGCCGCCAAAGCGGTTGCTGATGCTATTAGAACA
AGCCTTGGACCAAAAGGAATGGATAAAATGATTCAAGATGGAAAAGGTGATGTAACCATTACAAATGATGGTGCT
ACCATTCTGAAACAAATGCAAGTATTACATCCAGCAGCCAGAATGCTGGTGGAGCTGTCTAAGGCTCAAGATATA
GAAGCAGGAGATGGCACCACATCAGTAGTCATCATTGCTGGCTCCCTCTTAGATTCTTGTACCAAGCTTCTTCAG
AAAGGGATTTCATCCAACCATCATTCTGAGTCATTCCAGAAGGCCCTGGAAAAGGGCATTGAAATCTTGACTGAC
ATGTCTCGACCTGTGGAACTGAGTGACAGAGAACTTTGTAAATAGTGCAACCACTTCACTGAACTCAAAGGTG
GTTTCTCAGTATTCAAGTCTGCTTTCTCCAATGAGTGTAATGCAGTGATGAAAGTGATTGACCCAGCCACAGCC
ACCAGTGTAGATCTTAGAGATATTAAAATAGTTAAGAAGCTTGGTGGGACAATTGATGACTGTGAGTTGGTGGAA
GGGCTGGTTCTCACCCAAAAGTGTCAAATCTGGCATAACCAGAGTTGAAAAGGCCAAGATTGGGCTTATTCAG
TTTTGCTTATCTGCTCCCAAAACAGACATGGATAATCAAATAGTGGTTTCTGACTATGCCAGATGGACCGAGTG
CTGCGAGAAGAGAGAGCCTATATTTTAAATTTAGTGAAGCAAATTAACAAAACAGGATGTAATGTCCTTCTCATA
CAGAAATCTATTCTAAGAGATGCTCTTAGTGATCTTGCATTACACTTTCTGAATAAAATGAAGATCATGGTGATT
AAGGATATTGAAAGAGAAGACATTGAATTCATTTGTAAGACAATTGGAACCAAGCCAGTTGCTCATATTGACCAA
TTTACTGCTGACATGCTGGGTTCTGCTGAGTTAGCTGAGGAGGTCAATTTAAATGGTTCCTGGCAAACCTGCTCAAG
ATTACAGGCTGTGCCAGCCCTGGAAAAACAGTTACAATTGTTGTTCTGTTGTTCTAACAACCTGGTGATTGAAGAA
GCTGAGCGCTCCATTTCATGATGCCCTATGTGTTATTCGTTGTTTAGTGAAAGAGGGCTCTTATTGCAGGAGGT
GGTGCTCCAGAAATAGAGTTGGCCCTAGCATTAACTGAATATTCACGAACACTGAGTGGTATGGAATCCTACTGC
GTTCTGCTTTTTCAGATGCTATGGAGGTCATTCCATCTACACTAGCTGAAAATGCCGGCCTGAATCCCATTTCT
ACAGTAACAGAACTAAGAAACCGGCATGCCAGGGAGAAAAAACTGCAGGCATTAATGTCCGAAAGGGTGGTATT
TCCAACATTTTGGAGGAACTGGTTGTCCAGCCTCTGTTGGTATCAGTCAGTGCTCTGACTCTTGCAACTGAACT
GTTCCGAGCATTCTGAAAATAGATGATGIGGTAAACACTCGATAATCTGGATAACTGACTAGCACCATTATGATC
ACCAGTATTGTGGCTGGAATGGAAGAAGATCACCTTGGTGTTCCTTGTTTGAAGATTATTTCTCTGAATTTCT
GGGCTTGGTCTTCCAGTTGGCATTGCTGAAGTTGTATTGAAACAATTTAATGAAAATATTAAATATTTGGTTT
CAAAAGGCAGATTTATCTTCTCCCAACATTCTGTTATTTCTGATACTTTTGAAAACTAATAAACTAATAAAA
GAAGCGTA

816/6881
FIGURE 760

MPENVAPRSGATAGAAGGRGKGAYQDRDKPAQIRFSNISAACAVADAIRTSLGPKGMDKMIQDGKGDVTTITNDGA
TILKQMQLHPAARMLVELSKAQDIEAGDGTTSVVI IAGSLLDSC TKLLQKGIHPTI ISESFQKALEK GIEILTD
MSRPVELSDRETLLNSATTSLNSKVVSQYSSLLSPMSVNAV MKVIDPATATSVDLRDIKIVKKLGGTIDDCELVE
GLVLTQKVSNSGITRVEKAKIGLIQFCLSAPKTDMDNQIVSDYAQM DRVLREERAYILNLVKQIKKTGCNVLLI
QKSILRDALSD LALHFLNKM KIMVIKDIEREDIEFICKTIGTKPVAHIDQFTADMLGSAELAE EVNLNGSGKLLK
ITGCASPGKTVTIVVRGSNKLVI EEAERSIHDALCVIRCLVKKRALIAGGGAPEIELALALTEYSRTL SGMESYC
VRAFADAMEVIPSTLAENAGLNP ISTVTELRNRHAQGEKTAGINVRKGGISNILEELVVQPLLVSVSALT LATET
VRSILKIDDVVNTR

817/6881
FIGURE 761A

AGGAAGGAAGGAGCAGTTGGTTCAATCTCTGGTAATCT**ATG**CCAGCAATTATGACAATGTTAGCAGACCATGCGAG
CTCGTCAGCTGCTTGATTTTCAGCCAAAACTGGATATCAACTTATTAGATAATGTGGTGAATTGCTTATACCATG
GAGAAGGAGCCCAGCAAAGAATGGCTCAAGAAGTACTGACACATTTAAAGGAGCATCCTGATGCTTGGACAAGAG
TCGACACAATTTTGGAAATTTTCTCAGAATATGAATACGAAATACTATGGACTACAAAATTTTGGAAAATGTGATAA
AAACAAGGTGGAAGATTCTTCCAAGGAACCAGTGCGAAGGAATAAAAAAATACGTTGTTGGCCTCATTATCAAGA
CGTCATCTGACCCAACTTGTGTAGAGAAAGAAAAGGTGTATATCGGAAAATTAAATATGATCCTTGTTCAGATAC
TGAAACAAGAATGGCCCAAACATTGGCCAACTTTTATCAGTGATATTGTTGGAGCAAGTAGGACCAGCGAAAGTC
TCTGTCAAAATAATATGGTGATTCTTAAACTCTTGAGTGAAGAAGTATTGATTTCTCTAGTGGACAGATAACCC
AAGTCAAATCTAAGCATTTAAAAGACAGCATGTGCAATGAATTCTCACAGATATTTCAACTGTGTCAAGTTTGTA
TGGAAAATTCTCAAAATGCTCCACTTGTACATGCAACCTTGGAAACATTGCTCAGATTTCTGAACTGGATTCCCC
TGGGATATATTTTTGAGACCAAATTAATCAGCACATTGATTTATAAGTTCCTGAATGTTCCAATGTTTCGAAATG
TCTCTCTGAAGTGCCTCACTGAGATTGCTGGTGTGAGTGTAAAGCCAATATGAAGAACAATTTGTAACACTATTTA
CTCTGACAATGATGCAACTAAAGCAGATGCTTCCTTTTAAATACCAATATTCGACTTGCCTACTCAAATGGAAAAAG
ATGATGAACAGAACTTCATTCAAAATCTCAGTTTGTCTCTGACCTTTCTTAAGGAACATGATCAACTTATAG
AAAAAGATTAAATCTCAGGGAAAACCTTTATGGAGGCCCTTCATTATATGTTGTTGGTATCTGAAGTAGAAGAAA
CTGAAATCTTTAAAATTTGTCTTGAATACTGGAATCATTTGGCTGCTGAACTCTATAGAGAGAGTCCATTCTCTA
CATCTGCCTCTCCGTTGCTTTCTGGAAGTCAACATTTTGATGTTCCCTCCAGGAGACAGCTATATTTGCCCATGT
TATTCAGGTCCGTTTATTAATGGTTAGTCTGAATGGCTAAACCAGAGGAAGTATTGGTTGTAGAGAATGATCAAG
GAGAAGTTGTGAGAGAATTCATGAAGGATACAGATTCCATAAATTTGTATAAGAATATGAGGGAAACATTGGTTT
ATCTTACTCATCTGGATTATGTAGATACAGAAAGAATAATGACAGAGAAGCTTCACAATCAAGTGAATGGTACAG
AGTGGTCATGGAAAAATTTGAATACATTGTGTTGGGCAATAGGCTCCATTAGTGGAGCAATGCATGAAGAGGACG
AAAAACGATTTCTTGTACTGTTATAAAGGATCTATTAGGATTATGTGAACAGAAAAGAGGCCAAAGATAATAAAG
CTATTATTGCATCAAAATATCATGTACATAGTAGGTCAATACCCACGTTTTTTGAGAGCTCACTGGAAATTTCTGA
AGACTGTAGTTAACAAGCTGTTTGAATTCATGCATGAGACCCATGATGGAGTCCAGGATATGGCTTGTGATACTT
TCATTAAAATAGCCCAAAAATGCCGCAGGCATTTTCGTTTCAGGTTTCAGGTTGGAGAAGTGATGCCATTTATTGATG
AAATTTTGAACAACATTAACACTATTATTTGTGATCTTCAGCCTCAACAGGTTTCATACGTTTTTATGAAGCTGTGG
GGTACATGATTGGTGCACAAACAGATCAAACAGTACAAGAGCACTTGATAGAAAAGTACATGTTACTCCCTAATC
AAGTGTGGGATAGTATAATCCAGCAGGCAACCAAAAATGTGGATATACTGAAAGATCCTGAAACAGTCAAGCAGC
TTGGTAGCATTTTGAAAACAAAATGTGAGAGCCTGCAAAGCTGTTGGACACCCCTTTGTAATTCAGCTTGGAAAGAA
TTTATTTAGATATGCTTAATGTATACAAGTGCCTCAGTGAATAATTTCTGCAGCTATCCAAGCTAATGGTGAAA
TGGTTACAAAGCAACCATTGATTAGAAGTATGCGAACTGTAAAAAGGGGAAAACTTTAAAGTTAATATCTGGTTGGG
TGAGCCGATCCAATGATCCACAGATGGTTCGCTGAAAATTTTGTTCCTCTGTTGGATGCAGTTCTCATTGATT
ATCAGAGAAATGTCCAGCTGCTAGAGAACCAGAAGTGCTTAGTACTATGGCCATAATTGTCAACAAGTTAGGGG
GACATATAACAGCTGAAATACCTCAAATATTTGATGCTGTTTTTGAATGCACATTGAATATGATAAATAAGGACT
TTGAAGAATATCCTGAACATAGAACGAACCTTTTTCTTACTACTTCAGGCTGTCAATTCTCATTGTTTCCCAGCAT
TCCTTGCTATTCCACCTACACAGTTTAAACTTGTTTTGGATTCCATCATTGGGGCTTCAAACATACTATGAGGA
ATGTCGCAGATACGGGCTTACAGATACTTTTTACACTCTTACAAAATGTTGCACAAGAAGAAGCTGCAGCTCAGA
GTTTTTATCAAACCTTATTTTTGTGATATTCTCCAGCATATCTTTTCTGTTGTGACAGACACTTCACATACTGCTG
GTTTAAACAATGCATGCATCAATTCTTGCATATATGTTTAAATTTGGTTGAAGAAGGAAAAATAAGTACATCATTAA
ATCCTGGAAATCCAGTTAACAACCAAATCTTTCTTCAGGAATATGTGGCTAATCTCCTTAAGTCGGCCTTCCCTC
ACCTACAAGATGCTCAAGTAAAGCTCTTTGTGACAGGGCTTTTCAGCTTAAATCAAGATATTCCTGCTTTCAAGG
AACATTTAAGAGATTTCTAGTTCAAATAAAGGAATTTGCAGGTGAAGACACTTCIGATTTGTTTTTGGAAAGAGA
GAGAAATAGCCCTACGGCAGGCTGATGAAGAGAAACATAAACGTCAAATGTCTGTCCCTGGCATCTTTAATCCAC
ATGAGATTCAGAAAGAAATGTGTGAT**TAA**AATCCAAATTCATGCTGTTTTTTTTCTCTGCAACTCCGTTAGCAGA
GGAAAACAGCATGTGGGTATTTGTGACCAAAATGATGCCAATTTGTAAATTAAATGTACCTAGTGGCCCTTT
TTCTTATGTGTTTTTTTTGTATAAGAAATTTCTGTGAAATATCCTTCCATTGTTTAAAGCTTTTGTGTTGGTTCATC
TTTATTTAGTTTGCATGAAGTTGAAAATTAAGGCATTTTTAAAAATTTTACTTCATGCCCATTTTTGTGGCTGGG
CTGGGGGGGAGGAGGCAAATTCAAATTTGAACATATACTTGTAATTCTAATGCAAAATTATACAATTTTTCTCTGTAA

818/6881
FIGURE 761B

ACAATACCAATTTTAAATTAGGGAGCATTTTCCTTCTAGTCTATTTTCAGCCTAGAAGAAAAGATAATGAGTAAAA
CAAATTGCGTTGTTTAAAGGATTATAGTGCTGCATTGTCTGAAGTTAGCACCTCTTGGACTGAATCGTTTGCTA
GACTACATGTATTACAAAGTCTCTTTGGCAAGATTGCAGCAAGATCATGTGCATATCATCCCATTGTAAAGCGAC
TTCAAAAATATGGGAACACAGTTAGTTATTTTTACACAGTTCTTTTGTGTTTTGTGTGTGTGTGCTGTGCTTGT
CGACAACAGCTTTTTGTTTTCTCAATGAGGAGTGTTGCTCATTGTGAGCCTTCATTAACTCGAAGTGAAATGG
TTAAAAATATTTATCCTGTTAGAATAGGCTGCATCTTTTAAACAACCTCATTAAAAAACAAACAACCTCTGGCTTT
TGAGATGACTTATACTAATTTACATTGTTTACCAAGCTGTAGTGCTTTAAGAACACTACTTAAAAAGCAAAATAA
ACTTGGTTTACATTTAAAAAAA

819/6881
FIGURE 762

MPAINTMLADHAARQLLDFSQKLDINLLDNVNCCLYHGEGAQQORMAQEVLTHLKEHPDAWTRVDTILEFSQNMNT
KYYGLQILENVIKTRWKILPRNQCEGIKKYVVGLIIKTSSDPTCVEKEKVYIGKLN MILVQILKQEWPKHWPTFI
SDIVGASRTSESLCQNNMVILKLLSEEVDFDFSSGQITQVKS KHLKDSMCNEFSQIFQLCQFVMENSQNA PLVHAT
LETLLRFLNWIPLGYIFETKLISTLIYKFLNVPMFRNVSLKCLTEIAGVSVSQYEEQFVTLFTLTMMQLKQMLPL
NTNIRLAYSNGKDDEQNF IQNLSLFLCTFLKEHDQLIEKRLNLRETLM EALHYMLLVSEVEETE IFKICLEYWNH
LAAELYRESPFSTSASPLLSGSQHFDVPPRRQLYLPMLFKVRLLMVSRMAKPEEVLVVENDQGEVVREFMKD TDS
INLYKNMRETLVYLTHLDYVDTERIMTEKLNQVNGTEWSWKNLNTLCWAIGSISGAMHEEDEKRFLVTVIKDLL
GLCEQKRGKDNKAI IASNIMYIVGQYPRFLRAHWKFLKTVVNKLFEFMHETHDGVQDMACDTFIKIAQKCR RHV
QVQVGEVMPFIDEILNNINTIICDLQPQQVHTFYEA VGYMIGAQTDQTVQEH LIEKYMLLPNQVWDSIIQQATKN
VDILKDPETVKQLGSILKTNVRACKAVGHPFVIQLGRIYLDMLNVYKCLSENISAAIQANGEMVTKQPLIRSMRT
VKRETLKLISGWVSRSDPQMVAENFVPPLLD AVLIDYQRNVPAAREPEVLSTMAIIVNKLGGHITAEIPQIFDA
VFECTLMINKDFEEYPEHRTNFFLLLQAVNSHC FPAFLAIPPTQFKLVLD SIIWAFKHTMRNVADTGLQILFTL
LQNVAQEEAAAQSFYQTYFCDILQHIFSVVTDTSHTAGLTMHASILAYMFNLVEEGKISTSLNPGNPVNNQIFLQ
EYVANLLKSAPPHLQDAQVKLFVTGLFSLNQDIPAFKEHLRDFLVQIKEFAGEDTSDLFLEEREIALRQADEEKH
KRQMSVPGIFNPHEIPEEMCD

820/6881
FIGURE 763

GGCGGCGGCAGCAGCTGCTTGGGCGCCGTGCGGTGGTGA CTGAGCTACGAGCCTGGCAGCAGGTGTGCGCCGAGC
CCCGGCCTGGCCCGGCCCCGCGTGCTTCCAGGCTCCGCACCCCTGATGCTGCGCGGGTGCTGAGCCCACTTCG
GCCAGGACGATGGTTAAGTATTTCTTGGGCCAGAGCGTGCTCCGGAGTTCTTGGGACCAAGTGTTGCGCGCCTTC
TGGCAGCGGTACCCGAATCCCTATAGCAAACATGTCTTGACGGAAGACATAGTACACCGGGAGGTGACCCCTGAC
CAGAAACTGCTGTCCCGGCGACTCCTGACCAAGACCAACAGAATGCCACGCTGGGCCAAGCAACTATTTCTTGCC
AATGTTGCTCACTCGGTGTACATCCTGGAGGACTCTATTGTGGACCCACAGAATCAGACCATGACTACCTTCACC
TGGAACATCAACCACGCCCCGGCTGATGGTGGTGGAGGAACGATGTGTTTACTGTGTGAACTCTGACAACAGCGGC
TGGACTGAAATCCGCCGGGAAGCCTGGGTCTCTCTAGCTTATTTGGTGTCTCCAGAGCTGTCCAGGAATTTGGT
CTTGCCCAAGTTCAAAAGCAACGTGACCAAGACTATGAAGGGTTTTGAATATATCTTGACTAAGCTGCAAGGCGAG
GCCCCCTTCCAAAACACTTGAGACAGCCAAGGAAGCCAAGGAGAAGGCAGAGGAGACGGCACTGGCAGCTACAGAG
AAGGCCAAGGACCTCGCCAGCAAGGCGGCCACCAAGAAGCAGCAGCAGCAGCAACAGTTTGTGTAGCCAGCCAC
CACCACCACAGCAACCCAGACAGCTAGGCTTAGCCCCTCTGCCCTCCCTCCATTGTACTTTATCATTAAAAATCA
ACTTCCA

821/6881
FIGURE 764

CTGACTCTCTGAGGCTCATTGTCAGTTGTTGAAATTGTCCCGCAGTTTTCAATC**ATGT**CTGAACCAATCAGAG
TCCTTGTGACTGGAGCAGCTGGTCAAATTGCATATTCAGTGTACAGTATTGGAAATGGATCTGTCTTTGGTA
AAGATCAGCCTATAATTCTTGTGCTGTTGGATATCACCCCATGATGGGTGTCCTGGACGGTGTCTAATGGAAC
TGCAAGACTGTGCCCTTCCCCCTCCTGAAAGATGTCATCGCAACAGATAAAGAAGACGTTGCCTTCAAAGACCTGG
ATGTGGCCATTCTTGTGGGCTCCATGCCAAGAAGGGAAGGCATGGAGAGAAAAGATTTACTGAAAGCAAATGTGA
AAATCTTCAAATCCCAGGGTGCAGCCTTAGATAAAATACGCCAAGAAGTCAGTTAAGGTTATTGTTGTGGGTAATC
CAGCCAATACCAACTGCCTGACTGCTTCCAAGTCAGCTCCATCCATCCCCAAGGAGAACTTCAGTTGCTTGACTC
GTTTGGATCACAACCGAGCTAAAGCTCAAATTGCTCTTAAACTTGGTGTGACTGCTAATGATGTAAAGAATGTCA
TTATCTGGGGAAACCATTCTCGACTCAGTATCCAGATGTCAACCATGCCAAGGTGAAATTGCAAGGAAAGGAAG
TTGGTGTGTTATGAAGCTCTGAAAGATGACAGCTGGCTCAAGGGAGAATTTGTCACGACTGTGCAGCAGCGTGGCG
CTGCTGTCATCAAGGCTCGAAAACCTATCCAGTGCCATGTCTGCTGCAAAAGCCATCTGTGACCACGTCAGGGACA
TCTGGTTTGAACCCCAGAGGGAGAGTTTGTGTCCATGGGTGTTATCTCTGATGGCAACTCCTATGGTGTTCCTG
ATGATCTGCTCTACTCATTCCCTGTTGTAATCAAGAATAAGACCTGGAAGTTTGTGTAAGGTCTCCCTATTAATG
ATTTCTCACGTGAGAAGATGGATCTTACTGCAAAGGAAGTACAGAAGAAAAAGAAAGTGCTTTTGAATTTCTTT
CCTCTGCC**TGACT**AGACAATGATGTTACTAAATGCTTCAAAGCTGAAGAATCTAAATGTCGTCTTTGACTCAAGT
ACCAAATAATAATAATGCTATACTTAAATTACTTGTGAAAAACAACACATTTTAAAGATTACGTGCTTCTTGGTA
CAGGTTTGTGAATGACAGTTTATCGTCATGCTGTTAGTGTGCATTCTAAATAAATATATATTCAAATG

822/6881
FIGURE 765

MSEPIRVLVTGAAGQIAYSLLYSIGNGSVFGKDQPIILVLLDITPMMGVLDGVLMELODCALPLLKDVIATDKED
VAFKDLDVAILVGSMRREGMERKDLLKANVKIFKSQGAALDKYAKKSVKVIVVGNPANTNCLTASKSAPSIPKE
NFSCLTRLDHNRKAQIALKLGV TAN DVKNV I I WGNHSSTQYPDVNHAKVKLQKKEVG VYEALKDDSWLKGEFVT
TVQQRGA AVIKARKLSSAMSAKAICDHVRDIWFGTPEGEFVSMGVISDGNSYGV PDDLLYSFPVVIKNKTWK FV
EGLPINDFSREKMDLTAKELTEEKESAFEFLSSA

823/6881
FIGURE 766

TCTTTTAAGTATACTCTCTACTTATTAAAAAAGTCCTTTCCACGCTACCTGCAGAGGGGTCCATACG
GCGTTGTTCTGGATTCCCATCGTAACTTAAAGGGAACTTTACAAATGTCCGGAGCCCTTGATGTCCTGCAAATG
AAGGAGGAGGATGTCCTTAAGTTCCTTGCGCAGGAAGTCACTTAGGTGGCACCAATCTTGACTTCCAGATGGAA
CAGTACATCTATAAAAGGAAAAGTGATGGCATCTATATCATAAATCTGAAGAGGACCTGGGAGAAGCTTCTGCTG
GCAGCTCGTGCTATTGTTGCCATTGAAAACCCCTGCTGATGTCAGTGTTATATCCTCCAGGAATACTGGCCAGAGG
GCCGTGCTAAAGTTTGCTGCTGCCACTGGAGCCACTCCAATTGCTGGCCGCTTCACTCCTGGAACCTTCGCTAAC
CAGATCCAGGCAGCCTTCCGGGAGCCACGGCTTCTTGTTGGTTACTGACCCAGGGCTGACCACCAGCCTCTCATG
GAGGCATCTTATGTTAACCTACCTACCATTCGCTGTGTAACACAGATTCTCCTCTGCACTATGTGGACATTGCC
ATCCCATGCAACAACAAGGGAGCTCACTCAGTGGGTTTGATGTGGTGGATGCTGGCTCGGGAAGTTCTGCGCATG
CGTGGCACCATTTTCTGTGAACACCCATGGGAGGTCATGCCTGATCTGTACTTCTACAGAGATCCTGAAGAGATT
GAAAGAGAAGAGCAGGCTGCTGCTGAAAAGGCAGTGACCAAGGAGGAATTCAGGGTGAATGGACTGCTCCAGCT
CCTGAGTTCACTGTTACTCAGCCTGAGGTTGCAGACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCTATTCCC
TACTGAAGACGGGAGCGCTCAGCCTGCCACGGAAGACTGGTCTGCAGCTCCCACTGCTCAGGCCACTGAATGGGT
AGGAGCAACCACTGACTGGTCTTAAGCTGTTCTTGCATAGGCTCTTAAGCAACATGGAAAAATGGTTGATGGAAA
ATAAACATCAGTTTCT

824/6881
FIGURE 767

MSGALDVLQMKEEDVLKFLAAGTHLGGTNLDFQMEQYIYKRKSDGIYIINLKRTWEKLLLAARAIVAIENPADVS
VISSRNTGQRAVLKFAAATGATPIAGRFTPGTFANQIQAAFREPRLLVVTDPRADHQPLMEASYVNLPTIALCNT
DSPLHYVDIAIPCNNKGAHSVGLMWWMLAREVLRMRGTISCEHPWEVMPDLYFYRDPFEEIEREEQAAAEKAVTKE
EFQGEWTAPAPEFTVTQPEVADWSEGVQVPSVPIPY

825/6881
FIGURE 768

GCAGAGGGGTCCATACGGCGTTGTTCTGGATTCCCATCGTAACTTAAAGGGAACTTTCACAATGTCCGGAGCCC
TTGATGTCCTGCAAATGAAGGAGGAGGATGTCCTTAAGTTTCCTTGCAGCAGGAACTCACTTAGGTGGCACCAATC
TTGACTTCCAGATGGAACAGTACATCTATAAAAGGAAAAGTGATGGCATCTATATCATAAATCTGAAGAGGACCT
GGGAGAAGCTTCTGGCCGCTTCACTCCTGGAACCTTCGCTAACCAGATCCAGGCAGCCTTCCGGGAGCCACGGCT
TCTTGTGGTTACTGACCCCAGGGCTGACCACCAGCCTCTCATGGAGGCATCTTATGTTAACCTACCTACCATTGC
GCTGTGTAACACAGATTCTCCTCTGCACTATGTGGACATTGCCATCCCATGCAACAACAAGGGAGCTCACTCAGT
GGGTTTGATGTGGTGGATGCTGGCTCGGGAAGTTCTGCGCATGCGTGGCACCATTTTCCTGTGAACACCCATGGGA
GGTCATGCCTGATCTGTACTTCTACAGAGATCCTGAAGAGATTGAAAGAGAAGAGCAGGCTGCTGCTGAAAAGGC
AGTGACCAAGGAGGAATTTCAAGGTGAATGGACTGCTCCAGCTCCTGAGTTCACTGTTACTCAGCCTGAGGTTGC
AGACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGC

826/6881
FIGURE 769

MSGALDVLQMKEEDVLKFLAAGTHLGSTNLDFQMEQYIYKRKSDGIYIINLKRTWEKLLASLLEPSLTRSRQPSG
SHGFLWLLIPGLTTSLSQRHLKLTYPLLCVTQILLCAMWTLP SHATARELTQWV

827/6881
FIGURE 770

GGCCCAGCTGCTGAGAGGAGTTGCCTGAGAGTGACCTTTGCATCTGCCTGTCCAGCCAGCATGGAACCAAAGCGG
ATCAGAGAGGGCTACCTTGTGAAGAAGGGGAGCGTGTTCAATACGTGGAACCCATGTGGGTTGTATTGTTAGAA
GATGGAATTGAATTCTATAAGAAGAAAAGTGACAAACAGCCCCAAAGGAATGATCCCGCTGAAAGGGAGCACTCTG
ACTAGCCCTTGTCAAGACTTTGGCAAAAAGGATGTTTTGTGTTAAGATCACTACGACCAAACAGCAGGACCACTTC
TTCCAGGCAGCCTTCTCGGAGGAGAGAGATGCCTGGGTTCGGGATATCAAGAAGGCCATTAAATGCATTGAAGGA
GGCCAGAAATTTGCCAGGAAATCTACCAGGAGGTCCATTGACTGCCAGAAACCATTTGACTTAGGTGCCTTATAT
TTGTCCATGAAAGACACTGAAAAAGGAATAAAAGAACTGAATCTAGAGAAGGACAAGAAGATTTTTAATCACTGC
TTCACAGGTAACATGCGTCATTGATTGGCTGGTATCCAACCAGTCTGTTAGGAATCGCCAGGAAGGCCTCATGATT
GCTTCATCGCTGCTCAATGAGGGGTATCTGCAGCCTGCTGGAGACATGTCCAAGAGTGCAGTGGATGGAACCTGCT
GAAACCCCTTTTCTGGACAACCCCTGATGCCTTCTACTACTTTCCAGACAGTGGGTTCTTCTGTGAAGAGAATTCC
AGTGATGATGATGTGATTCTGAAGAAGAATTGAGAGGGGTCAATTATCAAGCAGGGATGTTTACTGAAGCAGGGG
CATAGAAGGAAAACTGGAAAGTGAGGAAGTTCATCTTGAGAGAAGACCCTGCCTACCTGCACTACTATGACCCT
GCTGGGGCAGAAGATCCCCTGGGAGCAATTCACCTTGAGAGGCTGTGTGGTGACTTCAGTGGAGAGCAACTCAAAT
GGCAGGAAGAGTGAGGAAGAGAACCTTTTTGAGATCATCACAGCAGATGAAGTGCCTATTTCTTGCAAGCAGCC
ACCCCAAGGAGCGCACAGAGTGGATCAGAGCCATCCAGATGGCCTCCCGAACTGGGAAGTAAAGAGACTCCTGC
ATTCTCTCTCCCCTCTGAGGGAAGCCCATGGACAAGCTCAGTCCAGGACCTGTCCACTTCTGTGACAAATCAAC
GGGAAACAGCCCAGGGGTGGGAAGTTTTTCATTTGCAGGGGGTCTGAATGTAACCTACCATGTGGTGTGCAAGGT
TCCCCTGCATTGTATTGCTCACTGCAGCCCCCTCTGCCCTATCCATGACCCCAAGCAGATATAACAAGCTGTGC
AGCCTCAGTAGGCTGCTTGCCCTCTCCAGGCCCTCAGGGCCTCTTCTGGAAAATGAAGAAATTCAACTAGTAGATT
CCTGAGGTCCCCCTAGCTTAAAAAATAAATACTGCCCCATGATTCTAACACTCGCAGTAGTGATAGTGTATC
TAGTTGTTCTGCTGGTGTCTTCTTGGCTAAGTCTTGGCCTTCAGTTATCTTCAAATGTACCAGAACCTGAGCC
AACGCCTCCCTGTGAACTGTTGCTGATCTGTAGTACAGTACCAGGAAGAAACCTCTTTTGTCTCTTTAGACAT
CTTCTACTTGCTCTTGGCCTTGAGATCGTGTAACAAAATGAAGGAGGGCTCTCTTCTTTCTTCTCATCTACTC
AAAAACTTCCCGAGAGCAGTGGTGGTTTTGAGGGTTTTGACTTCTATTACTTTTGGCAGCCTGGAAAGTTGTGTC
TTCTGGGAAAGAGACCTGGGGAGGCCAGGAGTAGCTGAGGGTCTTTTCTGTGCCCTTAAACCGCCCAGAGGAGCC
CTATTCCACTCTGGTTTTTAGGCTGATCTGAGAGGGTCTCCCTTTGTTCTTTCTGGAGCATTTCTCTAACGTTTA
TTACAATTAGGAGGGGGACCCACATCTGTGAGATTCTGTTTCATTTGAGGTTTACAGAAAAAAGTGGCCA
GATGTGTTCCCCCATGGGTGAGAGGCCCTGGGCAACTGCCTGGTGAATGTGTCTTGCGGCAGCTGCAGCAAGTGG
AGGGGCTGAACTACTGGCCAGCTCACTGGATGATGGGTAAATACAACAACCTGCACTGTAAGGACTCAGAGCCACA
CAGAACTTCTGAGAGGGGCTGTTAGCATTGCGCAGCATCTTCAGTTCTCCAGTAAATGATATTGCGTTCGTGCCT
CAGCTTTAAGCACAAGTAGCAGCAGCTCCTGCTTGAGTTCTGAGGGCATCATGGCCCTATGATTAACCAGAGTGA
TCTAACCTAGACTAAAATTGGGAACCTATTTGCAATTTTTGACCCTGACCACTAACTAGTGATTCTTCTCCAAAA
TTGAGAAAGACAGCACCCATTGAAGCAGATATGTGTGTGAAAGTATATTTTTCAATCCAGATTTTTAATTTTAA
GGCTCCAGGAAAGAAAGGAGAGTAGAACATTTTTCTCATTTTATCAAATCCTCTCTTGCCCTCCCTCAATTCCC
CTGTAAACATTCCCTGAAGCTGTTCCCACTCCAGATGGTTTTATCAATAGCCTAGAGGTAAAGAACTGTCTTTTC
TCTGATTCTTTAATAAATTATCTTTATAGAATATGCACAAGTTTTTCTACACTCAGTGTTAAAGTATTTATTAAT
GGGAAGTCAACTTAATGTTTTGAAATAAATATATGACTCTGTTTAAAT

828/6881
FIGURE 771

CTTTCGGGAGACTGGAGTCGAAGGCCGTGAGGTATTTTCTAAGXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXAACCCCGGAGGAGGGTGAGGAGCAGAGCTGGCCATAATGGCAGGTGAAGAAATTAATGAAGACTAT
CCAGTAGAAATTCACGAGTATTTGTCAGCGTTTGAGAATCCATTGGTGCTGTGGATGAGATGCTGAAGACCATG
ATGTCTGTTTCTAGAAATGAGTTGTTGCAGAAGTTGGATCCACTTGAACAAGCAAAAGTGGATTTGGTTTCTGCA
TACACATTAAATTCAATGTTTTGGGTTTATTTGGCAACCCAAGGAGTTAATCCTAAGGAACATCCAGTAAACAG
GAATTGGAAAGAATCAGAGTATATATGAACAGAGTCAAGGAAATAACAGACAAGAAAAAGGCTGGCAAGCTGGAC
AGAGGTGCAGCTTCAAGATTTGTAAAAATGCCCTCTGGGAACCAAAATCGAAAAATGCATCAAAAGTTGCCAAT
AAAGGAAAAAGTAAAGTTAACTTTTTGGTTTTGATGTACACATATTCAAAAAGTACATTAATATGTAAATTCAC
AGTAAATATGTAAAGCTAAATACTTTCCTCTCCAAAGATCATTATCTTTATTGATTAGCACTGAGGATTTTAAACA
TTGTGATATATTATATATTTATAATTTACCATCTCTTGATGAGACTCTTATTTCTTTATATAGGTCAGTCTTGCA
AGTACCATTTTATAAGCAGCTGTGAAATTTAAGTGAAATGTTCTTTGTAAACATTTGTACTATTTTAAATGAATA
ATGACCTTATGAAGTATGCTATCTGTAGGCTGAAATTATAGGTACATCTGTTTTCACTATATGATATTAAGAAAG
CGTGAAATGACTTAAATGTTCATTTTTTTTCTGTATAGATACTTTATCATGTTTTCATGATTTTAGGAATTACTGC
TTTGTTGATATTCAAAGTGTGAACTAAAACTTTATGGTTGTACTTTAATTCTTGGCATGTTGCCTCTATGTCCC
ATTTAAATAAAATACATTCTCATTAACTTTAGATGGGAAATAAGGTTGTATGTTGATGGATGAATTTGGCATG
ATGACTGTACTCTCAATAAAGGCTGAAATGTTGT

829/6881
FIGURE 772

CCTTCACTTCGCCCTCCAGCTGCTGCAGCTGCAGCCCGACCGCGAGCGTGCCAAGCGGCTTCAGCAGCTAGCGGA
GCGGTGGCGGCGGCCCCGCTCAGGAGACCACCAGATTCCCCTCTTCCCGCGGCCTCGCCATGGCGACCCACGGAC
AGACTTGCGCGCGTCCAATGTGTATTCCCTCCATCATATGCTGACCTTGGCAAAGCTGCCAGAGATATTTTCAACA
AAGGATTTGGTTTTGGGTGGTGAAACTGGATGTGAAAACAAAGTCTTGCAGTGGCGTGGAATTTTCAACGTCCG
GTTCACTCTAATACAGACACTGGTAAAGTTACTGGGACCCTGGAGACCAAATACAAGTGGTGTGAGTATGGTCTGA
CTTTCACAGAAAAGTGGAACACTGATAACACTCTGGGAACAGAAATCGCAATTGAAGACCAGATTTGTCAAGGTT
TGAAACTGACATTTGATACTACCTTCTACCAAATCAAAGCTGACAAGGAATAACTTTGCAGTGGGCTACAGGAC
TGGGGACTTCCAGCTACACACTAATGTCAATGATGGGACAGAATTTGGAGGATCAATTTATCAGAAAGTTTGTGA
AGATCTTGACACTTCAGTAAACCTTGCTTGGACATCAGGTACCAACTGCACTCGTTTTGGCATTGCAGCTAAATA
TCAGTTGGATCCCACTGCTTCCATTTCTGCAAAGTCAACAACCTCTAGCTTAATTGGAGTAGGCTATACTCAGAC
TC

830/6881
FIGURE 773

AGCTGCTGCAGCTGCAGCCCCGACCGCGAGCGTGCCAAAGCGGCTTCAGCAGCTAGCGGAGCGGTGGCGGCGGCCCC
GCTCAGGAGACCACCAGATTCCCCTCTTCCCGCGGCCTCGCCATGGCGACCCACGGACAGACTTGCGCGCGTCCA
ATGTGTATTCTCCATCATATGCTGACCTTGGCAAAGCTGCCAGAGATATTTTCAACAAAGGATTTGGTTTTGGG
TTGGTGAAACTGGATGTGAAAACAAAGTCTTGCAGTGGCGTGGAATTTTCAACGTCCGGTTCATCTAATACAGAC
ACTGGTAAAGTTACTGGGACCCTGGAGACCAAATACAAGTGGTGTGAGTATGGTCTGACTTTCACAGAAAAGTGG
AACACTGATAACACTCTGGGAACAGAAATCGCAATTGAAGACCAGATTTGTCAAGGTTTGAAACTGACATTTGAT
ACTACCTTCTCACCAAACACAGGAAAGAAAAGTGGTAAAATCAAGTCTTACAAGAGGGAGTGTATAAACCTTGGT
TGTGATGTTGACTTTGATTTTGTGGACCTGCAATCCATGGTTCAGCTGTCTTTGGTTATGAGGGCTGGCTTGCT
GGCTACCAGATGACCTTTGACAGTGCCAAATCAAAGCTGACAAGGAATAACTTTGCAGTGGGCTACAGGACTGGG
GACTTCCAGCTACACACTAATGTCAATGATGGGACAGAATTTGGAGGATCAATTTATCAGAAAAGTTTGTGAAGAT
CTTGACACTTCAGTAAACCTTGCTTGGACATCAGGTACCAACTGCACTCGTTTTGGCATTGCAGCTAAATATCAG
TTGGATCCCCTGCTTCCATTTCTGCAAAAGTCAACAACCTCTAGCTTAATTGGAGTAGGCTATACTCAGACTCTG
AGGCCTGGTGTGAAGCTTACACTCTCTGCTCTGGTAGACGGGAAGAGCATTAAATGCTGGAGGCCACAAGGTTGGG
CTCGCCCTGGAGTTGGAGGCTTAATCCAGCTGAAAGAAACCTTTGGGAATGGATATCAGAAGATTTGGCCTTAAT
ATATTTCCATTGTGACCAGCAGCAGGCTTTTTTCCCCAAGAAGATGATCAAAACAAAGGATGATCTCAACAAGA
GCTGTATTTTAAGTATTTAGACAGTTCTTTGTTAGCTGGTTTCTAGTTGAATTGGTTATCTAGTTACCAATGCTG
CAGTCCTGCAGTCACCTATACATTATTTAAATGTATTTAACTGTTAAATGCGCTACCCACCAATAATGAAATAGA
CCTTTATGAAAA

831/6881
FIGURE 774

MATHGQTCARPMCIPPSYADLGKAARDIFNKGFGFGLVKLDVKTCSGVEFSTSGSSNTDTGKVTGTLETYKW
CEYGLTFTEKWNTDNTLGTETIAIEDQICQGLKLTFDTTFSPNTGKKSGKIKSYKRECINLGCDVDFDFAGPAIHG
SAVFGYEGWLAGYQMTFDSAKSKLTRNNFAVGVRTGDFQLHTNVNDGTEFGGSIYQKVCEDLDTSVNLAWTSGTN
CTRFGIAAKYQLDPTASISAKVNNSLIGVGYTQTLRPGVKLTLSALVDGKSINAGGHKVGLALELEA

832/6881
FIGURE 775

ATGGTCTGACTTTCACAGAAAAGTGGAACTGATAACACTCTGGGAACAGAAATCGCAATTGAAGACCAGATTT
GTCAAGGTTTGAAACTGACATTTGATACTACCTTCTCACCAAACACAGGAAAGAAAAGTGTTAAAATCAAGTCTT
ACAAGAGGGAGTGTATAAACCTTGGTTGTGATGTTGACTTTGATTTTGCTGGACCTGCAATCCATGGTTCAGCTG
TCTTTGGTTATGAGGGCTGGCTTGCTGGCTACCAGATGACCTTTGACAGTGCCAAATCAAAGCTGACAAGGAATA
ACTTTGCAGTGGGCTACAGGACTGGGGACTTCCAGCTACACACTAATGTCAATGATGGGACAGAATTTGGAGGAT
CAATTTATCAGAAAGTTTGTGAAGATCTTGACACTTCAGTAAACCTTGCTTGGACATCAGGTACCAACTGCACTC
GTTTTGGCATTGCAGCTAAATATCAGTTGGATCCCCTGCTTCCATTTCTGCTGGTGTGAAGCTTACACTCTCTG
CTCTGGTAGACGGGAAGAGCATTAAATGCTGGAGGCCACAAGTTGGGCTCGCCCTGGAGTTGGAGGCTTAATCCA
GCTGAAAGAAACCTT

833/6881
FIGURE 776

GAGAAAACGGCCGGGCGGCGGTGGCTGTAGGTTGTGCGGCTGCAGCGGCTCTTCCCTGGGCGGACGATGGACAGC
CAGGGCAGGAAGGTGGTGGTGTGCGACAACGGCACC GG GTTGTGAAGTGTGGATATGCAGGCTCTAACTTTCCA
GAACACATCTTCCCAGCTTTGGTTGGAAGACCTATTATCAGATCAACCACCAAAGTGGGAAACATTGAAATCAAG
GATCTTATGGTTGGTGATGAGGCAAGTGAATTACGATCAATGTTAGAAGTTAACTACCCTATGGAAAATGGCATA
GTACGAAATTGGGATGACATGAAACACCTGTGGGACTACACATTTGGACCAGAGAACTTAATATAGATACCAGA
AATTGTAAATCTTACTCACAGAACCTCCTATGAACCCAACCAAAAACAGAGAGAAGATTGTAGAGGTAATGTTT
GAACTTACCAGTTTTCCGGTGATATGTAGCCATCCAGGCAGTTCTGACTTTGTACGCTCAAGGTTTATTGACT
GGTGTAGTGGTAGACTCTGGAGATGGTGTGACTCACATTTGCCAGTATATGAAGGCTTTTCTCTCCCTCATCTT
ACCAGGAGACTGGATATTGCTGGGAGGGATATAACTAGATATCTTATCAAGCTACTTCTGTTGCGAGGATACGCC
TTCAACCCTCTGCTGATTTTGAAACGGTTCGCATGATTAAAGAAAAACTGTGTTACGTGGGATATAATATTGAG
CAAGAGCAGAACTGGCCTTAGAAACCACAGTATTAGTTGAATCTTATACACTCCCAGATGGACGTATCATCAAA
GTTGGGGGAGAGAGATTTGAAGCACCAGAAGCTTTATTTAGCCTCACTTGATCAATGTTGAAGGAGTTGGTGT
GCTGAATTGCTTTTTTAACACAATTCAGGCAGCTGACATTGATACCAGATCTGAATTCTACAAACACATTGTGCTT
TCTGGAGGGTCTACTATGTATCCTGGCCTGCCATCACGGTTGGAACGAGAACTTAAACAGCTTTACTTAGAACGA
GTTTTGAAGGGTGATGTGAAAACTTTCTAAATTTAAGATCCGCATTGAAGACCCACCCCGCAGAAAGCACATG
GTATTCCTGGGTGGTGCAGTTCTAGCGGATATCATGAAAGACAAAGACAACTTTTGGATGACCCGACAAGAGTAC
CAAGAAAAGGGTGTCCGTGTGCTAGAGAACTTGGTGTGACTGTTGATAAACTCCAAAGCTTGTTCCCGTCATA
CCCGTAATGCTTTCTTTTTCTTTTATTGCCAATCTTTGAACTCATTCAACTCCAGGACATGGAAGAGGCCTCTC
TCTGCCCTTTGACTGGAAGGTCAAGTTTTATTCTGGTGTCTTGGGGAAGCTTTGTTAAATTTTTGTTAATGTGG
GTAAATCTGAGTTTAAATCAACTGCTTCCCTACATAGACTAGAGGGCTAAGGATTCTGTCTGCTGCTTTGTTTCT
TCTAAGTAGGCATTTAGATCATTCCCTATAGGCTTCCCTATTTTCACTTTACTGCTCTAATGCTGCTAGTCGTAGTC
TTTAGCACACTAGGTGGTATGCCTTTATTAGCATAAAACAAAAAACTTTAACAGGAGCTTTTACATATTACTG
GGATGGGGGTGGTTCCGGATGGGTGGGCAGCTGCTGAACCCTTTAGGGCATTTCCTCTGTAATGTGGCGCTTTC
AACTGTACTGCTGCAGCTTTAAGTACCTTAAAGCTTCTCCTGTGAACCTTCTTAGGGAAATGTTAGGTTTCAGAACT
AAAGTGTGTTTGGGTGGGTTTTGTTGCGGGGGGAGGGTAACAATGGGTGGTCTTCTGATTTTTATTTTTGAGGTT
TTGTCAACTGGAGTACGTAGAGGAACTTTATTTACAGTACTTTGATTGAGGAGGTTTTCTTCTACTTGTGCTCTG
CCTGGAGCTGTTTCCATATGATATAAAAAGCAAGTGTAGTATTCCATTACTATGTGGCTTAGGGATTTATTTGTT
TTTTAAATCAACCATGTTAGCTGGGATTAGACTCCCTACAGTCCCTCAATGGAAAAGTAACATTTAAAAATCCT
TTGGGTAATTCGAATTACAGATTTAAAAGAGCTTAAAGATCTGGIGTTTTGTTAATGCTTCTGTTTATTCCAGAAG
CATTAAGGTAACCCATTGCCAAGTATCATTCTTGCAAATTATTCTTTTATATAACTGACCAGTGCTTAATAAAAC
AAGCAGGTACTTACAAATAATTACTGGCAGTAGGTTATAATTGGTGGTTTAAAAATAACATTGGAATACAGGACT
TGTTGCCAATTGGGTAATTTTCATTAGTTGTTTTGTTTGTGTTTGAATTGAAACCTGGAAATACAGTAAATTTGA
CTGTTTAAATGTTGGCCAAAAAATCAAGATTTAATTTTTTTTATTTGTACTGAAAACTAATCATAACTGTAA
TTCTCAGCCATCTTTGAAGCTTGAAAGAAGAGTCTTTGGTATTTTGTAAACGTTAGCAGACTTTCCTGCCAGTGT
CAGAAAATCCTATTTATGAATCCTGTCGGTATTCCTTGGTATCTGAAAAAATACCAAATAGTACCATACATGAG
TTATTTCTAAGTTTGAAAAATAAAAAGAAATTGCATCACACTAATTACAAAATA

834/6881
FIGURE 777

ATGGAGACACTTGTACAAGTGAATCTCTTTAGAAAGAGAGATTTACGCCAGGTACGTGGAACACAGTCTGAGCAG
CACTGCACACCGTATCAAATCAGGTATCCTGTAGGAAGAGTACCTGGGGATGAAATCAACAAGTTCTTAGTGGA
TCTTCTCATTTCTTAGAATGTAATGTGGTTGGATGTTTGAAATTGGTACGAAAGGGGAGAATCCTTTCCCCAA
TTAGGAAAATGGGGAGTGGGGGCAGAGGAAATGAAGCCCAGGTTCTTCATCGGATGGAAGTTCTCTGGTCAGTGT
ACACAGTTTGCTCTTGAGAGGACTGATGGCCTGGGATATGTTATTGATGGTCCTGAAAGGGATCTGCGTTTGAAT
AGGTCAGAGAAGATGTTCTGGAAGTCTGGAGACTGGGATACGCTCCCTTCCCTACAGGCTCATTCATCCAGCGTT
CTGGCAGTACCCTCTGGTACCGCACAGACTTCAGGGGACCTTGAACAAGCTCCATTTTGTCTCCTGGAAGCTCAT
TCCACCAGGTTTGTAGTATGAGCTTCACCACTGGCTCCACCTTCTCCACCAACTACCAGTCCCTGGGCTCTGTCCA
GGTGCCAGCTAAGACGCTCGGCCAGTCAGCAGCATGACCAGTATCTCTGCAGGGGCTGGGGGCTCTGGTTCCCA
GATCTCCATGTCCCCCTCCACCAGCTTCTGGGGTGGCATGGGGTCTGGGGCCCTGGCCGTGGGGATGGCCAGGGT
TCTGGCAGGATGGAAGACATCCAGAACAAGAAGGAGACCATGCAAAGCCTGAATGACTGCCTGGCCTCCTACCTG
GACAGAGTGAGGAGACTGGATACCAAGAATCGGAAGCTGGAGAGCAAAATCCGGGAGCACCTGGAGAAGAAGGGA
CCCCAAGTCAGAGACTGGAGCCATTACTTCAAGACCGTGGAGGACCTGAGGGCTCAGATCTTCGCAAATACTGTG
GACAATGCCCCGCATCGTTCTGCAAGTCGACAATGCCATCTTGCTGATGACTTTAGAGTCAAGTATGTGACAGAG
CTGGCCATGCGCCAGTCTATGGAGAGCGACATCCATGGGCTCCGCAAGGTCATTGATGACACCAATGTCACTCGG
CTGCAGCTGGAAACAGAGATCGAGGCTCTCAAGGAGGAGCTGCTCTTCATGAAGAAGAACGAAGAAGGGGAAATA
AAAGGCCTACAAGCCCAGATTGCCAGCTCTGGGTTGACTGTGGAGGTAGATATCCCCAAATCTCAGGACCTTGCC
AAGCTCATGGCAGACATCTGGGCCCAATATGATGAGCTGGCTCGGAAGAGCCAAGAGGAGCTGGGCAAGTACTGG
TCTCAGCAGATTGAGGAGAGTATCACAGTAGTCACCATGCAGTCCACCGAGATGGAGCAGTTCAACAGGATCCTG
CTGCACCTGGAGTCAGAGCTGGCACAGACCTGGGCAGAGGGACAGTGCCAGGCCCAGGAGTACGAGGCCCTGCTG
AGCATCAGGGTCAAGCTGGAGGCTGAGATCGCCACCTACCACCACCTGCTGGAAGATACCACCACCGGCCGGATA
GTGGATGGCAAAGTGGGGTCTGAGACCAACAACACCAAAGTTCTGAGACATTAA

835/6881
FIGURE 778

METLVQVNLFRKRDLRQVRGTQSEQHCTPYQIRYPVGRVPGDEINKFLVESHFLECNVVGCLEIGTKGENPFPQ
LGKWGVGAEE MKPRFFIGWKFSGQCTQFALERTDGLGYVIDGPERDLRLNRSEKMFWKSGDWDTLPSLQAHSSSV
LAVPSGTAQTSGDLEQAPFCLEAHSTRFEYELHHS LHLHQLPVPGLCPGAQLRRSASQQHDQYLCRGWGLWFP
DLHVPLHQLLGWHGVWGPGRGDGQSGRMEDIQNKKETMQSLNDCLASYLDRVRRLDTKNRKLESKIREHLEKKG
PQVRDWSHYFKTVEDLRAQIFANTVDNARIVLQVDNAHLADDFRVKYVTELAMRQSMESDIHGLRKVIDDTNVTR
LQLETEIEALKEELLFMKKNEEGEIKGLQAQIASSGLTVEVDIPKSQDLAKLMADIWAQYDELARKSQEELGKYW
SQQIEESITVVTMQSTEMEQFNRI LLHLESELAQTWAEQGCAQEYEALLSIRVKLEAEIATYHHLLEDTTTGRI
VDGKVGSETNNTKVL RH

836/6881
FIGURE 779A

CGGTCCCTCGCCGCGCCGCCCGAGGGGCACTTCCGGCGGCGGTTCACTTCCTGGTTGGGTGGATGGAGCCGGGC
GGGAGCGCGCGCGGGGGAGGGGCGGCGGGTCAGTCTCCGCGCGGCGCTCCCGGGATCAGCTGGCGGGCGGGCGGG
AGCCGAGCGCGGCCCGGCTCTCGCTGCAGCGCCGCTCTTCTCTGCGTGCAGGCCGGCCGGCGGCCGTGACA
ATGTCGCGGGGCTGGTAGCAGGGCGCCGGCCGCCGAGCCGTCTCAAGTTTAAACTTACACGAATCGCTTTCTGGA
GGAGGAGGGGACCCGCTGCGCGATTGACACGCATATTCTATAGGCATCCTCCCTCAGCCCCACCCCCACGGCC
GGATTCGGGTGGCTCCTCTCCGAGGTGAAATCTGAGAAGAAATCCTTGGATCTCTTTTCTTAAAAAAAAAAAAA
AAAAAAAAAATCTAGAAACCATCGGTATTTTGCTTTGCTGCTCCCTATTTCGCAAGATGAAGAAGTTTTTCGACTC
CCGGCGAGAGCAGGGCGGCTCTGGCCTGGGCTCCGGCTCCAGCGGAGGAGGGGGCAGCACCTCGGGCTGGGCAG
TGGCTACATCGGAAGAGTCTTCGGCATCGGGCGACAGCAGGTACAGTGGACGAGGTGTTGGCGGAAGGTGGATT
TGCTATTGTATTTCTGGTGAGGACAAGCAATGGGATGAAATGTGCCTTGAAACGCATGTTTGTCAACAATGAGCA
TGATCTCCAGGTGTGCAAGAGAGAAATCCAGATAATGAGGGATCTTTCAGGGCACAAGAATATTGTGGGTTACAT
TGATTCTAGTATCAACAACGTGAGTAGCGGTGATGTATGGGAAGTGCTCATTCTGATGGACTTTTGTAGAGGTGG
CCAGGTGGTAAACCTGATGAACCAGCGCCTGCAAACAGGCTTTACAGAGAATGAAGTGCTCCAGATATTTTGTGA
TACCTGTGAAGCTGTTGCCGCGCTGCATCAGTGCAAACTCCTATTATCCACCGGGACCTGAAGGTTGAAAACAT
CCTCTTGATGACCGAGGCCACTATGTCCTGTGTGACTTTGGAAGCGCCACCAACAAATCCAGAATCCACAAAC
TGAGGGAGTCAATGCAGTAGAAGATGAGATTAAGAAATACACAACGCTGTCTATCGAGCACCAGAAATGGTCAA
CCTGTACAGTGGCAAAATCATCACTACGAAGGCAGACATTTGGGCTCTTGGATGTTTGTGTATAAATTATGCTA
CTTCACTTTGCCATTTGGGGAAAGTCAGGTGGCAATTTGTGATGGAACTTCACAATTCCTGATAATTCTCGATA
TTCTCAAGACATGCACTGCCTAATTAGGTATATGTTGGAACCAGACCCTGACAAAAGCCGGATATTTACCAGGT
GTCTACTTCTCATTTAAGCTACTCAAGAAAGAGTGCCCAATTCCAAATGTACAGAACTCTCCCATTCTGCAA
GCTTCCTGAACCAGTGAAAGCCAGTGAGGCAGCTGCAAAAAGACCCAGCCAAAGGCCAGACTGACAGATCCCAT
TCCCACCACAGAGACTTCAATTGCACCCCGCCAGAGGCCATAAGCTGGGCAGACTCAGCCGAACCCAGGAATCCT
TCCCATCCAGCCAGCGCTGACACCCCGGAAGAGGGCCACTGTTTCAGCCCCACCTCAGGCTGCAGGATCCAGCAA
TCAGCCTGGCCTTTTAGCCAGTGTTCCCCAACCAAAACCCCAAGCCCCACCCAGCCAGCCTCTGCCGCAAACCTCA
GGCCAAGCAGCCACAGGCTCCTCCCACTCCACAGCAGACGCCTTCTACTCAGGCCAGGGTCTGCCGCTCAGGC
CCAGGCCACACCCACAGCACCAGCAGCAACTCTTCCTCAAGCAGCAACAGCAGCAGCAACAGCCACCGCCAGCACA
GCAGCAGCCGGCAGGCACGTTTTACCAGCAGCAGCAGGCCCAGACTCAGCAGTTTCAGGCAGTACATCCAGCAAC
CCAGAAACCAGCAATTGCTCAGTTCCCTGTGGTGTCCCAAGGAGGCTCTCAACAGCAGCTAATGCAGAATTTCTA
CCAGCAGCAGCAGCAGCAACAACAGCAACAGCTGGCCACAGCCCTGCATCAACAACAGCTGAT
GACTCAGCAGGCTGCCTTGCAGCAAAAGCCCACTATGGCAGCAGGACAGCAGCCCCAGCCACAGCCAGCTGCAGC
CCCACAGCCAGCCCCTGCCAGGAGCCAGCGATTCAAGCCCCAGTAAGACAACAGCCAAAGGTTTCAGACAACCCC
ACCTCCTGCCGTCCAGGGGCAGAAAGTTGGATCTCTCACTCCACCTCATCCCCAAAACCCAACGTGCTGGGCA
CAGGCGTATTCTCAGTGACGTAACCCACAGTGCACTCTTTGGGGTCCCTGCCAGCAAATCAACCCAGCTGCTCCA
GGCAGCTGCAGCTGAGGCCAGTCTCAATAAGTCCAAGTCTGCAACCACCACTCCATCAGGCTCTCCTCGGACCTC
TCAACAAAACGTTTATAATCCTTCAGAAGGGTCTACGTGGAATCCCTTTGATGACGATAATTTCTCCAAACTCAC
AGCTGAAGAACTGCTAAACAAGGACTTTGCCAAGCTTGGGGAAGGCAAACATCCCAGAAAGCTTGGAGGCTCAGC
TGAGAGTTTGATCCAGGCTTTCAATCAACCCAAGGTGATGCTTTTGCTACGACCTCATTTTCTGCTGGAAGTGC
TGAAAAAAGGAAGGGTGGGCAGACTGTGGACTCTGGCCTCCCGCTTCTAAGCGTGTCTGATCCTTTCATTCTCT
TCAAGTACCTGATGCACCAGAAAACTAATTGAGGGACTCAAATCTCCTGACACTTCTCTTCTGCTCCCTGACCT
CTTGCTATGACAGATCCTTTTGGTAGCACTTCTGATGCTGTAATTGGTAAAGTCATCATCTCTGTTTCTTCACT
CATGCATGATATGTGTGCCTGTTTCAAGAAAGTACAGTACCTAGTTAAACCAATCCCTGGGGAATAGCCCTGCCAC
CCCAGAAGCCAAGGCTATTTAATCTCACTTGTATCACTCCAAATGAAGTGTTTTCTTCTGTTTTCGGGGTACAA
CGTCTATTTTTTGCCTTTCTTGATATCTGGAGATTTCTAGAGTGGATCTCTTATGAATGAGGAGGAATGTGGAAA
GTTTCACATTTAGTTAGAAGAACTTTAAAAAATTGGTTTCTAACTAGACTACCTTTACTGAACTTAATGAAATTT
AGCAGATTCTTCTTTTTTTTTTTTTTTGTTTGAGACAGAGTTTCACTCTTGTTGCTAGGCTGGAGTGCAATGGCA
AGATCTCAGCTCACTGCAACCTCCATCTCCCGGTTTCAAGCAATTCTCCTGCCTCAGCCTCCCGAGTAGCTGAGA
TTACAGGCATGCACCACCATGCCTGGCTAATTTTTATATTTTAGTAGAGATAGGTTTCTCCATGTTGGTCAGG
CTGGTCTCGAACTCCTGACCTCAGGTGATCCACCTGCCTTGGCCTCCCAAGTGCTGGGATTACAGGGGTGAGCC

837/6881
FIGURE 779B

ACCATGCCCAGCCCAGATTCTTCTTTAGAAAGGCCCATGTACATCCAGCTGCAGTGGGACGAGCCTGGGAAGCATA
GGAAGACCCCATCCCTACAAAAAAAATGTTGTTAGTTAGCCAGGTGTGGGGGTGCACACCTGTGCTACCAGCTCT
TTGGGAGGCTGAGACGGAAGATCACTTTGAGCCAGGGGGTTTGAGGCTGCAGTGAGCCCTGATCATGCCACTGCC
CTCCAGCTTAAGTGACAGAGACCCATCTTAAACAAAATTAAAAAATTTAAAAAGGTCCATGTATATACCAAGTAT
CAGTAACTGAGAAAACATTTTGCCCACTGGTTAAGCCCCATAAATAGAATCCAGGGCAGGGGCTTGGTCTGCTTC
CTCTCTCACATTTTCTATGTTCCAACAGCAAGGCAGGCAAGATTTGCAAAATGTCCAAGGCCCTGTACTCCAG
GAGGGTCCAATCATGAGGCACCTAATAATGCCTTTGGGCAGAAAGTCCTAGAACTCAGAAGTGCCATGACCTTGC
ATAGGGGTAGGCCTGCAGCTGAGGGGTGTCACGTGGTGCAAAAGGCCTCCCAGCTACATCCTGGGATGGGGTTTG
AGATGGATTAATGGCCTTTGCATGGCACAGAGGATGTTTGCCCCCAGGTTTATCCCTTAATAAAAGTGAAATTAC
CAGAAAAAATTAAGGTGCCTTTCAGCCCATCTCTTCTGACATGGAAGAGGTTTGCTGAGCGGCTTATGTTCTGAA
TTTGTTTATGAGAACTGATCATTAGTGAGACTGGCCACAGTATTTAACCTTGACATGCATGCTCAGTGAAGCCT
AGACATTTCAGAGCAGCAGAAATAAAGTAACTTATTTTTCTTTCCACCTTGCCTGAGACTGGCATTTTAGAGACCT
GTTAAAAGAAAGTCTTCACATGGCTGGGTGCAGTGGCTCACACTTGTAACCACAGGACTTTGGGAGGCCAAGGTG
GGATAGATCGCTTGAGCTCAGGAGCAAGACACCATCTCAAAAAATGAGAATT

838/6881
FIGURE 780

GCCCCAGGTGCGCTTCCCCTAGAGAGGGATTTTCCGGTCTCGTGGGCAGAGGAACAACCAGGAACTTGGGCTCAG
TCTCCACCCACAGTGGGGCGGATCCGTCCCGGATAAGACCCGCTGTCTGGCCCTGAGTAGGGTGTGACCTCCGC
AGCCGCAGAGGAGGAGCGCAGCCCGGCCTCGAAGAACTTCTGCTTGGGTGGCTGAACTCTGATCTTGACCTAGAG
TCATGGCCATGGCAACCAAAGGAGGTACTGTCAAAGCTGCTTCAGGATTCAATGCCATGGAAGATGCCCAGACCC
TGAGGAAGGCCATGAAAGGGCTCGGCACCGATGAAGACGCCATTATTAGCGTCCTTGCCCTACCGCAACACCGCCC
AGCGCCAGGAGATCAGGACAGCCTACAAGAGCACCATCGGCAGGGACTTGATAGACGACCTGAAGTCAGAACTGA
GTGGCAACTTCGAGCAGGTGATTGTGGGGATGATGACGCCACGGTGCTGTATGACGTGCAAGAGCTGCGAAGGG
CCATGAAGGGAGCCGGCACTGATGAGGGCTGCCTAATTGAGATCCTGGCCTCCCGGACCCCTGAGGAGATCCGGC
GCATAAGCCAAACCTACCAGCAGCAATATGGACGGAGCCTTGAAGATGACATTGCTCTGACACATCGTTTCATGT
TCCAGCGAGTGCTGGTGTCTCTGTGCTGCTGGTGGGAGGGATGAAGGAAATTATCTGGACGATGCTCTCGTGAGAC
AGGATGCCCAGGACCTGTATGAGGCTGGAGAGAAGAAATGGGGGACAGATGAGGTGAAATTTCTAACTGTTTCTCT
GTTCCCGGAACCGAAATCACCTGTTGCATGTGTTTTGATGAATACAAAAGGATATCACAGAAGGATATTGAACAGA
GTATTAAATCTGAAACATCTGGTAGCTTTGAAGATGCTCTGCTGGCTATAGTAAAGTGCATGAGGAACAAATCTG
CATATTTTGTGAAAAGCTCTATAAATCGATGAAGGGCTTGGGCACCGATGATAACACCCTCATCAGAGTGATGG
TTTCTCGAGCAGAAATTGACATGTTGGATATCCGGGCACACTTCAAGAGACTCTATGGAAAGTCTCTGTACTCGT
TCATCAAGGGTGACACATCTGGAGACTACAGGAAAGTACTGCTTGTTCTCTGTGGAGGAGATGATTAAATAAAA
ATCCCAGAAGGACAGGAGGATTCTCAACACTTTGAATTTTTTTAACTTCATTTTTCTACACTGCTATTATCATT
TCTCAGAATGCTTATTTCCAATTAAAACGCCTACAGCTGCCTCCTAGAATATAGACTGTCTGTATTATTATTAC
CTATAATTAGTCATTATGATGCTTTAAAGCTGTACTTGCATTTCAAAGCTTATAAGATATAAATGGAGATTTTAA
AGTAGAAATAAATATGTATTCCATGTTTTTAAAAGATTACTTTCTACTTTGTGTTTCACAGACATTGAATATATT
AAATTATTCCATATTTTCTTTTCAGTGAAAAATTTTTTAAATGGAAGACTGTTCTAAAATCACTTTTTTCCCTAA
TCCAATTTTTTAGAGTGGCTAGTAGTTTCTTCATTTGAAATTGTAAGCATCCGGTCAGTAAGAATGCCCATCCAGT
TTTCTATATTTCATAGTCAAAGCCTTGAAAGCATCTACAAATCTCTTTTTTTAGGTTTTGTCCATAGCATCAGTT
GATCCTTACTAAGTTTTTTCATGGGAGACTTCCTTCATCACATCTTATGTTGAAATCACTTTCTGTAGTCAAAGTA
TACCAAACCAATTTATCTGAACTAAATTCTAAAGTATGGTTATACAAACCATATACATCTGGTTACCAAACATA
AATGCTGAACATTCCATATTATTATAGTTAATGTCTTAATCCAGCTTGCAAGTGAATGGAAAAAAAAATAAGCTT
CAAAGTAGGTATTCTGGGAATGATGTAATGCTCTGAATTTAGTATGATATAAAGAAAACCTTTTTTGTGCTAAAAA
TACTTTTTTAAATCAATTTTGTGATTGTAGTAATTTCTATTTGCACTGTGCCTTTCAACTCCAGAAACATTCTG
AAGATGTACTTGGATTTAATTAAAAAGTTCACTTTGT

839/6881
FIGURE 781

MAMATKGGTVKAASGFNAMEDAQTLRKAMKGLGTDEDAIISVLAYRNTAQRQEIRTAYKSTIGRDLIDDLKSELS
GNFEQVIVGMMTPTVLYDVQELRRAMKGAGTDEGCLIEILASRTPEEIRRISQTYQQQYGRSLEDDIRSDTSFMF
QRVLVSL SAGGRDEGNYLDDALVRQDAQDLYEAGEKKWGTDEVKFLTVLCSRNRNHLHVFDEYKRISQKDIEQS
IKSETSGSFEDALLAIVKCMRNKSAYFAEKLYKSMKGLGTDDNTLIRVMVSRAEIDMLDIRAHFKRLYGKSLYSF
IKGDTSGDYRKVLLVLCGGDD

840/6881
FIGURE 782

CGCCACCGCCGCGCCCTCGCCCCACCCGCCCCGCCGCTCCCGGCCCCGCTCGCCCCCTCCGCCGCGCCGCCCC
GCCCCTGCGACTACGCTGCGGCCTCCCGCCCGCTCCCGCTCGCTCCCGCGGCCCTCGCTCGCCTCGCGCCGGCAG
TTTTGGGCCTACACCTCCCCCTCCCCCGCCAGCCGCCAAAGACTTGACCACGTAACGAGCCCAACTCCCCCGAAC
GCCGCCCCGCGCTCGCCATGGATGCCGGTGTGACTGAAAGTGGACTAAATGTGACTCTCACCATTGGGCTTCTTA
TGCACGGAAAGGAAGTAGGAAGCATCATTGGGAAGAAAGGGGAGTCGGTTAAGAGGATCCGCGAGGAGAGTGGCG
CGCGGATCAACATCTCGGAGGGGAATTGTCCGGAGAGAATCATCACTCTGACCGGCCCCACCAATGCCATCTTTA
AGGCTTTTCGCTATGATCATCGACAAGCTGGAGGAAGATATCAACAGCTCCATGACCAACAGTACCGCGGCCAGCA
GGCCCCCGGTACCCCTGAGGCTGGTGGTGCCGGCCACCCAGTGC GGCTCCCTGATTGGGAAAGGCGGGTGTAAGA
TCAAAGAGATCCGCGAGAGTACGGGGGCGCAGGTCCAGGTGGCGGGGGATATGCTGCCCCAACTCCACCGAGCGGG
CCATCACCATCGCTGGCGTGCCGCAGTCTGTACCGAGTGTGTCAAGCAGATTTGCCTGGTTCATGCTGGAGACGC
TCTCCAGTCTCCGCAAGGGAGAGTCATGACCATTCCGTACCAGCCCATGCCGGCCAGCTCCCCAGTTCATCTGCG
CGGGCGGCCAAGATCGGTGCAGCGACGCTGCGGGCTACCCCCATGCCACCCATGACCTGGAGGGACCACCTCTAG
ATGCCTACTCGATTCAAGGACAACACACCATTTCTCCGCTCGATCTGGCCAAGCTGAACCAGGTGGCAAGACAAC
AGTCTCACTTTGCCATGATGCACGGCGGGACCGGATTCGCCGGAATTGACTCCAGCTCTCCAGAGGTGAAAGGCT
ATTGGGCAAGTTTGATGCATCTACTCAAACCACCCATGAACCTCACCATTCCAAATAACTTAATTGGCTGCATAA
TCGGGCGCCAAGGCGCCAACATTAATGAGATCCGCCAGATGTCCGGGGCCCAGATCAAAATTGCCAACCCAGTGG
AAGGCTCCTCTGGTAGGCAGGTTACTATCACTGGCTCTGCTGCCAGTATTAGTCTGGCCCAGTATCTAATCAATG
CCAGGCTTTCCTCTGAGAAGGGCATGGGGTGAGCTAGAACAGTGTAGGTTCCCTCAATAACCCCTTCTGCTGT
TCTCCCATGATCCAACGTGTGAATTTCTGGTCAGTGATTCCAGGTTTTAAATAATTTGTAAGTGTTCAGTTTCTA
CACAACCTTTATCATCCGCTAAGAATTTAAAAATCACATTCTCTGTTTCAGCTGTTAATGCTGGGATCCATATTTAG
TTTTATAAGCTTTTCCCTGTTTTTAGTTTTGTTTTGGGTTTTTTGGCTCATGAATTTTATTTCTGTTTGTGCGATA
AGAAATGTAAGAGTGGAATGTTAATAAATTTAGTTTTAGTTCTGTAATGTCAAGAATTTAAGAATTAATAAACGG
ATTGGTTAAAAAATGCTTCATATTTGAAAAAGCTGGGAATTGCTGTCTT

841/6881
FIGURE 783

CCAAGCTGAACCAGGTGGCAAGACAACAGTCTCACTTTGCCATGATGCACGGCGGGACCGGATTGCGCGGAATTG
ACTCCAGCTCTCCAGAGGTGAAAGGCTATTGGGCAAGTTTGGATGCATCTACTCAAACCACCCATGAACTCACCA
TTCCAAATAACTTAATTGGCTGCATAATCGGGCGCCAAGGCGCCAACATTAATGAGATCCGCCAGATGTCCGGGG
CCCAGATCAAAATTGCCAACCCAGTGGAAGGCTCCTCTGGTAGGCAGGTTACTATCACTGGCTCTGCTGCCAGTA
TTAGTCTGGCCCAGTATCTAATCAATGCCAGGCTTTCCTCTGAGAAGGGCATGGGGTGCAGCTAGAACAGTG TAG
GTTCCCTCAATAACCCCTTCTGCTGTTCTCCCATGATCCAACGTGTAAATTTCTGGTCAGTGATTCCAGGTTTT
AAATAATTTGTAAGTGTTTCAGTTTCTACACAACTTTATCATCCGCTAAGAATTTAAGCTTTTCCTGTTTTTAGT
TTTGTTTTGGGTTTTTTGGCTCATGAATTTTA

842/6881
FIGURE 784

CGCAGAGCTCGCGCGTCGGTGTGGTTACAGCCGGCAGCCACGGCACCTCCTTCCGGCCGACTAGTCTCCAGGTCC
CGCGGTCTGGCCCCCTGGTCACCCGGCGCTGTCCCTCGTTCCTTGAAGATCTCCAGTGCTACCTTTTGTGGAACAT
CTCGAATACACCAAACCTTCTAGCTGCTAATACTCAGATTTATGGACAAGAAGTTATCATTGAAATTAAATGGTG
GCAGACATGTCCAAGGAATATTGCGGGGATTTGATCCCTTTATGAACCTTGTGATAGATGAATGTGTGGAGATGG
CGACTAGTGGACAACAGAACAAATATTGGAATGGTGGTAATACGAGGAAATAGTATCATCATGTTAGAAGCCTTGG
AACGAGTATAAATAATGGCTGTTCAGCAGAGAAAACCCATGTCCTCTCTCCATAGGGCCTGTTTTACTATGATGTA
AAAATTAGGTCATGTACATTTTCATATTAGACTTTTTGTTAAATAAACTTTTGTAATAGTCAAAAATGCTTTCTC
AGATGTTCTGAATATAGAATATCAGCTCTCATTCCAGTTTTTTCTAACATGAATTTTCCTGGTTGACATTGATTT
CAAAGGGTTTTATGCATTAAAGTGAAAGAATCTTATTAAATGTGAAACATGGCAAGGATTCCTTCTGTCCATCAT
CTTTCAACACTGAACAGATAAAGAAGTTACAAACATGAGTGAGTTTCTTCTAAAACACTAATTTTC

843/6881
FIGURE 785

GTACGCCGATTCCATATGGGCGCCGGCGCGGAGCGCCGCGGGGCAGCGCGGGGTCGCCATGGCTGAGCTGCAGCA
GCTCCGGGTGCAGGAGGCGATGGAGTCCATGGTGAAGAGTCTGGAAAGAGAGAACATCCGGAAGATGCAGGGTCT
CATGTTCCGGTGCAGCGCCAGCTGTTGTGAGGACAGCCAGGCCTCCATGAAGCAGGTGCACCAGTGCATCGAGCG
CTGCCATGTGCCTCTGGCTCAAGCCCAGGCTTTGGTCCACCAGTGAGCTGGAGAAGTTCAGGACCGCCTGGCCCC
GTGCACCATGCATTGCAATGACAAAGCCAAAGATTCAATAGATGCTGGGAGTAAGGAGCTTCAGGTGAAGCAGCA
GCTGGACAGTTGTGTGACCAAGTGTGTGGATGACCACATGCACCTCATCCCAACTATGACCAAGAAGATGAAGGA
GGCTCTCTTATCAATTGGAAAATAAAAGTATTTGCCAGTGGCCATCAGGCTGAGGGCAAGAATATATTTTTTATA
AGGAATTGGGAATTTTAGTCTTTTAAAGCAAAGTTTACGAATGAAGAAATGAAGGATGGCCACAAGCGTAAGGCAT
ATGTCACCTTGCCCTCTGGACACTGGTTATTTTATGTTTCAGTCCCTAAAAAATGAAATGGAAAAAAGTGGTGCTAA
ATCGAGTCAGAGATATTACAGGAGAGTTTTAGAGCTTATTATTTCTGTGGCCAGTGCTTGTCTTGGCAGTAAGG
CTCTCCCCTGTAACAAGCCAGAGCCCCCAAGGTACCAGACTCTTCTTACTACACAGGTACTAACAGGCTGGCAG
GTTAGAGTTGGTGGAGTCTGAGGAGAGATATTTTCTCTTTGTTGCCAACATCCTGTTTACCAAAAGTGTACCCCC
ACCATCTTCCATAAGCTGTGAAACAAAATCAATGAGGTCACTAACTTAGAAGGGAAAGAAAGTTTTCTGGGTCTT
TGTTTTCTTGATTTGGGGTAATTTATACAAGGGCATAACAAGTTGATTTTAAGATGTGGAACCTGGGAGGTAGACTA
GTTTGGATAAGAACTTTGAAATGTTCTTGTGGATCCCCATTTCTGGTCATCAAGATGTGGATGTACATTTCTTA
AAATTATTACATGCTGCATCTTTCAGCCTGGAGACTGTGCAGAAACATGAGAGGTGATGACACACTAATTATGGG
AAGCAGAATTACTGGCTGATGGCCCCCTGAGGCTGTGTGTAACAAAATGACAGGACAATCTTGCACTAACACTTTC
CCCTTGAAGAGAAGGGGGTTTTGATTGTGATATATACTAGTATCTAGGAATGAACAGTAAAAGAGGAGCAGTTGG
CTACTTGATTACAACAGAGTAAATGAAGTACTGGATTTGGGAAAACCTGGTTTTATTAGAACATATGGAATGAAA
GCCTACACCTAGCATTGCCTACTTAGCCCCCTGAATTAACAGAGCCCAATTGAGACAAACCCCTGGCAACAGGAA
ATTCAAGGGAGAAAAAGTAAGCAACTTGGGCTAGGATGAGCTGACTCCCTTAGAGCAAAGGAGAGACAGCCCCCA
TTACCAATAACATTTTTGCCTGGGGCTTGTGCAGCTGGCAGTGTTCTTGCCCCAGCATGGCACCTTATTGTTTT
GATAGCAACTTCGTTGAATTTTACCAACTTATTACTTGAAATTATAATATAGCCTGTCCGTTTGCTGTTTCCAG
GCTGTGATATATTTTCTAGTGGTTTGACTTTAAAAATAAATAAGGTTTAATTTTCTCCCC

844/6881
FIGURE 786

MAELQQLRVQEAMESMVKSLEARENIRKMQLMFRCASCCEDSQASMKQVHQCIERCHVPLAQAQALVTSELEKF
QDRLARCTMHCNDKAKDSIDAGSKELQVKQLDSCVTCKVDDHMHLPMTKKMKEALLSIGK

845/6881
FIGURE 787A

CAGACCCGCCCCGTGGCTGCAGCAGTGGTGTCCCATTTTAATGACTGCCCAGATTCCCACACTCAGTTCTGCTTCC
ATGGAACCTGCAGGTTTTTGGTGCAGGAGGACAAGCCAGCATGTGTCTGCCATTCTGGGTACGTTGGTGCACGCT
GTGAGCATGCGGACCTCCTGGCCGTGGTGGCTGCCAGCCAGAAGAAGCAGGCCATCACCGCCTTGGTGGTGGTCT
CCATCGTGGCCCTGGCTGTCTTATCATCACATGTGTGCTGATACTGCTGCCAGGTCCGAAAACACTGTGAGT
GGTGCCGGGCCCCATCTGCCGGCACGAGAAGCCAGCGCCCTCCTGAAGGGAAGAACCCTTGGTGGCACTCAG
AAACAGTGGTCTGAAGAGCCCAGAGGAGGAGTTTGGCCAGGTGGACTGTGGCAGATCAATAAAGAAAGGCTTCTT
CAGGACAGCACTGCCAGAGATGCCTGGGTGTGCCACAGACCTTCTACTTGGCCTGTAATCACCTGTGCAGCCTT
TTGTGGGCGCTTCAAACTCTGTCAAGAACTCCGTCTGCTTGGGGTTATTTCAGTGTGACCTAGAGAAGAAATCAGC
GGACCACGATTTCAAGACTTGTTAAAAAAGAACTGCAAAGAGACGGACTCCTGTTACCTAGGTGAGGTGTGTGC
AGCAGTTGGTGTCTGAGTCCACATGTGTGCAGTTGTCTTCTGCCAGCCATGGATTCCAGGCTATATATTTCTTTT
TAATGGGCCACCTCCCCACAACAGAATTCTGCCCAACACAGGAGATTTCTATAGTTATTGTTTTCTGTCAATTTGC
CTACTGGGGAAGAAAGTGAAGGAGGGGAAACTGTTTAATATCACATGAAGACCCTAGCTTTAAGAGAAGCTGTAT
CCTCTAACCACGAGACCCTCAACCAGCCCAACATCTTCCATGGACACATGACATTGAAGACCATCCCAAGCTATC
GCCACCTTGGAGATGATGTCTTATTTATTAGATGGATAATGGTTTTATTTTAACTCTCTTAAGTCAATGTAAAA
AGTATAAAACCCCTTCAGACTTCTACATTAATGATGTATGTGTTGCTGACTGAAAAGCTATACTGATTAGAAATG
TCTGGCCTCTTCAAGACAGCTAAGGCTTGGGAAAAGTCTTCCAGGGTGCAGGAGATGGAACCAGAGGCTGGGTTAC
TGGTAGGAATAAAGGTAGGGGTTTCAAGAAATGGTGCCATTGAAGCCACAAAGCCGGTAAATGCCTCAATACGTTCT
GGGAGAAAACCTTAGCAAATCCATCAGCAGGGATCTGTCCCTCTGTTGGGGAGAGAGGAAGAGTGTGTGTGTCTA
CACAGGATAAACCCTAACATATTGTACTGCTCAGTGATTAAATGGGTTCACTTCTCTGAGCCCTCGGTAAGT
ATGTTTAGAAATAGAACATTAGCCACGAGCCATAGGCATTTTCAGGCCAAATCCATGAAAGGGGGACCAGTCATTT
ATTTTCCATTTTGTGTGCTTGGTTGGTTTGTGCTTTATTTTTTAAAAGGAGAAGTTAACTTTGCTATTTATTTTC
GAGCACTAGGAAAACCTATTCCAGTAATTTTTTTTTTCCCTCATTTCATTTCAGGATGCCGGCTTTATTAACAAAAAC
TCTAACAAAGTCACCTCCACTATGTGGGTCTTCCCTTCCCTCAAGAGAAGGAGCAATTGTTCCCTGAGCATCTG
GGTCCATCTGACCCATGGGGCTGCCTGTGAGAAACAGTGGGTCCCTTCAAATACATAGTGGATAGCTCATCCCT
AGGAATTTTTCATTAAAATTTGGAAACAGAGTAATGAAGAAATAATATATAAACTCCTTATGTGAGGAAATGCTAC
TAATATCTGAAAAGTGAAAGATTTCTATGTATTAACCTCTTAAGTGCACCTAGCTTATTACATCGTGAAAGGTACA
TTTAAAAATATGTTAAATTGGCTTGAAATTTTTCAGAGAAATTTTGCTTCCCTAATTCTTCTTCCCTGGTCTGGAA
GAACAATTTCTATGAATTTTCTCTTTATTTTTTTTTTATAATTTCAGACAATTCTATGACCCGTGTCTTCATTTTTG
GCACTCTTATTTAACAAATGCCACACCTGAAGCACTTGGATCTGTTTCAGAGCTGACCCCTAGCAACGTAGTTGAC
ACAGCTCCAGGTTTTTAAATTACTAAAAATAAGTTCAAGTTTACATCCCTTGGGCCAGATATGTGGGTGAGGCTT
GACTGTAGCATCCTGCTTAGAGACCAATCAACGGACACTGGTTTTTTCAGCTCTATCAATCAGTAGTTAGCATCC
AAGAGACTTTGCAGAGGCGTAGGAATGAGGCTGGACAGATGGCGGAAGCAGAGGTTCCCTGCGAAGACTTGAGAT
TTAGTGTCTGTGAATGTTCTAGTTCCCTAGGTCCAGCAAGTCACACCTGCCAGTGCCCTCATCCTTATGCCTGTAA
CACACATGCAGTGAGAGGCCTCACATATACGCTCCCTAGAAGTGCCCTTCCAAGTCAGTCTTTGGAAACCAGCA
GGTCTGAAAAAGAGGCTGCATCAATGCAAGCCTGGTTGGACCATTGTCCATGCCTCAGGATAGAACAGCCTGGCT
TATTTGGGGATTTTTCTTCTAGAAATCAAATGACTGATAAGCATTGGATCCCTCTGCCATTTAATGGCAATGGTA
GTCTTTGGTTAGCTGCAAAAATACTCCATTTCAAGTTAAAAATGCATCTTCTAATCCATCTCTGCAAGCTCCCTG
TGTTTCCCTTGGCCTTTAGAAAATGAATTGTTCACTACAATTAGAGAATCATTTAACATCCTGACCTGGTAAGCTG
CCACACACCTGGCAGTGGGGAGCATCGCTGTTTCCAATGGCTCAGGAGACAATGAAAAGCCCCCATTTAAAAAAA
TAACAAACATTTTTTAAAAGGCCTCCAATACTCTTATGGAGCCTGGATTTTTCCCACTGCTCTACAGGCTGTGAC
TTTTTTTAAAGCATCCTGACAGGAAATGTTTTCTTCTACATGGAAAGATAGACAGCAGCCAACCCTGATCTGGAAG
ACAGGGCCCCGGCTGGACACACGTGGAACCAAGCCAGGGATGGGCTGGCCATTGTGTCCCCGAGGAGAGATGGG
CAGAAATGGCCCTAGAGTTCTTTTCCCTGAGAAAGGAGAAAAAGATGGGATTGCCACTCACCCACCCACACTGGTA
AGGGAGGAGAATTTGTGCTTCTGGAGCTTCTCAAGGGATTGTGTTTTGCAGGTACAGAAAACCTGCCTGTTATCTT
CAAGCCAGGTTTTTCAGGGCACATGGGTACCAGTTGCTTTTTTCAGTCAATTTGGCCGGGATGGACTAATGAGGC
TCTAACACTGCTCAGGAGACCCCTGCCCTCTAGTTGGTCTGGGCTTTGATCTCTTCCAACCTGCCAGTACAG
AAGGAGGAATGACTCAAATGCCCCAAAACCAAGAACACATTGCAGAAGTAAGACAAAACATGTATATTTTTAAATGT
TCTAACATAAGACCTGTTCTCTCTAGCCATTGATTTACCAGGCTTTCTGAAAGATCTAGTGGTTCACACAGAGAG

846/6881
FIGURE 787B

AGAGAGAGTACTGAAAAAGCAACTCCTCTTCTTAGTCTTAATAATTTACTAAAATGGTCAACTTTTCATTATCTT
TATTATAATAAACCTGATGCTTTTTTTTTAGAACTCCTTACTCTGATGCTGTATATGTTGCACTGAAAAGGTTAA
TATTTAATGTTTTAATTTATTTTGTGTGGTAAGTTAATTTTGATTTCTGTAATGTGTTAATGTGATTAGCAGTTA
TTTTCTTAATATCTGAATTATACTTAAAGAGTAGTGAGCAATATAAGACGCAATTGTGTTTTTCAGTAATGTGC
ATTGTTATTGAGTTGTACTGTACCTTATTTGGAAGGATGAAGGAATGAATCTTTTTTTCCT

847/6881

FIGURE 788A

ATTTCCTCCCAGCCTCGTGCGGGAAATGGCTTTAATTCTGACGGCAGGGCTGTGAGGGACTAGCGGGAACCCGAG
CCTTTTGTCAAGGAAGTGC GGCGTCCGGTGGCCAGTCATCCCCGCCGCCGCGGAGCCGCTGCACTGCTGGGGGATC
TCCAGCAGCTCTGACGAGCGCGGGCTGCAGCATGGGCAGAAAACGCTGCCCTGCAGATTAGCTGGGTGGATTTT
TTAAGCGCACCCCAACCCCAAAACCCATAAAATAACAAAACCAACCCGCAGTGGCCGACCGGAGATAGCTAAGAT
GCCGCGCAGGAGTTTCCACCTGGATGTTTGAGGTTGTGTAGATGTGGCCGGCACCCCTTGAGAGTGGAGCTAGGGG
GTGCAGACTGAGCAGTGAACAGAAGGAGCCTTGAGACAGGGCTGGGCCAGCCTCCCGAGTTCCAGGAGCGAATTGC
AAACCCACCGGGAAAATGAGCGAAGAGACGGTCCCCGAGGCTGCCTCGCCGCCGCCCGCCGAGGGGCAGCCTTAC
TTTGACCGCTTCTCAGAGGACGACCCCGAGTACATGCGCCTTCGCAACCGGGCGGGCGGACCTGCGGCAGGACTTC
AACCTGATGGAGCAGAAGAAGCGCGCTCACCATGATCCTGCAGAGTCCCTCTTTTCAGGGAGGAGCTGGAAGGCCTC
ATCCAGGAGCAGATGAAGAAGGGGAACAACCTCCTCCAACATCTGGGCCCTGCGACAGATCGCGGACTTCATGGCC
AGCACCTCCCACGCACTCTTCCCGACATCTTCCATGAATGTCTCCATGATGACGCCTATCAATGACCTCCACACA
GCTGACTCCCTGAACCTGGCCAAAGGGGAGCGGCTCATGCGGTGCAAGATCAGCAGTGTCTACCGACTCCTGGAC
CTCTATGGCTGGGCCAGCTGAGTGACACCTATGTACGTTGAGAGTCAGCAAGGAGCAGGACCACTTCTTGATC
AGCCCTAAGGGAGTTTCTTGCACTGAAGTCACAGCGTCCAGCCTGATCAAGGTGAACATTCTGGGAGAGGTGGTG
GAGAAGGGCAGCAGCTGCTTCCAGTGGACACCACAGGCTTCTGTCTGCACTCGGCCATCTATGCAGCGAGGGCC
GACGTGCGCTGCATCATCCACCTGCACACACCGGCCACAGCAGCGGTGTGCGCCATGAAGTGGGGCCTCCTGCCT
GTCTCCCAATGCCCTGCTGGTGGGGGACATGGCCTATTATGACTTCAATGGGGAAATGGAGCAGGAAGCCGAT
CGGATCAACCTGCAGAAGTGCTTGACCCACCTGCAAGATCCTGGTGCTAAGAAACCATGGAGTGGTTGCTCTG
GGTGACACGGTAGAGGAGGCATTTTACAAGATCTTCCACCTGCAGGCTGCATGTGAGATACAGGTGTGCGCTCTG
TCCAGTGCCGGGGGAGTGGAGAACCTCATCCTCCTGGAGCAGGAGAAGCACCGGCCCATGAGGTGGGCTCCGTG
CAGTGGGCCGGGAGCACCTTTGGGCCTATGCAGAAGAGTCGGCTGGGGGAGCATGAGTTGAGGCCCTCATGAGG
ATGCTGGACAACCTGGGCTACAGAACAGGTTACACGTATCGCCACCCCTTTGTTCAAGAGAAAACCAACACAAA
AGTGAGGTGGAGATTCCAGCCACGGTTCACAGCCTTCGTGTTTGAGGAGGACGGTGCCCCGGTGCCCCCCTGCGA
CAGCATGCCAGAAGCAGCAGAAGGAGAAGACCCGCTGGCTCAATACGCCCAACACCTACCTGCGGGTCAATGTG
GCCGATGAGGTCCAGAGGAGCATGGGCAGCCCCCGACCCAAGACCACGTGGATGAAGGTGACGAGGTGGAGAAA
TCCAGCAGTGGCATGCCGATTGCGATCGAAAACCCAAACCAATTTGTGCCTCTCTATACTGACCCCCAGGAAGTA
CTGGAGATGAGGAACAAGATTGAGAGAACAACCAAGGACCAAGATGTGAAGTCAGCGGGGCTCAGTCCCAGCTCCTG
GCGAGCGTCATTGCGGAGAAGAGCCGAAGCCCGTCTACAGAGAGCCAGCTGATGTCCAAGGGAGACGAGGATACC
AAAAGACGATTCCAGAGGAGACGGTGCCCAACCCCTTCAGCCAACCTCACTGACCAGGAGTTGGAGGAGTACAAGAAA
GAGGTGGAGAGGAAGAACTAGAACTTGATGGAGAGAAAGAACTGCCCCAGAAGAGCCTGGCTCACCTGCAAG
TCTGCACCTGCTTCTCCAGTGCAGAGCCAGCGAAGGAGGCAGAGACAAAGAGCCCTTTAGTCTCTCCTTCCAAG
TCTTTAGAGGAAGGTACTAAGAAGACAGAAACAAGCAAAGCCGCCACCACAGAGCCCCGAAACAACCCAGCCGGAA
GGGTGGTGGTCAACGGGAGGGAGGAGGAGCAGACGGCAGAGGAAATCCTCAGCAAAGGCCCTGAGCCAGATGACC
ACCACTGCTGACACGGATGTTGATACCTCTAAGGACAAAACCGAGTCGGTCACCAGCGGCCCATGTCCCCAGAG
GGCTCACCTTCCAAGTCTCCCTCAAAGAAGAAAAAGAAATTCCGAACCCCTCCTTCTGAAAAAGAGCAAAAAG
AAGGAGAAAGTGGAGTCTGATTGATGACACCCTTGGGCTCCCTCCTGCCTCCTCTCTCCTCCCCTTCCCTTC
TCCATCTCTGTCCCTGCAAGCACAGGGCTAAGGAGGGATAGAGTAGGACCCTGGACCACATTGCGAAGGGGAAC
TTAGAGATCACCCGACCAACCCCTTCGTTTTACAGTTGCCCAAGAGAAATCAGGTGACTTGCCCAAGGTCACACAG
CTAGTTAGCGGCAGAGCCTGCACTCGAATTCAGGTCTCCTGACTTCCAGTCCAGTGCTCCTTCTACTACACAACA
CTGCCTAGTTGTGGGCTGCCTTTGTTGGATGCTGTCCACCAATCTGAGCCTAGGGCAAGAAGGCCAGAAATGGG
CCGTGAGCTCTCACAGGCTCAGACTAAATCAGAGGTCAAGGCTTCCCCTGAGTAAGGTCCATTTCTTCCCAGGAA
TCCAATCTCCTGTGGATGGAGCTATCTCTACATTTAAAAATCTCTTCTCTTTTCCACTTTGGGTCCCTGCCCTGC
TGCTCAAAGTGACTAGCCAAATTGACCCCTCCAACAGAAAGTAATCTTTGTTCCCAAGGGCTGATGGCTTAGCTT
GTACTACCCCAACATTAACCCCTGAGCTTTCTTCATGGAACCTCTTGAATGATGGATGGAAGAGCTATAAGAGGT
GGTAGGCATAGGGGCAAGCCATGTAAGCTGAGGATTGGGGATGGTTTCATCAACATAAGAGGCCAGGAACCTTGAC
CCCTTTGAATTGTGCATCTCAGGCACTTCAAACTAAAACCAAAATTTAGCATAGGAAAAAGTTGTTTAATGCTCA
GGGCAGAAATTTGGGGAAGTTGAAATCCTCTGTTGGCTTTGGGTTGTATAAGGAGGATCAAAACAACAGAGGAAA
TGCTGACTTTCTAGCTTTGCATGACACCTGGAGCAATGCACTGTACCTGCCTCACTCCTGTCCAGTGGTCAGGTT

848/6881

FIGURE 788B

TCCCCTGACCTTCCCTCACCCCCAGAAACACTTGCTTACAGACCGAAACTGGCATCTTACTCTTGGCACCTTGAC
TTGCACCCCTCTGAGGTTCCAACCTCAGTCATTCTTTGTCCAGCAGAGGAGAATCAGAAATGAGCCCTTCAGGATTA
ATCCTCTTGCACCAGCTCTCAGAGAAATGCTGGGTATCCCTGTCCTTGTCCCTATCTGTCCATCCTGGGGCCTGG
TAATGGCCACAGTTATTGTTTTAAATGCCAACACTGTCCTTCATGTTCTTCCGTGGGGCATTGATTAATGAGCA
TTTGTTGGCTCCTAAAAATTAGACAATCCATTCTCTTG

849/6881
FIGURE 789

GGCACGAGGCGGAGAACAGGAGCATGGAGGGCGGGCTGGGGCGTGCTGTGTGCTTGCTGACCGGGGCCTCCCGCG
GCTTCGGCCGGACGCTGGCCCCGCTCCTGGCCTCGCTGCTGTGCGCCGGCTCCGTGCTTGCTCCTTAGCGCCCCGA
ACGACGAGGCACTGCGCCAGCTGGAGGCCGAGCTGGGCGCCGAGCGGTCTGGCCTGCGCGTGGTGCGGGTGCCCCG
CCGACCTGGGCGCCGAGGCCGGCTTGCAGCAGCTGCTCGGCGCCCTGCGCGAGCTCCCCCGGCCCAAGGGGCTGC
AGCGACTGCTGCTTATCAACAACGCGGGCTCTCTTGGGGATGTGTCCAAAGGCTTCGTGGACCTGAGTGACTCCA
CTCAAGTGAACAACACTACTGGGCACTGAACTTGACCTCCATGCTCTGCCTGACTTCCAGCGTCCTGAAGGCCTTCC
CGGACAGTCCTGGCCTCAACAGAACCGTGGTTAACATCTCGTCCCTCTGTGCCCTGCAACCTTTCAAAGGCTGGG
CGCTGTACTGTGCAGGAAAGGCTGCTCGTGATATGCTGTTCCAGGTCCCTGGCGCTGGAGGAACCTAATGTGAGGG
TGCTGAACTATGCCCCAGGTCCCTCTGGACACAGACATGCAGCAGTTGGCCCCGGGAGACCTCCGTGGACCCAGACA
TGCGAAAAGGGCTGCAGGAGCTGAAGGCAAAGGGGAAGCTGGTGGATTGCAAGGTGTCAGCCCAGAACTGCTGA
GCTTACTGGAAAAGGACGAGTTCAAGTCTGGAGCCACGTGGACTTCTATGACAAATAAGCCCATGTTTTTGGCT
TCCTGAACCTTTTTTGCCCCACTTTTAGACATACCCCAGAGCCCTGTGGCTCCCCACACCCTGCCATAGGGGCAG
TCCTGCCTTACACATAGAAGCATTCATGCCTGCTGCCCTGCCCTCAGGCACAGCCAGCTGTGAGCTCCAGGTCA
TTGGCCTTACCAGTTGTCAGGAGTCTGTGCTGTGCACCCTGGGTTATAAGGAGGCTTAGGAGAGAGGTTATGGGT
ATTGGTGTCTCTATCCCCAGGAATAGAACTTAAGGGGTGGGAAGAACAGGAAAAGAAGCTGGAACACAGAAGAGA
GGAGGTTGTGTCTCTTGCTCATAGCAAGCCTGTGGGTAGAGGAAAGAGTGATCTGGTGTGCAATAGGAGGACCCA
TGTAGATTGCGAGATGGCCTGGATGGGAGGAAGGGCAGACGGTACATGTCCCAGCCCACATAGATGCCCTTGCT
GAGGGTAGCAGGACCTTCTGTTGAACTTTGTGTCCTCACTCTGATGTCTCCTTCCTTCAGAATCTACCACCCCTC
CCCCAGGCTGGGAGAAGGGGCTCCTGGGTGTCTGTATACACGCCAAAGGCAGATACAAATAAAATACAGATTGTC
CTTTAAAAAAAAAAAAAAAAAAAA

850/6881
FIGURE 790

MEGGLGRAVCLITGASRGFGRTLAPLLASLLSPGSVLVLSARNDEALRQLEAELGAERSGLRVVRVPADLGAEAG
LQQLLGALRELPRPKGLQRLLLINNAGSLGDVSKGFVDLSDSTQVNNYWALNLTSMCLTSSVLKAFPDSFGGLNR
TVVNISSLALQPFKGWALYCAGKAARDMLFQVLALEEPNVRVLNYAPGPLDTDMQQLARETSVDPDMRKGLQEL
KAKGKLVDCKVSAQKLLSLLEKDEFKSGAHVDFYDK

851/6881
FIGURE 791

GGAGCATGGAGGGCGGGCTGGGGCGTGCTGTGTGCTTGCTGACCGGGGCCTCCCGCGGCTTCGGCCGGACGCTGG
CCCCGCTCCTGGCCTCGCTGCTGTGCGCCCGGCTCCGTGCTTGTCCTTAGCGCCCGCAACGACGAGGCACTGCGCC
AGCTGGAGGGCCGAGCTGGGCGCCGAGCGGTCTGGCCTGCGCGTGGTGCGGGTGCCCGCCGACCTGGGCGCCGAGG
CCGGCTTGCGAGCAGCTGCTCGGCGCCCTGCGCGAGCTCCCCCGGCCCAAGGGGCTGCAGCGACTGCTGCTTATCA
ACAACGCGGGTAAGACCCCGGGGCTGGAGCGGACTCCCCATGTGAGCGCCCACTTCCTCCACCGCTGGGGAATTT
AAGGGCTACTCCTAGGGGTCAGATAGGACGCCTAGAAATCTAAAGCCCTAGTTGTTCCAGCTTGAGTAGCAAGTG
GAGGCGAGGTGTACAGGAAGACTCGGTGCCGTCGGGACAACAGTCTGCCCCCACTTCCTGGAAAATTGGCCAGCC
GGGTTTTCCAAAGCGCCTGTAGAACTTTCCCGAGCCCCCTTGCTCTGCGCCCTCTGGCGGAGGCCTGAGTCAGGGC
TTGGAGTCTCCAAACAAGTAACTCTCTGCTTCTCCAAAGGACCGCTAGAGCTTTCCTTCAGCCCCACGGCAAGG
GCTCTCTTGGGGATGTGTCCAAAGGCTTCGTGGACCTGAGTGACTCCACTCAAGTGAACAACACTACTGGGCACTGA
ACTTGACCTCCATG

852/6881
FIGURE 792

GTTCCAAGGTTTTCGGCCCCGGTCTCGGAGAAGAGGGGAGAGTGGAGGGCCGCTGAATAAGCTTCCAAAATGATGC
CCACACCAGTTATCCTATTGAAAGAGGGGACTGATAGCTCCCAAGGCATCCCCCAGCTTGTGAGTAACATCAGTG
CCTGCCAGGTGATTGCTGAGGCTGTAAGAACTACCCCTGGGTCCCCGTGGCATGGACAAGCTTATTGTAGATGGCA
GAGGCAAAGCAACAATTTCTAATGATGGGGCCACAATTCTGAAACTTCTTGATGTTGTCCATCCTGCAGCAAAGA
CTTTGGTAGACATTGCCAAATCCCAAGATGCTGAGGTGGGTGATGGCACCACCTCAGTGACCTTGCTGGCTGCAG
AGTTTCTGAAGCAGGTGAAACCCCTATGTGGAGGAAGGTTTACACCCCCAGATCATCATTCGAGCTTTCCGCACAG
CCACCCAGCTGGCAGTTAACAAGATCAAAGAGATTGCTGTGACCGTGAAGAAGGCAGATAAAGTGGAGCAGAGGA
AGCTGCTGGAAAAGTGTGCCATGACCGCTCTGAGCTCCAAGCTGATCTCCCAGCAGAAAAGCTTTCTTTTGCTAAGA
TGGTGGTGGATGCAGTGATGATGCTCGATGATTTGCTGCAGCTTAAAATGATTGGAATCAAGAAGGTACAGGGTG
GAGCCCTCGAGGATTCTCAGCTGGTAGCTGGTGTTCATTCAAGAAGACTTTCTCTTACGCTGGGTTTGAAATGC
AACCCTAAAAGTACCACAATCCCAAGATTGCCCTTTTGAATGTCGAGCTCGAGTTGAAAGCTGAGAAAGACAATG
CTGAGATAAGAGTCCACACAGTTGAGGATTATCAGGCAATTGTTGATGCTGAGTGGAACATTCTCTATGACAAGT
TAGAGAAGATCCATCATTCTGGAGCCAAAGTTGTCTTGTCCAAACTCCCCATTGGGGATGTGGCCACCCAGTACT
TTGCTGACAGGGACATGTTCTGTGCTGGCCGAGTACCTGAGGAGGATCTGAAGAGGACAATGATGGCCTGTGGAG
GCTCAATCCAGACCAGTGTGAATGCTCTGTCAGCAGATGTGCTGGGTGATGCCAGGTGTTTGAAGAGACCCAGA
TTGGAGGCGAGAGGTACAATTTTTTTTACTGGCTGCCCCAAGGCCAAGACATGCACCTTCATTCTCCGTGGCGGCG
CCGAGCAGTTTATGGAGGAGACAGAGCGGTCCCTGCATGATGCCATCATGATCGTCAGGAGGGCCATCAAGAATG
ATTAGTGGTGGCTGGTGGCGGGGCCATTGAGATGGAACCTCTCCAAGTACCTGCGGGATTACTCAAGGACTATTTC
CAGGAAAACAGCAGCTGTTGATTGGGGCTTATGCCAAGGCCTTGGAGATTATCCCACGCCAGCTGTGTGACAATG
CTGGCTTTGATGCCACAAACATTCTCAACAAGCTGCGGGCTCGGCATGCCAGGGGGGTACATGGTATGGAGTAG
ACATCAACAACGAGGACATTGCTGACAACCTTTGAAGCTTTTCGTGTGGGAGCCAGCTATGGTGC GGATCAATGCGC
TGACAGCAGCCTCTGAGGCTGCGTGCCTGATCGTGTCTGTAGATGAAACCATCAAGAACCCCCGCTCGACTGTGG
ATGCTCCACAGCAGCAGGCCGGGGCCGTGGTCTGTGGCCGCCCCACTGAGAGGCACCCACCCATCAGATGGCT
GGCTGGCTGCTGGGTGCACTTACCCTCCTTGGCTTGGTTACTTCATTTTACAAGGAAGGGGTAGTAATTGGCCCA
CTCTCTTCTTACTGGAGGCTATTTAAATAAAATGTAAGACTTCAAAAAAAAAAAAAAAAAAAAAA

853/6881
FIGURE 793

MMPTPVILLKEGTDSSQGIPQLVSNISACQVIAEAVRTTLGPRGMDKLIVDGRGKATISNDGATILKLLDVVHPA
AKTLVDIAKSQDAEVGDGTTSVTLAAEFLKQVKPYVEEGLHPQIIIRAFRTATQLAVNKIKEIAVTVKKADKVE
QRKLLKCAMTALSSKLISQQKAFFAKMVVDVMMMLDDLQLKMIGIKKVQGGALDSQLVAGVAFKKTFSYAGF
EMQPKKYHNPKIALLNVELELKAEKDNAEIRVHTVEDYQAIVDAEWNILYDKLEKIHHSKAKVVLKLPIGDVAT
QYFADRD MFCAGRVPEEDLKRTMMACGGSIQTSVNALSADVLGRCQVFEETQIGGERYNFFTGC PKAKTCTFILR
GGAEQFMEETERSLHDAIMIVRRAIKNDSVVAGGGAIEMELSKYLRDYSRTIPGKQQLLIGAYAKALEIIPRQLC
DNAGFDATNILNKLRRARHAQGGTWYGVDINNEDIADNFEAFVWEPAMVRINALTAASEAACLIVSVDETIKNPRS
TVDAPTAAGRGRGRGRPH

854/6881
FIGURE 794

ATATAACCGCGTGGCCCGCGCGCGCTTCCCTCCCGGCGCAGTCACCGGCGCGGTCTATGGCTGCGACTTCTCT
AATGTCTGCTTTGGCTGCCCCGGCTGCTGCAGCCCGCGCACAGCTGCTCCCTTCGCCTTCGCCCTTTCCACCTCGC
GGCAGTTCGAAATGAAGCTGTTGTCAATTTCTGGAAGGAACTGGCCCAGCAGATCAAGCAGGAAGTGCGGCAGGA
GGTAGAAGAGTGGGTGGCCTCAGGCAACAAACGGCCACACCTGAGTGTGATCCTGGTTGGCGAGAATCCTGCAAG
TCACTCCTATGTCTCAACAAAACCAGGGCAGCTGCAGTTGTGGGAATCAACAGTGAGACAATTATGAAACCAGC
TTCAATTTTCAGAGGAAGAATTGTTGAATTTAATCAATAAACTGAATAATGATGATAATGTAGATGGCCTCCTTGT
TCAGTTGCCTCTTCCAGAGCATATTGATGAGAGAAGGATCTGCAATGCTGTTTCTCCAGACAAGGATGTTGATGG
CTTTCATGTAATTAATGTAGGACGAATGTGTTTGGATCAGTATTCATGTTACCGGCTACTCCATGGGGTGTGTG
GGAAATAATCAAGCGAACTGGCATTCCAACCCTAGGGAAGAATGTGGTTGTGGCTGGAAGGTCAAAAAACGTTGG
AATGCCCATTGCAATGTTACTGCACACAGATGGGGCGCATGAACGTCCCGGAGGTGATGCCACTGTTACAATATC
TCATCGATATACTCCCAAAGAGCAGTTGAAGAAACATAACAATTCCTGCAGATATTGTAATATCTGCTGCAGGTAT
TCCAAATCTGATCACAGCAGATATGATCAAGGAAGGAGCAGCAGTCATTGATGTGGGAATAAATAGAGTTCACGA
TCCTGTAAC TGCCAAACCCAAGTTGGTTGGAGATGTGGATTTTGAAGGAGTCAGACAAAAAGCTGGGTATATCAC
TCCAGTTCCTGGAGGTGTTGGCCCCATGACAGTGGCAATGCTAATGAAGAATACCATTATTGCTGCAAAAAAGGT
GCTGAGGCTTGAAGAGCGAGAAGTGCTGAAGTCTAAAGAGCTTGGGGTAGCCACTAATTAACTACTGTGTCTTCT
GTGTCACAAACAGCACTCCAGGCCAGCTCAAGAAGCAAAGCAGGCCAATAGAAATGCAATATTTTAAATTTATTC
TACTGAAATGGTTTTAAATGATGCCTTGATTTTATTGAAAGCTTAAATGGGTGGGTGTTTCTGCACATACCTCTG
CAGTACCTCACCAGGGAGCATTCCAGTATCATGCAGGGTCTGTGATCTAGCCAGGAGCAGCCATTAACCTAGTG
ATTAATATGGGAGACATTACCATATGGAGGATGGATGCTTCACTTTGTCAAGCACCTCAGTTACACATTGCCTT
TTCTAGGATTGCATTTCCCAAGTGCTATTGCAATAACAGTTGATACTCATTTTAGGTACCAGACCTTTTGAGTTC
AACTGATCAAACCAAAGGAAAAGTGTGCTAGAGAAAATTGGGGAAAAGGTGAAAAAGAAAAATGGTAGTAATT
GAGCAGAAAAAAATTAATTTATATATGTATTGATTGGCAACCAGATTTATCTAAGTAGAACTGAATTGGCTAGGA
AAAAAGAAAAACTGCATGTTAATCATTTTCCTAAGCTGTCCTTTTGAGGCTTAGTCAGTTTATTGGGAAAATGTT
TAGGATTATTCCTTGCTATTAGTACTCATTTTATGTATGTTACCCTTCAGTAAGTTCTCCCCATTTTAGTTTTCT
AGGACTGAAAGGATTCTTTTCTACATTATACATGTGTGTTGTCATATTTGGCTTTTGCTATATACTTTAACTTCA
TTGTTAAATTTTTGTATTGTATAGTTTCTTTGGTGTATCTTAAACCTATTTTGA AAAACAACTTGGCTTGAT
AATCATTTGGGCAGCTTGGGTAAGTACGCAACTTACTTTCCACCAAAGAACTGTCAGCAGCTGCCTGCTTTTCT
GTGATGTATGTATCCTGTTGACTTTTCCAGAAATTTTTTAAGAGTTTGAGTTACTATTGAATTTAATCAGACTTT
CTGATTAAAGGGTTTTCTTTCTTTTTTAATAAAACACATCTGTCTGGTATGGTA

855/6881
FIGURE 795

MSALAARLLQPAHSCSLRLRPFHLAAVRNEAVVISGRKLAQQIKQEVQRQEVEEWVASGNKRPHLSVILVGENPAS
HSYVLNKTRAAAVVGINSETIMKPASISSEELLNLINKLNDDNDVGLLVQLPLPEHIDERRICNAVSPDKDVDG
FHVINVGRMCLDQYSMLPATPWGVWEIIKRTGIPTLGKNVVVAGRSKNVGMPIAMLLHTDGAHERPGGDATVTIS
HRYTPKEQLKKHTILADIVISAAGIPNLITADMIKEGAVIDVGINRVHDPVTAKPKLVGDVDFEGVRQKAGYIT
PVPGGVGPMTVAMLMKNTIIAAKKVLRLEEREVLKSKELGVATN

856/6881
FIGURE 796

GGAAAATTTGTCACAGCAGCCAGAGGGGTTTAAACAGGAGTGCAGAGGGATAAGGGCAGCTTCTGCCCTCTGCCCA
AGAGCTGGCCACCTCTTTAAAGACTGAGGGAACAGTGGGAGGAGGAAGTGTGGGACAGTGTGGTACCTATCTGTC
CCCCCTCTGGAGGGGTTGACAAGGGAAAGGGCACCGGGGGGCACAGAGATGCAGGACAGATTGCACATCCTGGAG
GACCTGAATATGCTCTACATTCGGCAGATGGCACTCAGCCTGGAGGACACGGAGTTGCAGAGGAAGCTAGACCAT
GAGATCCGGATGAGGGAAGGGGCTGTAAAGCTGCTGGCAGCCTGCTCCCAGCGAGAGCAGGCTCTGGAGGCCACC
AAGAGCCTGCTAGTGTGCAACAGCCGCATCCTCAGCTACATGGGCGAGCTGCAGCGGCGCAAGGAGGCGCAGGTG
CTGGGGAAGACAAGCCGGCGGCCTTCTGACAGTGGCCCGCCGCTGAGCGCTCCCCCTGCCGCGGCCGGGTCTGC
ATCTCTGACCTCCGGATTCCACTCATGTGGAAGGACACAGAATATTTCAAGAACAAAGGTGACTTGACCCGCTGG
GCTGTGTTCTCTGCTGCTGCAGCTGGGGGAACACATCCAGGACACAGAGATGATCCTAGTGGACAGGACCCTCACA
GACATCTCCTTTTCAAGCAATGTGCTCTTCGCTGAGGCGGGGCCAGACTTTGAACTGCGGTTAGAGCTGTATGGG
GCCTGTGTGGAAGAAGAGGGGGCCCTGACTGGCGGCCCAAGAGGCTTGCCACCAAACTCAGCAGCTCCCTGGGC
CGTCTCTCAGGGAGGCGTGTCCGGGCATCGCTGGACAGTGTGGGGGTTTCAGGGAGCAGTCCCATCTTGCTCCCC
ACCCAGTTGTTGGTGGTCTCTGTTACCACCTCTTGGCTCACACCACACTCACCTTGGCAGCAGTGAAGATGGA
TTCCGCACACATGACCTCACCTTGCCAGTCATGAGGAGAACCCTGCCTGGCTGCCCCCTTTATGGTAGCGTGTGT
TGCCGTCTGGCAGCTCAGCCTCTCTGCATGACTCAGCCCACTGCAAGTGGTACCCTCAGGGTGCAGCAAGCTGGG
GAGATGCAGAACTGGGCACAAGTGCATGGAGTTCTGAAAGGCACAAACCTCTTCTGTTACCGGCAACCTGAGGAT
GCAGACACTGGGGAAGAGCCGCTGCTTACTATTGCTGTCAACAAGGAGACTCGAGTCCGGGCAGGGGAGCTGGAC
CAGGCTCTAGGACGGCCCTTACCCCTAAGCATCAGTAACCAGTATGGGGATGATGAGGTGACACACACCCTTCAG
ACAGAAAGTCGGGAAGCACTGCAGAGCTGGATGGAGGCTCTGTGGCAGCTTTTCTTTGACATGAGCCAATGGAAG
CAGTGTGTGATGAAATCATGAAAATTGAACTCCTGCTCCCCGGAACCAACCCCAAGCACTGGCAAAGCAGGGG
TCCTTGTTACCATGAGATGGCTATTGAGCCGCTGGATGACATCGCAGCGGTGACAGACATCCTGACCCAGCGGGAG
GGCGCAAGGCTGGAGACACCCCCACCCTGGCTGGCAATGTTTACAGACCAGCCTGCCCTGCCTAACCCCTGCTCG
CCTGCCCTCAGTGGCCCCAGCCCCAGACTGGACCCACCCCTGCCCTGGGGGAGACCCCGAACCTTTTCCCTGGAT
GCTGTCCCCCAGACCACTCCCCTAGGGCTCGCTCGGTTGCCCCCTCCACCTCAGCGATCCCCACGGACCAGA
GGCCTCTGCAGCAAAGGCCAACCTCGCACTTGGCTCCAGTACACAGTGTGAGAGAGAAAGGTGCTGGCATAGGAT
CTGCCCAGAAGAGAAAATGACCCATGCGCAGTTGGGCTCTGGATACGGCGCTGTCTATAGCAAGTTGGCCAGTCT
GGCCTCCTGTTCTCTGCTGGACCTGGGGTAGGCTGCAGGGGTGGGCAGAAGCCCCCTTTAAATTGTGGTTGCCA
TGGTACCGAGGACTCATTCTGGGGCTCGCTGGGACCTCCCTAAACCTTCTTGGAAGAAAAGTGAACCAACT
CTGCCCTACCTCCCTGCATAACCAGCTTTGAGGATGGCACTGAAGAACCCTTGGAGCAAACATACCTCCCTTGT
GACTCCACATCAACCATTAAAGTTATTTAACAGCAAAAAAAAAAAAAA

857/6881
FIGURE 797

MQDRLHILEDLNMLYIROMALSLEDTELQRKLDHEIRMREGACKLLAACSQREQALEATKSLLVCNSRILSYMGE
LQRRKEAQVLGKTSRRPSDSGPPAERSPCRGRVCISDLRIPLMWKDTEYFKNKGDLHRWAVFLLLQLGEHIQDTE
MILVDRTLTDISFQSNVLF AEAGPDFELRLELYGACVEEEGALTGGPKRLATKLSSSLGRSSGRRVRASLDSAGG
SGSSPILLPTPVVGPRYHLLAHTTLTAAVQDGFRTDHLTASHEENPAWLPLYGSVCCRLAAQPLCMTQPTAS
GTLRVQQAGEMQNWAQVHGVLKGTNLF CYRQPEDADTGEEPLLTIAVNKETRV RAGELDQALGRPFTLSISNQYG
DDEVTHLTQTESREALQSWMEALWQLFFDMSQWKQCCDEIMKIETPAPRKPPQALAKQGSLYHEMAIEPLDDIAA
VTDILTQREGARLET PPPW LAMFTDQPALPNPCSPASVAPAPDWTHPLPWGRPRTFSLDAVPPDHSPRARSVAPL
PPQRSPTTRGLCSKGQPRTWLQSPV

858/6881
FIGURE 798

GACTACGTGGGTCTGGAGCTGACTGCCGTCCTGACACGTCCTAGAGCTGCAAGTCCTGCCAGAGAGCCACCATGA
CCTCTCAGCCTCTCAGGCTAGCAGAAGAGTATGGCCCAAGTCCTGGGGAGTCTGAACTGGCTGTGAACCCCTTTG
ATGGGCTTCCCTTCTCTTCCCGCTACTATGAGCTGCTGAAGCAGCGCCAAGCCTTGCCCATCTGGGCTGCTCGCT
TTACCTTCTTGGAGCAGTTGGAGAGTAACCCCACTGGAGTGGTGTCTGGTGTCTGGGGAGCCTGGTTCTGGCAAGA
GCACCCAGATCCCTCAGTGGTGTGCAGAGTTTGCCTGGCCAGAGGGTTCCAGAAAGGACAGGTTACTGTTACTC
AGCCCTACCCTCTTGCAGCCCGGGAGCCTGGCTCTGCGGGTTGCTGATGAGATCGACCTGACCCCTGGGTGCTGAG
GTTGGATCCAGCATCCCCAGGAGGACTGCACGGGGCCCAACACCCTGCTCAGGTTCTGCTGGGACAGGCTGCTT
CTGCAGGAGGTGGCCTCGACCCGAGGCACTGGAGCCTGGGGCGTGCTGGTACTAGATGAGGCTCAGGAGCGGTGCG
GTGGCATCAGATTCACTCCAGGGGCTACTGCAAGATGCCAGGCTGGAAAAAATTCCGGGGGACCTCAGAGTGGTT
GTGGTTACTGACCCAGCCCTTGAACCTAAGCTCCGAGCTTTCTGGGGCAATCCTCCTATTGTGCATATACCCAGA
GAGCCTGGTGAGAGACCTTCCCCCATCTACTGGGACACCATCCACCTGATCGGGTGGAAGCTGCCTGCCAAGCA
GTGCTTGAATTGTGTGCGGAAGGAGCTTCCAGGAGATGTGCTAGTGTTCCTGCCAGTGAGGAGGAAATTTCCCTG
TGCTGTGAATCCTTGTCCAGGGAGGTAGAGTCCTTGCTTCTCCAAGGGCTTCCACCACGAGTACTGCCCTTCAC
CCAGACTGTGGACGAGCCGTTCAAGCTGTGTATGAGGACATGGATGCCCGAAAGGTTGTGGTCACTCACTGGCTG
GCTGACTTCTCCTTCTCCCTCCCTTCCATCCAACATGTCATCGACTCAGGACTGGAGCTCCGAAGTGTTTACAAT
CCTAGGATCCGAGCAGAATTCCAAGTGTGAGGCCAATCAGCAAGTGTGAGGACAGGCAAGACGATTGCGAGCA
AGAGGGTTCACCAGGATCCTGCCTCTGCCTGTATCCTAAGTCCTTCTTAGAACTAGAAGCTCCACCATTGCCA
CAACCAGGGTGTGTGAGGAGAATCTGAGTCCCTGGTGTACTACTAAAAAGGAGACAGATTGCAGAGCCAGGG
GAGTGTCACTTCTGGACCAGCCTGCTCCAGAAGCACTGATGCAAGCCCTGGAAGATTTAGACTATCTGGCAGCC
CTGGATGATGATGGGGACCTGTCAGATCTGGGTGTCATACTATCAGAATTCCTCTGGCCCCCTGAGCTGGCCAAA
GCCCTGCTGGCCTCATGCGAGTTTGACTGTGTGGACGAGATGCTCACCCCTGGCTGCCATGCTCACAGCTGCCCT
GGGTTTACCCGTCCTCCACTCAGTGCAGAAGAAGCTGCCCTGCGTCGGGGCCCTGGAACACACGGATGGTGACCAC
AGTTCTCTGATCCAGGTGTATGAAGCCTTTATACAAAGTGGAGCAGATGAGGCTTGGTGCCAGGCTCGAGGTCTG
AATTGGGCAGCATTGTGCCAAGCCCATAACTTCGGGGGAGAACTCCTAGAACTCATGCAACGAATTGAACCTCCC
TTGTCCCTACCAGCCTTTGGCTCTGAGCAGAATCGCAGAGACCTTCAGAAAGCACTGGTGTGAGAATACTTTCTC
AAGGTGGCCAGAGACACAGACGGGACTGGAAATTACCTTCTCCTAACCATAAGCATGTGGCCCAGCTCTCCTCA
TACTGCTGCTACCGAAGCCGAGAGCTCCTGCCAGACCCCCACCATGGGTGCTCTACCACAATTTACCATATCC
AAAGACAACCTGCCTCTCCATTGTTTCTGAGATTCAACCACAGATGCTGGTGGAATTGGCCCCCTCCATACTTCCTG
AGTAACTTGCCTCCAGTGAGAGCAGAGACCTTCTGAACCAGCTAAGGGAAGGAATGGCAGATTCTACAGCAGGG
AGCAAATCATCCTCAGCCAGGAGTTTCAAGATCCCTGTGTCCTGCAGTGAACCTGCCTGCTATGGAATGGAGCT
GGGTTTATCTCATCACATTAGATTATCCCTCAGGGTGACACCAAGCACCCAGACAGATTTAGAAGCCCAAAGTT
TAGGGTCAAATGTAAACCCTGGAACCTGAGTCCCAAGAAATGGTAGACTGGGAATGGAAGAATGGGGTAAACCA
CAGTCTACATAGGGAAGGACTCTTTCCTTAGCCTTCTCTTATTGATTGGAGAGGGACTGACATGCTCCTCATTCT
CTTAACCTTTGCCAAACCCATTCTTGTAATCCTTGTGATCTATAAAAGATTTTCTATGATGCCAAAAAAAAAA
AAAAAAAAA

859/6881
FIGURE 799

MDLTIGHEVGSSIPQEDCTGPNLTLLRFCWDRLLLQEVASTRGTGAWGVLVLDQAQERSVASDSLQGLLDARLEK
LPGDLRVVVVTDPALEPKLRAFWGNPPIVHIPREPGERPSPYWDTIPPDRVEAACQAVLELCRKELPGDVLVFL
PSEEEISLCCESLSREVESLLLQGLPVRVLPDHPDCGRAVQAVYEDMDARKVVVTHWLADFSFSLPSIQHVIDSG
LELRSVYNPRIRAEFQVLRPISKQAEARRLRARGFPPGSCLCLYPKSFLELEAPPLPQPRVCEENLSSLVLLK
RRQIAEPGECHFLDQPAPEALMQALEDLDYLAALDDDGDLSDLGVILSEFPLAPELAKALLASCEFDVDEMLTL
AAMLTAAPGFTRPPLSAEEAALRRALEHTDGDHSSLIQVYEAFIQSGADEAWCQARGLNWAALCQAHKLRGELLE
LMQRIELPLSLPAFGSEQNRRDLQKALVSEYFLKVARDTDGTGNVLLTHKHVAQLSSYCCYRSRRAPARPPWV
LYHNFTISKDNCLSIQVSEIQPQMLVELAPPYFLSNLPPSESRLNQLREGMADSTAGSKSSAQEFRDPCVLQ

860/6881
FIGURE 800

CGAAAATGGCGGCGGCGGCGACGGCCGGGCGCTCCTGAAGCAGCAGTTATGGAGCTTCCCTCAGGGCCGGGGCCG
GAGCGGCTCTTTGACTCGCACCGGCTTCCGGGTGACTGCTTCCTACTGCTCGTGCTGCTGCTCTACGCGCCAGTC
GGGTTCTGCCTCCTCGTCCTGCGCCTCTTTCTCGGGATCCACGTCTTCCTGGTCAGCTGCGCGCTGCCAGACAGC
GTCCTTCGCAGATTTCGTAGTGCGGACCATGTGTGCGGTGCTAGGGCTCGTGGCCCCGCGAGGAGTCCGGACTC
CGGGATCACAGTGTGAGGGTCCCTCATTTCCAACCATGTGACACCTTTTCGACCACAACATAGTCAATTTGCTTACC
ACCTGTAGCACCCCTCTACTCAATAGTCCCCCAGCTTTGTGTGCTGGTCTCGGGGCTTCATGGAGATGAATGGG
CGGGGGGAGTTGGTGGAGTCACTCAAGAGATTCTGTGCTTCACGAGGCTTCCCCCACTCCTCTGCTGCTATTCT
CCTGAGGAAGAGGCCACCAATGGCCGGGAGGGGCTCCTGCGCTTCAGTTCCCTGGCCATTTTCTATCCAAGATGTG
GTACAACCTCTTACCCTGCAAGTTCAGAGACCCCTGGTCTCTGTGACGGTGTGAGATGCCTCCTGGGTCTCAGAA
CTGCTGTGGTCACTTTTCGTCCCTTTCACGGTGTATCAAGTAAGGTGGCTTCGTCTGTTTCATCGCCAACTAGGG
GAAGCGAATGAGGAGTTTGCCTCCGTGTACAACAGCTGGTGGCCAAGGAATTGGGCCAGACAGGGACACGGCTC
ACTCCAGCTGACAAAGCAGAGCACATGAAGCGACAAAGACACCCCAAGATTGCGCCCCCAGTCAGCCCACTCTTCT
TTCCCTCCCTCCCTGGTCTTCTCCTGATGTGCAACTGGCAACTCTGGCTCAGAGAGTCAAGGAAGTTTGGCC
CATGTGCCATTGGGTGTATCCAGAGAGACCTGGCCAAGACTGGCTGTGTAGACTTGACTATCACTAATCTGCTT
GAGGGGGCCGTAGCTTTCATGCCTGAAGACATCACCAAGGGAAGTCAAGTCCCTACCCACAGCCTCTGCCTCCAAG
TTTCCCAGCTCTGGCCCGGTGACCCCTCAGCCAACAGCCCTAACATTTGCCAAGTCTTCTGGGGCCGGCAGGAG
AGCCTGCAGGAGCGCAAGCAAGCACTATATGAATACGCAAGAAGGAGATTACAGAGAGACGAGCCCAAGGAGCT
GACTGAGCTCAAAGGAACAGGATGGCACCCAGAGCCGAGGACGGAGACTGGGGGCAGCCCTCACCCAACTCACA
ACAGGCTGGATGGGTGGGTGGTAAAAAGGGAAGGATGAGGCTCCCCCAATGTCACATTAAATTCATGGTTTTTCAT
TC

861/6881
FIGURE 801

CGTGGATCCCGAGAAAGAGGCGCAGGACGAGGAGGCAGAACCCGACTGGCGCGTAGAGCAGCAGCACGAGCAGTA
GGAAGCAGTCACCCGGAAGCCTGGGGGCGAGAGGCGAAGTGGTCAGGCGCCGAAGGCCGAGAGCACGCGGGGATC
GGTCTCTTCCCGCCGGGTCTCTTACCGGTGCGAGTCAAAGAGCCGCTCCGGCCCCGGCCCTGAGGGAAGCTCCAT
AACTGCTGCTTCAGGAGCGCCCCGGCCGTCGCCGCCGCCGCCATTTTCGCGCCCCGGCCGCAGGGGCTCTTGGGAAG
GCGGAGTCTTTGGGCATCCGCCCGGGGTGAGGGGACCCGAAGTCTTGAGGCGCGCCGAAGGGCTAGCGGTCCCA
GCATACCCCGCGGCCCTTGGGCGCTCTCACAACCTCGCGTCCGGCGGAGACCACAATTCGCGGCATTTCGTGGGGC
AGGGAGGAGTCGGCCTCCCGGAATCCTGGTCCCGGCGTGCATTCTGAAGGACTTCAGGTACCGGCGTGCCCCG
GTCCTACTGTCCGCCTGCTCGCGTCTGGGTGCCGCTCTGAGTAGGGCGGGCGAGGAGGCAGCCAAGGCGGAGC
TGATGGCTGCGCCGAGGGCGGGGCGGGGTGCAGGCTGGAGCCTTCGGGCATGGCGGGCTTTGGGGGGCATTTCGCT
GGGGGAGGAGACCCCGTTTGACCCCTGACCTCCGGGCCCTGCTGACGTCAGGAATTCTGACCCCGGGCCCCGAG
TGACTTATGGGACCCCCAGTCTCTGGGCCCCGTTTGTCTGTTGGGGTCACTGAACCCCGAGCATGCCTGACGCTCTG
GGACCCCGGGTCCCCGGGCACAACCTGACTGCGGTGACCCAGATACCAGGACCCGGGAGGCCTCAGAGAACTCTG
GAACCCGTTTCGCGCGCGTGGCTGGCGGTGGCGCTGGGCGCTGGGGGGGCAGTGCTGTTGTTGTTGTTGGGGCGGGG
GTCGGGGTCTCCGGCCGTCCTCGCCGCCGTCCTAGCCCGCCGCCCGCTTCTCCCCGGAGTCAGTACAACCTTCA
TCGCAGATGTGGTGGAGAAGACAGCACCTGCCGTGGTCTATATCGAGATCCTGGACCGGCACCCTTTCTTGGGCC
GCGAGGTCCCTATCTCGAACGGCTCAGGATTCTGTGGTGGCTGCCGATGGGCTCATTGTACCAACGCCCATTGTGG
TGGCTGATCGGCGCAGAGTCCGTGTGAGACTGCTAAGCGGCGACACGTATGAGGCCGTGGTCACAGCTGTGGATC
CCGTGGCAGACATCGCAACGCTGAGGATTGAGACTAAGGAGCCTCTCCCCACGCTGCCTCTGGGACGCTCAGCTG
ATGTCCGGCAAGGGGAGTTTGTGTTGCCATGGGAAGTCCCTTTGCACTGCAGAACACGATCACATCCGGCATTG
TTAGCTCTGCTCAGCGTCCAGCCAGAGACCTGGGACTCCCCCAAACCAATGTGGAATACATTCAAACCTGATGCAG
CTATTGATTTTGAAAACCTCTGGAGGTCCCCTGGTTAACCTGGATGGGGAGGTGATTGGAGTGAACACCATGAAGG
TCACAGCTGGAATCTCCTTTGCCATCCCTTCTGATCGTCTTCGAGAGTTTCTGCATCGTGGGGAAAAGAAGAATT
CCTCCTCCGGAATCAGTGGGTCCCAGCGGCGCTACATTGGGGTGATGATGCTGACCCTGAGTCCCAGCATCCTTG
CTGAACCTACAGCTTCGAGAACCAAGCTTTCCCGATGTTTCAGCATGGTGTACTCATCCATAAAGTCATCCTGGGCT
CCCCTGCACACCGGGCTGGTCTGCGGCCTGGTGATGTGATTTTGGCCATTGGGGAGCAGATGGTACAAAATGCTG
AAGATGTTTATGAAGCTGTTTGAACCCAATCCCAGTTGGCAGTGCAGATCCGGCGGGGACGAGAAACACTGACCT
TATATGTGACCCCTGAGGTCACAGAA**TGA**ATAGATCACCAAGAGTATGAGGCTCCTGCTCTGATTTCTCCTTGC
CTTTCTGGCTGAGGTTCTGAGGGCACCGAGACAGAGGGTTAAATGAACCAGTGGGGGAGGTCCCTCCAACCACC
AGCACTGACTCCTGGGCTCTGAAGAATCACAGAAACACTTTTTATATAAAATAAAATTATACCTAGCAACATATT
ATAGTAAAAAATGAGGTGGGAGGGCTGGATCTTTTCCCCACCAAAAGGCTAGAGGTAAAGCTGTATCCCCCTAA
ACTTAGGGGAGATACTGGAGCTGACCATCCTGACCTCCTATTAAAGAAAATGAGCTGCTGAAAAAAAAAAAAAA
A

862/6881
FIGURE 802

MAAPRAGRAGWSLRAWRALGGIRWGRRPRLTPDLRALLTSGTSDPRARVTYGTPSLWARLSVGVTEPRACLTSG
TPGPRAQLTAVTPDTRTREASENSGTRSRRAWLAVALGAGGAVLLLLLWGGGRGPPAVLAAVPSPPPASPRSQYNFI
ADVVEKTAPAVVYIEILDRHPFLGREVPISNGSGFVVAADGLIVTNAHVVADRRRVVRLLSGDTYEAVVTAVDP
VADIATLRIQTKEPLPTLPLGRSADVRQGEFVAMGSPFALQNTITSGIVSSAQRPARDLGLPQTNVEYIQTDA
IDFGNSGGPLVNLDGEVIGVNTMKVTAGISFAIPSDRLREFLHRGEKKNSSSGISGSQRRYIGVMMLTSLPSILA
ELQLREPSFPDVQHGVLIHKVILGSPAHRAGLRPGDVILAIGEOMVQNAEDVYEAVRTQSQLAVQIRRGRETTL
YVTPEVTE

863/6881
FIGURE 803

GCAACGCGAGTGGGAGCACCAGGATCTCGGGCTCGGAACGAGACTGCACGGATTGTTTTAAGAAAATGGCAGACA
AACCAGACATGGGGGAAATCGCCAGCTTCGATAAGGCCAAGCTGAAGAAAACGGAGACGCAGGAGAAGAACACCC
TGCCGACCAAAGAGACCATTGAGCAGGAGAAGCGGAGTGAAATTTCCTAAGATCCTGGAGGATTCCTACCCCCG
TCCTCTTCGAGACCCCAGTCGTGATGTGGAGGAAGAGCCACCTGCAAGATGGACACGAGCCACAAGCTGCACTGT
GAACCTGGGCACTCCGCGCCGATGCCACCGGCCTGTGGGTCTCTGAAGGGACCCCCCCCCAATCGGACTGCCAAA
TTCTCCGGTTTGCCCCGGGATATTATAGAAAATTATTTGTATGAATAATGAAAATAAAACACACCTCGTGGCATG
GCA

864/6881
FIGURE 804

MADKPDMGGEIASFDKAKLKKTETQEKNLPTKETIEQEKRSLS

865/6881
FIGURE 805

CACCAAATGGCGGATGACGCCGGTGCAGCGGGGGGGCCAGAGCCCTGGTGGCCATGGGATAGGGAACCGCGGTG
GCTTCCACGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGTCGCGGGAGTGGACGGGGCCGTGCCGAGGCCGCGG
AGCTCGCGGAGGCAAGGCCGAGGATAAGGAGTGGATGCCTGTCACCAAGCTGGGCGCTTGGTCAAGGACATGAA
GATCAAGTCCCTGGAGGAGATCTATCTCTTCTCCCTGCCATTAAGGAATCTGAGATCATTGATTTCTTCCTGGG
GGACTCTCTCAAGGATGAGGTTTTGAAGATTATGCCGGTGCAGAAGCAGACCCGTGCCGGCCAGCGCACCAGGTT
CAAGGTGACAGGCCGCTGCGGCTCTGTGCTGGTGCGCCTCATCCCTGCACCCAGGGGCACTGGCATCGTCTCCGC
ACCTGTGCCCAAGAAGCTGCTCATGATGGCTGGTATCGATGACTGCTACACCTCAGCCCGGGGCTGCACTGCCAC
CCTGGGCAACTTCGCCAAGGCCACCTTTGATGCCATCTCTAAGACCTACAGCTACCTGACCCCCGACCTCTGGAA
GGAGACTGTATTTACCAAGTCTCCCTATCAGGAATTCAGTACCACCTCGTCAAGACCCACACCAGAGTCTCGGT
GCAGCGGACCCAGGCTTCAGATGTGGCTACAACATAGGGTTTTTATACAAGAAAAATAAAGTGAATTAAGCCTG

866/6881
FIGURE 806

CGCAGGCTGGAAGGAAGACGAACCTACGAAGCAGAGATCTGAAGACAGCATGTACACAGCCATTCCCCAGAGTGG
CTCTCCATTCCCAGGCTCAGTGCAGGATCCAGGCCTGCATGTGTGGCGGGTGGAGAAGCTGAAGCCGGTGCCTGT
GGCGCAAGAGAACCAGGGCGTCTTCTTCGCGGGGACTCCTACCTAGTGCTGCACAATGGCCCAGAAGAGGTTTC
CCATCTGCACCTGTGGATAGGCCAGCAGTCATCCCGGGATGAGCAGGGGGCCTGTGCCGTGCTGGCTGTGCACCT
CAACACGCTGCTGGGAGAGCGGCCTGTGCAGCACCGCGAGGTGCAGGGCAATGAGTCTGACCTCTTCATGAGCTA
CTTCCCACGGGGCCTCAAGTACCAGGAAGGTGGTGTGGAGTCAGCATTTACAAGACCTCCACAGGAGCCCCAGC
TGCCATCAAGAACTCTACCAGGTGAAGGGGAAGAAGAACATCCGTGCCACCGAGCGGGCACTGAACTGGGACAG
CTTCAACACTGGGGACTGCTTCATCCTGGACCTGGGCCAGAACATCTTCGCCTGGTGTGGTGGAAAGTCCAACAT
CCTGGAACGCAACAAGGCGAGGGACCTGGCCCTGGCCATCCGGGACAGTGAGCGACAGGGCAAGGCCCAGGTGGA
GATTGTCACTGATGGGGAGGAGCCTGCTGAGATGATCCAGGTCTTGGGCCCCAAGCCTGCTCTGAAGGAGGGCAA
CCCTGAGGAAGACCTCACAGCTGACAAGGCAAATGCCCAGGCCCGAGCTCTGTATAAGGTCTCTGATGCCACTGG
ACAGATGAACCTGACCAAGGTGGCTGACTCCAGCCCCTTTGCCCTTGAAGTCTGATATCTGATGACTGCTTTGT
GCTGGACAACGGGCTCTGTGGCAAGATCTATATCTGGAAGGGGCGAAAAGCGAATGAGAAGGAGCGGCAGGCAGC
CCTGCAGGTGGCCGAGGGCTTCATCTCGCGCATGCAGTACGCCCCGAACACTCAGGTGGAGATTCTGCCTCAGGG
CCGTGAGAGTCCCATCTTCAAGCAATTTTTCAAGGACTGGAAATGAGGGGTGGGCGTCTTCCTGCCCCATGCTCCC
CTGCCCCCACCACCTGCCTGCTTGCTTCTCTGGCTGCCTGGTCAGTGCAGAGGTGCCCCCTGCAGATGTTCAAT
AAAGGAGACAAGTGCTTTCCC

867/6881
FIGURE 807

MYTAIPQSGSPFPQSVQDPGLHVWRVEKLKVPVPAQENQGVFFSGDSYLVLHNGPEEVSHLHLWIGQQSSRDEQG
ACAVLAVHLNLTLLGERPVQHREVQGNESDLFMSYFPRGLKYQEGGVESAFHKTSTGAPAAIKKLYQVKGKKNIRA
TERALNWDSFNTGDCFILDGQNIFAWCGGKSNILERNKARDLALAIRDSERQGKAQVEIVTDGEEPAEMIQVLG
PKPALKEGNPEEDLTADKANAAALYKVSDATGQMNLTQVADSSPFALELLISDDCFVLDNGLCGKIYIWKGRK
ANEKERQAALQVAEGFISRMQYAPNTQVEILPQGRESPIFKQFFKDWK

868/6881
FIGURE 808

GGCACGAGGCGCCCGCCTGCTACGAGTAGAACGCTGTCCGCAGCTTGCGCATTTCGCAGCCGCTGCCGCCCTCGCC
GCTGCTCCTTCGTAAAGGCCACTTCCGCACACCGACACCAACATGAACGGACAGCTCAACGGCTTCCACGAGGCGT
TCATCGAGGAGGGCACATTCCCTTTTACCTCAGAGTCGGTCGGGGAAGGCCACCCAGATAAGATTTGTGACCAAA
TCAGTGATGCTGTCTTGATGCCCACCTTCAGCAGGATCCTGATGCCAAAGTAGCTTGTGAACTGTTGCTAAAA
CTGGAATGATCCTTCTTGCTGGGGAAATTACATCCAGAGCTGCTGTTGACTACCAGAAAGTGGTTCGTGAAGCTG
TTAAACACATTGGATATGATGATTCTTCCAAAGGTTTTGACTACAAGACTTGTAACGTGCTGGTAGCCTTGGAGC
AACAGTCACCAGATATTGCTCAAGGTGTTTCATCTTGACAGAAATGAAGAAGACATTGGTGTCTGGAGACCAGGGCT
TAATGTTTGGCTATGCCACTGATGAACTGAGGAGTGTATGCCCTTAAACCATTGTCTTGGCACACAAGCTAAATG
CCAACTGGCAGAACTACGCCGTAATGGCACTTTGCCTTGGTTACGCCCTGATTCTAAAACCTCAAGTTACTGTGC
AGTATATGCAGGATCGAGGTGCTGTGCTTCCCATCAGAGTCCACACAATTGTTATATCTGTTTCAGCATGATGAAG
AGGTTTTGTCTTGATGAAATGAGGGATGCCCTAAAGGAGAAAGTCATCAAAGCAGTTGTGCCTGCGAAATACCTTG
ATGAGGATACAATCTACCACCTACAGCCAAGTGGCAGATTTGTTATTGGTGGGCCTCAGGGTGATGCTGGTTTGA
CIGGACGCAAAATCATTGTGGACACTTATGGCGGTTGGGGTGCTCATGGAGGAGGTGCCTTTTCAGGAAAGGATT
ATACCAAGGTCGACCGTTTCAGCTGCTTATGCTGCTCGTTGGGTGGCAAAATCCCTTGTTAAAGGAGGTCTGTGCC
GGAGGGTTCTTGTTTCAGGTCTCTTATGCTATTGGAGTTTTCTCATCCATTATCTATCTCCATTTTCCATTATGGTA
CCTCTCAGAAGAGTGAGAGAGAGCTATTAGAGATTGTGAAGAAGAATTTTCGATCTCCGCCCTGGGGTCATTGTCA
GGGATCTGGATCTGAAGAAGCCAATTTATCAGAGGACTGCAGCCTATGGCCACTTTGGTAGGGACAGCTTCCCAT
GGGAAGTGCCCAAAAGCTTAAATATTGAAAGTGTTAGCCTTTTTTCCCCAGACTTGTTGGCGTAGGCTACAGAG
AAGCCTTCAAGCTCTGAGGGAAAGGGCCCTCCTTCTAAATTTTCTGTCTCTTTTCAGCTCCTGACCAGTTGCA
GTCACTCTAGTCAATGACATGAATTTTAGCTTTTGTGGGGGACTGTAAGTTGGGCTTGCTATTCTGTCCCTAGGT
GTTTTGTTCACCATTATAATGAATTTAGTGAGCATAGGTGATCCATGTAAGTGCCTAGAAACAACACTGTAGTAA
ATAATGCTTTGAAATGAACCTTTGTGCCCTATCACCCAACGTCCTCAAAGTCATAATTGCATTGACTTTCCCCAC
CAGATGCTGAAAATGTCCTTGTGATGTGCACGTAAAGTACTTGTAGTTCCACTTATAGCCTCTGTCTGGCAATGC
CACAGCCCTGTCAGCATGAATTTGTAATGTCTTGAGCTCTATTATGAATGTGAAGCCTTCCCCTTATCCTCCCTG
TAACTTGATCCATTTCTAATTATGTAGCTCTTTGTGAGGAGTGTTCCCTATCCAATCAATCTTGCATGTAACGC
AAGTTCCCAGTTGGAGCTCCAGCCTGACATCAAAAAAGGCAGTTACCATTAAACCATCTCCCTGGTGCTTATGCT
CTTAATTGCCACCTCTAACAGCACCAAATCAAAATCTCTCCACTTTTCAGCTGTCTTTTGGAGGACGTACGTAATA
AGGTTTTAATTTAGTAAACCAATCCTATGCATGGTTTTCAGCACTAGCCAAACCTCACCAACTCCTAGTTCTAGAA
AAACAGGCACTTGGCAGCCTTGTGATGTACATACAGAGAAGTCACAGGGCAGTACCTGAGGGTCTGTAGGTTGCAC
ACTTTGGTACCAGATAACTTTTTTTTTTCTTTATAAGAAAGCCTGAGTACTCCACACTGCACAATAACTCCTCCC
AGGGTTTTAACTTTGTTTTATTTTCAAAACCAGGTCCAATGAGCTTTCTGAACAGCTGGTGTAGCTACAGAGAAA
CCAGCTTCCCTTCAGAGAGCAGTGCTTTTGGCGGGGAGGAGGAAATCCCTTCATACTTGAACGTTTTCTAATTGCT
TATTTATTGTATTCTGGGGTATGGCGTAAGTACAGAGAAGCCATCACCTCAGATGGCAGCTTTTAAAAGATTTTT
TTTTTTTCTCTCAACACCATGATTCTTTTAAACAACATGTTTCCAGCATTCCCAGGTAGGCCAAGGTGTCCTACAG
AAAAACCTTGGGTTAGACCTACAGGGGGTCTGGCTGGTGTTAACAGAAGGGAGGGCAGAGCTGGTGCGGCTGGCC
ATGGAGAAAGCTGACTTGGCTGGTGTGGTACAGAGAAGCCAGCTTGTTTACATGCTTATTCCATGACTGCTTGCC
CTAAGCAGAAAGTGCTTTTCAGGATCTATTTTTGGAGGTTTATTACGTATGTCTGGTTCTCAATTCCAACAGTTT
AATGAAGATCTAAATAAAATGCTAGGTTCTACCTTAAAAAAAAAAAAAAAAAAAA

869/6881
FIGURE 809

MNGQLNGFHEAFIEEGTFLFTSESVGEGHPDKICDQISDAVLDAHLQQDPDAKVACETVAKTGMILLAGEITSRA
AVDYQKVVREAVKHIGYDDSSKGFYKTCNVLVALEQQSPDIAQGVHLDRNEEDIGAGDQGLMFGYATDETEECM
PLTIVLAHKLNAKLAELRRNGTLPWLRPDSKTQVTVQYMQDRGAVLP IRVHTIVISVQHDEEVCLDEMRDALKEK
VIKAVVPAKYLDEDTIYHLQPSGRFVIGGPQGDAGLTGRKIIVD TYGGWGAHGGGAFSGKD YTKVDRSAAYAARW
VAKSLVKGGLCRRVLVQVSYAIGVSHPLSISIFHYGTSQKSERELLEIVKKNFDLRPGVIVRDLDLKKPIYQRTA
AYGHFGRDSFPWEVPKKLKY

870/6881
FIGURE 810

[illegible]

871/6881
FIGURE 811

MKHIPVLEDGPWKTVCKELNGLKKLKRKGKEPARRANGYKTFRLDLEAPEPRAVATNGLRDRTTHRLQPVPVPVP
VPVPVAPAVPPRGGTDTAGERGGSSRAPEVSDARKRCFALGAVGPGLPTPPPPPPPPAPQSQAPGGPEAQPFREPGP
RPRILLCAPPARPAPSAPPAPPAPPESTVRPAPPTRPGESSYSSISHVIYNNHQDSSASPRKRPGEATAASSEIK
ALQQTRRLLANARERTRVHTISAAFEALRKQVPCYSYGQKLSKLAILRIACNYILSLARLADLDYSADHSNLSFS
ECVQRCTRTLQAEGRAKKRKE

872/6881
FIGURE 812

GGCACGAGGGATGGCGGTTGTATCTGCTGTTTCGCTGGCTGGGCCTCCGCAGCAGGCTTGGCCAGCCGCTGACGGG
TCGGCGGGCGGGTTTGTGTGAACAGGCACGCAGCTGCAGATTTTATTCTGGTAGTGCAACCCTCTCAAAGGTTGA
AGGAACTGATGTAACAGGGATTGAAGAAGTAGTAATTCCAAAAAGAAAACCTGGGATAAAGTAGCCGTTCTTCA
GGCACTTGTCATCCACAGTAAACAGGGATACCACAGCTGTGCCTTATGTGTTTCAAGATGATCCTTACCTTATGCC
AGCATCATCTTTGGAATCTCGTTCATTTTTACTGGCAAAGAAATCCGGGGAGAATGTGGCCAAGTTTATTATTAA
TTCATACCCCAAATATTTTCAGAAGGACATAGCTGAACCTCATATACCGTGTTAATGCCTGAGTACTTTGAACC
TCAGATCAAAGACATAAGTGAAGCCGCCCTGAAGGAACGAATTGAGCTCAGAAAAGTCAAAGCCTCTGTGGACAT
GTTTGATCAGCTTTTGCAAGCAGGAACCACTGTGTCTCTTGAAACAACAAATAGTCTCTTGGATTTATTGTGTTA
CTATGGTGACCAGGAGCCCTCAACTGATTACCATTTTCAACAACTGGACAGTCAGAAGCATTGGAAGAGGAAAA
TGATGAGACATCTAGGAGGAAAGCTGGTCATCAGTTTGGAGTTACATGGCGAGCAAAAAACAACGCTGAGAGAA
CTTTTCTCTAATGCCAGAGAAAAATGAACATTCCTATTGCACAATGATCCGAGGAATGGTGAAGCACCGAGCTTA
TGAGCAGGCATTAAACTTGTACACTGAGTTACTAAACAACAGACTCCATGCTGATGTATACACATTTAATGCATT
GATTGAAGCAACAGTATGTGCGATAAATGAGAAATTTGAGGAAAAATGGAGTAAATACTGGAGCTGCTAAGACA
CATGGTTGTCACAGAAGGTGAAACCAATCTTCAGACTTTTAAATACCATTTCTGAAATGTCTCCGAAGATTTTCATGT
GTTTGCAAGATCGCCAGCCTTACAGGTTTTACGTGAAATGAAAGCCATTGGAATAGAACCCTCGCTTGCAACATA
TCACCATATTATTTCGCTGTTTGATCAACCTGGAGACCCTTTAAAGAGATCATCCTTCATCATTTATGATATAAT
GAATGAATTAATGGGAAAGAGATTTTCTCAAAGGACCCGGATGATGATAAGTTTTTTTCAGTCAGCCATGAGCAT
ATGCTCATCTCTCAGAGATCTAGAAGTTGCCTACCAAGTACATGGCCTTTTAAAAACCGGAGACAACTGGAAAT
CATTGGACCTGATCAACATCGTAATTTCTATTATTCCAAGTTCTTCGATTTGATTTGTCTAATGGAACAAATTGA
TGTTACCTTGAAGTGGTATGAGGACCTGATACCTTCAGCCTACTTTCCCACTCCCAACAATGATACATCTTCT
CCAAGCATTGGATGTGGCCAATCGGCTAGAAGTGATTCTTAAATTTGGAAAGATAGTAAAGAATATGGTCATAC
TTTCCGCACTGACCTGAGAGAAGAGATCCTGATGCTCATGGCAAGGGACAAGCACCCACCAGAGCTTCAGGTGGC
ATTTGCTGACTGTGCTGCTGATATCAAATCTGCGTATGAAAGCCAACCCATCAGACAGACTGCTCAGGATTGGCC
AGCCACCTCTCTCAACTGTATAGCTATCTCTTTTTAAGGGCTGGGAGAACTCAGGAAGCCTGGAAAATGTTGGG
GCTTTTTCAGGAAGCATAATAAGATTCTTAGAAGTGAGTTGCTGAATGAGCTTATGGACAGTGCAAAAGTGCTAA
CAGCCCTTCCAGGCCATTGAAGTAGTAGAGCTGGCAAGTGCCCTCAGCTTACCTATTTGTGAGGGCCTCACCCA
GAGAGTAATGAGTGATTTTGCAATCAACCAGGAACAAAAGGAAGCCCTAAGTAATCTAACTGCATTGACCAGTGA
CAGTGATACTGACAGCAGCAGTGACAGCGACAGTGACACCAGTGAAGGCAAATGAAAGTGGAGATTTCAGGAGCAG
CAATGGTCTCACCATAGCTGCTGGAATCACACCTGAGAACTGAGATATACCAATATTTAACATTGTTACAAAGAA
GAAAAGATACAGATTTGGTGAATTTGTTACTGTGAGGTACAGTCAGTACACAGCTGACTTATGTAGATTTAAGCT
GCTAATATGCTACTTAACCATCTATTAATGCACCATTAAAGGCTTAGCATTTAAGTAGCAACATTGCGGTTTTCA
GACACATGGTGAGGTCCATGGCTCTTGTTCATCAGGATAAGCCTGCACACCTAGAGTGTGCGGTGAGCTGACCTCAC
GATGCTGTCTCTGCTGCGATTGCCCTCTCTGCTGCTGGACTTCTGCCTTTGTTGGCCTGATGTGCTGCTGTGATG
CTGGTCTTTCATCTTAGGTGTTTCATGCAGTTCTAACACAGTTGGGGTTGGGTCAATAGTTTCCCAATTTTCAGGAT
ATTTTCGATGTGAGAAATAACGCATCTTAGGAATGACTAAACAAGATAATGGCAGTTTAGGCTGCACAACTGGTAA
AATGACTGTAGATAAAATGTTGTAATTAGTGTACACGTTTGTATTTTTGTTAATATAGCCGCTGCCATAGTTTTCT
AACTTGAACAGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAA

873/6881
FIGURE 813

MVAQKVKNLQTFNTILKCLRRFHVFAFARSPALQVLREMKAIGIEPSLATYHHIIRLFDQPGDPLKRSSFIIYDIM
NELMGKRFSPKDPDDDKFFQSAMSSICSSLRDLELAYQVHGLLKTGDNWKFIGPDQHRNFYYSKFFDLICLMEQID
VTLKWYEDLIPSAYFPHSQTMIHLLQALDVANRLEVIPKIWKDSKEYGHTFRSDLREEILMLMARDKHPPPELQVA
FADCAADIKSAYESQPIRQTAQDWPATSLNCIAILFLRAGRTQEAWKMLGLFRKHNKIPRSELLNELMDSAKVSN
SPSQAIIEVVELASAFSLPICEGLTQRVMSDFAINQEKEALSNLTALTSDDSDTDSSSDSDSDTSEGK

874/6881
FIGURE 814

ACGCGGGGCACGCACACACGGAAGCACGCCTCCACTTAACTCGCGCCGCCCGCGGCAGCTCGAGTCCACCAGCAGCG
CCGTCCGCTTGACCGAGATGCTGCGGGCCGTGTCAGTTATCGGGTGTGACCGCCGCCGCCAGAGTTGTCTCTGTG
GGAAGTTTGTCTCCGTCCATTGCGACCATGCCGCAGATACTCTACTTCAGGCAGCTCTGGGTTGACTACTGGCA
AAATTGCTGGAGCTGGCCTTTTGTGTTGTTGGTGGAGGTATTGGTGGCACTATCCTATATGCCAAATGGGATTCCC
ATTTCCGGGAAAGTGTAGAGAAAACCATACCTTACTCAGACAAACTCTTCGAGATGGTTCTTGGTCCTGCAGCTT
ATAATGTTCCATTGCCAAAGAAATCGATTTCAGTCGGGTCCACTAAAAATCTCTAGTGTATCAGAAGTAATGAAAG
AATCTAAACAGTCTGCCTCACAACCTCCAAAAACAAAAGGGAGATACTCCAGCTTCAGCAACAGCACCTACAGAAG
CGGCTCAAATTATTTCTGCAGCAGGTGATACCCTGTGCGTCCCAGCCCCCTGCAGTTCAGCCTGAGGAATCTTTAA
AACTGATCACCTGAAATTGGTGAAGGAAAACCCACACCTGCACCTTTCAGAAGAAGCATCCTCATCTTCTATAA
GGGAGCGACACCTGAAGAAGTTGCAGCTCGCCTTGACACAACAGGAAAAACAAGAACAAGTTAAATTGAGTCTC
TAGCCAAGAGCTTAGAAGATGCTCTGAGGCAAACCTGCAAGTGTCACTCTGCAGGCTATTGCAGCTCAGAATGCTG
CGGTCCAGGCTGTCAATGCACACTCCAACATATTGAAAGCCGCCATGGACAATTCTGAGATTGCAGGCGAGAAGA
AATCTGCTCAGTGGCGCACAGTGGAGGGTGCATTGAAGGAACGCAGAAAGGCAGTAGATGAAGCTGCCGATGCCC
TTCTCAAAGCCAAAGAAGAGTTAGAGAAGATGAAAAGTGTGATTGAAAAATGCAAAGAAAAAGAGGTTGCTGGGG
CCAAGCCTCATATAACTGCTGCAGAGGGTAAACTTCACAACATGATAGTTGATCTGGATAATGTGGTCAAAAAGG
TCCAAGCAGCTCAGTCTGAGGCTAAGGTTGTATCTCAGTATCATGAGCTGGTGGTCCAAGCTCGGGATGACTTTA
AACGAGAGCTGGACAGTATTACTCCAGAAGTCCTTCCTGGATGGAAAAGGAATGAGTGTTTCAGACTTAGCTGACA
AGCTCTCTACTGATGATCTGAACTCCCTCATTGCTCATGCACATCGTCTGATTGATCAGCTGAACAGAGAGCTGG
CAGAACAGAAGGCCACCGAAAAGCAGCACATCACGTTAGCCTTGGAGAAAACAAAAGCTGGAAGAAAAGCGGGCAT
TTGACTCTGCAGTAGCAAAAAGCATTAGAACATCACAGAAGTGAAATACAGGCTGAACAGGACAGAAAGATAGAAG
AAGTCAGAGATGCCATGGAAAATGAAATGAGAACCAGCTTCGCCGACAGGCAGCTGCCACACTGATCACTTGC
GAGATGTCCTTAGGGTACAAGAACAGGAATTGAAGTCTGAATTTGAGCAGAACCTGTCTGAGAACTCTCTGAAC
AAGAATTACAATTTGTCGTCTCAGTCAAGAGCAAGTTGACAACCTTACTCTGGATATAAATACTGCCTATGCCA
GACTCAGAGGAATCGAACAGGCTGTTTCAGAGCCATGCAGTTGCTGAAGAGGAAGCCAGAAAAGCCCACCAACTCT
GGCTTTTCAGTGGAGGCATTAAAGTACAGCATGAAGACCTCATCTGCAGAAACACCTACTATCCCGCTGGGTAGTG
CAGTTGAGGCCATCAAAGCCAACTGTTCTGATAATGAATTCACCCAAGCTTTAACCGCAGCTATCCCTCCAGAGT
CCCTGACCCGTGGGGTGTACAGTGAAGAGACCCTTAGAGCCCGTTTCTATGCTGTTCAAAAAGTGGCCGAAGGG
TAGCAATGATTGATGAAACCAGAAATAGCTTGTACCAGTACTTCTCTCCTACCTACAGTCCCTGCTCCTATTCC
CACCTCAGCAACTGAAGCCGCCCCAGAGCTCTGCCCTGAGGATATAAACACATTTAAATTACTGTATATGCTT
CCTATTGCATTGAGCATGGTGTATCTGGAGCTAGCAGCAAAGTTTGTCAATCAGCTGAAGGGGGAATCCAGACGAG
TGGCACAGGACTGGCTGAAGGAAGCCCGAATGACCCTAGAAACGAAACAGATAGTGGAATCCTGACAGCATATG
CCAGCGCCGTAGGAATAGGAACCACTCAGGTGCAGCCAGAGTGAGGTTTAGGAAGATTTTCATAAAGTCATATTT
CATGTCAAAGGAAATCAGCAGTGATAGATGAAGGGTTCGACGCGAGAGTCCCGGACTTGTCTAGAAATGAGCAGG
TTTACAAGTACTGTTCTAAATGTTAACACCTGTTGCATTTATATTCTTTCCATTTGCTATCATGTGAGTGAACGC
CAGGAGTGCTTTCTTTGCAACTTGTGTAACATTTTCTGTTTTTTCAGGTTTTACTGATGAGGCTTGTGAGGCCAA
TCAAAATAATGTTTGTGATCTCTACTACTGTTGATTTTGCCTCGGAGCAAACCTGAATAAAGCAACAAGATG

875/6881
FIGURE 815

MLRACQLSGVTAAQSCLCGKFVLRPLRPCRRYSTSGSSGLTTGKIAGAGLLFVGGGIGGTILYAKWDSHFRESV
EKTIPYSDKLFEMVLGPAAYNVPLPKKSIQSGPLKISSVSEVMKESKQSASQLQKQKGDTPASATAPTEAAQIIS
AAGDTLSVPAPAVQPEESLKTDPHPEIGEGKPTPALSEEASSSSIRERPPEEVAARLAQQEKQEQVKIESLAKSLE
DALRQTASVTLQAIAAQNAAVQAVNAHSNILKAAMDNSEIAGEKKSAQWRVTEGALKERRKAVDEAADALLKAKE
ELEKMKSVIENAKKKEVAGAKPHITAAEGKLHNMIVDLDNVVKKVQAAQSEAKVVSQYHELVVQARDDFKRELD
ITPEVLPGWKGMVSVDLADKLSTDDLNSLIAHAHRRIDQLNRELAEQKATEKQHITLAEKQKLEEKRAFDSAVA
KALEHHRSEIQAEQDRKIEEVRDAMENEMRTQLRRQAAAHTDHLRDVLRVQEQELKSEFEQNLSEKLSEQELQFR
RLSQEQVDNFTLDINTAYARLRGIEQAVQSHAVAEAEARKAHQLWLSVEALKYSMTSSAETPTIPLGSAVEAIK
ANCSDNEFTQALTAaipPESLTRGVYSEETLRARFYAVQKLARRVAMIDETRNSLYQYFLSYLQSLLLFPPQQLK
PPPELCPEDINTFKLLSYASYCIEHGDLELAAKFVNQLKGESRRVAQDWLKEARMTLETQIVEILTAYASAVGI
GTTQVQPE

876/6881
FIGURE 816

TAGTGCCGCCGCTCCCTACTCTGGGGGTTGGGACTACCTCCTTTTCCGCGGGCCCCGCCAGGCGGCTGCCCCGTG
ACCTGCCTGGGCGCGGGGAACTGAAAGCCGGAAGGGGCAAGACGGGTTTCAGTTCGTTCATGGGGCTGTTTGGAAAG
ACCCAGGAGAAGCCGCCCAAAGAACTGGTCAATGAGTGGTCATTGAAGATAAGAAAGGAAATGAGAGTTGTTGAC
AGGCAAATAAGGGATATCCAAAGAGAAGAAGAAAAAGTGAAACGATCTGTGAAAGATGCTGCCAAGAAGGGCCAG
AAGGATGTCTGCATAGTTCTGGCCAAGGAGATGATCAGGTCAAGGAAGGCTGTGAGCAAGCTGTATGCATCCAAA
GCACACATGAACTCAGTGCTCATGGGGATGAAGAACCAGCTCGCGGTCTTGCGAGTGGCTGGTTCCTGCAGAAG
AGCACAGAAGTGATGAAGGCCATGCAAAGTCTTGTGAAGATTCCAGAGATTCAGGCCACCATGAGGGAGTTGTCC
AAAGAAATGATGAAGGCTGGGATCATAGAGGAGATGTTAGAGGACACTTTTGAAAGCATGGACGATCAGGAAGAA
ATGGAGGAAGAAGCAGAAATGGAAATTGACAGAATTCTCTTTGAAATTACAGCAGGGGCCCTTGGGCAAAGCACCC
AGTAAAGTGACTGATGCCCTTCCAGAGCCAGAACCTCCAGGAGCGATGGCTGCCTCAGAGGATGAGGAGGAGGAG
GAAGAGGCTCTGGAGGCCATGCAGTCCCGGCTGGCCACACTCCGCAGCTAGGGGCTGCCTACCCCGCTGGGTGTG
CACACACTCCTCTCAAGAGCTGCCATTTTATGTGTCTCTTGCCTACACCTCTGTTGTGAGGACTACCATTTTGG
AGAAGGTTCTGTTTGTCTCTTTTCATTCTCTGCCCAGGTTTTGGGATCGCAAAGGGATTGTTCTTATAAAAGTGG
CATAAATAAATGCATCATTTTTAGGAGTATAGACAGATATATCTTATTGTGGGGAGGGGAAAGAAATCCATCTGC
TCATGAAGCACTTCTGAAAATATAGGTGATTGCCTGAATGTGCAAGACTCTACTTTTGTCTATAAAACACTATAT
AAATGAATTTTAATAAATTTTGTCTTAGCACTTGGCCCCATTGTAGATTGCCCTGTGCAGTAACTTTCAAGGT
GTCGGCTGCCCCAGATTGCTTCATTTGCTGGGTGTGGAAAGAGTTGCTATGGCCAGGCATATGGGATTTGGAAGC
TCAGCAGAAGTGACTTCTGCTCTGTGGTTGCTGCTCCCCGGCTTTACAGACATGGTATGGCAGCCATTCTTTTA
TCTATTTAACCAAGAGGATGCTGGGGAATTGTGCTGCTTGTCTGTTGGCTGGTGGCTGCATTATGTCTGGGGT
GTGCATGTGGGTCTATTTAGAGCTTCTGTCCCTTCCTTCCATTGCAAGTTGCACCCAGATGAGACAGCTGTAGT
ACTAGGTCTCTTTACCTCTCATTGCCTGTCCCTGCTTCGAGCTGGTGTCTTGTGCGTGGGACATGGGCCTTCC
TATCTGTGTTTTCTCAAAGTCAGGAGCTGACCAGGAGCACACTAAGGTGTGGTCATGCATCATAACCAACATTCA
CTCATCTGGGACATTCTTAAGATACATTTATAAATCATTTACAGCAGTAGTACTTTGTATGTGTTGAGAGTTTACA
GAGCTCTTTGACATACGCGATCTTAGTCTTTACAAATAAGGAAAACAGCTCAGTTTGGGAAGTATCAGAGATGGG
ATTCAAACCCAGATCCTCTGGTCCAAGTTGTATGTGCACTGAACTAATCAGGCAGGAAAAAGCCCAGCCACTGT
CTCACAGATTGTTTTTTGTATATTGTAGCAAAATCCTGAAACAATGGGGTCCTTCCAGTCTCATCATAAAAATG
GCAATCTTGGCTGGGTGCGGTGGTTCATGCCTATAATCCAGTGCTTTACAAGGCTGAGGCAGGAGGCTCTCTTG
AGAATAGGAGTTCAAGACCAGCCTGGGCAACATAGCAAGATCCTGTCTCTCCAAAAAAAAAAAAAAAAAAAAA
AAAATTTTCATTTTTTGAGTCCAGAGGACCCTCCTATTACTCTTGATTTTCATCTTCAGAGTGTAGTTAAAAAATTAT
TTTAAATAATTATTTTTTTTAAATCAGTTGTAGGTTACAGCAAAAAGTGGACAAAAGAAATTTCTCATATATCCC
CTGCCCTCACACATGCATAGCCTCCCACTATCAGTATCCACACCAGAGTGGTACATTTGTTACAATCAATA
AACCTCCATTGACACATCATTATCACCCAAAGTCCATAGTTTACATGAAGATTCAGTCTGGTGTGTACATTGTA
TGGGCTTAGACAAATGTATGATGATATCTACAATTATAGAATCATAACAGAATAGTTTCACTGCCCTAAAACTTCT
CTATGCTTCACCTGTTTCATCCCTTTCTTCCCTAATCCCTTGCAACCCTTTAAAAAATAATTAGGTTTCAGGGG
GTACATGTGCAGGTAACTCGTGACAAGGGGGTTTGTATACAGATTATTTAGTGACCCAGGTACTAAGCCTAGT
ACCAATAGTTACTTTTCTGGTCCTGTCCCTTTTCCACCTCCACCTCAGGTAGGCCCCAGTATGTTATTCCT
TTGTGTCCATGTTATTTCACTCCCACTTGTGAGAACATGGAATATTTGGTTTCTGTTCTATGTTAGTTTGTTA
AGGATAATGGCCTCCAGCCCCATCCATGTTTCTGCAAAGGACATGATCTTTCTTTGGCAACCCTTTTTACTGTC
GCCATAGTTCTTCTTTTCTAGAATGTATATTGGAATCATATAGTATGTAGCCTTTTCAGACTGGCTTCTTTCA
CTTAATAATATGCAATTAAGGTTCCCTCCATGTCAATTCATGGCTTAATAGTGCATTTATTTTTAGCACTGAATAA
TACTCCATTGTCTAGATGAATAGTTTATCCATTACCTATTGAAAGACTTCTTGGTGGTTTCCAAGTTTGGCAA
TTATGAATAAAGCTGTTGTAAACATCTTTGTGCAGGTTTTCTATGGGCATGTTTTTAATTCATTGAATAAATA
CCAAGAGCTTCAGTGCTGGATCATA

877/6881
FIGURE 817

CAGGACACAGCATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCCAAAT
GTGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGG
CCAGTCAGAGTATTAGTAGCTGGTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATA
AGGCGTCTAGTTTAGAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACCTCTACCA
TCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTATTCTCCACATGGACGT
TCGGCCAAGGGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATG
AGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT
GGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCT
ACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCC
ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCACCTGC
TCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTCCACAGGGGACCTACCC

878/6881
FIGURE 818

GCGGCCGTTACGGCGCTCAGGCGTCTCGACGCGCGGATTTAAACCAGCTCAGGAGACGCCAAGGAAAGATGGG
ACCTCCCGGGCCAGCACTGCCAGCCACAATGAATAACTCTTCTTCAGAGACGCGAGGACACCCCCACAGTGCCTC
CTCTCCTTCAGAGCGTGTGTTCCCGATGCCCCCTGCCAGGAAGGCGCCTCTCAATATTCTTGGCACCACAGTCCCT
CGAAGACTTTCCTCAGAATGACGATGAGAAGGAGCGGCTGCAGCGGAGGCGCTCGAGGGTCTTTGATCTGCAGTT
CAGCACTGACTCACCTCGCTTATTGGCCTCCCCCTCCAGCAGGAGTATTGACATTTTCAGCTACTATCCCCAAGTT
TACAAACACGCAGATTACGGAACATTACTCCACCTGTATCAAACCTGTCCACTGAAAATAAAATCACTACCAAGAA
TGCTTTTGGTTTGCACCTTGATTGATTTTATGTGAGAGATTCTTAAACAGAAAGACACCGAACCAACCAACTTTAA
AGTGGCTGCGGGTACTCTGGATGCCAGCACCAAGATCTATGCTGTGCGCGTGGATGCCGTCCATGCCGATGTATA
CAGAGTCCTTGGGGGGCTGGGCAAAGATGCACCGTCTTTGGAAGAAGTAGAAGGCCATGTTGCTGATGGAAGTGC
TACTGAAATGGGAACAACCAAAAAAGGCTGTAAAGCCAAAGAAGAAGCACTTACACAGAACTATTGAGCAGAACAT
AAACAACCTCAATGTCTCCGAAGCAGATCGGAAGTGTGAGATTGATCCCATGTTTCAGAAGACAGCAGCCTCATT
TGATGAGTGCAGCACAGCAGGGGTGTTTCTGTCCACTCTCCACTGCCAGGACTACAGAAGTGAAGTGTGTTTCC
CTCTGATGTCCAGACTCTCTCCACGGGAGAACCTCTCGAGTTGCCAGAGTTAGGTTGTGTAGAAATGACAGATTT
AAAAGCGCCCTTGCAGCAGTGTGCAGAAGATCGCCAGATCTGCCCTTCCCTGGCCGGGTTCAGTTTACACAGTG
GGACAGTGAAACACATAATGAGTCTGTGTGCGCCCTGGTAGACAAGTTTAAAGAAGATGACCAGGTATTTGACAT
CAATGCTGAAGTTGACGAGAGTGAAGTGTGAGACTTCCCCGATGGGTCCCTGGGGGATGACTTTGATGCCAACGA
TGAACCTGACCACACCGCAGTTGGGGATCATGAAGAGTTTCAGGAGCTGGAAGGAGCCCTGCCAGGTTTCAGAGCTG
CCAGGAAGAAATGATTTCCCTTGGGGATGGAGACATCAGGACCATGTGCCCCCTTCTGTCTATGAAACCTGGAGA
ATATTCTTATTTAGTCTCGGACCATGTGATGTGGCTGGCCCCGATCACTGGCGCTTTAGGCCTCGACGCAA
ACAAGATGCTCCTTCCCAATCAGAAAACAAAAAGAAGGTACAAAAAAGATTTTGAATTTGACTTTGAAGATGA
TATTGACTTTGATGTATATTTTAGAAAAACAAAGGCTGCTACTATTCTGACCAAGTCCACTTTGGAGAACCAGAA
TTGGAGAGCTACCACCCTTCCTACAGATTTCACTACAATGTTGACACTCTGGTCCAGCTTACCTCAAACCAGG
CACCAGGTTACTTAAGATGGCCCAGGGCCATAGGGTAGAGACTGAGCATTATGAAGAAATTGAAGACTATGATTA
CAACAACCCTAACGACACCTCCAACTTTTGCCCTGGATTACAGGCTGCTGACAGTGATGATGAAGATTTGGATGA
CTTATTTGTGGGACCTGTTGGGAACTCTGACCTCTCACCTTATCCTTGCCATCCACCTAAGACAGCACAAACAGAA
TGGTGACACTCCAGAAGCCCAAGGATTAGACATCACAACATATGGGGAGTCAAACCTGGTAGCTGAGCCTCAGAA
GGTAAATAAAATTGAAATTCATATGCCAAGACTGCCAAAAAGATGGACATGAAGAACTGAAGCAGAGCATGTG
GAGTCTGCTGACAGCGCTCTCCGGAAAGGAGGCAGATGCAGAGGCAAACCACAGGGAAGCTGGAAAAGAAGCGGC
CCTGGCAGAAGTGGCTGACGAGAAGATGCTTAGCGGGCTCACGAAGGACCTGCAGAGGAGCCTGCCCCCTGTCTAT
GGCTCAGAACCTCTCCATACCTCTGGCTTTTGCCTGTCTCTACATTTAGCCAATGAAAAGAATCTAAACTGGA
AGGAACAGAGGACCTCTCTGATGTTCTTGTGAGGCAAGGAGATTGAGTTCACTATGGAGAAGTCAGCAGCAGGAG
GCCCATCCCTTACTCAGTTGCCGGGACATCCCCAGTCTCGGGGGAAGAAGATGCCATGGGCTTATACCCAGGCTG
TAGCCAACCTACCAACGTGCCTGTTTGTGTTGCTCTTCTCTCTCCATCATAGTCTGGGTGCCAGCGCCCTG
AAGCTCCGTGCTCAACTGATTAACTTTACTGCCCTATGGTGACCATCTAGGAGAGGGGAGGGCAGAGGGGTGA
GGGTACTATTCTGGATTGAGAAAACCTATATCCATTCTTTATATCAATGTATAGTTTTAGTCTCCTAAATTGATC
TGTTATTTTCCAACTATTCTCTTGTAGAAAATTTTCCAGTGGGCACTTAATGGTGCCCTTGAAGAAGTTCTTAA
TCCATGTACATAAAATACATCATATGTACACTTATAAATGTATATAGAATGCTCAAAAATAAAATTCTTAATAAT
AGAACTGGCAAATA

879/6881
FIGURE 819

MGPPGPALPATMNNSSSETRGHPHSASSPSERVFPMLPRKAPLNIPGTPVLEDFPQNDDEKERLQRRRSRVFDL
QFSTDSPRLASPSSRSIDISATIPKFTNTQITEHYSTCIKLSTENKITTKNAFGLHLIDFMSEILKQKDTEPTN
FKVAAGTLDASTKIYAVRVDAVHADVYRVLGGLGKDAPSLEEVEGHVADGSATEMGTTKKAVKPKKKHLHRTIEQ
NINNINVSEADRKCEIDPMFQKTAASFDECSTAGVFLSTLHCQDYRSELLFPSDVQTLSTGEPLLELPELGCVEMT
DLKAPLQQCAEDRQICPSLAGFQFTQWDSETHNESVSALVDKFKKNDQVFDINAEVDESDCGDFPDGSLGDDFDA
NDEPDHTAVGDHEEFRSWKEPCQVQSCQEEMISLGDGDIRTMCPLLSMKPGEYSYFSPRTMSMWAGPDHWRFRPR
RKQDAPSQSENKKKSTKKDFEIDFEDDIDFDVYFRKTKAATILTKSTLENQNRATTLPDFFNYNVDTLVQLHLK
PGTRLLKMAQGHRVETEHYEEIEDYDYNPNPNDTSNFCPGLQAADSDDDLDDLFVGPVGNSDLSPYPCHPPKTAQ
QNGDTPEAQGLDITTYGESNLVAEPQVKNKIEIHYAKTAKKMDMKKLKQSMWSLLTALSGKEADAEANHREAGKE
AALAEVADEKMLSGLT KD LQ RSLPPVMAQNLSIPLAFACLLHLANEKNL KLEGTEDLS DVLVRQGD

880/6881
FIGURE 820A

TTCCAAGAAGAAGGATTTGCACCCTCGGGATATTGATGCATTTTGGCTGCAGCGGCAGCTCAGTCGTTTCTATGA
TGATGCCATCGTGTGCGAGAAGAAGGCAGATGAAGTATTGGAGATTTTGAAGACGGCCAGTGATGATCGGGAATG
TGAAAATCAGCTGGTTCTGCTGCTTGGTTTCAACACCTTTGATTTTCATTAAAGTGTTGCGGCAGCACAGGATGAT
GATTTTATACTGTACCTTGCTGGCCAGTGCACAAAGTGAAGCTGAAAAGGAAAGGATTATGGGAAAGATGGAAGC
TGACCCAGAGCTATCCAAGTTCCTCTACCAGCTTCATGAAACCGAGAAGGAGGATCTGATCCGAGAGGAAAGGTC
CCGGAGAGAGCGAGTGCCTCAGTCTCGAATGGACACAGATCTGGAAACCATGGATCTCGACCAGGGTGGAGAGGC
ACTGGCTCCACGGCAGGTTCTGGACTTGGAGGACCTGGTTTTTACCCAAGGGAGCCACTTTATGGCCAATAAACG
CTGTCAGCTTCCTGATGGATCCTTCCGTCGCCAGCGTAAGGGCTATGAAGAGGTGCATGTGCCTGCTCTGAAGCC
CAAGCCCTTTGGCTCAGAAGAACAACCTGCTTCCAGTGGAAAAGCTGCCAAAGTATGCCCAGGCTGGGTTTGGAGG
CTTCAAAACACTGAATCGGATCCAGAGTAAGCTCTACCGTGCTGCCCTTGAGACGGATGAGAATCTGCTGCTGTG
TGCTCCTACTGGTGCTGGGAAAGACCAACGTGGCCCTGATGTGCATGCTCCGAGAGATTGGGAAACACATAAACAT
GGACGGCACCATCAATGTGGATGACTTCAAGATTATCTACATTGCCCCCATGCGCTCCTTGGTGAGGAGATGGT
GGGCAGCTTTTGGAAAGCGCTGGCCACTTATGGCATCACTGTTGCTGAACTGACTGGGGACCACCAGCTGTGCAA
AGAAGAGATCAGTGCCACTCAGATCATCGTCTGCACCCCCGAGAAGTGGGACATCATCACCCGCAAGGGTGGTGA
GCGCACCTACACCCAGCTGGTGCGGCTCATCATTCTGGATGAGATTTCATCTTCTCCACGATGACAGAGGTCTCTGT
CTTAGAAGCTTTAGTGGCCAGGGCCATCCGAAACATTGAGATGACCCAAGAGGATGTCCGACTCATTGGTCTCAG
TGCCACCCTACCCAACATATGAAGATGTAGCCACCTTTCTACGTGTTGACCCCTGCCAAGGGTCTCTTTTACTTTGA
CAACAGCTTCCGTCCAGTGCCTCTGGAACAGACATATGTGGGTATCACAGAGAAAAAAGCTATCAAGCGTTTCCA
GATCATGAATGAAATCGTCTATGAAAAATCATGGAACATGCTGGAAAAAATCAGGTGCTGGTGTGTTGTCCACTC
CCGGAAGGAGACTGGAAAGACAGCCAGGGCCATCCGGGACATGTGCCTAGAAAAGGACACTCTGGGTCTGTTTCT
GAGGGAGGGCTCAGCCTCCACAGAAGTCTGCGAACAGAAGCTGAGCAGTGCAAGAACCTAGAGCTGAAGGATCT
TCTGCCTTATGGCTTTGCTATTTCATCACGCAGGCATGACCAGGGTTGACCGAACACTCGTGGAGGATCTTTTTGC
TGATAAACATATTAGGTTTTAGTTTCCACAGCAACTCTAGCTTGGGGTGTGAATCTCCCTGCACATACAGTCAT
CATCAAAGGCACCCAGGTGTACAGTCCAGAGAAGGGGCGTTGGACAGAACTGGGAGCACTGGACATTCTGCAGAT
GCTGGGACGTGCCGGAAGACCCAGTATGACACCAAGGGTGAAGGCATACTCATCACATCTCATGGGGAGCTACA
GTACTACCTGTCCCTCCTCAATCAACAACCTTCTATTGAAAGCCAGATGGTTTTCAAAGCTTCTGACATGCTCAA
TGCAGAAATCGTGCTAGGAAATGTCCAGAATGCCAAGGATGCGGTGAACTGGCTGGGCTATGCCTACCTCTATAT
CCGAATGCTGCGATCCCCAACCTCTATGGCATCTCTCATGATGACCTCAAGGGAGATCCCCTGCTGGACCAGCG
CCGACTAGATCTGGTTCATACAGCTGCCCTGATGCTGGACAAGAACAATCTGGTCAAGTACGACAAGAAGACGGG
CAACTTCCAGGTGACAGAACTGGGCCGTATAGCCAGCCACTACTACATCACCAATGATACAGTGCAGACTTACAA
CCAGCTGCTGAAGCCCACCTGAGTGAGATTGAGCTTTTTCAGGGTCTTCTCATTGTCTCTGAGTTCAAGAACAT
CACAGTGAGAGAGGAGGAGAAGCTGGAGCTGCAGAAGTTGCTGGAGAGGGTGCCTATCCCTGTAAAGGAGAGCAT
TGAGGAACCCAGTGCTAAGATCAACGTTCTTCTGCAAGCCTTCATCTCACAGCTGAAATTGGAGGGCTTTGCACT
GATGGCTGACATGGTGTATGTACACAGTCGGCTGGCCGGTTGATGCGAGCGATATTTGAAATTGTCCTGAACCG
AGGTTGGGCACAGCTTACAGACAAGACCCTGAACCTCTGCAAGATGATCGACAAACGCATGTGGCAGTCCATGTG
TCCTCTGCGCCAGTTCCGGAAACTCCCTGAGGAAGTAGTGAAGAAGATTGAGAAGAAGAATTTCCCTTTTGAGCG
TCTGTACGACCTGAATCATAATGAGATTGGGGAGCTTATCCGCATGCCAAAGATGGGGAAGACCATCCACAAATA
TGTCCATCTGTTTCCCAAGTTGGAGTTGTCTAGTGCACCTGCAGCCTATCACACGCTCCACCCTGAAGGTGGAGCT
GACCATCACGCCAGACTTCCAGTGGGATGAAAAGGTGCATGGTTTCATCCGAGGCTTTTTGGATTCTGGTGGAGGA
TGTGGACAGCGAGGTGATTCTGCACCATGAGTATTTTCTCCTCAAGGCCAAGTACGCCCAGGACGAGCACCTCAT
TACATTCTTCGTGCCTGTCTTTGAACCGCTGCCCCCTCAGTACTTCATCCGAGTGGTGTCTGACCGCTGGCTCTC
TTGTGAGACCCAGCTGCCTGTCTCCTTCCGGCACCTGATCTTGCCGGAGAAGTACCCCCCTCAACCGAACTTTT
GGACCTGCAGCCCTTGCCGTGTCTGCTCTGAGAAACAGTGCCTTTGAGAGTCTTTACCAAGATAAATTTCTTT
CTTCAATCCCATCCAGACCCAGGTGTTTAACTGTATACAACAGTGACGACAACGTGTTTGTGGGGGCCCCCAC
GGGCAGCGGGAAGACTATTTGTGCAGAGTTTGCCATCCTGCGAATGCTGCTGCAGAGCTCGGAGGGGCGCTGTGT
GTACATCACCCCATGGAGGCCCTGGCAGAGCAGGTATACATGGACTGGTACGAGAAGTTCCAGGACAGGCTCAA
CAAGAAGGTGGTACTCCTGACAGGCGAGACCAGCACAGACCTGAAGCTGCTGGGCAAAGGGAACATTATCATCAG
CACCCCTGAGAAGTGGGACATACTTTCCGGCGATGGAAGCAGCGCAAGAACGTGCAGAACATCAACCTCTTCGT

881/6881
FIGURE 820B

GGTGGATGAGGTCCACCTTATCGGGGGCGAGAATGGGCCTGTCTTAGAAGTGATCTGCTCCCGAATGCGCTACAT
CTCCTCCCAGATTGAGCGGCCCATTCGCATTGTGGCACTCAGCTCTTCGCTCTCCAATGCCAAGGATGTGGCCCA
CTGGCTGGGCTGCAGTGCCACCTCCACCTTCAACTTCCATCCCAATGTGCGTCCCGTCCCTTGGAGCTGCACAT
CCAGGGCTTCAACATCAGCCATACACAAACCCGCTGCTCTCCATGGCCAAGCCTGTGTACCATGCTATACCAA
GCACTCGCCCAAGAAGCCTGTCAATTGTCTTTGTGCCGTCTCGCAAGCAGACCCGCTCACTGCCATTGACATCCT
CACCACCTGTGCAGCAGACATCCAACGGCAGAGGTTCTTGCACTGCACCGAGAAGGATCTGATTCCGTACCTGGA
GAAGCTAAGTGACAGCAGCTCAAGGAAACGCTGCTAAATGGGGTGGGCTACCTGCATGAGGGGCTCAGCCCCAT
GGAGCGACGCCCTGGTGGAGCAGCTCTTCAGCTCAGGGGCTATCCAGGTGGTGGTGGCTTCTCGGAGTCTCTGCTG
GGGCATGAACGTGGCTGCCCACCTGGTAATCATCATGGATACCCAGTACTACAATGGCAAGATCCACGCCTATGT
GGATTACCCCATCTATGACGTGCTTCAGATGGTGGGCCACGCCAACCGCCCTTTGCAGGACGATGAGGGGCGCTG
TGTCATCATGTGTGTCAGGGCTCCAAGAAGGATTTCTTCAAGAAGTTCTTATATGAGCCATTGCCAGTAGAATCTCA
CCTGGACCACTGTATGCATGACCACTTCAATGCTGAGATCGTCACCAAGACCATTGAGAACAAGCAGGATGCTGT
GGACTACCTCACCTGGACCTTTCTGTACCGCCGCATGACACAGAACCCCAATTACTACAACCTGCAGGGCATCTC
CCATCGTCACTTGTGCGGACCACTTGTGAGAGCTGGTGGAGCAGACCCTGAGTGACCTGGAGCAGTCCAAGTGCAT
CAGCATCGAGGACGAGATGGACGTGGCGCCTCTGAACCTAGGCATGATCGCCGCTACTATTACATCAACTACAC
CACCATTGAGCTCTTCAGCATGTCCCTCAATGCCAAGACCAAGGTGCGAGGGCTTATCGAGATCATCTCCAATGC
AGCAGAGTATGAGAACATTCCCATCCGGCACCATGAAGACAATCTCCTGAGGCAGTTGGCTCAGAAGGTCCCCCA
CAAGCTGAATAACCCTAAGTTCAATGATCCGCACGTCAAGACCAACCTGCTCCTGCAGGCTCACTTGTCTCGCAT
GCAGCTGAGTGCTGAGTTGCAGTCAGATACGGAGGAAATCCTTAGTAAGGCAATCCGGGCTCATCCAGGCCTGCGT
GGATGTCCTTTCCAGCAATGGGTGGCTCAGCCCTGCTCTGGCAGCTATGGAACGGCCAGATGGTCAACCAAGC
CATGTGGTCCAAGGACTCATACTGAAGCAGCTGCCACACTTCACCTCTGAGCATATCAAACGTTGCACAGACAA
GGGAGTGGAGAGTGTTCGACATCATGGAGATGGAGGATGAAGAACGGAACGCGTTGCTTCAGCTGACTGACAG
CCAGATTGCAGATGTGGCTCGCTTTTGTAAACCGCTACCCTAATATCGAACTATCTTATGAGGTGGTAGATAAGGA
CAGCATCCGCAGTGGCGGGCCAGTTGTGGTGTGGTGCAGCTGGAGCGAGAGGAGGAAGTACAGGCCCTGTCTAT
TGCGCCTCTCTTCCCGCAGAAACGTGAAGAGGGCTGGTGGGTGGTGAATTGGAGATGCCAAGTCCAATAGCCCTCAT
CTCCATCAAGAGGCTGACCTTGCAGCAGAAGGCCAAGGTGAAGTTGGACTTTGTGGCCCCAGCCACTGGTGGCCCA
CAACTACACTCTGTACTTCATGAGTGACGCTTACATGGGATGTGACCAGGAGTACAAATTCAGCGTGGATGTGAA
AGAAGCTGAGACAGACAGTGATTTCAGATTGAGTCTGAGGCATTTACTTTTGGGTAAAGGAGAGTTGAGCCTGAA
TTAGGAATGTGTACATTGTAGGAATCCTGGTTGTGGGGACCAGGTCTGTGGGCCTCAGGTCTGGCCAGCCAGGGC
TGGTGTGTCCCCGCTACCTCCACTTCCTTTCCCTTGCTCACTCTGGATCCAGTGACAGCAGGTGTCTATGGGTC
AAGCATAAATCATATATAGCATTTTCAGGCATGTTCTGTTAGTCTGAGTCTGACATTCTAATAAAATAAT
TTGTAGAAACC

882/6881
FIGURE 821

MADV TARS LQY EYKANS NLVLQADRSLIDRTRRDEFTGEVLSLVGKLEGTRMGDKAQRTPQM QEERRAKRRKRD
EDRHDINKMKG Y TLLSEGIDEMVG I IYKPKTKETRETYEVLLSFIQAALGDQPRDILCGAADEVLA VLKNEKLRD
KERRKEIDLLLGQTDDTRYHVLVNLGKKITDYGGDK EIQNMDDNIDETYG VNVQFESDEEEGEDDVYGEVREEAS
DDDMEGDEAVVRCTLSANLVASGELMS SKKKDLHPRDIDAFWLQRQLSRFYDDAIVSQKKADEVLEILKTASDDR
ECENQLVLLLGFNTFDFIKVLRQHRMMILYCTLLASAQSEAEKERIMGKMEADPELSKFLYQLHETEKEDLIREE
RSRRERVRQSRMDTDLETMDLDQGGEALAPRQVLDLEDLVFTQGS HFMAN KRCQLPDG SFRRQRKG YEEVHVPA L
KPKPFGSEEQLLPVEKLPKYAQAGFEGFKTLNRIQSKLYRAALETDENLLL CAPTGAGKTINVALMCMLREIGKHI
NMDGTINVD DFKI IYIAPMRS LVQEMVGSFGKRLATYGITVAELTGDHQLCKEEISATQIIVCTPEKWDIITRKG
GERTYTQLVRLIILDEIHLHDDRGPVLEALVARAIRNIEMTQEDVRLIGLSATLPNYEDVATFLRVDPAGLIFY
FDNSFRPVPLEQTYVGITEKKAIKRFQIMNEIVYEKIMEHAGKNQVLV FVHSRKETGKTARAI RDMCLEKDTLGL
FLREGSASTEVLRTEAEQCKNLELKDLLPYGFAIHHAGMTRVDR TLVEDLFADKHIQVLVSTATLAWGVNLP AHT
V I I KGTQVYSPEKGRWTEL GALDILQMLGRAGR PQYDTKGE GILITSHGELQYYLSLLNQQLPIESQMVS KL PDM
LNAEIVLGNVQNAKDAVNWLGYAYLYIRMLRSPTLYGISHDDLKGDPLLDQRRDLVHTAALMLDKNNLVKYDKK
TGNFQVTELGRIASHYYITNDTVQTYNQLLKPTLSEIELFRVFSLSSEFKNITVREEEKLELQKLLERVPIPVKE
SIEEPSAKINVLQAFISQLKLEGFALMADMVYVTQSAGRLMRAIFEIVLNRGWAQLTDKTLNLCKMIDKRMWQS
MCPLRQFRKLPEEVVKKIEKKNFPERLYDLNHNEIGELIRMPKMGKTIHKYVHLFPKLELSVHLQPI TRSTLKV
ELTITPDFQWDEKVHGSSEAFWILVEDVDSEVILHHEYFLLKAKYAQDEHLITFFVPVFEPLPPQYFIRVVS DRW
LSCETQLPV SFRHLILPEKYPPPTELLDLQPLPVSALRNSAFESLYQDKFPFFNP IQTQVFNTVYNSDDNVFVGA
PTGSGKTICAEFAILRMLLQSSEGRCVYITPMEALAEQVYMDWYEFQDR LNKKVLLTGETSTDLKLLGKGNII
ISTPEKWDILSRRWKQRKNVQNINLFVVDEVHLIGGENGPVLEVICS RMRYISSQIERPIRIVALSSSL SNAKDV
AHLWGCSATSTFN FHPNVRPVPLELHIQGFNISHTQIRLLSMAKPVYHAITKHSPKKPVIVFVPSRKQTR LTAID
ILTTCAADIQRQRF LHCTEKDLIPYLEKLS DSTLKETLLNGVGYLHEGLSPMERRLVEQLFSSGAIQVVVASRSL
CWGMNVA AHLVIIMDTQYYNGKIHAYVDYPIYDVLQMVGHANRPLQDDEGRCVIMCQGSKKDFFKKFLYEPLPVE
SHLDHCMHDHFN AEIVTKTIENKQDAVDYLTWTFLYRRMTQNP NYYNLQGISHRHLS DHLS ELVEQTLSDLEQSK
CISIEDEM DVAPLNLGMIAAYYYINYTTIELFSMSLNAKTKVRGLIEIISNAAEYENIPIRHHEDNLLRQLAQKV
PHKLNNPKFNDPHVKTNLLLQAHL SRMQLSAELQSDTEEILSKAIRLIQACVDVLSSNGWLSPALAAMELAQMVT
QAMWSKDSY LKQLPHFTSEHIKRCTDKGVESVFDIMEMEDEERNALLQLTDSQIADVARFCNRYPNIELSYEVVD
KDSIRSGGPVVVLVQLERE E E V TGPVIAPLFPQKREEGWVWVIGDAKSNSLISIKRLTLQQKAKVKLDFVAPATG
AHNYTLYFMSDAYMGCDQEYKFSVDVKEAETDSDSD

883/6881
FIGURE 822

GTTTCCATCCCTCCTCTGGAGGCTTTTGAAGTCACCGGGAGACAGATGTGCTCTGTGGCAGGCAGGGGAGTGGGG
GTGCTCAGGCACCTTGGGAGGTCTGGGAGCTCCTCAGTGTGACCGCTGGGACCCACCAGGACTTTTTTCCTTTGTCA
GAAGCCTTTGGTTGCTTTTGCTGCTCTGCATGTGTCACTGTGGAGGGGCAATAGAGCAAGGCCTTACATGGCATGG
TCATTTCTCGGGCCCAGGAGGCTTAGAGGCCTGCCCCTGGCGCTCAAGTATTGAACCAGAACCATGGGGTGGCAC
TGAAGCCTCCTCACCACATCATGATAAATAACGGGGACATTACAGAGCAGGCACCTGTTTCCTCAGTCCATGGCT
GAGTACATCACCGGTGTTTTCTCTCTTATTCTCTCCATCAAGCCTAAAAGGAATCTCTATTGGAGATACTGCCAT
TAGTGTTCCCTTTTATAGGTGAGGAACTGAGGCATAGAGGGTTCCCCAGTTGAACCAACTGATAAATAGTAGAACT
TGGATTTTAATTACAGTCTTGATGCCAGGGATAAGGCTCTTACTTTCTACCTTAGGCTATTTCTAGGAAACGCAGG
AGAGTGTTGAAGGGGCAGAGAAAGGGATCCAGTTCCTTTCTGTCCCGCATCCTAGTCCCTGAGAAGCAAAGAAGA
AIGTGTTGGCTTCTTTTGCTTTGCTTTTGTGTGTCATCCACACATCTCCAGGGGACCTGGGCTCTTGATCTTGGCC
TCTTCCCCTTTAACTGTAAAGTGGGAGCAGGTAAGGGGTACAGTAGGGCTGGCCTGGAGTTAGAGGCTTGGATG
CCTTAGCTCCTCTGTCTGCACTCCAGAACTGCCTGACTTCATTTTCGTATGTTGTCCTTTGTTTTGACAATTGATC
CATGTCCCAGTCCGTCTCTTCTTCTTCTTGATACTTACACTGCTTCTTCTGTTGGTTTTCCAGTGTTTAACT
GTATACAACAGTGACGACAACGTGTTTGTGGGGGCCCCACGGGCAGCGGGAAGACTATTTGTGCAGAGTTTGCC
ATCCTGCGAATGCTGCTGCAGAGCTCGGAGGGGCGCTGTGTGTACATCACCCCATGGAGGCCCTGGCAGAGCAG
GTATGACGTGGCGCTGTGTGATGTGAATTTCCCAAGAAGCATTTTCATCTGTGATTCCGTATGAAGGCTTTCTAAG
CCCTGAAATTTGCAGGGTCATTTCTCAGTTTGTGTATTAAAGAAAAGCTGCCCCAGCCAAGCGTGGTGGCTCAC
GCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGCAGATCTCCGGAGATCAGGAGTTTCGAGACCAGCCTGGCC
AACATGGTGAAACCTGTCTCTACTAAAAATACAGAAATTAGCTGGGCGTGGTGGTGTGCGCCTGTAATCCCAGC
TACTTGGAAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGTTCCGCAACCACT
GCACTCCAGCCTGGGCAACAAGAGCGAGACTTCATCTCA

884/6881
FIGURE 823

GCGGAAGGCGCGGGAGCTTGCGTGCTGCTGGGCCTGAGCTGTCTGTCTCGTTTCTGTCCGCGCGCCCTGCATCCC
GGCCCCGGGCGCCCCGCTGGAGGTCGCCGAGGAGCCACAGGGCTGACTGGTCTGCTGCCCGGGCCAGGAGTGCCCT
GGTGTAGCAGTCGCGGAGCCATCCCGGCGTCTGCTGCCATGACCGACTCTCCCCTCAGAGGAGACTCTTCCTCAG
CGGTGGCTGCAGAGACAGATGAGCGGCGGCTCCTGGCCGCGGGACCGTGAGACGGGTTCTGTGGCCGGCCATTTAG
GGGACGCTGCGACCAACGCTGCGCCCCCTCCGACTGGTTCCCTTGGGCCCCGGAAGCTCGCGGCGGGCCCTGCG
GGAGGCGGCATGCTCCCGCGGAGGCTGCTGGCCGCCTGGCTGGCGGGGACGCGGGGCGGGGCGCTGCTGGCGCTT
CTGGCCAATCAGTGCCGCTTCGTACGGGCCTGCGCGTGCGGCGCGCGCAGCAGATCGCGCAGCTCTACGGCCGC
CTCTACTCCGAGAGCTCACGCCGCGTTCCTCTCGGCCGCTCTGGCGCCGGCTGCACGGCCGCTCTGGCCATGCC
TCTGCCTTGATGGCGGCGTTAGCCGGCGTCTTCGTTTGGGACGAGGAGAGGATCCAGGAGGAGGAGTTGCAGAGA
TCTATTAATGAGATGAAGCGGTTGGAAGAAATGTCAAATATGTTTCAGAGCTCTGGAGTCCAGCACCACCTCCA
GAACCAAAAGCCCAACAGAAAGGAATGAAGATTAGAGGGCAAAGAGCAACGTTGGGAAATGGTGATGGATAAG
AAACACTTTAAGCTGTGGCGGCGCCCAATTACAGGCACCCACCTTTACCAGTACCGAGTTTTTGGAACTACACA
GATGTGACACCTCGGCAGTTCTTCAATGTTTCACTGGACACAGAGTATAGAAAAAATGGGATGCCCTGGTAATC
AAGCTGGAGGTGATTGAGAGGGATGTGGTTAGTGGTTCCGAGGTTCTTCACTGGGTAACCCATTTTTCTTATCCA
ATGTACTCACGGGATTATGTTTATGTTTCGGCGGTATAGTGTGGATCAGGAAAACAACATGATGGTGTGGTGTGCG
CGTGCTGTGGAGCATCCGAGTGTGCCAGAGTCTCCAGAATTCGTCAGGGTCAGATCATATGAATCCCAAATGGTT
ATCCGTCACCAAGTCATTTGATGAGAATGGCTTTGACTACTTACTAACATACAGTGACAATCCCCAAACGGTG
TTTCTCGCTACTGTGTTAGTTGGATGGTTTTCCAGTGGCATGCCAGATTTCTTGGAGAAGCTGCACATGGCCACT
CTGAAAGCCAAGAATATGGAGATTAAAGTAAAGGACTACATCTCAGCTAAGCCTCTGGAAATGAGTAGTGAAGCC
AAGGCCACCAGCCAGTCTCTGAGCGAAAGAACGAGGGCAGCTGTGGCCCTGCTCGGATTGAGTATGCTTGACAG
GCTTTGGGATAAGAAGGGACAAGGTGCTTCTAGCCCTGTCTCAGTCCGTTATCACTCTGCTGTAGAAGGGGGACA
TGCCACATGTATTAGAAGGCATCTGCTGTAACTTCCAGTGCAAGATAATTCAATAACTGATGTCCCATTTTCATTC
AGAGCCCTTATTGCTCTTATCAAAACAGAAGAAGGCTACATTTGTGGGAGTGTGTGCATATTCTCAGGCCAACTG
TTTTGAAATTCGGTATCTCACTGAGCTAATCTGGAACAAACCTCTCACCTCAGGCCAGAAGGGGATGACCTCCAT
TTGCTTCTCTGAGTAGTTTCTCTGCTGACATTCCAAATCCACCATCGATTGTGCAGCGCTTTGGATTTCTTTC
AGTTCTCCAGGTCCACCTGGAAAGTATAGTTGGCCAGTTGAGTCTCTCAAATGAGGGGCTACTGGGAGTGCTCTT
GGTAACAATCATGATGTGAATGGGTGTGAACGATACTTGGCTATGTTAAGTGCCTTGTCCGCACCTTGCTTTTAT
CTCTAGAGACATGAAGTTATTATTAATTTTTTTTTTTTTTAAAGTAGAGATGGAGTTTCACTCTGTTTCCCAGGCT
GGTCTTGAACCTCGGCCATGCCTGGCCAGGGACATGAATTTGTACAAAGAAATTTCCCTCCCTGCCTGCACAA
TATACCCATTGACTCACCTTATCCAAAGCAAGTTTCTGTGAATCGGCCAGTTCTTCTATATTTCATTGGATCAT
TGCTCCTTCCCTAACCTTCCCCATTTACCAAGAACTGGGAGACTAATCCTTTTAGATAGTAGCTTTTTTGATGC
TCAAAACATCACATTTAAATTTAGTTTAAAAATTTTTTAACTTTTGTGTCAAATAGGAGTTGAGGAATTGAGCAG
GATTCTACCTAGTCCGATTGTATAGAAAACACCATTTTGATTCAGGTATTATTTTTTCATATTTAGGTTTGACT
TGTTCTTTTTCAGAAAGGCTAAAGTCAGAGGAATGGGGGCTGGGCCACTCCCTTGGAGCTCTCAGATCTACAGACAA
GCTGTGTGAATGCATAGATGTAATCTTGTCTCAAATACTAATACAGTGGAGATTTGGTTTATGTTACCATTAAAGT
TCCTCTAAAAAGTTTTTCTTCTCTTTCAGAGCCAAAATAAAAGTGAACCTACACTGTTTTCAGATAAGGTCACAAT
CTGATGCTGTGAGTTTGACCGAGCTGGTTTTGCTTATGGTCATGCTGCAATTTGTTAGAATAATAGGGATCAAGT
TTTAAATCCTCCTCCTTCCCTTTTTTCTGGAGTCTTGAGGGCCAGAGTTTTTGTGTTTTGTTTTGTTTTGTTTT
CCTGCTTGCTACTGTTTTGTGGTGTGAAAAGTGGTTTAAACCTGAGACTAAGTAAACACTTCCCTTGACCTTCT
TGTTGCCTGTTTCAATTTTGTGCCAAGGAAGTAGCTGCCCCAGTGATGTCTTGCCTTCTCCGCGTCATTGTTGGA
AGAGGAGAGATGCATCGAGCAGTCCCAGCTGCTTTTCAATTTACTTCTTCTTCCAGGACCTGACAGAAGTCA
GGGAAGAGTCCCTGGGTTATGTCCAACTTAGCACCTGCAATTTGTGGGATGTGGATGGATGTGTGCATAAGAGA
GAGAGAGAATATGTGTGTGTGTGTGCGTCTGCGAGCGCACACATGCACAAGTGCGAAGGAGTTGCGGTTGC
TCCATGTTCTGACTTAGGGCAATTTGATTCTGCACTTGGGGTCTGTCTGTACAGTTACTCATGTTCATTGTAATGA
TTTCACTCCTAACTGTGACATTTTTATCAAATGTGTGAATAAATACATAAAGATTGGTAC

885/6881
FIGURE 824A

CGCGCTTAGGGATCCGGCCGTGGCCGAGCGCGCGGCCGTAAGACCGCGGGTGACTAGCATGCAGATACCCATGCT
CTGACTTTCTGCCCCCTCCACTGACATGGCCACCGGGGTGGGGAGAGGGACTTCCAGACTTCAGCTCGACGCATG
GGCACCTCGCTGCTCTTCCAGCTTTTCAGTGCATGAACGGGAGCTGGACCTGGTTTTTCTGGATCATAGCTATGCC
AAGCCTTGGAGTGCCCAACCCAGATGCCAGTAGTGCCCGCCCCACCCGCATGCTCTTTGTCACTCCCCGGCGGCAG
CACGAAAGTACCATTGAATCAGACGTCCCAATAGATGTGGAGACGGTCACATCAACGCCTATGCCACTCTATGAC
AATCAGAAGGCACGCAGCGTGATGAATGAGTGTGAACGGCATGTCATCTTTGCCAGGACTGATGCAGATGCCCTT
CCTCCACCAGAGGACTGGGAGGAGCATGTCAACAGGACTGGCTGGACAATGGCCAGAACAAGCTATTCAACAAG
ATCCTCAAAGCCCTGCAGTCTGACCGGCTTGCCCGCTTGCCCAACGAAGGGGCTTGTAATGAGCCAGTGCTGCGC
CGTGTGTCTGTGGACAAGTGTGCAAGGAGAGTGCAGGAGGCTCTGGCAAGTGTGAGCTGGGATACCAAGCTGATC
CAGTGGCTGCACACCACCTTGTGGAGACCTTGAGTCTGCCCATGCTGGCAGCCTACCTGGATGCTTTGCAGACG
CTGAAGGGGAAGATCCCAACCTTGATTGACCGGATGCTTGTGTCTATCCAACACAAAGACTGGGGCTGCAGGAGCT
GAGGCCTTGTCTCTCTACTGAAGAGGCCCTGGGACCCTGCTGTGGGTGTGCTTTCTCATAACAAACCAAGCAAA
CTCCCTGGCTCTCCGCTGATTCTCATCGCCTCCTCTGGTCCCTCCAGCTCTGTGTTTCCACTTCACGCCGCCAC
CGCTTCTGGCAATCTCAGCTGTCTGCTTGGGCAAGGTATCCCTGTAGCCACCCATCTGCTGAACAATGGCAGT
GGGGTAGGAGTTCTACAGTGTCTCGAGCATATGATTGGGGCAGTGAGAAGCAAAGTGTGGAGATTACAGCCAT
TTCCACACAAACCCATTATCTTGATTGGCTGGAACACAGGAGCTTTGGTGGCCTGTCTGTGTCTAGTAATGGAG
TATGTCACTGCAGTTGTCTGCCTTGGGTTTCTCTGCTTACTGTGGATGGCCCCAGAGGGGATGTAGATGATCCC
CTCTTGGATATGAAAGACTCCAGTCTCTTTGTCAATTGGTCAGAAATCCCTTCAATGTACCCCTGAAGCCATGGAG
GACTTCCGGGAGAAAGATTGAGCTGAGAACAGCTTGGTGGTGGTTGGGGGAGCTGATGACAATCTCAGAATAAGC
AAAGCAAAGAAGAAATCAGAAGGGTTGACTCAGAGCATGGTGGACAGATGTATTTCAGGATGAGATTGTGGACTTT
CTGACTGGAGTGCTCACTCGTGCTGAGGGTCACATGGGCTCTGAACCTCGGGATCAGGATGCTGAGAAGAAGAAG
AAGCCCCGCGATGTGGCCCGCAGAGACTTGGCCTTTGAAGTCCCTGAGCGGGGAGTGCACCTGCCTCCCCAGCT
GCCAAGCTGCCCCGCTCACCTCAGGCTCAGAGGATCTCTCCAGTGTGTCCAGCAGCCCCACCTCCAGTCCCCAAG
ACCAAAGTGACCACAGTGACCTCTGCCCAGAAGTCCAGTCAGATTGGAAGTTCTCAGCTGCTGAAGAGACATGTG
CAGCGGACAGAAGCTGTGCTGACCCACAAACAAGCTCAAGCACAGTTTGCTGCTTTTCTGAAACAAAATATGCTG
GTGAGGAAAGCTCTTCTCCTGGCACCTCCTCTGTCTCTTTGTTCCCATTTTCATCAGAACACCAGAGGAAGGA
GAGAAAGAGGATCTTAGGGTTTCAGCTGAAGCGACACCATCCCTCGAGTCCCTTCTGGCAGTAAGACCTCCAAA
CGACCGAAGATCAAGGTGTCCCTTATCTCCCAAGGGGACACAGCTGGAGGGCCTTGTGCTCCTTCCCAAGGAAGT
GCTCCAGAAGCTGCAGGTGGGAAGCCCATACCATGACACTGGGGCAGGCTTCAGCAGGGGCCAAGGAGCTCACA
GGACTTCTCACCACAGCCAAGTCCAGTTCTTCTGAAGGTGGAGTCTCAGCCAGCCAGTCCCTTCAGTGGTCTCC
AGCAGCACTGCACCCAGTGCCTTGCACACACTGCAGAGCCGCTGGTGGCCACATCTCCTGGCAGCTCCCTCCCA
GGGGCCACATCAGCCAGCAGCCTCCTCCAAGGCCTCAGCTTCAGCTTGCAGGATATCAGCAGCAAGACCTCTGGC
CTTCCAGCAAATCCCTCCCCAGGACCAGCCCCACAGGCTTGAAGGTCCCCACCACCATTACTCTGACACTTCGTG
GCCAGCCGAGCAGGATCACTACACTGAGCCCTATGGGCTCAGGAGCAGCCCCATCCGAGGAGTCTCTTCCCAGG
TGCTGCCCTCCAGCTCACAGCGCCTGCCTCCAGCACCTGAAGATGCTGTGTGATATGTCTCTTACCAAGTTG
GTGATGGCTGCCTCATGGTGGGCCCTGGACAGGTGTGTGGTCCCTGCTGAGCTGTCCACGTGTGGAAGACCTGTT
TAAGACAGTCATTTTTGCCTCTCCGCCAACTGTCTTCAGAGAAACCATTAGGTTAGGTGATACGGTGCCAGCAAG
GGAAGCACCATCGTCCAGGATCTGCAAATCTGGTTCTGGGAACCCAGACTCCTCAGCAGATCTGGCTGTACAT
GGATCAGAACCCTTCTTCCCCCGCTTAAGCTGTGGTTTGACCCAAGGGTCAGCATATAGGACTGCCTGCTGCAT
TTAATGAAGGTGTTTTCTTTTGAAGTCTGTGCTACCTCTGCGCCTAGTTGGGAGGAGACATCCATCTGGTCTG
GGATTTCCGGGAGTTAGAATGGAAGCTCTTTGTCTAAAGACTGGAGTCATCCTGGCCTGCCAACTGGTGGTTTCTG
GCCGGACGGGCTTGTTTTGGACATCACTGTTGCCTTCACTCAGCAGCCACGGGAGAGTGTCCCCATGCAACTCC
ACCTTAGAAACCACGTGAGTACTGAGTAGCTTGTGACTCCTGGAACTTCTGGTTTTTGTAGTATCATAATG
AAGGCAAAGAGAACTAGGCTGTCTCTTTAGCCTCTTTGACTTACTCTAGATGTTGGGAGCAGTGGTTGCCAGG
TGAAACCTGGGCCCTTTGTCTTTTACCATGCTTTGGGCAGTTTCTGTATCCAGAGAGTCCGCAGGTTTCAGATA
AGCTGAAGAAGAGTAATAGAACAGCAAAGGAAGTGGCTTGAAGGATGTGCTAGTAAGCCCTGTGGTTTGTGCTTA
GGTCTCTGCTCTGCTACCCAAGGAAGTGGTGGTTTCAGCTGGAGATAAAAAGAAGAATTTGCCAAGTCAGAGAAGA
AACCCCAACCCCGGAAAATCCTCTGTCTCCAGTCTCTGGAGGTGAAGCAGGGACAATAAGCTAAGGTAGTATCTT

886/6881
FIGURE 824B

GGCCATCCCAGGAAACTTGTGGCATTAGGACGATGAAGGCCATGCTTCAGTGTTTTTCGTTTCTATTTTCATGAGAC
TTTTTGTCTTCCTGCTTACAAGTGGGAAGATGATTGACAGTGAAGTCTACTATGCAGGGCTGTTGGTACCAACCTG
AGCCCTATAGGTGGCAGTCCCTGGAGAAGTGGTCACAGAAGATGGAGCTCTGATCCCCTGCTTACCTCTTCACAA
CACTTGTGTGCAAAGATAGTTTTAGATTTGGTTTAGAAGCTATCCTCCAGAACAGGCTCCCATACTTAGAATGTT
TCTAGTTAAGGTAATAAAATTAGGCAACCCAAGTGTGACTCCACTCAAGTGTCTTTTTCTGTAGGCAGGAAGGGCC
CACAACATGGCTTAAAAATGTAGTCCATGGTTCTGGCCACAGTACAGTGTGTATCTATACCAGGTCACCTGTGTT
CAATCTGGGAGCCTTCCTGGCCAGTCTGAGTGGCAGCCAGAAGGGAGCTCATAGTGTCTAGGAGTCTCAGGCAAG
GTAGGTCAGGGTACTGTGGGCAGGGGGGATGTGTGTGATAGGAGAGGGTACCCTAAACCCCATACCTTCCCTCCC
TGACCTGAAAAGCTGATCTCAACAGGGATTACACAGAAATTAGGCTGTGTTTTTGCATTAGCTGGTAGGTGACTT
TCTCAAAATTCTTAAATTCAGAAAGTATTTAGTAACTTGAGGAAGGTATGAAATCTGGAGGAGGCATCCAGGAC
CCAGGGGTTTGATAGCTTTACAGGTAGGATCATACCACACCAAAAAGAGCAGTGGACAATAAGACTATATGAGCTA
TATGAAGCTTTTAGGAATCATTAGGACAGACAGAGCCCTAAACAACCCATTTCATGACTTAAGTTGTTGGCTCAG
TGTATGCTGGGGACAAAGAAAACTAACAAGCCGACCTGCCTTTATGATAAATTCTAGTGTGCTTACAAGGGATG
ACTTCCTGAGGTGTGATCTGTCCACCTTGAAGAACTCCACAAGTGAAGAAGGGGAGCTGTGAGAACGTGGATTGT
TCTACAAGTGTGACAGGGTAACAGAGGAAGTGGCTGAGGCCTAGAGTCACGTTTTCCAGTTCCCTTCGCAAACTA
TATTTCTTGGAACGCGAAAGGAAGCTTTACCTATTTTCATAGAAGACCTGGAATCCATAACCTCAGAAGGCAATAT
TATTGATAGAAAATGTGGAAGGATCAGGAAGTTCTTAGATTCTTGGATGACAGATGCATGTTGATGCCCTATGGA
GATGTCCTTGTGTTTTGAGGTCACTGAGGTAGGAAGACCTGTCTACTCTTGGTTTCACCACTAGAACAGTCTTGG
GCTGGATGGGTTATAGAGCTGAGCGGCTGTGATGGTTCTGTTTTTACATTAACAAAACAATTAAAAACACCAAA
AAC

FIGURE 825

CACACCCCTGCAGGACACCTCTCTGGCACAACACCACCTTCTTTGGGGTTTTTTCAAGCACAGTGGGGTGACATGTAC
CTGTTCGGCCATCTGTGAGTACCAGTTGGAAGAGATCCAGCGGGTGTTTGAGGGCCCCCTATAAGGAGTACCATGAG
GAAGCCCAGAAGTGGGACCGCTACACTGACCCTGTACCCAGCCCTCGGCCTGGCTCGTGCATTAACAACCTGGCAT
CGGCGCCACGGCTACACCAGCTCCCTGGAGCTACCCGACAACATCCTCAACTTCGTCAAGAAGCACCCGCTGATG
GAGGAGCAGGTGGGGCCTCGGTGGAGCCGCCCTGCTCGTGAAAGAAGGGCACCAACTTCACCCACCTGGTGGCC
GACCGGGTTACAGGACTTGATGGAGCCACCTATACAGTGCTGTTTCATTGACACAGGAGACGGCTGGCTGCTCAAG
GCTGTGAGCCTGGGGCCCTGGGTTACCTGATTGAGGAGCTGCAGCTGTTTGACCAGGAGCCCATGAGAAGCCTG
GTGCTATCTCAGAGCAAGAAGCTGCTCTTTGCCGGCTCCCGCTCTCAGCTGGTGCAGCTGCCCGTGGCCGACTGC
ATGAAGTATCGCTCCTGTGCAGACTGTGTCTCGCCCGGGACCCCTATTGCGCCTGGAGCGTCAACACCAGCCGC
TGTGTGGCCGTGGGTGGCCACTCTGGATCTCTACTGATCCAGCATGTGATGACCTCGGACACTTCAGGCATCTGC
AACCTCCGTGGCAGTAAGAAAGTCAGGCCCACTCCCAAAAACATCACGGTGGTGGCGGGCACAGACCTGGTGTCTG
CCCTGCCACCTCTCCTCCAACCTTGGCCCATGCCCGCTGGACCTTTGGGGGGCCGGGACCTGCCTGCGGAACAGCCC
GGGTCTTCTCTACGATGCCCGGCTCCAGGCCCTGGTTGTGATGGCTGCCAGCCCCGCCATGCCGGGGCCTAC
CACTGCTTTTTCAGAGGAGCAGGGGGCGCGGCTGGCTGCTGAAGGCTACCTTGTGGCTGTCTGTGGCAGGCCCGTCTG
GTGACCTTGGAGGCCCGGGCCCCCTGGAAAACTGGGGCTGGTGTGGCTGGCGGTGGTGGCCCTGGGGGCTGTG
TGCTGGTGTCTGCTGCTGCTGGTGTCTGTCATTGCGCCGGCGGCTGCGGGAAGAGCTGGAGAAAGGGGCCAAGGCT
ACTGAGAGGACCTTGGTGTACCCCTGGAGCTGCCCAAGGAGCCACCAGTCCCCCTTCCGGCCCTGTCTCTGAA
CCAGATGAGAAACTTTGGGATCCTGTGCGTTACTACTATTTCAGATGGCTCCCTTAAGATAGTACCTGGGCATGCC
CGGTGCCAGCCCGGTGGGGGGCCCCCTTCGCCACCTCCAGGCATCCAGGCCAGCCTCTGCCTTCTCCAACCTCGG
CTTCACCTGGGGGGTGGGCGGAACTCAAATGCCAATGGTTACGTGCGCTTACAACCTAGGAGGGGAGGACCGGGGA
GGGCTUGGGCACCCCTGCCTGAGCTCGCGGATGAACTGAGACGCAAACCTGCAGCAACGCCAGCCACTGCCCGAC
TCCAACCCCGAGGAGTCATCAGTATGAGAGGGGAACCCCCACCGCGTTCGGCGGGAAGCGTGGGAGGTGTAGCTCCTA
CTTTTGCACAGGCACCAGCTACCTCAGGGACATGGCACGGGCACCTGCTCTGTCTGGGACAGATACTGCCAGCA
CCCACCCGGCCATGAGGACCTGCTCTGCTCAGCACGGGCACCTGCCACTTGGTGTGGCTCACCAGGGCACCAGCCT
CGCAGAAGGCATCTTCTCCTCTCTGTGAATCACAGACACGCGGGACCCAGCCGCCAAAACCTTTTCAAGGCAGA
AGTTTTCAAGATGTGTGTTTGTCTGTATTTGCACATGTGTTTGTGTGTGTGTATGTGTGTGTGCACGCGCGTGC
GCGCTTGTGGCATAGCCTTCTGTTTCTGTCAAGTCTTCCCTTGGCCTGGGTCTCCTGGTGTAGTCATTGGAGCT
ATGAAGGGGAAGGGGTGCTATCACTTTGTCTCTCTACCCCCACTGCCCGAGTGTGCGGCAGCGATGTACATAT
GGAGGTGGGGTGGACAGGGTGTGTGCCCCCTTCAGAGGGAGTGCAGGGCTTGGGGTGGGCCTAGTCTCTGCTCCTA
GGGCTGTGAATGTTTTTCAGGGTGGGGGGAGGGAGATGGAGCCTCCTGTGTGTTTGGGGGAAGGGTGGGTGGGGC
CTCCCACTTGGCCCCGGGGTTCAGTGGTATTTTTATACTTGCCTTCTTCTGTACAGGGCTGGGAAAGGCTGTGTG
AGGGGAGAGAAGGGGAGAGGGTGGGCCTGCTGTGGACAATGGCATACTCTCTTCCAGCCCTAGGAGGAGGGCTCCT
AACAGTGTAACTTATTGTGTCCCCGCGTATTTTATTGTGTGAAATATTTGAGTATTTTTATATTGACAATAAAAT
GGAGAAAATGAAAAAAAAAAAAAAAAAAAAA

888/6881
FIGURE 826

MYLSAICEYQLEEIQRVFEGPYKEYHEEAQKWDRYTDPVPSRPFGSCINNWHRRHGYTSSLELPDNILNFVKKHP
LMEEQVGPRWSRPLLVKKGTFNTHLVADRVGTGLDGATYTVLFIDTGDGWLLKAVSLGPVWHLIEELQLFDQEPMR
SLVLSQSKKLLFAGSRSQVLVQLPVADCMKYRSCADCVLARDPYCAWSVNTSRCVAVGGHSGSLLIQHVMTSDTSG
ICNLRGSKKVRPTPKNITVVAGTDLVLPCHLSSNLAHARWTFGGRDLPAEQPGSFLYDARLQALVVMQAQPRHAG
AYHCFSEEQGARLAAEGYLVAVVAGPSVTLEARAPLENLGLVWLAVVALGAVCLVLLLLVLSLRRRLREELEKGA
KATERTLVYPLELPKEPTSPFFRPCPEPDEKLWDPVGYYSYSDGSLKIVPGHARCQPGGGPPSPPPGIPGQPLPSP
TRLHLGGGRNSNANGYVRLQLGGEDRGGLGHPLPELADELRRKLQQRQPLPDSNPEESSV

889/6881
FIGURE 827

CGGAAGTTTTGCTGCTAGTCGCGGACGCAATGGCTTCAAGGTTACTTCGCGGAGCTGGAACGCTGGCCGCGCAGG
CCCTGAGGGGCTCGCGGCCCCAGTGGCGCGGCCGCGATGCGCTCCATGGCATCTGGAGGTGGTGTTCCTACTGATG
AAGAGCAGGCGACTGGGTGGAGAGGGAGATCATGCTGGCTGCAAAGAAGGGACTGGACCCATACAATGTACTGG
CCCCAAAGGGAGCTTCAGGCACCAGGGAAGACCCTAATTTAGTCCCCCTCCATCTCCAACAAGAGAATAGTAGGCT
GCATCTGTGAAGAGGACAATACCAGCGTCGTCTGGTTTTGGCTGCACAAAGGCGAGGCCAGCGATGCCCCCGCT
GTGGAGCCCATTACAAGCTGGTGCCCCAGCAGCTGGCACACTTGAGCACCTGCACTAAATTACTCAAAATGTGCTG
TAAAGTTTCTTCTTTCCAGTAAAGACTAGCCATTGCATTGGCTCCTTCTCCATAAAAAAAAAAAAAAAAAAAAA

890/6881
FIGURE 828

MASRLLRGAGTLAAQALRARGPSGAAAMRSMASGGGVPTDEEQATGLEREIMLAACKGLDPYNVLAPKGASGTRE
DPNLVPSISNKRIIVGCICEEDNTSVVWFWLHKGEAQRCPRCGAHYKLVPQQLAH

891/6881
FIGURE 829

TTGCAGCCGCCGGCAGCTACTGCAAGGCAAAAGCCGGAGTGGACGTGTCTTTTGAAACTGCTGCTCTTTCACTTC
TCAGGCGTCAACGAGAGCTCAGCACCCAGGCTGAACTCTGTACCATTGGAAGAATCGGAAGCTGATGCATCTGTT
GACATGTTTTCCAAAGTCCTGGAGCATCAGCTGCTTCAGACTACCAAACTGGTGGGAAGAACATTTGGATTCTGAA
ATTCAAAAACCTGGATCAGATGGATGAGGATGAATTGGAACGCCTTAAAGAAAAGAGACTCCAGGCACTAAGGAAA
GCTCAACAGCAGAAAACAAGAATGGCTTTCTAAAGGACATGGGGAATACAGAGAAATCCCTAGTGAAAGAGACTTT
TTTCAAGAAGTCAAGGAGAGTGAAAATGTGGTTTGCCATTTCTACAGAGACTCCACATTCAGGTGTAAAATACTA
GACAGACATCTGGCAATATTGTCCAAGAAACACCTCGAGACCAAAATTTTGAAGCTGAATGTGGAAAAAGCACCT
TTCCTTTGTGAGAGACTGCATATCAAAGTCATTCCACACTAGCACTGCTAAAAGATGGGAAAACACAAGATTAT
GTTGTTGGGTTTACTGACCTAGGAAATACAGATGACTTCACCACAGAACTTTAGAATGGAGGCTCGGTTCTTCT
GACATTCTTAATTACAGTGGAAATTTAATGGAGCCACCATTTCAGAACCAAAAGAAATTTGGAACAAACTTCACA
AAGCTGGAAAAGAAAACCTATCCGAGGAAAGAAATATGATTACAGACTCTGATGATGATAGAGCTCAATAATTCTT
TGTAATTGCTCTTTTTTTTTCTGCTTCAGATTTAATGTGTTTTTAAATTTCTATTAATGTCTATACATTGGTCA
CCTAAATACTCATATTCTCGAGTTTTATACAGTTGTATCACATCGAAAAGTGTCTTTACTGTTTTCTGTGTGGCC
ATCATGTTTAAGTTGAGGAAAACCTCAGTTCTTAATTATCTGGGAAGGGTCTGGATTCTCTATTTTTGAGATTGA
CTTTATCACAATATGATTCTTACATCTTTATAACCATTACAAATTGTGTTTTAGATCTACAGAGTTAGAAATTCGA
AACTATTCCAGGACTAATTCTTAATCGGCATTATTTATACAAGAGGTCAAGTAACATTTACTAGCGCAATACTG
CACTTGTAATGAATTATAAACGCTCTTCTGGAATATATTTAAATAACCATTAAAGAACTGCTTATTCATTCTGG
ACACTGCATGTTGATGTTGAATCAACTGATGCCAGCAGAAAGCTATTTTGATTTGTGAACATACTGCCTTATTTA
AAGGGTCCTGATTGCTTGTATTTAAGACATTCATTAATAAGAAACCAGGAAACACTTTTGAAATAACAGCATAA
GGAACCTTCACTGTCTCTGCTCAATAAAATACCTGTAACTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

892/6881
FIGURE 830

MEADASVDMFSKVLEHQLLQTTKLVEEHL DSEIQKLDQMD EDELERLKEKRLQALRKAQQQKQEWLSKGHGEYRE
IPSERDFFQEVKESENVVCHF YRDSTFRCKILDRHLA ILSKKHLET KFLKLNVEKAPFLCERLHIKVIPTLALLK
DGKTQDYVVGFTDLGNTDDFTTETLEWRLGSSDILNYS GNLMEPPFQNKKF GTNFTKLEKKTIRGKKYDS DSDD
D

893/6881
FIGURE 831A

CGCGGGTCTGTGGAGAGCCGGGTGCGAGCGGCGGCAGCACGAGGGGAAAAAGAGCTGAGCGGAGACCAAAGTCAGC
CGGGAGACAGTGGGTCTGTGAGAGACCGAATAGAGGGGCTGGGGCCACGAGCGCCATTGACAAGCAATGGGGAAAG
AAACAGAAAAACAAGAGCGAAGACAGCACCAAGGATGACATTGATCTTGATGCCTTGGCTGCAGAAATAGAAGGA
GCTGGTGTGCCAAAGAACAGGAGCCTCAAAAGTCAAAAGGGAAAAAGAAAAAGAGAAAAAAAGCAGGACTTT
GATGAAGATGATATCCTGAAAGAACTGGAAGAATTGTCTTTGGAAGCTCAAGGCATCAAAGCTGACAGAGAACT
GTTGCAGTGAAGCCAAACAGAAAAACAATGAAGAGGAATTCACCTCAAAAGATAAAAAAAGAAAGGACAGAAAGGC
AAAAACAGAGTTTTGATGATAATGATAGCGAAGAATTGGAAGATAAAGATTCAAAATCAAAAAAGACTGCAAAA
CCGAAAGTGGAAATGTACTCTGGGAGTGATGATGATGATGATTTTAACTTCTTCTAAAAAGCTAAAGGGAAA
GCTCAAAATCAATAAGAAGTGGGATGGGTGAGAGGAGGATGAGGATAACAGTAAAAAATTAAAGAGCGTTCA
AGAATAAATTCTTCTGGTGAAAGTGGTGATGAATCAGATGAATTTTGCATCTAGAAAAGGACAGAAAAAAAT
CAGAAAAACAGCCAGGTCCTAACATAGAAAGTGGGAATGAAGATGATGACGCCTCCTTCAAATTAAGACAGTG
GCCCCAAAAGAAGGCAGAAAAGAAGGAGCGCGAGAGAAAAAGCGAGATGAAGAAAAGCGAAACTGCGGAAGCTG
AAAGAAAAAGAAGAGTTAGAAACAGGTAAAAAGGATCAGAGTAAACAAAAGGAATCTCAAAGGAAATTTGAAGAA
GAACTGTAAATCCAAAGTACTGTTGATACTGGAGTAATTCCTGCCTCTGAAGAGAAAGCAGAGACTCCCACA
GCTGCAGAAGATGACAATGAAGGAGACAAAAAGAAGAAAGATAAGAAGAAAAGAAAGGAGAAAAGGAAGAAAAA
GAGAAAGAGAAGAAAAAGGACCTAGCAAAGCCACTGTTAAAGCTATGCAAGAAGCTCTGGCTAAGCTTAAAGAG
GAAGAAGAAAGACAGAAGAGAGAAGAGGAAGAACGTATAAACGGCTTGAAGAATTAGAAGCCAAGCGTAAAGAA
GAGGAACGATTGGAACAAGAAAAAGAGAAAGGAAAAAGCAAAAAGAAAAAGAAAGAAAGAACGCTTGAAAAAA
GAAGGGAACTTTTAACTAAATCCCAGAGAGAAGCCAGAGCCAGAGCCGAAGCTACTCTTAACTGCTACAAGCT
CAGGGTGTTGAAGTGCCATCAAAGACTCTTTGCCAAAGAAGAGGCCAATTTATGAAGATAAAAAGAGGAAAAAA
ATACCACAGCAGCTAGAAAGTAAAGAAGTGTCTGAATCAATGGAATTATGTGCTGCTGTAGAAGTTATGGAACAA
GGAGTACCAGAAAAAGGAGAGACACCACCTCCTGTTGAACCAGAAAGAAAGATACTGAGGATGCTGGATTG
GATGATTGGGAAGCTATGGCCAGTGATGAGGAGACAGAAAAAGTAGAAGGAAACAAAGTTCATATAGAAGTAAAA
GAAAACCTGAAGAGGAGGAGGAGGAGGAAGAAGAGGAAGAAAGATGAAGAAAGTGAAGAAGAGGAGGAAGAG
GAGGGAGAAAGTGAAGGCAGTGAAGGTGATGAGGAAGATGAAAAGGTGTCAGATGAGAAGGATTGAGGGAAGACA
TTAGATAAAAAGCCAAAGTAAAGAAATGAGCTCAGATTCTGAATATGACTCTGATGATGATCGGACTAAAGAAAGAA
AGGGCTTATGACAAAGCAAAACGGAGGATTGAGAAACGGCGACTTGAACATAGTAAAAATGTAAACACCGAAAAAG
CTAAGAGCCCCCTATTATCTGCGTACTTGGGCATGTGGACACAGGGAAGACAAAAATTCTAGATAAGCTCCGTCAC
ACACATGTACAAGATGGTGAAGCAGGTGGTATCACACAACAAATTGGGGCCACCAATGTTCTCTTGAAGCTATT
AATGAACAGACTAAGATGATTAAAAATTTTGATAGAGAGAATGTACGGATTCCAGGAATGCTAATTATTGATACT
CCTGGGCATGAATCTTTCAGTAATCTGAGAAATAGAGGAAGCTCTCTTTGTGACATTGCCATTTTAGTTGTTGAT
ATTATGCATGGTTTGGAGCCCCAGACAATTGAGTCTATCAACCTTCTCAAATCTAAAAATGTCCCTTCATTGTT
GCACTCAATAAGATTGATAGTTATATGATTGAAAAAGAGTCTGACTCTGATGTGGCTGCTACTTTAAAGAAG
CAGAAAAAGAATACAAAAGATGAATTTGAGGAGCGAGCAAAGGCTATTATTGTAGAATTTGCACAGCAGGGTTG
AATGCTGCTTTGTTTTATGAGAATAAAGATCCCCGCACTTTTGTGTCTTTGGTACCTACCTCTGCACATACTGGT
GATGGCATGGGAAGTCTGATCTACCTTCTTGTAGAGTTAACTCAGACCATGTTGAGCAAGAGACTTGCACACTGT
GAAGAGCTGAGAGCACAGGTGATGGAGGTTAAAGCTCTCCCGGGGATGGGCACCACTATAGATGTCATCTTGATC
AATGGGCGTTTGAAGGAAGGAGATACAATCATTGTTTCTGGAGTAGAAGGGCCATTGTAACCTCAGATTGAGGC
CTCCTGTTACCTCCTCCTATGAAGGAATTACGAGTGAAGAACCAGTATGAAAAGCATAAAGAAGTAGAAGCAGCT
CAGGGGGTAAAGATTCTTGAAAAGACCTGGAGAAAACATTGGCTGGTTTACCCCTCCTTGTGGCTTATAAAGAA
GATGAAATCCCTGTTCTTAAAGATGAATTGATCCATGAGTTAAAGCAGACACTAAATGCTATCAAATTAGAAGAA
AAAGGAGTCTATGTCCAGGCATCTACACTGGGTTCTTTGGAAGCTCTACTGGAATTTCTGAAAACATCAGAAGTG
CCCTATGCAGGAATTAACATTGGCCCAGTGCATAAAAAAGATGTTATGAAGGCTTCAGTGATGTTGGAACATGAC
CCTCAGTATGCAGTAATTTTGGCCTTCGATGTGAGAATTGAACGAGATGCACAAGAAATGGCTGATAGTTTAGGA
GTTAGAATTTTTAGTGAGAAATTTTATCATTTTATTTGATGCCCTTTACAAAATATAGACAAGACTACAAGAAA
CAGAAACAAGAAGAATTTAAGCACATAGCAGTATTTCCCTGCAAGATAAAAAATCCTCCCTCAGTACATTTTTAAT
TCTCGAGATCCGATAGTGATGGGGGTGACGGTGGAAGCAGGTGAGGTGAAACAGGGGACACCCATGTGTGTCCCA
AGCAAAAATTTTGTGACATCGGAATAGTAACAAGTATTGAAATAAACCATAAACAAGTGATGTTGCAAAAAA

894/6881
FIGURE 831B

GGACAAGAAGTTTGTGTAAAAATAGAACCTATCCCTGGTGAGTCACCCAAAATGTTTGGAAGACATTTTGAAGCT
ACAGATATTCTTGTTAGTAAGATCAGCCGGCAGTCCATTGATGCACTCAAAGACTGGTTCAGAGATGAAATGCAG
AAGAGTGACTGGCAGCTTATTGTGGAGCTGAAGAAAGTATTTGAAATCATCTAATTTTTTCACATGGAGCAGGAA
CTGGAGTAAATGCAATACTGTGTTGTAATATCCCAACAAAATCAGACAAAAAATGGAACAGACGTATTTGGACA
CTGATGGACTTAAGTATGGAAGGAAGAAAAATAGGTGTATAAAATGTTTTCCATGAGAAACCAAGAACTTACAC
TGGTTTGACAGTGGTCAGTTACATGTCCCCACAGTTCCAATGTGCCTGTTCACCTCACCTCTCCCTTCCCCAACCC
TTCTCTACTTGGCTGCTGTTTTAAAGTTTGCCCTTCCCCAAATTTGGATTTTTATTACAGATCTAAAGCTCTTTC
GATTTTATACTGATTAAATCAGTACTGCAGTATTTGATTAACC

895/6881

FIGURE 832

CTTCCTTTCCAACCTGGACGCTGCAGAA**ATG**GCTCCCGCAAAGAAGGGTGGCGAGAAGAAAAAGGGCCGTTCTGCC
ATCAACGAAGTGGTAACCCGAGAATACACCATCAACATTCACAAGCGCATCCATGGAGTGGGCTTCAAGAAGCGT
GCACCTCGGGCACTCAAAGAGATTTCGGAAATTTGCCATGAAGGAGATGGGAACTCCAGATGTGCGCATTGACACC
AGGCTCAACAAAGCTGTCTGGGCCAAAGGAATAAGGAATGTGCCATACCGAATCCGTGTGCGGCTGTCCAGAAAA
CGTAATGAGGATGAAGATTCACCAAATAAGCTATATACTTTGGTTACCTATGTACCTGTTACCACTTTCAAAAAT
CTACAGACAGTCAATGTGGATGAGAAC**TAA**TCGCTGATCGTCAGATCAAATAAAGTTATAAAATTGC

896/6881
FIGURE 833

MAPAKKGGEKKKGRSAINVVTREY TINIHKRIHGVGFKKRAPRALKEIRKFAMKEMGTPDVRI DTRLNKAVWAK
GIRNVFYRIRVRLSRKRNEDEDSPNKLYTLVTYVPVTTFKNLQTVNV DEN

897/6881
FIGURE 834

ATGCCCCGGCGGAGGGGCGAGCGCGGCGTCTGGCCGGCTTCTCACCGCCGCGGAGCAAAGAGGGTCCCGGGAAGCG
GCAGGGTCGGCGTCCAGGAGCGGCTTCGGGGGCTCCGGCGGCGGCAGAGGCGGAGCAAGCGGCCCGGGTCCGGG
AGCGGAGGCCCTGGGGGCCCCGCGGGCAGGATGAGCTTGACCCCGAAGGAGCTCTCGAGCCTGCTGAGCATCATA
TCGGAGGAGGCGGGCGGCGGCAGCACCTTCGAGGGCCTGTCCACCGCCTTCACCACTACTTCAGCAAGGCCGAC
CACTTCCGCCTGGGCTCGGTGCTCGTCATGCTGCTCCAGCAGCCCGACCTGCTGCCTAGCGCGGCGCAGCGCCTC
ACGGCGCTCTACCTGCTCTGGGAGATGTACCGCACCGAGCCGCTGGCCGCCAACCCCTTCGCCGCCAGCTTCGCG
CACCTGCTCAACCCCGCGCCGCCCGCCGCGGGCGGCCAGGAACCCGACCGCCCTCCGCTCTCAGGATTTTTACCT
CCTATAACTCCACCAGAAAAGTTTTTTCTTTCCAGCTGATGCTGGCACCCCCACGGGAACTCTTCAAAAAGACG
CCTCGCCAGATTGCACTGATGGACGTTGGAAACATGGGCCAGTCTGTGGACATTAGTGGGCTTCAGTTAGCCTTG
GCCGAACGCCAATCTGAATTGCCAACGCAAAGCAAAGCGAGCTTCCCCAGTATTCTCAGTGACCCAGACCCGGAT
TCTTCTAATTCTGGATTTGACAGCTCAGTTGCCTCTCAGATCACAGAAGCTTTAGTCAGCGGACCAAAGCCACCT
ATTGAAAGCCATTTTCGACCAGAGTTTATTCGTCCACCGCTCCACTCCACATTTGTGAGGATGAACTTGCTTGG
CTAAACCCCAACGGAGCCTGACCACGCGATCAGTGGGATAAATCGATGTGTGTTAAGAATAGCACTGGTGTGGAG
ATCAAACGAATAATGGCCAAAGCCTTCAAAAGCCCCCTTATCCTCTCCCCAACAAACACAGCTACTTGGTGAGTTG
GAAAAAGACCCCAAACCTTGCTACCATATTGGCCTCACCCCAAGCCAAACTTCCTGACCTTGTTGGAAAAACAACCT
TTAGTCGCTATAGAAATGTTGCTGAAATTAATGCAGTCAAGCCAGATCACTGAGTATTTCTCTGTCTGGTCAAT
ATGGACATGTCTTTACATTCAATGGAAGTTGTAAATCGACTAACTACAGCTGTTGATCTACCTCCTGAATTTATT
CACCTTTATATATCAAATTGCATCTCTACTTGTGAACAGATTAAGGATAAATATATGCAGAATCGGTTGGTGCGT
CTTGTTGTGTGTTTCTCCAATCCTTGATCCGTAACAAAATTATTAATGTACAGGATTTGTTTATAGAAGTGCAG
GCATTCTGTATTGAATTCAGTAGGATACGAGAAGCTGCTGGTCTTTTCCGGTTGTTGAAGACATTGGATACTGGG
GAAACACCTTCTGAGACCAAAATGTCAAAATAA

898/6881
FIGURE 835

MPGGGASAASGRLLTAAEQRGSREAAGSASRSGFGGSGGGRGGASGPGSGSGPGGPAGRMSLTPKELSSLLSII
SEEAGGGSTFEGLSTAFHHYFSKADHFRLGSVLVMLLQQPDLLPSAAQRLTALYLLWEMYRTEPLAANPFAASFA
HLLNPAPPARGGQEPDRPPLSGFLPPITPPEKFFLSQLMLAPPRELFKKTPRQIALMDVGNMGQSVDISGLQLAL
AERQSELPTQSKASFPSILSDPDPDSSNSGFDSSVASQITEALVSGPKPPIESHFRPEFIRPPPPLHICEDELAW
LNPTEPDHAIQWDKSMCVKNSTGVEIKRIMAKAFKSPLSSPQQTQLLGELEKDPKLVYHIGLTPAKLPDLVENNP
LVAIEMLLKLMQSSQITEYFSVLVNMDMSLHSMEVVNRLTTAVDLPPEFIHLYISNCISTCEQIKDKYMQNRLVR
LVCVFLQSLIRNKIINVQDLFIEVQAFCIEFSRIREAAGLFRLKTLDTGETPSETKMSK

899/6881
FIGURE 836

AGGGTACGGGCGGGACCGCCGCAGCCCCGGGGCGGGGGCACGGCAACCGCGAGGCCTGGGGGCGCCCGCCCCCG
CGCCCCACGCCCCGGTGCCAGCGAGCCGAGGCGTGTCATCTCCTTATATGGTCAAATGACACGGCGGGGTTTCTCGA
GGGCGGGAGCTGCGCAGCGCTCCACTCGGCCGGCAGCGGAGCCGCAGCCACCAGCCGCCCGCGCCCTCCAGCCCC
GTCCGGGAGTCCCCGGCCCCGCTGCGGTGCCGTGAGTACCTCCAACCCCTGCGCCCCGGAGGGAGGCCGAGGGGC
TTAGCCACCAGGGCTCGGAAGTGGGGGCCGAATCCGGTGCGAGACCCAAGGAGAGGGGAGCAGAGCCGGAGTTGG
GGAGACTGTGGCTGAAAACCTGTGTCTTCTGGAGACTAGGCTGGCATTTTGACTTTGGGACGGAGTCTCGCTTTG
TCGCCCAGGCTGGAGTGCAGTGGCACGATCTCAGCTCACTGCAAGCTCTACCTCTTGGTTACGCCATTCTCCTG
CCCCAGCCTCCCAAGTAGCTGGGACTACAGGTTGCTGAAAAGCCAGGAGTCAAAATGACTGAGCGCTTTGACTGC
CACCATTGCAACGAATCTCTCTTTGGCAAGAAGTACATCCTGCGGGAGGAGAGCCCCCTACTGCGTGGTGTGCTTT
GAGACCCTGTTTCGCCAACACCTGCGAGGAGTGTGGGAAGCCCATCGGCTGTGACTGCAAGGACTTGTCTTACAAG
GACCGGCACTGGCATGAAGCCTGTTTCCACTGCTCGCAGTGCAGAACTCACTGGTGGACAAGCCCTTTGCTGCC
AAGGAGGACCAGCTGCTCTGTACAGACTGCTATTCCAACGAGTACTCATCCAAGTGCCAGGAATGCAAGAAGACC
ATCATGCCAGGTACCCGCAAGATGGAGTACAAGGGCAGCAGCTGGCATGAGACCTGCTTCATCTGCCACCGCTGC
CAGCAGCCAATTGGAACCAAGAGTTTCATCCCCAAAGACAATCAGAATTTCTGTGTGCCCTGCTATGAGAAACAA
CATGCCATGCAGTGC GTTCAGTGC AAAAGCCCATCACCACGGGAGGGGTCACTTACCGGGAGCAGCCCTGGCAC
AAGGAGTGTCTTCGTGTGCACCGCCTGCAGGAAGCAGCTGTCTGGGCAGCGCTTCACAGCTCGCGATGACTTTGCC
TACTGCCTGAACTGCTTCTGTGACTTGTATGCCAAGAAGTGTGCTGGGTGCACCAACCCCATCAGCGGACTTGGT
GGCACAAAATACATCTCCTTTGAGGAACGGCAGTGGCATAACGACTGCTTTAACTGTAAGAAGTGTCCCTCTCA
CTGGTGGGGCGTGGCTTCCTCACAGAGAGGGACGACATCCTGTGCCCCGACTGTGGGAAAGACATCTGAATTCAA
CACAGAGAAGTTGCTGCTTGTGATCTCACACACAGATTTTTATGTTTTCTTTCTCACCAGGCAATCTTGCTTC
TGTTTTCTTCCAGCCACATTGAGACTTTCTTCTAGTGCTTTTCAGTGATACTCACGTTTGCTTAAACCCTTTAGT
GCTTTGTGATAGTTCAGTCCCAGGGAAAGAGAAAACCTCGCCCTAGGCCCTAGGTGGGAAGATGGTTTGAAATTTT
TGTAATCGAGTAAGGCACACCCAAATGTAAAAATCCTTTTGAATGATGCCTTTATAAATCTTTCTCTCACIGTCT
ATTTAAGTGCAATTAACATATGTCACGAACCTGAAAGTTTTCTAAACTCAATAAGGTAATGACCAGTTGTTATTT
ACAGCTCTGTAACCTCCCGTTGCGTCAAGTCTAAACCAAGATTATGTGACTTGCAATAAAGTTATTTCAGAACAGA
AAAAAAAAAAAAAAAAAAAA

900/6881
FIGURE 837

MTERFDCHHCNESLFGKKYILREESPYCVVCFETL FANTCEECKPIGCDCKDLSYKDRHWHEACFHCSQCRNSL
VDKPFAAKEDQLLCTDCYSNEYSSKCQECKKTIMPGRKMEYKGSSWHETCFICHRCQQPIGTKSFIPKDNQNF C
VPCYEKQHAMQCVQCKKPIITGGVTYREQPWHKECFVCTACRKQLSGQRFTARDDFAYCLNCFCDLYAKKCAGCT
NPISGLGGTKYISFEERQWHNDCFNCKKCSLSLVGRGFLTERDDILCPDCGKDI

901/6881
FIGURE 838

AGTCTTCTGGCCCCGAGAGGGAGAGGTGGGGATAGGACCTTCCTTTAGTCCCCTCCGTAGTGGAACGAAGGATTCTTTATGGTCATCTGTGGTGTTCAATTCGTAAAGAAGCATCTGCAGGGTAAGAAGGAAAAACGTCCACCTTGCAAAATATATCCCAGGCACATGCCTCCTGAGAAGTGACCCCTCCTCCCTCCGCCTCCCCGGGCACGTCTGGGGCTTCTCCAGTCTCCCGCTCCTGGGACCAGGCAGAGATCCCGGCGTGGGCAGACCCCTGCCACCGCGCCCCAGGCCTCGTCCGAAACTCGCGCCCCGAGAGCCACGCCGGAGGCGACGCTCCCGATAACTACTGTGCTCCCAAGACCCGGAGGGCACGAAGAAAGGAGCCCTGGCAAACAAAGGGTTGCTGAAAAGCCAGGAGTCAAAATGACTGAGCGCTTTGACTGCCACCATTTGCAACGAATCTCTCTTTGGCAAGAAGTACATCCTGCGGGAGGAGAGCCCCTACTGCGTGGTGTGCTTTGAGACCCTGTTGCGCAACACCTGCGAGGAGTGTGGGAAGCCCATCGGCTGTGACTGCAAGGTACCTGCTGCGGGCCTCTGCGGGTCCCCGGCGCTCCCTAGGAAACACGGGTTTCTCTGTGGTTTGTGCTGAAGCCCTGATCCACCACTGAAGTCTGTCTCTTGAGCCCCCTCTGAGGGGCGTGGACCCTGCGTGTAGCCTTTCGGAAGCTTCTTCCCTCTAGCGAATGTGATCTCTGCCCACAAGCACTGGGTGAGGGCCTTGCCAGGACTTTTGTGCTTAGTATCTCTAAGTACATTTCTGTATTCTAGCAATTAGTGCCCTTATCTAACTACCCAGCTGCCTACCAATACTGGAACCTTCTTAAGGGTGGTGCTCTCTTCCTCTTGCTGTTTGGCCCGTGGTGAGTAACGTGGAGCAGGTGCTGTGCTCAGTCAATATTTGATGAATGAATGTGTACATGAGAGAACCAGAGTTGGTTCCTGGATAAATGGGCACATAAAAGCACAAAGTCCTTGG

902/6881
FIGURE 839

AAGGACTCCATGAAAGATGACAGAAGAAGTTATTGTGATAGCCAAGTGGGACTACACCGCCCAGCAGGACCAGGA
GCTGGACATCAAGAAGAACGAGCGGCTGTGGTTGCTGGACGACTCCAAGACGTGGTGGCGGGTGAGGAACGCGGC
CAACAGGACGGGCTATGTACCGTCCAACCTACGTGGAGCGGAAGAACAGCCTGAAGAAGGGCTCCCTCGTGAAGAA
CCTGAAGGACACACTAGGCCTCGGCAAGACGCGCAGGAAGACCAGCGCGCGGGATGCGTCCCCACGCCCAGCAC
GGACGCCGAGTACCCCGCCAATGGCAGCGGCGCCGACCGCATCTACGACCTCAACATCCCGGCCCTTCGTCAAGTT
CGCCTATGTGGCCGAGCGGGAGGATGAGTTGTCCCTGGTGAAGGGGTCGCGCGTCACCGTCATGGAGAAGTGCA
CGACGGTTGGTGGCGGGGCAGCTACAACGGGCAGATCGGCTGGTTCCCTCCAACCTACGTCTTGAGGAGGTGGA
CGAGGCGGCTGCGGAGTCCCCAAGCTTCCTGAGCCTGCGCAAGGGCGCCTCGCTGAGCAATGGCCAGGGCTCCCG
CGTGCTGCATGTGGTCCAGACGCTGTACCCCTTCAGCTCAGTCACCGAGGAGGAGCTCAACTTCGAGAAGGGGGA
GACCATGGAGGTGATTGAGAAGCCGGAGAACGACCCCGAGTGGTGAAATGCAAAAATGCCCGGGGCCAGGTGGG
CCTCGTCCCCAAAACCTACGTGGTGGTCCTCAGTGACGGGCCTGCCCTGCACCCTGCGCACGCCCCACAGATAAG
CTACACCGGGCCCTCGTCCAGCGGGCGCTTCGCGGGCAGAGAGTGGTACTACGGGAACGTGACGCGGCACCAGGC
CGAGTGCGCCCTCAACGAGCGGGGCGTGGAGGGCGACTTCCTCATTAGGGACAGCGAGTCCTCGCCAGCGACTT
CTCCGTGTCCCTTAAAGCGTCAGGGAAGAACAACACTTCAAGGTGCAGCTCGTGGACAATGTCTACTGCATTGG
GCAGCGGCGCTTCCACACCATGGACGAGCTGGTGAACACTACAAAAGGCGCCCATCTTCACCAGCGAGCACGG
GGAGAAGCTCTACCTCGTCAGGGCCCTGCAGTGACGGCGCCCCGGCCCCACACTCGCCTCCCGGGCCCCACGGTG
GAGCTGCCCGCCCGGCCTTGTGGCAGAGGCTCCTCCGCGGGGACGGCCCCGACGGCTTCTCTG

903/6881
FIGURE 840

MTEEVIVIAKWDYTAQQDQELDIKKNERLWLLDDSKTWVRVNAANRTGYVPSNYVERKNSLKKGSLVKNLKDITL
GLGKTRRKTSARDASPTPSTDAEYPANGSGADRIYDLNIPAFVKFAYVAEREDLSLVKGSRVTVMEKCSDGWWR
GSYNGQIGWFPSNYVLEEVDEAAAESPFLSLRKGASLSNGQGSRLHVVTLYPFSSVTEEEELNFEKGETMEVI
EKPENDEPEWWKCKNARGQVGLVPKNYVVLSLSDGPALHPAHAPQISYTGPFSSSGRFAGREWYYGNVTRHQAECALN
ERGVGDFLIRDSESSPSDFSLSLKASGKNKHFKVQLVDNVYCIGQRRFHTMDELVEHYKKAPIFTSEHGEKLYL
VRALQ

904/6881
FIGURE 841

TGGAACCATGCTGCTTGAGGCTCTGGACTGCATCCTACCACCAACTCGTCCAACCTGACAAGCCCTTGACCTGCC
TCTCCAGGATGTCTACAAAATTGGTGGTATTGGTAGTGTTCTGTTGGCCGAGTGGAGACTGGTGTTCTCAAACC
TGGTATGGTGGTCACCTTTGCTCCAGTCAACGTTACAACAGAAGTAAAAATCTGTCGAAATGCACCATGAAGCTTT
GAGTGAAGCTCTTCCTGGGGACAATGTGGGCTTCAATGTCAAGAATGTGTCTGTCAAGGATGTTTCGTCATGGCAA
CGTTGCTGGTGACAGCAAAAATGACCCACCAATGGAAGCAGCTGGTTTCACTGCTCAGGTGATTATCCTGAACCA
TCCAGGCCAAATAAGCACTGGCTATGCCCCTGTATTGGATTGCCACACGGCTCATATTGCATGCAAGTTTGCTGA
GCTGAAGGAAAAGATTGATCACCGTTCTGGTAAAAAGCTGGAAGATGGCCCTAAATTCCTTTGGGTTGCTTTG
CTGTTTCGTGATATGAGACAGATAGTT

905/6881
FIGURE 842

AAAAGCCAAAATGGGAAAGGAAAAGACTCATACCAACATTGTCGTCATTGGACACATAGATTCGGGCAAGTCCAC
CACTACTGGCCATCTGATCTACAAAGGCGGTGGCATCGACAAAAGAACCATTGAAAAATTTGAGAAGGAGGCTGC
TGAGATGGGAAAGGGCTCCTTCAAGTATGCCTGGGTCTTGGATAAACTGAAAGCTGAGTGTGAACATGGTATCAC
CATTGATACCTCCTTGTGGAAATTTGAGACCAGCAAGTACTATGTGACTATCGTTGATGCCCCAGGACACAGAGA
CTTCATCAAAAACATGATTACAGAGACATCTCAGGCTGACTGTGCTGTCCTGATTGTTGCTGCTGGTGTGGTGA
ATTTGAAGCTGGTATCTCCAAGAATGGGCAAACCCAAGAGCATGCCCTTCTGGCTTACACACTGGGTGTGAAACA
ACTAATTGTTGGTGTTAACAAAATGGATTCTACTGAGCCACCCTACAGCCAGAAGAGATATGAGGAAACTACAAA
ATTGGTGGTATTGGTAGTGTTCCTGTTGGCCGAGTGGAGACTGGTGTTCCTCAAACCTGGTATGGTGGTCACCTTT
GCTCCAGTCAACGTTACAACAGAAGTAAAATCTGTCGAAATGCACCATGAAGCTTTGAGTGAAGCTCTTCCTGGG
GACAATGTGG

906/6881
FIGURE 843

AACAGATCTTC**ATGA**ATGTCGCTATCTTTGAGGATGAAGTTTTTGCTGGAGTTACCACACACCAGGAACCTCTTTC
CACACAGCCTGCTGAGTGTGATTGCCAACTTCATCCCTTTCTCTGATCTCAACCAGAGTCCACGGAACATGTACC
AATGCCAGATGGGTAAGCAAACCTATGGGCTTTCCACTTCTCACTTATCAAGACCGATCGGATAACAAACTGTATC
GTCTTCAGACTCCTCAGAGTCCCTTGGTGAGACCCTCCATGTATGATTATTATGACATGGATAACTATCCAATTG
GGACCAATGCCATCGTTGCTGTGATTCTTACACTGGCTATGATATGGAAGATGCCATGATTGTGAATAAGGCCT
CTTGGGAACGAGGCTTTGCCCATGGAAGTGTCTACAAGTCTGAGTTTCATAGACCTCTCTGAAAAATTAAACAAG
GAGATAGTAGCCTGGTGTGTTGGCATCAAACCTGGTGACCCACGCGTTCTGCAGAAGTTAGATGACGATGGATTGC
CGTTTATAGGAGCAAACTGCAGTACGGAGATCCGTATTACAGCTACCTCAACCTCAACACCGGGGAAAGTTTTG
TGATGTACTATAAGAGTAAAGAAAATTGTGTTGTGGATAACATCAAAGTGTGCAGTAATGACACTGGGAGTGGAA
AATTCAAGTGTGTTTGCATCACTATGAGAGTGCCTCGGAACCCAACTATCGGAGATAAATTTGCCAGTCGCCATG
GGCAGAAGGGCATTTTAAGCAGATTGTGGCCGGCTGAGGACATGCCTTTTACTGAGAGTGGGATGGTCCCAGACA
TTCTGTTCAATCCCCATGGTTTTCCATCCCGCATGACCATTGGGATGTTAATTGAGAGTATGGCCGGGAAGTCTG
CAGCTTTGCATGGTCTCTGCCATGATGCTACACCCTTCATCTTCTCAGAGGAGAACTCGGCCTTAGAATACTTTG
GTGAGATGTTAAAGGCTGCTGGCTACAATTTCTATGGCACCGAGAGGTTATATAGTGGCATCAGTGGGCTAGAAC
TGGAAGCAGACATCTTCATAGGAGTGGTTTATTATCAGCGCTTACGCCATATGGTCTCAGACAAATTTCAAGTAA
GGACAACCTGGAGCCCGAGACAGAGTCACCAACCAGCCTATTGGGGGAAGAAATGTCCAGGGTGAATCCGTTTTG
GGGAGATGGAACGGGATGCGCTTTTAGCTCATGGTACATCTTTCTCCTTCATGACCGCTCTTCAACTGCTCAG
ATCGGTCGGTAGCCCATGTGTGTGAAGTGTGGCAGTTTACTCTCTCCACTGTTGGAGAAGCCACCCCTTCTTGG
TCTGCCATGCGCAACAGAAAATACAACCTGTACTCTGTG**TAGT**CGCAGTGACACTATCGATACTGTTTCTGTGCCT
TATGTTTTTTCGGTATTTTGTAGCTGAACCTGGCAGCTATGAACATCAAAGTGAACTGGATGTTGTTTAACTTGAT
GTTGACCTTTTGGATTAAGGGGACTATCAGATTAAAGCAAATGTAATTTTAATTCAATGAAGATATCATTACCA
GGTACTCTTGAGATTTTCAACGGTGTAGAACTCTCAACCAAGACCTGAAAACCAAGTATGCAAGGTTTCTGA
ATCTCTCTGGTAGATTAACTATTGACAATGATTTTCTGTTATCTTTGTTCAAAAAGTTCATGTCTTCTCAAAAATA
TGAAATATTGATAAATGGAAGAGCATACGGTGACAAGTCTCCTTTCCAACCCAGGTTCCCTACACCCTGCTCTC
AGCAGGCAGTGAGTGTACACACCTGTTAATCCATCTTGAGCAGGACAGTACTATACAAATAGAATGCAAGCTGT
AATGTAATTTTATATTTTCTTATAGCCACGTTGAAGTAAAAACAAACAGGTACAGTGTGTTTTTACCAGCTTTATA
GAAGTACAGTTGTTACATATTTAATGAATACAATTTGATGGGTCTGACTATATGCACACACCTTTGATAACCATCA
CCACAATCAGGGTAATAAACATACCTGTCATCTCCACAAGTTTTCTCCTGCCCTTTGTTTTTGGTTTTTGGTT
GCTGTTGAGTTTTTGTGTTTGTCTTCTGTGTTAAGAACCTTAACTCAAGACCTACCCTCTTAACAAATCTTTAAG
TGCACGATATAGTATTGTTAATTCCAGGCACCATGTTGTACAACAGATCTTTAGACCTTACTTGTCTTGATAAC
TGAAGCTTTATACCTGTTGAACAACCTCTCCATTTCCCTGGCCCCCTAGCAACCACCTTCTACCCTGTTTCTATGA
GTTTGACTATTACAGATATCTCATATAGTGGGATCATGCAATATTTGTCTGTGACTGGCTTATTTCACTTAGCA
TAGTGAAATAAGATTCAATTTTGAAGCCAGGCATGGTGTCTGTGCATCTATAGTCCCTGCTATTTGAGAGGC
TGAGGTGGGAGGATCATTTGAGTGCAGGAGTTCAAGGACAGCCTGGGTAATATAGGAAGACCCTGTCTTGAAGAC
CCTGACCTCAAGTGATCCACCCACCTCGGCCTCCGAAAGTGCTAGGATTACAGGTGTGAGCCACTGTGCCTGGCC
TCCGGTGAGTATTTTATATTTAGTCTACACTTCCATACTTGGCTTTTTTCTGCTTTTATGTTGATCTGCTTTCAT
AGCAGTGTGTAGAGTGCCACTTATGTTTTCTTCTTGTGTACAGTATTTTATTGTATGGATTTACCATCCCCTGT
GTATTTAAGTTGTTCCATTCTTTGGCCATTATAACTTTTTTCTGCAAATATTCTGGTGACTTATCTTTGGCCATT
ATAAACTGTTGATAATAAAAAAAAAAAAAAAAAAAAA

907/6881
FIGURE 844

MNVAIFEDEVFAGVTTHQELFPHSLLSVIANFIPFSDLNQSPRNMYQCQMGKQTMGFPLITYQDRSDNKLYRLQT
PQSPLVRPSMYDYYDMDNYP IGTNAIVAVISYTG YDMEDAMIVNKASWERGFAHG SVYKSEFIDLSEKIKQGDSS
LVFGIKPGDPRVLQKLDDDGLPFIGAKLQYGD PYYSYLNLTGESFVMYYKSKENC VVDNIKVCSNDTGSGKF KC
VCITMRVPRNPTIGDKFASRHGQKGILSRLWPAEDMPFTESGMVPDILFNPHGFPSRMTIGMLIESMAGKSAALH
GLCHDATPFI FSEENSALEYFGEMLK AAGYNFYGTERLYSGISGLELEADIFIGV VYYQRLRHMVSDKFQV RTTG
ARDRV TNQPIGGRNVQGGIRFGEMERDALLAHGTSFLLHDRLFNCSDRSVAHVCEVWQFTLSTVGEATPFLVCHA
QQKIQLYSV

908/6881
FIGURE 845

GAGCTGTCCCCGGTGCCGCCGACCCGGGCCGTGTGCCCGTGGCTCCAGCCGCTGTGCGCTCGATCTCCTCGTCTC
CCGCTCCGCCCTCCCTTTTCCCTGGATGAACTTGCGTCCTTTCTCTTCTCCGCCATGGAATTCTGCTCCGTGCTT
TTAGCCCTCCTGAGCCAAAGAAACCCAGACAACAGATGCCCATACGCAGCGTATAGCAGTAACTCCCCAGCTCG
GTTTCTGTGCCGTAGTTTACAGTATTTAATTTTATATAATATATATTATTTATTATAGCATTTTTGATACCTCAT
ATTCTGTTTACACATCTTGAAAGGCGCTCAGTAGTTCTCTTACTAAACAACCACTACTCCAGAGAATGCGCAACGC
TGATTACCAGTACTACAGCTGCTACCGCCGCTTCTGGTCCTTTGGTGGACTACCTATGGATGCTCATCCTGGGCT
TCATTATTGCATTTGTCTTGGCATTCTCCGTGGGAGCCAATGATGTAGCAAATTCCTTTGGTACAGCTGTGGGCT
CAGGTGTAGTGACCCTGAAGCAAGCCTGCATCCTAGCTAGCATCTTTGAAACAGTGGGCTCTGTCTTACTGGGGG
CGAAAGTGAGCGAAACCATCCGGAAGGGCTTGATTGACGTGGAGATGTACAACCTCGACTCAAGGGCTGCTGATGG
CCGGCTCAGTCAGTGCTATGTTTGGTTCGTCTGTGTGGCAACTCGTGGCTTCGTTTTGAAGCTCCCTATTTCTG
GAACCCATTGTATTGTTGGTGCAACTATTGGTTTCTCCCTCGTGGCAAAGGGGCAGGAGGGTGTCAAGTGGTCTG
AACTGATAAAAAATTGTGATGTCTTGGTTCGTGTCCCACTGCTTTCTGGAATTATGTCTGGAATTTTATTCTTCC
TGGTTCGTGCATTCATCCTCCATAAGGCAGATCCAGTTCCCTAATGGTTTGCAGCTTTGCCAGTTTTCTATGCCT
GCACAGTTGGAATAAACCTCTTTTCCATCATGTATACTGGAGCACCGTTGCTGGGCTTTGACAACTTCCTCTGT
GGGGTACCATCCTCATCTCGGTGGGATGTGCAGTTTTCTGTGCCCTTATCGTCTGGTTCCTTTGTATGTCCAGGA
TGAAGAGAAAAATTGAACGAGAAATAAAGTGTAGTCCTTCTGAAAGCCCTTAATGGAAAAAAGAATAGCTTGA
AAGAAGACCATGAAGAAACAAAGTTGTCTGTTGGTGATATTGAAAACAAGCATCCTGTTTCTGAGGTAGGGCCTG
CCACTGTGCCCTCCAGGCTGTGGTGGAGGAGAGAACAGTCTCATTCAAACCTGGAGATTTGGAGGAAGCTCCAG
AGAGAGAGAGGCTTCCCAGCGTGGACTTGAAAGAGGAAACCAGCATAGATAGCACCGTGAATGGTGCAGTGCAGT
TGCCTAATGGGAACCTTGTCCAGTTCAGTCAAGCCGTGACGAACCAAATAAACTCCAGTGGCCACTACCAGTATC
ACACCGTGCATAAGGATTCCGGCCTGTACAAAGAGCTACTCCATAAATTACATCTTGCCAAGGTGGGAGATTGCA
TGGGAGACTCCGGTGACAAACCTTAAGGCGCAATAATAGCTATACTTCCCTATACCATGGCAATATGTGGCATGC
CTCTGGATTCAATCCGTGCCAAAGAAGGTGAACAGAAGGGCGAAGAAATGGAGAAGCTGACATGGCCTAATGCAG
ACTCCAAGAAGCGAATTCGAATGGACAGTTACACCAGTTACTGCAATGCTGTGTCTGACCTTCACTCAGCATCTG
AGATAGACATGAGTGTCAAGGCAGAGATGGGTCTAGGTGACAGAAAAGGAAGTAATGGCTCTCTAGAAGAATGGT
ATGACCAGGATAAGCCTGAAGTCTCTCTCCTCTTCCAGTTCCCTGCAGATCCTTACAGCCTGCTTTGGGTCATTCCG
CCCATGGTGGCAATGACGTAAGCAATGCCATTGGGCCTCTGGTTGCTTTATATTTGGTTTTATGACACAGGAGATG
TTTCTTCAAAAAGTGGCAACACCAATATGGCTTCTACTCTATGGTGGTGTGGTATCTGTGTTGGTCTGTGGGTTT
GGGGAAGAAGAGTTATCCAGACCATGGGGAAGGATCTGACACCGATCACACCCTCTAGTGGCTTCAGTATTGAAC
TGGCATCTGCCCTCACTGTGGTGATTGCATCAAATATTGGCCTTCCCATCAGTACAACACATTGTAAAGTGGGCT
CTGTTGTGTCTGTGTTGGCTGGCTCCGGTCCAAGAAGGCTGTTGACTGGCGTCTCTTTTCGTAAACATTTTTATGGCCT
GGTTTGTACAGTCCCCATTTCTGGAGTTATCAGTGCTGCCATCATGGCAATCTTCAGATATGTCATCCTCAGAA
TGTTGAAGCTGTTTGAGATTAAAATTTGTGTCAATGTTTGGGACCATCTTAGGTATTCTCTGCCCTGAAGAATG
ATTACAGTGTTAACAGAAGACTGACAAGAGTCTTTTTATTTGGGAGCCAGAGGAGGGAAGTGTTACTTGTGCTAT
AACTGCTTTTGTGCTAAATATGAATTGTCTCAAATTAGCTGTGTAAATAGCCCGGGTTCCACTGGCTCCTGCT
GAGGTCCCCTTTCTTCTGGGCTGTGAATTCCTGTACATATTTCTCTACTTTTTGTATCAGGCTTCAATTCATT
ATGTTTTAATGTTGTCTCTGAAGATGACTTGTGATTTTTTTTTCTTTTTTTTAAACCATGAAGAGCCGTTTGACA
GAGCATGCTCTGCGTTGTTGGTTTCACCAGCTTCTGCCCTCACATGCACAGGGATTTAACAACAAAAATATAACT
ACAACCTCCCTTGTAGTCTCTTATATAAGTAGAGTCCTTGGTACTCTGCCCTCCTGTGCTAGTGGCAGGATCTA
TTGGCATATTCCGGAGCTTCTTAGAGGGATGAGGTTCTTTGAACACAGTGAAAATTTAAATTAGTAACTTTTTTG
CAAGCAGTTTATTGACTGTTATTGCTAAGAAGAAGTAAGAAAGAAAAAGCCTGTTGGCAATCTTGGTTATTTCTT
TAAGATTTCTGGCAGTGTGGGATGGATGAATGAAGTGAATGTGAACTTTGGGCAAGTTAAGTGGGACAGCCTTC
CATGTTCAATTTGTCTACCTCTTAACTGAATAAAAAAGCCTACAGTTTTTTAG

909/6881

FIGURE 846

MATLITSTTAATAASGPLVDYLWMLILGFIIAFVLAFSVGANDVANSFGTAVGSGVVTLKQACILASIFETVGSV
LLGAKVSETIRKGLIDVEMYNSTQGLLMAGSVSAMFGSAVWQLVASFLKLPISGTHCIVGATIGFSLVAKGQEGV
KWSELIKIVMSWFVSPLLSGIMSGILFFLVRAFILHKADVPVNGLRALPVFYACTVGINLFSIMYTGAPLLGFDK
LPLWGTILISVGCAVFCALIVWFFVCPRMKRKIEREIKCSPSESPLEKKNSLKEDHEETKLSVGDIENTKHPVSE
VGPATVPLQAVVEERTVSFKLGDLEEAPERERLPSVDLKEETSIDSTVNGAVQLPNGNLVQFSQAVSNQINSSGH
YQYHTVHKDSGLYKELLHKLHLAKVGDCMGDSGDKPLRRNNSYTSYTMAICGMPLDSFRAKEGEQKGEEMEKLW
PNADSKKRIRMDSYTSYCNAVSDLHSASEIDMSVKAEMGLGDRKGSNGSLEEWYDQDKPEVSLLFQFLQILTACF
GSFAHGGNDVSNAGPLVALYLVYDTGDVSSKVATPIWLLLYGGVGICVGLWVGRRVIQTMGKDLTPITPSSGF
SIELASALTVVIASNIGLPISTTHCKVGSVSVGWLRSKKAVDWRLFRNIFMAWFVTVPISGVISAAIMAFRYV
ILRM

910/6881
FIGURE 847

ACCAACCTCTTCGAGGCACAAGGCACAACAGGCTGCTCTGGGATTCTCTTCAGCCAATCTTCATTGCTCAAGTGT
CTGAAGCAGCC**ATG**GCAGAAGTACCTGAGCTCGCCAGTGAAATGATGGCTTATTACAGTGGCAATGAGGATGACT
TGTTCTTTGAAGCTGATGGCCCTAAACAGATGAAGTGCTCCTTCCAGGACCTGGACCTCTGCCCTCTGGATGGCG
GCATCCAGCTACGAATCTCCGACCACCACTACAGCAAGGGCTTCAGGCAGGCCGCGTCAGTTGTTGTGGCCATGG
ACAAGCTGAGGAAGATGCTGGTTCCTGCCACAGACCTTCCAGGAGAATGACCTGAGCACCTTCTTTCCCTTCA
TCTTTGAAGAAGAACCTATCTTCTTCGACACATGGGATAACGAGGCTTATGTGCACGATGCACCTGTACGATCAC
TGAAGTGACGCTCCGGGACTCACAGCAAAAAAGCTTGGTGATGTCTGGTCCATATGAACTGAAAGCTCTCCACC
TCCAGGGACAGGATATGGAGCAACAAGTGGTGTCTCCATGTCTTTGTACAAGGAGAAGAAAGTAATGACAAAA
TACCTGTGGCCTTGGGCCTCAAGGAAAAGAATCTGTACCTGTCTGCGTGTTGAAAGATGATAAGCCCACTCTAC
AGCTGGAGAGTGTAGATCCCAAAAATTACCCAAAGAAGAAGATGGAAAAGCGATTTGTCTTCAACAAGATAGAAA
TCAATAACAAGCTGGAATTTGAGTCTGCCAGTTCCCCAACTGGTACATCAGCACCTCTCAAGCAGAAAACATGC
CCGTCTTCCTGGGAGGGACCAAAGGCGGCCAGGATATAACTGACTTCACCATGCAATTTGTGTCTTCC**TAA**AGAG
AGCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGGAACAGAAAGGTTTT
TGAGTACGGCTATAGCCTGGACTTTCTGTGTGTCTACACCAATGCCCAACTGCCTGCCTTAGGGTAGTGCTAAGA
GGATCTCCTGTCCATCAGCCAGGACAGTCAGCTCTCTCCTTTCAGGGCCAATCCCCAGCCCTTTTGTGTAGCCAG
GCCTCTCTCACCTCTCCTACTCACTTAAAGCCCGCCTGACAGAAACCACGGCCACATTTGGTTCTAAGAAACCTT
CTGTCATTTCGCTCCACATTCTGATGAGCAACCGCTTCCCTATTTATTTATTTATTTGTTTGTGTTTATTCA
TTGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTAAAAGAGCCTAGTTTTTAAATAGCTATGGAAT
CAATTCAATTTGGACTGGTGTGCTCTCTTTAAATCAAGTCCTTTAATTAAGACTGAAAATATATAAGCTCAGATT
ATTTAAATGGGAATATTTATAAATGAGCAAATATCATACTGTTCAATGGTTCTGAAATAAACTTCTCTGAAG

911/6881
FIGURE 848

MAEVP ELASEMMAYYS GNEDDLFF EADGPKQMKCSFQDL DLCPLDGGIQLRISDHHYSKGFRQAASVVVAMDKLR
KMLVPCPQTFQENDLSTFFPFIFEEEP IFFDTWDNEAYVHDAPVRS LNCTLRDSQQKSLVMSGPYELKALHLQGQ
DMEQQVVF SMSFVQGEESNDKIPVALGLKEKNLYLSCVLKDDKPTLQLESVDPKNYPKKKMEKRFVFNKIEINN K
LEFESAQFPNWIISTSQ AENMPVFLGGTKGGQDITDFTMQFVSS

912/6881

FIGURE 849

AGGCACCATGACTCCTGTGAGGATGCAGCACTCCCTGGCAGGTCAGACCTATGCCGTGCCCCTCATCCAGCCAGA
CCTGCGGTGAGAGGAGGCCGTCCAGCAGATGGCAGATGCCCTGCAGTACCTGCAGAAGGTCTCTGGAGACATCTT
CAGCAGTGAGAGCGGCCTTGCTGCGGCCAAAGAACATGGAAAAGCATGAGTGGGGTGATGTGTGCCTTAAAGCAT
CAGACACTTGGGCCTCGGGCATCAGGAGCCAGCCACAGGGATGTCTGGGGAAATGGCGTTCCATGAGATGCAAGC
ACACAAGAATGCACTTGGCACATCTGGGGAACAGCAGGCAGCTGATATCACTGGGCCCCACCCTGCACCAGGGAGG
ATGGAAGCAGGTAGAGCAGAGCCGGAGCCAGGTGCAGGCCATTGGAGAGAAGGTCTCCTTGGCCCAGGCCAAGAT
TGAGAAGATCAAGGGCAGCAAGAAGGCCATCAAGGTGTTCTCCAGTGCCAAGTACCCTGCTCCAGAGCGCCTGCA
GGAATATGGCTCCATCTTCACGGGCGCCCAGGACCCTGGCCTGCAGAGACGCCCCCGCCACAGGATCCAGAGCAA
GCACCGCCCCCTGGACGAGCGGGCCCTGCAGGAGAAGCTGAAGGACTTTCCTGTGTGCGTGAGCACCAAGCCGGA
GCCCCAGGACGATGCAGAAGAGGGACTTGGGGGTCTTCCCAGCAACATCAGCTCTGTCAGCTCCTTGCTGCTCTT
CAACACCACCTAGAACCT

913/6881
FIGURE 850

AGCGCGGGGAACCGGAGGCTGCAGGATGGTCAAGCTGACGGCGGAGCTGATCGAGCAGGCGGCGCAGTACACCA
ACGCAGTGCGGACCGGGAGCTGGACCTCCGGGGGTATAAAATTCCTCGTCATTGAAAATCTAGGTGCTACGTTAG
ACCAGTTTGATGCTATTGATTTTTCTGACAATGAGATCAGGAACTGGATGGTTTTCTTTGTTGAGAAGACTGA
AAACATTGTTAGGGAACAACAACAGAATATGCCGTATAGGTGAGGGACTTGATCAGGCTCTGCCCTGTCTGACAG
AACTCATTCTCACCAATAATAGGCTCGTGGAAGTGGGTGATCTGGACCCTCTGGCATCTCTCAAATCGCTGACTT
ACCTAAGTATCCTAAGAAATCTGGTAACCAATAAGAAGCATTACAGATTGTATGTGATTTATAAAGTTCCGCAAG
TCAGAGTACTGGATTTCCAGAAAGTGAACTAAAAGTTTTAATCCAGGTGCTGGTTTGCCAACTGACAAAAAGAA
AGGTGGGCCATCGCCAGGGGATGTAGAAACAATCAAGAATGCTATAGCAAATGCTTCAACTCTGGCTGAAGTGGA
GCGGCTGAAGGGGTTGCTGCAGTCTGGTCAGATCCCTGGCAGAGAACGCAAATCGGGGCC

914/6881
FIGURE 851A

GATGGGCTGTGCAAAGGGCGCGGCTGCTGAGGACAGGGCTGTGGCTGGAGAACCTGCTGCTTCCTGAAGCCGAGC
CCCACCCTAAAGGACCGAGAGCACAGGCCATGGGAGAGGAATCGAGTAGGGATGCAGAGCCTGGTGGCACTGTCC
TGAGAGAGGAGGAGGCTGGGCAGGGCCCCGGCGCTGGAGAGGTGCCCTGCATATGGGACCTCTCAGAGGTGCACA
AGAGCTGTGTGCCCAGGTACCCCTGTCTCCTCTCCTCCTCCAGCCCCCAGCCTACTCTCCTAATGGTCTGTGTCT
TTCAGGGATGAGATTTACTGCCAGATCTGCAAGCAGCTCTCGGAGAACTTCAAAACAAGCAGCCTGGCCCCGGGGC
TGGATCCTGCTCAGCCTCTGCCTCGGCTGCTTCCCACCCTCAGAGAGGTTTCATGAAGTATCTACTGAACTTCATC
GGCCÀAGGGCCGGCGACCTACGGCCCCCTTCTGTGCCGAGCGCCTGAGACGCACCTATGCCAATGGGGTGCCTGCG
GAGCCCCCACCTGGCTGGAGCTGCAGGCTGTCAAGTCCAAGAAGCACATCCCCATCCAAGTCATCTTGGCCACT
GGAGAGAGCCTAACCCTCCCCGTGGACTCAGCCTCCACATCTCGGGAAATGTGCATGCACATCGCTCACAAGCAG
GGCCTCAGCGACCACCTGGGCTTCTCCCTCCAGGTCGCCGTGTACGACAAGTTCTGGTCCCTGGGCAGCGGGCGC
GACCACATGATGGATGCCATCGCCCCGTGTGAGCAGATGGCCAGGAGAGGGGCGAGAGCCAGCGCCAGTCACCC
TGGCGCATCTACTTCCGGAAGGAATTCTTACCCCCCTGGCACGACTCCCGGGAGGACCCCTGTCAGCACCGAGCTT
ATTTACCGCCAAGTCCTCCGAGGAGTCTGGTCTGGCGAGTACAGCTTCGAGAAGGAGGAAGAGCTGGTTGAGCTG
CTGGCCCCGGCACTGCTACGTGCAGCTCGGCGCCTCAGCAGAGAGCAAGGCTGTCCAGGAGCTGCTGCCCAGCTGC
ATCCCCCAACAAGCTGTACAGGACCAAGCCCCCAGACAGGTGGGCGAGCCTCGTCACTGCCGCCTGCGCCAAGGCC
CCATACACTCAGAAGCAAGTCACACCCTGGCCGTGCGAGAGCAGGTGGTGGACGCCGCCCGCCTGCAGTGGCCG
CTGCTCTTCTCCCGGCTCTTCAAGTCATCACACTCTCAGGCCCCCGCCTGCCAAGACGCAGCTGATCTTGGCT
GTTAACTGGAAGGGGCTTTGCTTCTGACCAGCAGGAGAAGATGCTGCTGGAACCTCTCTTCCAGAGGTCATG
GGTCTGGCCACCAACAGGGAGGCCAGGGCGGGCAGAGGCTGCTGCTCTCCACGATGCATGAGGAGTACGAGTTT
GTGTACCCAGCAGTGTGGCCATCGCTGAGCTGGTGGCCCTGTTCTGAGGGCCTGAAGGAGAGGTCCATTTTC
GCCATGGCCCCTGACAGGACAGGAAGGCCACAGATGACACCACCCTCCTGGCCTTCAAGAAGGGGGACCTGTTGGTC
CTCACAAGAAGCAGGGGCTGCTGGCCTCTGAGAACTGGACCCTCGGCCAGAACGACAGGACAGGCAAGACGGGG
CTGGTGGCCATGGCCTGCCTCTACACCATCCCCACGGTCACTAAGCCCTCGGCACAGCTGCTGAGCTTGCTTGCC
ATGTACACCAGAGAAGAGGAAGCTGGCGGCTCAGGAGGGGCAGTTCACAGAGCCACGTCCTGAGGAGCCACCCAAG
GAAAAGCTGCACACCCTGGAGGAGTTCTCCTATGAGTTCTTCAGGGCTCCAGAGAAGGACATGGTGAGCATGGCC
GTGCTGCCCCCTGGCCCGTGCCCGTGGCCACCTGTGGGCTATTCTGCGAGCCGCTGCGACAGCCGCTGCTCAAG
CGAGTCCACGCCAACGTCGACCTCTGGGACATCGCCTGCCAGATCTTGTGCGCATCCTCCGGTACATGGGCGAC
TACCCTTCTCGGCAGGCTGGCCACCCTGGAGCTCACCGACCAGATCTTCACACTGGCCCTGCAGCACCCGGCC
CTCCAGGACGAGGTCTACTGCCAGATCCTGAAGCAGCTGACGCACAACCTCCAACAGGCACAGCGAAGAGCGGGGC
TGGCAGCTGCTGTGGCTGTGCACGGGCCTCTTCCCGCCCAGCAAGGGGCTGCTGCCCCATGCCCAGAAGTTTATA
GACACTCGGAGGGGGGAAGCTGCTGGCCCCGACTGCAGCCGCCGAATCCAGAAGGTCTGAGGACGGGGCCCCGG
AAGCAGCCCCCGCACCAGGTGGAGGTGGAGGCCGAGAGCAGAACGTCCTCCGCATCTGCCACAAGATCTACTTC
CCCAATGACACCAGTGAGATGCTGGAGGTGGTTGCCAACACACGGGTGCGGGATGTGTGTGACAGCATTGCCACC
AGGCTGCAGCTGGCCTCCTGGGAGGGCTGCAGCCTCTTCATCAAGATTTTCAGACAAGGTGGGCGGGGCTGGGGCT
GGGCAGACGGTGGGCGGACGGGCAGTGAGCGAGGCCCTAGGTGCTGCCTGTGGGGGCTCAGCCTACCAGGGGCA
CCCATGCTGGACCAGGCTGCACGGCCAGGGCTGCTGGGACAGAGGTAGGTGGGGTCTGGAGCAGAGCCAGCTCC
ACACGCCAATAGCCCACGCACAGCCGACTCCAGCGCAGCACCCAGGCCGTAGGCGGCCACTGGACCAGAACCAG
CAGGTTCTCAGGAGGACAGTCCCCGGAAGCCACCAACTTCCCTGTACCTTCCCCTTCCCAGGTCATCAGCCAG
AAGGAGGGAGACTTCTTCTTTGATTCTTGAGGGAGGTGTCTGACTGGGTGAAGAAGAACAAGCCCCAGAAAGAA
GGGGCCCCCGTGACGCTCCCCCTACCAGGTGTACTTCATGCGGAAATTGTGGCTCAACATATCTCCAGGGAAGGAT
GTGAATGCAGACACCATACTCCATTACCACCAGGAGCTGCCAAGTACCTGCGCGGATTCCACAAGTGTTCGCGG
GAGGATGCCATCCACCTGGCGGGCCTCATCTACAAGGCCAGTTCAACAACGACCGGTCCCAGCTGGCTAGTGTC
CCCAAGATCCTGAGGGAACCTGGTGCCTGAGAACCTCACACGCTGATGTCTCGGAGGAGTGAAAAAGAGCATC
CTTCTAGCCTATGACAAGCATAAGGACAAGACAGTGGAGGAGGCCAAGGTGGCCTTCTGAAGTGGATCTGCCGG
TGGCCACCTTCCGATCCGCCTTCTTCGAGGTGAAGCAAACCTCGGAGCCTTCTTACCCGGACGTCATCCTCATC
GCCATCAACCGACATGGGGTTCTGCTCATCCACCCCAAGACCAAGGACCTGCTCACCACCTATCCCTTCACCAAG
ATCTCCAGCTGGAGCAGCGGCAGCACCTACTTCCACATGGCGCTGGGGAGCCTGGGCCGTGGCAGCCGCTGCTG
TGCGAGACCTCCCTGGGCTATAAGATGGATGACCTGCTGACCTCATATGTGCAGCAGCTCCTGAGTGCCATGAAC

915/6881
FIGURE 851B

AAGCAGCGGGGCTCCAAGGCCCCAGCCCTGGCCAGCACCTAGCAGCGGATGCTGGCGTGTCTGCTCAGGCGCCCT
TCCCGACCTCTAGCCTGGCGGCACCTTCCAGGCCCTCTCAACCCAGGGCCTGTCCTTGGCGGGCAGCCTTCCAT
GCTGCCCCCATACAAAGCCCACCTCAGCCCCGCAGGCGGCCCCCTCTGTCCTGGGCGCTGCCCAGGGAGGCCAAA
AGACGGGCCCAGAATGGGGTCGGGAGTCTCGGACCCCCAGGCTATTGGTGGATGACTGACTGACAGGACACCTCC
CAACCCACCCACCCACCAGAATGTTCAATAAAAACTCCTGGAGCAGGA

916/6881
FIGURE 852

MKYLLNFIGQGPATYGPFCERLRRTYANGVRAEPPTWLELQAVKSKKHIPIQVILATGESLTPVDSASTSREM
CMHIAHKQGLSDHLGFSLQVAVYDKFWSLGSGRDHMDAIARCEQMAQERGESQRQSPWRIYFRKEFFTPWHDSR
EDPVSTELIYRQVLRGVWSGEYSFEKEEELVELLARHCYVQLGASAESKAVQELLPSCIPHKLRYTKPPDRWASL
VTAAACAKAPYTQKQVTPLAVREQVVDAARLQWPLLFSLFEVITLSGPRLPKTQLILAVNWKGLCFDQQEKMLL
ELSFPEVMGLATNREAQGGQRLLLSTMHEEYEFVSPSSVAIAELVALFLEGLKERSIFAMALQDRKATDDTTLLA
FKKGDLLVLTKKQGLLASENWTLGQNDRTGKTGLVPMACLYTIPTVTKPSAQLLSLLAMSPEKRKLAAQEGQFTE
PRPEEPPKEKLHTLEEFSEYEFFRAPEKDMVSMVLPALARARGHLWAYSCPELRQPLLKRVHANVDLWDIACQIFV
AILRYMGDYPSRQAWPTLELTDQIFTLALQHPALQDEVYCQILKQLTHNSNRHSEERGWQLLWLCTGLFPPSKGL
LPHAQKFIDTRRGKLLAPDCSRRIQKVLRTGPRKQPPHQVEVEAAEQNVSRICKIYFPNDTSEMLEVVANTRVR
DVCDSIATRLQLASWEGCSLFIKISDKVGRAGAGQTVGGRAVSEALGAACGGLSLPGAPMLDQAARPGLLGQR

917/6881
FIGURE 853

AAGTGCATGACTCAGGACTGGGTGGGAGGGGGCTGTCCCTGAGGCCCTGGTCTCCCCAGCCAAGTCCTGGCAGG
GGGATGCTGTTCTTCAGGATCCCATGACCTGGGGCTCTTGGGGAGCCCCAGCCCGGAGAGTGACCTGTGGCTTTG
CTGGGGAAAGGGGCTTGAGGGTACAGGGCAGTGTCCAGGATTGCAGTCTCAAATCCGAGGCCCCACAGGGGAGCT
GCCTCTGTGATCGCCATTAAGGCTGTGGCCTGGGGTCTCAGGGCAGCCCAGGAACCAAAAATAGCCTGTAACTTG
TCACTTTGTAAGTCCTGCCCTCCAGACACACTTCCCTTTCTTCTCCCCAAGCCTCTCTTCCCAGTTAGCTCCCCCT
GACTTGGAGTCACCTCTAAGCCTTGGCCCAGGCCCTCTGCAGTGAGATGGAGGGACTCATCCCCCGGAGAGTGG
CATCTGCAGGCCCCTGGCTGCCTGTGGTCACCCCCTAGGGTTCTAGCGGGGCTGCCTCCCATTTTTCTCAGAGC
ATCCCTGCCAGCTGGCTGGTTCTCACTCTCTGTCTTTCTAGGAAAAGAAAGTGGGGAGAGACAGGAACAGGGTCC
GGAGCAGCCCCAGCAGCAGCATTGAGGTGGAGCAATATGTCCGACGCCTTGGCCAACGCCGTGTGCCAGCGCTGC
CAGGCCCCGCTTCTCCCCCGCCGAGCGCATTGTCAACAGCAATGGGGAGCTGTACCATGAGCACTGCTTCGTGTGT
GCCCAGTGCTTCCGGCCCTTCCCCGAGGGGCTCTTCTATGAGTTTGAAGGCCGGAAGTACTGCGAACACGACTTC
CAAATGCTGTTTGCTCCGTGCTGTGGATCCTGCGGTGAGTTCATCATTGGCCGCGTCATCAAGGCCATGAACAAC
AACTGGCACCCGGGCTGCTTCCGCTGCGAGCTGTGTGATGTGGAGCTGGCTGACCTGGGCTTTGTGAAGAATGCC
GGCAGGCATCTCTGCCGGCCTTGCCACAACCGTGAGAAGGCCAAGGGCCTGGGCAAGTACATCTGCCAGCGGTGC
CACCTGGTCATCGACGAGCAGCCCCTCATGTTTCAAGGAGCGACGCCTACCACCCTGACCACTTCAACTGCACCCAC
TGTGGGAAGGAGCTGACAGCCGAGGCCCCGAGCTGAAGGGTGAGCTCTACTGCCTGCCCTGCCATGACAAGATG
GGCGTCCCCATCTGCGGGGCTGCGGCCGGCCCATCGAGGGCCGAGTGGTCAACGCGCTGGGCAAGCAGTGGCAC
GTGGAGCACTTTGTCTGTGCCAAGTGTGAGAAGCCATTCTGGGGCACCGGCACTATGAGAAGAAGGGCCTGGCC
TACTGCGAGACTCACTACAACCAGCTCTTCGGGGACGTCTGCTACAACCTGCAGCCATGTGATTGAAGGCGATGTG
GTGTGCGCCCTCAACAAGGCCTGGTGTGTGAGCTGCTTCTCCTGCTCCACCTGCAACAGCAAGCTCACCCCTGAAG
AACAAGTTTGTGGAGTTCGACATGAAGCCCGTGTGTAAGAGGTGCTACGAGAAGTTCCCGCTGGAGCTGAAGAAG
CGGCTGAAGAAGCTGTCCGAGCTGACCTCCCGCAAGCCCAGCCCAAGGCCACAGACCTCAACTCTGCCTGAAGGC
CCTCTTGCGCAGTGCCCTCTCGGCCCTCCGCCTTCTCCCCTCCTGCTGTCCATGCTTGGCCCCCTCGTCCCCATC
CACCTGTGCCCTCCGCATCTTACCCTCCCTTTCTCTTTCTCCTCATTGCCTTCTCCCTTCTGTTCCCTCATCTCTG
CCTTCCCCATGTCTCTCCTCTCCTTGGCCGTGGCTTCTGTCTGTGAGGAGGCAGGAGCTGGGGAGTGGGAGCCTA
TGACCCACAGTCTGACAGCCATGTCCACCTGTGCCCACAGCTTCCGCCCACAGACCTCCAGGGACAGGAGCAAAAT
TGCACCACAGCTCCCCGCTGGCCTGGCCCTCCCCAGGCGGCTCAGTGGCTCATGCTGTCTGTGAGAGCCCCCTG
CCCCAGAGCGGCCCCACTAAGCGCATGTGGCTCCTGGGCTACCCACAGCCAGGGCAGCCTGCTGGAGCCACAGGG
CCAGGGCCATGCAGATGGAGGCCTCTGGGAGCCACCTCCAATCCCTCACCCTCACTCAACCAGTGGCACAGTGT
CCTTGTGCCCACACTGAGCCAGCAAGTCCTGCTGTCCACACCCACAAGCTACCTGGAGGGACAGGACCCACCTCC
ATCCTTTCGGAAGGCCTTCTTGGAATCCACCTTGGCCTCCGCCCTCGGTTCCGCCCCGCCCTCTCCCCCGACC
TTGGGGCTTGTGTGAGCCCTTGGGTGGGGCCAGGAGGAGGTGATGGCGTCAGAGGAGGTGTGGTCAGAGGTGAC
TTGTTCCACCTCCAGGGAGGACGCTTCGTCTTCGGCCAGCGCAGACCTGGTGTGTTGTTGTTGGGCTCACGCTT
GCACAATGAAGGCTTGTTCACAC

918/6881
FIGURE 854

CCGACACCCACGGGCGGAGATCACCTGCTGCCCCGCAGACCCCTGTCCCTTCCTCCCGGACCAGCAGCTAGAGGA
TGTCCAAACGGAGTTGGTGGGCTGGATCCAGAAAGCCCCCAAGAGAGATGCTGAAACTCTCAGGCTCTGACTCCA
GCCAAAGCATGAATGGCCTTGAAGTGGCTCCCCCAGGTCTGATCACCAACTTCTCCCTGGCCACGGCAGAGCAAT
GTGGCCAGGAGACGCCACTGGAGAACATGCTGTTGCGCTCCTTCTACCTTCTGGATTTTATCCTGGCTTTAGTTG
GCAATACCCTGGCTCTGTGGCTTTTCATCCGAGACCACAAGTCCGGGACCCCGGCCAACGTGTTCTGATGCATC
TGGCCGTGGCCGACTTGTCGTGCGTGCTGGTCCTGCCCCACCCGCTGGTCTACCACTTCTCTGGGAACCACTGGC
CATTTGGGGAAAATCGCATGCCGTCTCACCGGCTTCCTCTTCTACCTCAACATGTACGCCAGCATCTACTTCCTCA
CCTGCATCAGCGCCGACCGTTTCCTGGCCATTGTGCACCCGGTCAAGTCCCTCAAGTCCGCGAGGCCCCCTCTACG
CACACCTGGCCTGTGCCTTCCTGTGGGTGGTGGTGGCTGTGGCCATGGCCCCGCTGCTGGTGAGCCACAGACCG
TGCAGACCAACCACACGGTGGTCTGCCTGCAGCTGTACCGGGAGAAGGCCTCCCACCATGCCCTGGTGTCCCTGG
CAGTGGCCTTTCACCTTCCCGTTTCATCACCACGGTCACCTGCTACCTGCTGATCATCCGCAGCCTGCGGCAGGGCC
TGCGTGTGGAGAAGCGCCTCAAGACCAAGGCAGTGCGCATGATCGCCATAGTGCTGGCCATCTTCCTGGTCTGCT
TCGTGCCCTACCACGTCAACCGCTCCGTCTACGTGCTGCACTACCGCAGCCATGGGGCCTCCTGCGCCACCCAGC
GCATCCTGGCCCTGGCAAACCGCATCACCTCCTGCCTCACCAGCCTCAACGGGGCACTCGACCCCATCATGTATT
TCTTCGTGGCTGAGAAGTTCGCGCCACGCCCTGTGCAACTTGCTCTGTGGCAAAGGCTCAAGGGCCCGCCCCCA
GCTTCGAAGGGAAAACCAACGAGAGCTCGCTGAGTGCCAAGTCAGAGCTGTGAGCGGGGGGCGCCGTCCAGGCCG
AGCGCAGACTGTTTAGGACTCAGCAGACCCAGCAAGAGGCATCTGCCCTTTCCTCCAGCCACCTCCCCAGCAAGCA
ACCTGAAATCTCAGCAGATGCCACCATTCTCTAGATCGCCTAGTCTCAACCCATAAAAAGGAAGAACTGACAA
AGGGGATCCATCGGCCACCCCTCTGCAGGGGCTTGTGATGGCTACAATGGCTCCTAGACACTCAACGACTTCATC
TGTGGCAGGGAGAGAGGAGGCCGGAAGAACAACCCCTGAACAATGGAGGCCTTCTTTCCCGCTAGGCTCCCAGC
CTCCTTCCCGCTACAGAATCGCTCATCGGCGAGGCTCAGCAGAAAGACCCTGAAGGCAGGCTGCAAATGACCCAG
AAGAGGGACCTGGGAGTCCTGGTGGGGACGGGGAGGGAGTCTCAATACTCCTTTGCAGCGCAAGGTACTCTGAGT
CCCCCTCTGTAGTGCCTCTGCCAGACACACACTGCCTGAGTTGAAGAGACACAGGCCACACATTTAGGCTGGTTG
CCAGCGGACGTACGACTCACGGCCTGCGGGGACTCAGCACAGCTCTGGATTCTGGATCTCTCCTGCTGTAAACC
CACGCACAAGCCTGCAACCCCCAGAGCTCTTTGACAGGCTCCCAGGCCTCCCAGTCCTGGACAAGCATGTGCAGT
CACGGGAGCTCAGCTCAGGCCAGGGCTGGGCTGTGCACCTGCCTCCCAGTACCCAGACCCACTTCCTCCAGAGA
GGCCTCTCTCCGCTGAGCTATTTCCCTTGCTAGTGTGCAGATATTTCCCTAACATGTCCTTTTTTTGTATTTGTT
TGTACGGACCATAAAATATAACTGTAGCTTTAAGACTAAAAAAAAA

919/6881
FIGURE 855

MSKRSWWAGSRKPPREMLKLSGSDSSQSMNGLEVAPPGLITNFSLATAEQCGQETPLENMLFASFYLLDFILALV
GNTLALWLFIRDHKSGTPANVFLMHLAVADLSCVLVLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFL
TCISADRFLAIVHPVKSLKLRRLYLAHLACAFWVVAVAMAPLLVSPQTVQTNHTVVCLQLYREKASHHALVSL
AVAFTFPFITTVTCTYLLIIRSLRQGLRVEKRLKTKAVRMIAIVLAIFLVCFVPYHVNRSVYVLHYRSHGASCATQ
RILALANRITSCLTSLNGALDPIMYFFVAEKFRHALCNLLCGKRLKGPPPSFEGKTNESSLSAKSEL

920/6881
FIGURE 856A

GGGGAAGATGGCGGCTGCTCCTTTGGAGGAGCGGGATTGAGAGGATCGGGGTGGGGAGACCAAACAAGAGAGACA
TTTCTGGCTCTGAAGGCGAACGCTTCGCTGGCCATTTAGGAGCTCTGCTCAAAGCCAGACGTATCCTAGAAGGAA
AACATCACCATGGCTACAGAAATTGGTTCTCCTCCTCGTTTTTTTCCATATGCCAAGGTTCCAGCACCAGGCACCT
CGACAGCTGTTTTATAAGCGACCTGATTTTGCACAACAGCAAGCAATGCAACAGCTTACTTTTGATGGAAAACGA
ATGAGAAAAGCTGTGAACCGAAAAACCATAGACTACAATCCATCTGTAATTAAGTATTTGGAGAACAGAATATGG
CAAAGAGACCAGAGAGATATGCGGGCAATTCAGCCTGATGCAGGTTATTACAATGATCTGGTCCCACCTATAGGA
ATGTTGAATAATCCTATGAATGCAGTAACAACAAAATTTGTTCCGACATCAACAAATAAAGTAAAGTGTCCTGTA
TTTGTGTTAGGTGGACTCCAGAAGGAAGACGCTTGGTCACTGGAGCTTCTAGTGGGGAGTTTACCCTGTGGAAT
GGACTCACTTTCAATTTTGAACAATATTACAGGCTCACGACAGCCAGTGAGGGCCATGACGTGGTCACATAAT
GACATGTGGATGTTGACAGCAGACCACGGAGGATATGTGAAATATTGGCAGTCGAACATGAACAACGTCAAGATG
TTCCAGGCACATAAGGAGGCGATTAGAGAGGCCAGTTTCTCACCACGGATAATAAATTTGCTACATGCTCTGAT
GACGGCACTGTTAGAATCTGGGACTTTCTTCGTTGCCATGAGGAAAGAATTCTCCGAGGGCATGGTGCTGATGTG
AAATGTGTAGACTGGCATCCAACCAAAGGGTTAGTTGTTTCAGGAAGTAAAGATAGTCAACAGCCAATCAAGTTC
TGGGATCCCAAGACTGGGCAGAGTCTTGCAACACTTCATGCCCATAAAAACACAGTAATGGAAAGTGAAATTAAC
CTCAATGGCAATTGGCTACTCACAGCATCACGTGATCATCTCTGTAAACTTTTTTGATATCAGAAAACCTAAAAGAA
GAGCTTCAAGTCTTCCGAGGTCATAAGAAAAGAGCCACAGCTGTGGCCTGGCATCCTGTTTCATGAAGGACTTTTT
GCCAGTGGAGGGTCTGATGGTTCTTTGTTATTCTGGCATGTTGGGGTAGAGAAGGAAGTGGGTGGGATGGAGATG
GCTCACGAAGGGATGATCTGGAGTCTGGCTTGGCATCCTCTTGGGCATATTCTCTGCTCAGGCTCAAATGACCAT
ACTAGCAAATTTCTGGACTCGAAACCGACCAGGTGATAAATGCGAGATCGATATAATCTAAACCTTTTACCTGGA
ATGTCTGAAGATGGAGTAGAATATGATGACCTCGAACCTAATAGCCTGGCAGTAATTCCAGGAATGGGAATACCA
GAACAATAAATTTAGCTATGGAACAAGAACAGATGGGGAAAGATGAATCAAATGAAATTGAAATGACAATTCCA
GGTTTAGAATTGGGGAATGGAGGAAGTGATGCAAAAGGATCAGAAAAAGTACCTCAGAAGAAAGTCTCTTATGCA
AAACCCATTCCTGCTCAGTTCCAGCAGGCTTGGATGCAAAATAAAGTTCCAATTCTGCTCCAAATGAGGTGCTG
AATGACAGAAAAAGAAGACATTAAATTGGAAGAGAAGAAAAAACACAAGCAGAAATTGAGCAAGAAATGGCTACA
TTACAATATACTAACCACAACTTCTGGAGCAACTTAAATTTGAAAGACTTGACAGAAACAAGTTGAGCAAATTT
CAGCCTCCTCCCTCATCTGGCACCCCTCTCCTCGGACCCACGCTTTTCCAGGACAAGGTCCAATGTCTCAGATT
CCTCAAGGTTTTTCAACAGCCCCATCCATCTCAGCAGATGCCAATGAACATGGCTCAAATGGGGCCTCCAGGTCCA
CAGGGACAGTTTTAGGCCTCCTGGACCCAGGGACAAATGGGACCACAAGGTCTCTCACTGCATCAGGGAGGTGGG
GGGCCACAAGGATTCATGGGACCACAGGGGCCCCAGGGCCCGCCCCAGGGGTTGCCACGGCCTCAGGACATGCAT
GGGCCCCAAGGAATGCAGAGGCATCCTGGACCTCATGGCCCTTTGGGACCTCAAGGGCCACCTGGACCACAAGGT
AGTTCTGGTCTCAAGGTTCATATGGGTCTCAGGGTCCACCTGGCCACAGGGTCACATAGGCCCCCAAGGCCCG
CCTGGCCCTCAGGGTCACTTGGGCCCACAGGGGCTCCGGGTACTCAAGGTATGCAAGGGACCACCTGGTCCCAGA
GGAATGCAAGGGCCTCCTCATCTCATGGGATCCAAGGCGGACCAGGGTCTCAAGGGATCCAAGGTCTGTGTCT
CAGGGACCTCTGATGGGATTGAATCCAAGAGGAATGCAGGGGCCCTCAGGGCCCCGGGAGAACAGGGTCTGTCT
CCCCAAGGGATGATTATGGGCCACCCGCTCAAGAGATGAGAGGACCTCACCTCCAGGTGGACTACTGGGACAC
GGCCCTCAGGAAATGAGAGGTCTCAGGAGATCCGAGGCATGCAGGGGCCCTCCACCCCAAGGATCAATGCTGGGA
CCTCCCCAGGAATTGCGAGGGCCTCCAGGCTCACAAAGTCAGCAGGGGCCCGCCCCAGGGCTCTTTAGGACCTCCA
CCCCAGGGTGGCATGCAAGGACCCCCCGGACCTCAGGGACAGCAGAACCAGCAAGAGGGCCACATCCATCTCAA
GGGCCAATAACCATTCAGCAACAGAAAACGCCTCTGCTAGGTGATGGGGCCCCGGGCCCCCTTCAACCAGGAAGGA
CAGAGCACAGGCCCCCACCCTGATACCAGGCCTAGGGCAGCAGGGAGCACAAGGTTCGATTCCCCCTCTGAAC
CCCGGACAAGGACCTGGCCCCAACAAAGTTTCAGAAGAGGAGCCCCGCGGAGGCATGAGGGCCGTGCTCCCCCA
GAGGAAGGGATGGTTTTCTTGGTCTCTGAAGACTTTGGTCCAGAGGAGAATTTTGATGCTTCTGAGGAAGCGGCC
GAGGACGAGATCTCAGAGGTGAGGTGCGGGTACCCACAGGAGGAAGGAAGGGTTTACTTCCCACTCTTGACG
AGTTCCCTCGCTTTGAAGGAGGGCGGAAGCCAGATTCTTGGGATGGAAACAGAGAGCCTGGGCCAGGTCTATGAAC
ATTTTCGTGATACTCCCCGCTGATCATCCCCCTCACGACGGTCATTCCCAGCCAGCAGAGAACGCTCCTCTT
CTCTCCAAGGCATGGACATGGCATCCCTACCTCCCCGAAAGCGCCCCCTGGCATGATGGCCAGGCACCTCTGAGC
ACAGAGAGATGGAGGCCCCAGGAGGCCCTTCTGAAGACCGAGGAGGCAAAGGCCGAGGGGGCCAGGACCTGCTC
AGAGAGTGCCCAATCTGGGCGTTCCAGCTCCTTAGACGGAGAGCACCACGATGGATACCACAGAGATGAACCTT

921/6881
FIGURE 856B

TTGGGGGCCCTCCAGGCAGTGGCACCCCTTCTCGAGGGGGCCGGAGTGGCAGTAACTGGGGTAGAGGGAGTAACA
TGAACCTCTGGCCCGCCGAGGCGAGGAGCTTCACGGGGTGGTGGAAAGGGTCGGTAGAAGCTGGAACCTGAGTACCC
TGAGGCCTCTCTGGACAGTATGTAAGAACTTCTTGTGGACTCACCAAGAGAAAACAAAAGGAAGCCTGCACCATTG
TAGCCCTGAACCTTTTTCTGGGCACCTGAATCCCAGGAACCCCTCAATGAGGTCTTCAAGATGAAGAGACTGCTGC
CAGCTACCAGCCTGGCTGGCCCTGTCCTGTCCACCCTCATTGCCCCAACTCCCATGTTGTTTTGTGAAGATAAAA
GCTGGGATCTTTTTCTTTTTTTTAAAGTCTCACAAGACATGGGGCATCTCCACAAATTTAAGTTCCTGTCCATTG
GAAATTTGTTTCTATGTGTACAGTTTGTGAGAGAAAAACAAAGTTTTTGTATGAATACAGAATGTGATTTACGCA
AGAATTGACAGAAAAGTAGTTGTGAAGTGCTTGCCCTTAAGGAAACCTTTGGTTTCCATCGCATCCCATCTGCCAA
GGAATGCACGGTTGTTGCTGATGTTTCATGAGCATATTAACCACTAGGTTATCTAAATTAATCTCAGCTGTGAACT
TTGTGTTTTTCAACACATTCTGTACACCATTTTTGTGACAGAAAAATACTTGAAAATTATTCTAATGTAGTTTG
TAGTAGGTTCAAATTTTTATTTCAGACATGCTCTGACAGATGGAAAAATTGTAAGAGAAAAATGCAATCTTC
TGGATGTCCAACGAGGGAGCTTCCCCTTGGAAGCATCTCCTAAGAATCACAGTTTAGGTTTGAATCGCCTTGTTA
TGATGAGGAGAGGAACTTGATGTTAGTCAGAAATAAAGTCACATGCCCTTTAGATAACTTGAAATCACACATGGA
GTTGATAAGGAATGGACCAAAATAGGTCCTCAAACAATTTTGCAACACTTAATTAAGTTTTCTCTCTTCTCTT
CCATACTATGTGGAAATACCAGTGTTACGGCAGGGCGTACTTCTAACTCACAGTAAGCCAGATAGATCTTGTCCA
TGGCAAATTCCTTGTTTAAAATAAACATAACCATTTAGCCAGTTTGGATTGGAAGCCAAAAATTCAGTTTGTAT
ATACCCCATGATACTTTCTATACTGACCTTTATTTTGGTTTTACATGGAAGCTTTTATTAAAGGACTGTCTTAT
GGCCACCTTAACATTTTATTACATTGGCAGCTTCAGTTTTGGCATCAGTCAAATTTATTTGGCAAATTTAGTGGT
GCTGGAAGTTTCTTTTTTCTTTTCTTTTTTGACAGAGTCTTGCTCTGTCACCCAGCCAGGAGTGCAGTGGTGC
AATCACGGCTCACTTCAGCTTTGACCCTGCCTCAGCCTCCCTAGTAGCTAGGACTACAGGCATATGCCACCATGC
CCAGCTAATTTTTTGTGTGTGTGTTTTTTGTAGAGATGGAGTTTACCACCTTTGTCTATGCTGGTTTCAAACCTC
TGGGCTCAAGCGGTCCACCTGCTGTGGCCTCCCAAAGTGCTGGGATTGCAGATCTGAGCCACAGTACCTGGCCGC
TGGTGCTGGAAGTTTCAATGGTTGCTTAGAAAAGGCATACTGATATAGTTTAAACAGGATATGAAAATTTAACTGG
TTCTCTATGAATGTAAAAAACAGCAAAAGCTAATTGATTTCTGTGGAGTGAGAAAATGTCAGCCATATACACTGC
TTTTCAGTGTTAGAATCTAGAGACTATTTTTTTTTTAACTTTGAAATTACAGCTTATTTAATCAGCGCTCCACCA
TAAACATGCTATTAGGAGGCTCAAGATTGCTTTAGGTTATGGGTATTTCTTCACTCACCCCCAACTGGTATAGCT
TAAAGAGAGAGAACTGTAATCAAATTTTCATGAAGCTAAAACCGGATCCAGAGACCAAACCCATATCAAGATTAG
ACTTTTTTTTCCCTGAGATTCTAGTGAAAAATTTTCATTATTTGGGCTTTAACTTTAGAAACATAGTATCTCAG
TAAGCAGATAACCAGATCACATTTAAAAATTTTCATTTTACCTTGAAGCTCTACTGGACTTGACAGATCACATT
TGAGAGTGAATTCATTTAAACAATAAACCTCTACATTATACTTAT

922/6881
FIGURE 857

AGAACATCCAGTCACGGATAAAAATGAGCTGGTTTCTGAGAGGCCAACTGGCCGAGCAGGCTGAGCAATATGATGA
CATGGCAGCCTGCATGAAGTCTGTAAGTCAAGGAGCTGAATTATCCAATGAGGAGAGGAATCTTCTCTCAGT
TGCTTATAAAAATGTTGTAGGAGCCCGTAAGTCATCTTGGAGGGTCGTCTCAAGTATTGAACAAAAACGGAAGG
TGCTGAGAAAAACAGCAGATGGCTCGAGAACACAGAGAGAAAAATTGAGACGGAGCTAAGAGATATCTGTAATGA
TGTATTGTCTCTTTTGGAAAAGTTCTTGATCCCCAATGCTTCACAAGCAGAGAGCAAAGTCTTCTATTTGAAAAAT
GAAAGGAGATTACTACCGTTACTTGACTGAGGTTACTGCTGGTGATGACAAGATAGGGATTGTGGATCAGTCACA
ACAAGCATACCAAGAAGCTTTTGAATCAGCAAAAAAGAAATGCAACCAACACATCCTGTCTCAGATTGGGTCTGGC
CCTTAACTTCTGTGTTCTATTATGAGATTCTGAACTCCCCAGAGAAAAGCCTGCTGTCTTGCAAAGACCGCTTTTG
ATGAAGCCATTGCTGAACTTGATACATTAAGTGAAGAGTCATACAAAAGACAGCATGCTAATAATGCAATTACTGA
GAGACAACCTTGACATTGTGGACATCGGATACCCAAGGAGACGAAGCTGAAGCAGGAGAAGGAGGGGAAAAATTAAC
CGGCCTTCCAACCTTTTGTCTGCCTCATTCTAAAATTTACACAGTAGACCATTTGTCTCATCCATGCTGTCCACAAA
TAGTTTTTTGTTTATGATTTATGACAGGTTTTATGTTACTTCTATTTGGATTTCTATATTTCCCATGTGGTTTTTA
TGTTTAATATTAAGGGAGTAGAGCCAGTCAACATTTAGGGAGGTATCTGTTTTCATCTTGAGGTGGCCAATATTG
GGATGTGGAATTTTTATACAAGTTATAAATGTTTGGCATAGTACTTTTGGTACATTGTGGCTTCACAAGGGCCAG
TGTAAGTCTGCTTCCATGTCTAAGCAAAGAAAAGTGCCTACATATTGGTTTGTCTGGTGGAGAATAAAAGGGAT
CATTGATTCCAGTCAGAGGTGTAGTAATTGTGGGTACTTTTAAGGTTTGGAGCACTTTACAAGGCTGTGGTAGAA
ACATACCCCATGGATACCACATGTTAAACCATGTATATCTGTGGAATACTCAGTCTCATTGTGCACACCTTTGAC
TACAGCTGCAGAAGTTTCTTTTAGATAAAGTTGTGACCCATTTTACTCTGGATAAGGGCAGAAACAGTTCACAT
TCCATTATTTGTAAAGTTACCTGCTGTTAGCTTTTATTATTTTGTCTACACTCATTTTATTTGTATTTAAATGTT
TTAGGCAACCTAAGAACAAATGTAAGTAAAGATGCAGTAAAAATGAATTGCTTGGTATTGCTTTCATGTA
TATCAAGCACAGCAGTAAAAACAAAACCCATGTATTTAACTTTTTTTTAGGTTTTTTGCTTTTGTGATTTTTTTT
TGATACTTGCCTAACATGCATGTGCTGTAAAAATAGTTAACAAGGAAATAACTTGAGATGATGGCTAGCTTTGTT
TAATGTCTTATGAAATGTTTCGTGGATAATCCAAGCATAATTGTTAAGAACACGTGTATTAAATTCATGTAAGTGG
AATAAAAGTTTTATGAATGGACTTTTCACTACTTTCTCTACAGCTTTTCGTGTAAATTAGTCTTTTGGTTCTGA
AATTTCTCTAAAGGAAATTTGTACATTTTTGAAATTTATTCCTTATTCCCTCTTGGCAGCTAATGGGCTTTTAGTA
AGTTTAAACAAAAAATTTATCATAACAACAAAAATACTACTAATAATACTACTGTTTCCATGTCCCATGATCCC
GTCTCTTCTCCCTCCCTGAAAAAATGAGTTCTATTTTTTCTGGGAGAGGGGAGATTAAATTGAAAAAATG
TTAATATGTTCCATTTAAATTTTGGTATATGGCATTCTTAACTTAAGAAGCCACAATGTTCTTGGCCCATCAT
GACAATGGGTAGCATTAAGTATAAGTTTGTGCTTCCAAATCACTTTTCGGTTTTTAAGAATTTCTTGATACTCC
TACAGCCTGCCTTCGATTTTGTATCCTTTATTCTGTTTGTGAGGTGCACAAGATTACCTTCCTTTTTTAGCCATCT
GTCTTGTACCAACCATTCCTACTTGGTGGCCATGTACTTGGAAAAAGGCCGCATGATCTTTCTGGCTCCACTCA
ATGTCTAAGGCACCTGCTTCCTTTGCTTGCATCCACAGACTATTTCCCTCATCCTATTTACTGCAGCAATTGT
CTCCTTAGTTGACGAGATTGTGTTTATCTCCCTTTAAACCCCTACCTATCCTGAATGATCTGTCTATTGTCTGCCT
TTAAATCCTTCCTCTTTCTTCTTCTCTATTCTCTAAATAATGATGGGGCTAAATTATACCCAAAGCTCACTTT
ACAAAATATTTCTCAGTACTTTGCAGAAAACACCAAAACAAAAATGCCATTTTAAAGAGGTGTATTTTTCTTT
TAGAATGTTAGAATGTAAGCTCCTCAAAGCAGGGACAATGTTTTCCGTATGTTCTACTGTGCCTAGTATACTGT
AAATGCTCAATAAATACTGATGATGGGAGGCAGTGAGTCTTGATGATAAGGGTGAGAAACCGAAATCCC

923/6881
FIGURE 858

GATGACATGGCAGCCTGCATGAAGTCTGTAACTAAGCAAGGAGCTGAATTATCCAATGAGGAGAGGAATCTTCTC
TCAGTTGCTTATAAAAAATGTTGTAGGAGCCCGTAAGTCATCTTGGAGGGTCGTCTCAAGTATTGAACAAAAAACG
GAAGGTGCTGAGAAAAACAGCAGATGGCTCGAGAACACAGAGAGAAAATTGAGACGGAGCTAAGAGATATCTGT
AATGATGTATTGTCTCTTTTGAAAAGTTCTTGATCCCCAATGCTTCACAAGCAGAGAGCAAAGTCTTCTATTTG
AAAATGAAAGGAGATTACTACCGTTACTTGACTGAGGTACTGCTGGTGATGACAAGATAGGGATTGTGGATCAG
TCACAACAAGCATACCAAGAAGCTTTTGAAATCAGCAAAAAAGAAATGCAACCAACACATCCTGTCAGATTGGGT
CTGGCCCTTAACTTCTGTGTTCTATTATGAGATTCTGAACTCCCCAGAGAAAGCCTGCTGTCTTGCAAAGACCGC
TTTTGATGAAGCCATTGCTGAACTTGATACATTAAGTGAAGAGTCATACAAAGACAGCATGCTAATAATGCAATT
ACTGAGAGACAACCTTGACAATGTGGTTTTTATGTTTAATATTAAGGGAGTAGAGCCAGTCAACATTTAGGGAGGT
ATCTGTTTTTCATCTTGAGGTGGCCAATATTGGGATGTGGAATTTTTATACAAGTTATAAATGTTTGGCATAGTAC
TTTTG

924/6881
FIGURE 859A

TTTTCGGCGCCGTGGCGGAATGGCGGCTTCCATCTCTGAGGCGAGCGACGCTATGGATCCACAGTGGTTTGCTA
AGAAGGCCATTTTCAACTCTCCACTGGAGGCTGCTATGGCGTTCCCTCACCTGCAGCAGCCCAGCTTTCTACTGG
CTAGCCTGAAAGCTGACTCTATAAATAAGCCCTTTGCACAGCAGTGCCAAGACTTGGTTAAAGTCATTGAGGACT
TTCCAGCAAAGGAGCTGCACACCATCTTCCCATGGCTGGTAGAAAGCATTTTGGCAGCCTAGATGGTGTCTCTCG
TTGGCTGGAACCTCCGCTGCTTACAGGGGCGCGTGAATCCTGTGGAGTACAGCATCGTGATGGAATTTCTCGACC
CTGGTGGCCCAATGATGAAGTTGGTTTATAAGCTTCAAGCTGAAGACTATAAGTTCGACTTTCCTGTCTCCTACT
TGCCTGGTCTGTGAAGGCGTCCATCCAGGAGTGCATCCTCCCTGACAGTCCTCTGTACCACAACAAGGTCCAGT
TCACCCCTACTGGGGGCTTGGTCTGAAGTTGGCCCTGAATCCGTTTCGAGTATTACATATTCTTCTTTGCCTTGA
GCCTCATCACTCAGAAAGCCACTTCCCTGTGTCCCTCCACGTCCGTACTTCAGACTGTGCCTATTTTCATCCTGGTGG
ACAGGTACCTGTCTATGGTTCCCTGCCCACCGAAGGCAGTGTGCCCCCACCCTCTCCTCCAGCCCAGGGGGGACCA
GCCCCCTACACACCTCCCAGGACACCAGCCATACCCTTTGCTTCCTATGGCCTCCACCACACTAGCCTCCTAAAGC
GACACATCTCTCATCAGACGCTCTGTGAATGCAGACCCCGCCTCCCACGAGATCTGGAGGTGAGAACTCTGTCTCC
AGGTTTTTTGTTGAAATGTGGCTTCATCACTATTCCCTTGAGATGTATCAAAAAATGCAGTCCCCTCATGCCAAGG
AGTCGTTTACGCCTACTGAGGAGCATGTGTTGGTGGTGCGCCTGCTGCTGAAGCACCTGCACGCCTTTGCCAACA
GCCTGAAGCCAGAGCAGGCCTCACCTCCGCCACTCCCACGCCACCAGCCCCCTGGAGGAGTTCAAACGGGCTG
CTGTCCCGAGGTTTCGTCCAGCAGAACTCTACCTCTTCTTGCAGCATTGCTTTGGCCACTGGCCCCCTGGACGCAT
CGTTTCAGAGCTGTCTTGAGATGTGGCTGAGCTACCTGCAGCCGTGGCGGTACGCGCCTGACAAGCAGGCTCCGG
GCAGCGACTCCCAGCCCCGGTGTGTGTCGGAGAAATGGGCACCCTTTGTCCAGGAGAACCTGCTGATGTACACCA
AGTTGTTTGTGGGCTTTCTGAACGCGCGCTCCGCACAGACCTGGTCAGCCCCAAGCACGCGCTCATGGTGTTC
GAGTGGCCAAAGTCTTTGCCAGCCCAACCTGGCTGAGATGATTAGAAAAGGTGAGCAGCTATTCTGGAGCCAG
AGCTGGTCATCCCCCACCAGCCAGCACCGACTCTTACGGCCCCCACATTCACTGGGAGCTTCTGTACCCCTGGC
CACCAGCGTCACTGATGCCTCCTTCAAGGTGAAGAGCCACGTCTACAGCCTGGAGGGCCAGGACTGCAAGTACA
CCCCGATGTTTGGGCCCCGAGGCCCGCACCTGGTCTGCGCCTCGCTCAGCTCATCACACAGGCCAAACACACAG
CCAAGTCCATCTCCGACCAGTGTGCGGAGAGCCCGCTGGCCACTCCTTCTCTCATGGCTGGGCTTTAGCTCCA
TGGACACCAATGGCTCCTACACAGCCAACGACCTGGACGAGATGGGGCAAGACAGTGTCCGGAAGACAGATGAAT
ACCTGGAGAAGGCCCTGGAGTACCTGCGCCAGATATTCCGGCTCAGCGAAGCGCAGCTCAGGCAGTTCACACTCG
CCTTGGGCACCAACCAGGATGAGAATGGA AAAAAGCAACTCCCCGACTGCATCGTGGGTGAGGACGGAAGTCAATCC
TTACGCCCTGGGGCGGTACCAGATCATCAATGGGCTGCGAAGGTTTGAAATTGAGTACCAGGGGGACCCGGAGC
TGCAGCCCATCCGGAGCTATGAGATCGCCAGCTTGGTCCGCACACTCTTTAGGCTGTCTGTCTGCCATCAACCACA
GATTTGCAGGACAGATGGCGGCTCTGTGTTCCCGGGATGACTTCTCCTCGGCAGCTTCTGTCTGCTACCACCTCACAG
AACCTGGGCTGGCCAGCAGGCACCTGCTGAGCCCTGTGGGGCGGAGGCAGGTGGCCGGCCACACCCGCGGCCCA
GGCTCAGCCTGCGCTTCTCTGGGCAGTTACCGGACGCTGGTCTCGCTGCTGCTGGCCTTCTCTCGTGGCCTCTCTGT
TCTGCGTGGGGCCCTCCCATGCACGCTGCTGCTCACCTGGGCTATGTCTCTACGCCTCTGCCATGACACTGC
TGACCGAGCGGGGAAGCTGCACCAGCCCTGAAGGTGTGAGCTGCCTTCAGAGCAGGCTGGAGGGATTTGCCACA
CAGCCCCACCCTTGGGCTGAGAGGACCTGGGAAGCCCTCCAGGAGGGAACACGGTCATCCTCGGGCTTCTGGAG
CGGGGTTCTGTCAGCCGCAGAGGCATCTGGAGGAAACGCAACCAAGAAAGGAAGGCAGGTGGGCCCCAGCAAAGG
AGTAGCTGCCAGGGCTCAACAGCTACGCTCTGTGACAGCGCAGAGCTCAGCGGCGGCCTTTCCCTCCCTCCGCCA
AGGACTCACGGCCAAGCCAGCTCTCGGGGCCTTTTTTCCACTGCCATTGAGTACTCTGCTGCACCAAGCTTGG
GAGCCAGCCTGCCAACAGCCACCTGGGCCTGGCCTCCCCACTGGCTGGCCTTGAGGTTGGCAGAGTGGGTTGTGG
CGCTTCTCTCTCTGTGTGGGACCAGGACAGTGGCTTAAGTCTCCACTCCAGGAAAGAATCAAAGTTTCTAGAGT
TGTGAGAAAACAGAGAGTGGCTGTCTGATTCTTCACTGTGAGGGGCGTCTTCATGTTCTCCAGCTGTTCCA
AGACTGGGCGGTAGAAATCCATGTTTCAGGAGCCTAAGACCCTCCCAGAGCCCAGGGGCTTACCCGACAGCCCCA
AGCCATTGAGCACATACCCAAAGCAGTGGCCAAACATCGCGGACCCCTGTGCCTTGTACAGATGGGTGCTGGTC
CTCAGGCGTTGGGGACACTGCTGGGTGATGGGGTCGATTCTGCCAGTTTCTGCTCTGCAGCCAAAGATGGTCA
GAAGCATTGTCACTTCAAGTAACATCAAGTGCTCAAAGACATGGCAACCGTTCAAGTGGTACTTAAGTATTCAAAT
ATACAACACAGATTCTCTGACAGAAACCAGCACGGGGTCTTACCTTCATTACCCACAGGCGACATGCGAGG
GAGAACAGCATCTCAGTGGTGATTTCCAAACCAAGCCTTTGTTTTCGGTGTGGGGTTTTGGGGGTTTTGCTTTAAT
GTTTTGAAATTGTAAATGTTGGGCTTTGTATTTTGATGTAAACTGAGCATAATGGCATTTTAGGGCCTGTGACC

925/6881
FIGURE 859B

AAAATGAAGCTTGTAACGACCCATGGATCTGAATAAACATGTCCTTGCTTCTGAAAAAAAAAAAAAAAAAAAAA
AAAAAA

926/6881
FIGURE 860

MAFPHLQQPSFLLASLKADSINKPFAQQCQDLVKVIEDFPAKELHTIFPWLVESIFGSLDGVLVGWNLRLCLQGRV
NPVEYSIVMEFLDPGGPMMKLVYKLQAEDYKFDFPVSYLPGPVKASIQECILPDSPLYHNKVQFTPTGGLGLNLA
LNPFEYYIFFFALSLITQKPLPVSLHVRTSDCAYFILVDRYLSWFLPTEGSVPPPLSSSPGGTSPSPPPRTPAIP
FASYGLHHTSLLKRHISHQTSVNADPASHEIWRSETLLQVFVEMWLHHYSLEMYQKMQSPHAKESFTPTTEHVLV
VRLLLKHLHAFANSLKPEQASPSAHSHATSPLEEFKRAAVPRFVQQKLYLFLQHCFGHWPLDASFRVLEMWLSY
LQPWRYAPDKQAPGSDSQPRCVSEKWAPFVQENLLMYTKLFVGFLNRALRTDLVSPKHALMVFRVAKVFAQPNLA
EMIQKGEQLFLEPELVIPHRQHRLFTAPTFTGSFLSPWPPAVTDASFVKVSHVYSLEGQDCKYTPMFGPEARTLV
LRLAQLITQAKHTAKSISDQCAESPAGHSFLSWLGFSSMDTNGSYTANDLDEMGQDSVRKTDEYLEKALEYLRQI
FRLSEAQLRQFTLALGTTQDENGKKQLPDCIVGEDGLILTPLGRYQIINGLRRFEIEYQGDPELQPIRSYEIASL
VRTLFRLLSSAINHRFAGQMAALCSRDDFLGSFCRYHLTEPGLASRHLLSPVGRRQVAGHTRGPRLSLRFLGSYRT
LVSLLLAFFVASLFCVGPLPCTLLLLTLGYVLYASAMTLLTERGKLHQP

927/6881
FIGURE 861

GGCGCCGAGTAGCCGGGCGGGCCGGAGCGCGGGCGGGCGGAGGCAGCTGCGCCCGCGCCTCCTGCCCTCCCA
GGCCCCGCGCCCCGCGCCCGGGCCCCGGCGATGGTGACACATGCGGCGGGCGCGCCGGCGGCAGGACCATGGT
TGAGCGCGCCAGCAAGTTCGTGCTGGTGGTGGCGGGCTCGGTGTGCTTCATGCTCATCTTGTACCAGTACGCGGG
CCCAGGACTGAGCCTGGGCGCGCCCGGGCGGCGCGCGCCCGCCGACGACCTGGACCTGTTCCCCACGCCCCGACCC
CCACTACGAGAAGAAGTACTACTTCCCGGTCCGCGAGCTGGAGCGCTCGCTGCGCTTCGACATGAAGGGCGACGA
CGTGATCGTCTTCCTGCACATCCAGAAGACGGGCGGCACCACTTCGGCCGCCACCTCGTGACAGAACGTACGCCT
CGAGGTGCCGTGCGACTGCCGGCCCGGCCAGAAGAAGTGACCTGCTACCGGCCCAACCGCCGCGAGACTTGGCT
CTTCTCCCGCTTCTCCACCGGCTGGAGCTGCGGGCTGCACGCCGACTGGACCGAGCTACCAACTGCGTGCCCGG
CGTGCTGGACCGCCGCGACTCCGCCGCGCTGCGCACGCCAGGAAGTTCTACTACATCACCTGCTACGAGACCC
CGTGTCCTCGCTACCTGAGCGAGTGGCGGCATGTGCAGAGGGGTGCCACGTGGAAGACGTGCTTGATATGTGTGA
TGGGCGCACGCCCCAGCCTGAGGAGCTGCCGCCCTGCTACGAGGGCACGGACTGGTCGGGCTGCACGCTACAGGA
GTTTCATGGACTGCCCGTACAACCTGGCCAACAACCGCCAGGTGCGCATGCTGGCCGACCTGAGCCTGGTGGGCTG
CTACAACCTGTCTTCATCCCCGAGGGCAAGCGGGCCAGCTGCTGCTCGAGAGCGCCAAGAAGAACCTGCGGGG
CATGGCCTTCTTCGGCCTGACCGAGTTCCAGCGCAAGACGCAGTACCTGTTTCGAGCGGACGTTCAACCTCAAGTT
CATCCGGCCCTTCATGCAGTACAATAGCACGCGGGCGGGCGGCGTGGAGGTGGATGAAGACACCATCCGGCGCAT
CGAGGAGCTCAACGACCTGGACATGCAGCTGTACGACTACGCCAAGGACCTCTTCAGCAGCGCTACCACTACAA
GCGGCAGCTGGAGCGCAGGGAGCAGCGCCTGAGGAGCCGCGAGGAGCGTCTGCTGCACCGGGCCAAGGAGGCACT
GCCGCGGGAGGATGCCGACGAGCCGGGCGCGTGCCCAACGAGGACTACATGAGCCACATCATTGAGAAGTGGTA
GTGGCGGTGGTGGCCACGGGGAGGCCTCTTGGGGGGTGTGGGGGATAAAACAGGACAGACGACAGGTCCACCCAA
GACTGTCAAGGGATGAGCATCCCAAACCTGCTCCACAGAGGTAGCTGCGTCTTGAAAAAAACAGAGCAGGGATG
TAGTGGGGCTGGGCAGGGATGGGGGCTTGAGAAATCAACAGGTGCAGCCAGTGGGTGAGAGGAAAGCGTGCTCG
AAGGATGCCATGGTCAGGGCAGGGCCTCCAGAGCAGGTGTTGTGCCTGGAGCTGCTCTCTGGCCTCCTTGATT
TATCGCAAAAACCTGAAGTTTTCGCAAGAGACGAGGACAGCGGAAAGTGGACCTGCCAGGCCGGGAGTGTGTCCC
TCACCAACTATGCACACAGCACTCGCTCTTAGCTCCTCTGTCCGGGCTACTAGGAGTGAGACCAGCTTCTGGCAA
CTGCCCCAGCTCCAGGCCATCCCATAGCCCCTCCTCTTCTGGCTGCCCCCAATGCCCCGAGGCCTGGGGAGCCCC
CAGCTCACCCATCTGTAGCTCCCTCAAAGTCAGGGCCCAACCCATCTGAGGCAGAGAAGACTCGAGTCCAGCCCC
CAGGAAGCCTGCTCCCTCTCTGGCCCATGGTCCTGCTTCATGCTTTGGGTGAGGAGGCCAAAGCTGATGTTTCAG
GCCCCACCCACTCCCTACAGTCCTCAGACC

928/6881
FIGURE 862

GACTGCCCCGTACAACCTGGCCAACAACCGCCAGGTGCGCATGCTGGCCGACCTGAGCCTGGTGGGCTGCTACAAC
CTGTCTCTTCATCCCCGAGGGCAAGCGGGCCCAGCTGCTGCTCGAGAGCGCCAAGAAGAACCTGCGGGGCATGGCC
TTCTTCGGCCTGACCGAGTTCCAGCGCAAGACGCAGTACCTGTTTCGAGCGGACGTTCAACCTCAAGTTCATCCGG
CCCTTCATGCAGTACAATAGCACGCGGGCGGGCGGGCTGGAGGTGGATGAAGACACCATCCGGCGCATCGAGGAG
CTCAACGACCTGGACATGCAGCTGTACGACTACGCCAAGGACCTCTTCCAGCAGCGCTACCAGTACAAGCGGCAG
CTGGAGCGCAGGGAGCAGCGCCTGAGGAGCCGCGAGGAGCGTCTGCTGCACCGGGCCAAGGAGGCACTGCCGCGG
GAGGATGCCGACGAGCCGGGCGCGTGGCCACCGAGGACTACATGAGCCACATCATTGAGAAGTGGTTAGTGGCGG
TGGTGGCCACGGGGAGGCCTCTTGGGGGGTGTGGGGGATAAAAAACAGGACAGACGACAGGTCCACCCAAGACTGTC
AAGGGATGAGCATCCCCAACCTGCTCCACAGAGGTAGCTGCGTCTTGAACAAAAACAGAGCAGGGATGTAGTGGG
GCTGGGCAGGGATGGGGGGCTTGAGAAATCAACAGGTGCAGCCCAGTGGGTTCAGAGGAAAGCGTGCTCGAAGGATG
CCATGGTTCAGGGCAGGGCCTCCAGAGCAGGTGTTGTGCTGGAGCTGCTCTCCTGGCCTCCTTGGATTATATCGCA
AAAATGAAAGTTTTCGCAAGAGACGAGGACAGCGGAAAGTGGACCTGCCAGGCCGGGAGTGTGTCCCTCACCAA
CTATGCACACAGCACTCGCTCTTAGCTCCTCTGTCCGGGCTACTAGGAGTGAGACCAGCTTCTGGCAACTGCCCC
AGCTCCAGGCCATCCCATAGCCCCCTCCTCTTCTGGCTGCCCCCAATGCCCGAGGCCTGGGGAGCCCCCAGCTCA
CCCATCTGTAGCTCCCTCAAAGTCAGGGCCCCACCCCATCTGAGGCAGAGAAGACTCGAGTCCAGCCCCCAGGAAG
CCTGCTCCCCCTCTCTGGCCCATGGTCTGTCTTCATGCTTTGGGTTCAGGAGGCCAAAGCTGATGTTTCAGGCCCCAC
CCACTCCCTACAGTCCCTCAGACCAAGGAGGGGTTTGGGTAGTAGGCCCGAGCTGCATTGCCGGCCTTCTCGGGC
CAACTGGCAGCCAGGAGTGGGGAGGCTTTGGCCAGGGATGCTGCCACTTGTGCGTGAGTCCGCGGCTGGCCCTT
GGAGGTGACCATCCAGGCAGGCCTGGCTCAGACTGGAAGGGCTGGGGACCGAGGGCTCCCCTGCCTCTGTTCTCC
TTTCTGACCCACTGGGATTTGCTAGCAGGCTGCCCCAGCCCCATCACCGAAACACATACTCAAGAGCTCAAATAC
CACTGCTCCCACCAGCGTACGGATTAAGTTTCATCAGGCTTCCATCGGCTGGAGCATGGGACCATAGCCCCTGCCC
AGGAGCCGTACCCTCGGACCACAGTGGCTCTGTATGGCCAGGAACCTGGGACTCGAGCTTTTCAGATTCTCAACTAG
CCTTGGCAAAACAGCTGTAGGTGGCCTCCCTGACAACAGACACTCAGCCCTCCCCACCCTGGCTCTCCTTGCAAT
TCCCCATGCTCCCCACCCCCTGGCAAAAGGCTGGCCATGCTCTGTTCCAGCAGCCGCGCAGGTTTCCCCACTGG
CTGCAATGGCCCTACCAAAAGCCATGTTGCATATCCGTTGTAAGCACGTGCCCTGTGCCCTGTCCCCATTCTTA
TGCCCTAGGAGGCCAAGCTGGTGTCTCTAGGAGGGCCACACAGGCACCCTGGATCCCCCAGAGAGTAGATTGGT
GTGCTCAGGCCGCGAGGCTGACTCAGAGGTAGGGCAGTGGGCTCTGCAGGCCACCTGGCTGGGGTTGGTGGGGGTC
CTCTCTCCTGCCCCAGCTTCCACTCAGCCACCACAGTTGCCACACCATGGGGTGGAGACGTGGGTACACCACGGGC
TTGGGAGCAAGCGCCTTCTGCAGCACAGGAAGCCGAAGCTGGGGTCAGGTGAGGTGCTACCCCTGGAGGTCTGG
CATAAGGGCCCCACCCCTCAGGTCTCCTACACTGGCCCCATTTTACTTTGGGGTCCAAGGACAGGATGGTCAACAG
GGCAGGGTGGACAGCGTGCCAGCGCCGCGCAGGGCCACCTCCCTGGGTGGATGCATCACACTAAGGAAGTGAGTG
CCAAGGGGATTTAGTGGTGTGGTTCTTTCAAAGGGAGGTTCAGGGTCAATGGGAATCTGCTCGGACACTCAACATG
GGGGTGGGTGCACCTCCTTGGAGGAGGAGGAACACGTTTCAGGGGATTGTGAGGTCTTGACAAGCCACGTGGGGCA
CCTTGGCTTCCCGGCAGGAGGTGGACACCCAGCCAGAGGCCTGGCTCAAGGTGACCTCACCTTACCATGGGCTT
CCTGGGTGCGCGGGCCTGAGCGCAGGTTGTTTTGTACATATTGGAATATGTGTTAACTTATGCCCCGCATCCCAA
CTCACACGGAAGCACGGGTCTTGTCTCAGTCTCTTCGCTGCATTTGGAAAGCAGTCTCCTCTCGGGCCAGCGCCG
GGCTGAGGTGTCCAGAGGCGGCGGCAGCTGGCAGTGCCCTCAGCCCCCAAGTGTCCAGCCTGGCACTTCCCATTC
AGGCCACCTGCTTTGGGTCAACAGTTCTTTGCCAGCAGCATCTCCTAAATTGTAAGGACTCTGTCCACCGGGGC
CCTCCCAGGGCTGTGAGGACGGAACAGGCAGGGAGTGGAGCTAACAGCTTAGTCACCAGGACCCCCAGACCTGC
AAACGTCCCCCTCCTGGAAGGGGAAGCCAGGAACAGCAGAACTGCCCAAAAACAAGGCTGTGAACTTTTCGGGAA
CTGGAACGTGTTTAACTTGAACCCAGGATTGTTTAAAGCTTTATTTATTTATAGCTTCTTCTTAAAAAAAGTGTT
GAAGAAATTTTTTGGTTATTATACAAAAAATGAGTTGATGATGGAAAAAGCAAGTCATAATCATCTAATTGTTT
TTGTCTAGGTTCGAGAATGAATGTTAGCTGATGAAATAAACCTGACAAGG

929/6881
FIGURE 863

MLADLSLVGCYNLSFIPEGKRAQLLLESAKKNLRGMAFFGLTEFQRKTQYLFERTFNLKFIRPFMQYNSTRAGGV
EVDEDTIRRIEELNDLDMQLYDYAKDLFQQRYQYKRQLERREQRLRSREERLLHRAKEALPREDADPEGRVPTED
YMSHIEKW

930/6881
FIGURE 864

GGAAAAAAGCGACTTGTGGCGGTCGAGCGTGGCGCAGGCGAATCCTCGGCACTAAGCAAAT**ATGG**ACCTCGCGGC
GGCAGCGGAGCCGGGCGCCGGCAGCCAGCACCTGGAGGTCCGCGACGAGGTGGCCGAGAAGTGCCAGAACTGTT
CCTGGACTTCTTGAGGAGTTTCAGAGCAGCGATGGAGAAATTAAATACTTGCAATTAGCAGAGGAACTGATTCCG
TCCTGAGAGAAACACATTGGTTGTGAGTTTTGTGGACCTGGAACAATTTAACCAGCAACTTTCCACCACCATTCA
AGAGGAGTTCTATAGAGTTTACCCTTACCTGTGTGGGCTTGAAAACATTTCGTCAAAGACCGTAAAGAGATCCC
TCTTGCCAAGGATTTTTATGTTGCATTCCAAGACCTGCCTACCAGACACAAGATTTCGAGAGCTCACCTCATCCAG
AATTGGTTTGCTCACTCGCATCAGTGGGACGGTGGTGCGGACTCACCCAGTTCCACCCAGAGCTTGTGAGCGGAAC
TTTTCTGTGCTTGGACTGTCTAGACAGTGATCAGGGATGTAGAACAGCAGTTCAAATACACACAGCCAAACATCTG
CCGAAATCCAGTTTTGTGCCAACAGGAGGAGATTCTTACTGGATACAAATAAATCAAGATTTGTTGATTTTCAAAA
GGTTTCGTATTCAAGAGACCCAAGCTGAGCTTCCTCGAGGGAGTATCCCCCGCAGTTTAGAAGTAATTTTAAGGGC
TGAAGCTGTGGAATCAGCTCAAGCTGGTGACAAGTGTGACTTTACAGGGACACTGATTGTTGTGCCTGACGTCTC
CAAGCTTAGCACACCAGGAGCACGTGCAGAACTAATTCCCGTGTGAGTGGTGTGATGGATATGAGACAGAAGG
CATTTCGAGGACTCCGGGCCCTTGGTGTAGGGACCTTTCTTATAGGCTGGTCTTTCTTGCCTGCTGTGTTGCGCC
AACCAACCCAAGTTTTGGGGGAAAGAGCTCAGAGATGAGGAACAGACAGCTGAGAGCATTAGAACCATAATGAC
TGTGAAAGAATGGGAGAAAGTGTGTGAGATGAGTCAAGATAAAAAATCTATACCACAATCTTTGTACCAGCCTGTT
CCCTACTATACATGGCAATGATGAAGTAAACGGGGTGTCTGCTGATGCTCTTTGGTGGCGTTCCAAAGACAAC
AGGAGAAGGGACCTCTCTTCGAGGGGACATAAATGTTTGCATTGTTGGTGACCCAAGTACAGCTAAGAGCCAATT
TCTCAAGCACGTGGAGGAGTTCAGCCCCAGAGCTGTCTACACCAGTGGTAAAGCGTCCAGTGCTGCTGGCTTAAC
AGCAGCTGTTGTGAGAGATGAAGAATCTCATGAGTTTGTGATTGAGGCTGGAGCTTTGATGTTGGCTGATAATGG
TGTGTGTTGTATTGATGAATTTGATAAGATGGACGTGCGGGATCAAGTTGCTATTTCATGAAGCTATGGAACAGCA
GACCATATCCATCACTAAAGCAGGAGTGAAGGCTACTCTGAACGCCCCGACGTCCATTTTGGCAGCAGCAAACCC
AATCAGTGGACACTATGACAGATCAAATCATTGAAACAGAATATAAATTTGTCAGTCCCATCATGTCCCGATT
CGATCTCTTCTTTATCCTTGTGGATGAATGTAATGAGGTTACAGATTATGCCATTGCCAGGCGCATAGTAGATTT
GCATTCAAGAATTGAGGAATCAATTGATCGTGTCTATTCCCTCGATGATATCAGAAGATATCTTCTCTTTGCAAG
ACAGTTTAAACCCAAGATTTCCAAAGAGTCAGAGGACTTCATTGTGGAGCAATATAAACATCTCCGCCAGAGAGA
TGGTTCTGGAGTGACCAAGTCTTCATGGAGGATTACAGTGCGACAGCTTGAGAGCATGATTTCGTCTCTCTGAAGC
TATGGCTCGGATGCACTGCTGTGATGAGGTCCAACCTAAACATGTGAAGGAAGCTTTCCGGTTACTGAATAAATC
AATCATCCGTGTGGAACACCTGATGTCAATCTAGATCAAGAGGAAGAGATCCAGATGGAGGTAGATGAGGGTGC
TGGTGGCATCAATGGTTCATGCTGACAGCCCTGCTCCTGTGAACGGGATCAATGGCTACAATGAAGACATAAATCA
AGAGTCTGCTCCCAAAGCCTCCTTAAGGCTGGGCTTCTCTGAGTACTGCCGAATCTCTAACCTTATTGTGCTTCA
CCTCAGAAAGGTGGAAGAAGAAGAGGACGAGTCAGCATTAAAGAGGAGCGAGCTTGTTAACTGGTACTTGAAGGA
AATCGAATCAGAGATAGACTCTGAAGAAGAACTTATAATAAAAAAAGAATCATAGAGAAAGTTATTCATCGACT
CACACACTATGATCATGTTCTAATTGAGCTCACCCAGGCTGGATTGAAAGGCTCCACAGAGGGAAGTGAGAGCTA
TGAAGAAGATCCCTACTTGGTAGTTAACCTAACTACTTGCTCGAAGAT**TGAG**ATAGTGAAAGTAAGTACCAGAG
GCTGAGGAAGTGTGGCACAGCACCTCGTGGCCTGGAGCCTGGCTGGAGCTCTGCTAGGGACAGAAGTGTTCCTGG
AAGTGATGCTTCCAGGATTTGTTTTTCAGAAACAAGAATTGAGTTGATGGTCCTATGTGTACATTTCATCACAGGT
TTCATAACCAACACAGGCTTCAGCACTTCCTTTGGTGTGTTTCCTGTCCCAGTGAAGTTGGAACCAATAATGTGT
AGTCTCTATAACCAATACCTTTGTTTTTCATGTGTAAGAAAAGGCCCATTAATTTAAGGTATGTGCTGTCTATT
GAGCAAATAACTTTTTTTCAATTGCCAGCTACTGCTTTTATTCATCAAAATAAAATAACTTGTTCCTG

931/6881
FIGURE 865

MDLAAAEPGAGSQHLEVRDEVAEKCQKFLDFLEEFQSSDGEIKYLQLAEELIRPERNTLVVSFVDLEQFNQQL
STTIQEEFYRVYPYLCRALKTFVKDRKEIPLAKDFYVAFQDLPTRHKIRELTSSRIGLLTRISGQVVRTHPVHPE
LVSGTFLCLDCQTVIRDVEQQFKYTQPNICRNPVCANRRRFLDDTNKSRFVDFQKVRIQETQAEIPRGSIPRSLE
VILRAEAVESAQAGDKCDFGTGLIVVPDVSKLSTPGARAETNSRVSGVDGYETEGIRGLRALGVRDLSYRLVFLA
CCVAPTNPFRFGGKELRDEEQTAESIKNQMTVKEWEKVFEMSQDKNLYHNLCTSLFPTIHGNDEVKRGVLLMLFGG
VPKTTGEGTSLRGDINVCIVGDPSTAKSQFLKHVEEFSRAVYTSKGASSAAGLTAAVRDEESHEFVIEAGALM
LADNGVCCIDEFDKMDVRDQVAIHEAMEQQTISITKAQVKATLNARTSILAAANPISGHYDRSKSLKQNINLSAP
IMSRFDLFFILVDECNEVTDYAIARRIVDLHSRIEESIDRVYSLDDIRRYLLFARQFKPKISKESEDFIVEQYKH
LRQRDGSGVTKSSWRITVRQLESMIRLSEAMARMHCCDEVQPKHVKEAFRLNKSIIIRVETPDVNLQEEEEIQME
VDEGAGGINGHADSPAPVNGINGYNEDINQESAPKASLRIGFSEYCRISNLIVLHLRKVEEEEDSALKRSELVN
WYLKEIESEIDSEELINKKRIIEKVIHRLTHYDHVLIELTQAGLKGSTEGSESYEEDPYLVVNPNYLLED

932/6881
FIGURE 866

CCGGGATCTCGAGATAGCCGCAGCTCTCGCGATCTTTCTGGAGCCGCACCTCCACGCGGAGTCCGAGCGCGTGTG
CTGAGACCCCAGGGTCGGGAGGGCGGAGACTGGGAGGGAGGGAGAAGCCCCTTTGGCCTGCCTTACGGAAGCCCTG
CGAGGGAGGGTGGTGTCCACTGCCCAGTTCGGTGTCCCGATGCCCAGCGCCAGCGCCAGCCGCAAGAGTCAGGAG
AAGCCGCGGGAGATCATGGACGCGGCGGAAGATTATGCTAAAGAGAGATATGGAATATCTTCAATGATACAAATCA
CAAGAAAAACCAGATCGAGTTTTGGTTTCGGGTTAGAGACTTGACAATACAAAAAGCTGATGAAGTTGTTTGGGTA
CGTGCAAGAGTTTACATAAGCAGAGCTAAAGGGAAACAGTGCTTCTTAGTCCTACGTCAGCAGCAGTTTAAATGTC
CAGGCTCTTGTGGCGGTGGGAGACCATGCAAGCAAGCAGATGGTTAAATTTGCTGCCAACATCAACAAAGAGAGC
ATTGTGGATGTAGAAGGTGTTGTGAGAAAAGTGAATCAGAAAAATTGGAAGCTGTACACAGCAAGACGTTGAGTTA
CATGTTTCAGAAAGATTTATGTGATCAGTTTTGGCTGAACCCCGTCTGCCCTGCAGCTGGATGATGCTGTTTCGGCCT
GAGGCAGAAGGAGAAGAGGAAGGAAGAGCTACTGTTAACCAGGATACAAGATTAGACAACAGAGTCATTGATCTT
AGGACATCAACTAGTCCAGGAGTCTTCCGTCTCCAGTCTGGCATCTGCCATCTCTTCCGAGAACTTTAATTAAC
AAAGGTTTTGTGAAATCCAACTCCTAAATATTATTCAGCTGCCAGTGAAGGAGGAGCCAATGTTTTTACTGTG
TCATATTTTAAAAATAATGCATACCTGGCTCAGTCCCCACAGCTATATAAGCAAATGTGCATTTGTGCTGATTTT
GAGAAGGTTTTCTCTATTGGACCAGTATTCAGAGCGGAAGACTCTAATACCCATAGACATCTAACTGAGTTTGT
GGTTTGGACATTGAAATGGCTTTTAATTACCATTACCACGAAGTTATGGAAGAAATTGCTGACACCATGGTACAA
ATATTCAAAGGACTTCAAGAAAGGTTTCAGACTGAAATTCAAACAGTGAATAAACAGTTCCCATGTGAGCCATTC
AAATTTTTTGGAGCCAACTCTAAGACTAGAATATTGTGAAGCATTGGCTATGCTTAGGGAAGCTGGAGTCGAAATG
GGAGATGAAGACGATCTGAGCACACCAAATGAAAAGCTGTTGGGTCATTTGGTAAAGGAAAAGTATGATACAGAT
TTTTATATTCTTGATAAATATCCATTGGCTGTAAGACCTTTCTATACCATGCCTGACCCAAGAAATCCCAAACAG
TCCAACCTCTTACGATATGTTTCATGAGAGGAGAAGAAATATTGTCAGGAGCTCAAAGAATACATGATCCTCAACTG
CTAACAGAGAGAGCTTTACATCATGGAATTGATTTGGAGAAAATTAAGGCTTACATTGATTCCTTCCGCTTTGGA
GCCCCCTCTCATGTGTTGGTGGAGGCATTGGATTGGAACGAGTTACTATGCTGTTTCTGGGATTGCATAATGTTTCGT
CAGACCTCCATGTTCCCTCGTGATCCCAAACGACTCACTCCTTAAATTCACACTTTGCCACTTAACTCCAGTGTG
GATGACAGAGCGAGACCCCTGCCTCAAAAAAAAAAAAAAAAAAGAAAAGCCACACTTATTCTTTTCAGTAACCTGC
TAGTGACAGGCTGTACTTTAGGTACTTAAAATATGCACTAGAATAAAATTTGCAAGGCCCTAAAATATCACTGTT
ATTTTTGGAGTAATTCAGTATAGGTTTCGTTTTAAAGAGATTTTTATAACTTCAGACATGCATCAGTAGGAAATAA
CTTGAGAAATTCATATGGTTATGTTACAAATTCATATTCTGTTACTACAGTAAACGTTAAGAGTTTTAAACAGTT
AAGATTGTACAATTTTTCTTCTTTTCTATATTACAAGGGCCCCAGTGTTAATGTCTTAGATTTTCAGTATTTGAA
CTTATTTTTTTTAAATTCGTGATTGAGATAAGAATAATTCAGGTAGCATCTGAAATTTTAAATGAATGTATAATTG
GCATATCATGGAAAATTAACCAGAAAGTATCAGTTCTTAAAAGTTATGCCTAGAAATTATGTAAAGCTAAACTAC
TGTTTAGAAAGTATTCAGTGTAATATTGIATTAATTTGTTAAATTCTAAACTTGAATTTCAATAAAATTTTAAAG
CT

933/6881
FIGURE 867

ATGACAAAGAAAAATGCCTGCATGGGCCTTGTTTTCCAGATTCAATCAAGGCTCAAAGCTTTTATCTTGTTCTTA
ATAGCACCTTGACCCGATAGAGCCCGCAAGGCTTTGCGGGCCTTAATTATTTCCCAAGATCGATGAGACCCCT
CAGCCCCCTGGGCAGCAGCATCCCACGGCAGTTTTCCAGATGGATGAGCTGCGTCGAAAGCTGCAGAGCAGACAG
GGATGCAGACAAGGTCCAGCACGCCCAGCAGAGCCTGCGGCCTGCGGGTTCCTCGGGCGGATGGCACTGCAAAAT
TCAGCCCTTAATTCAATCAATATGTGCCTTCGAGGAGTTTATAGTCATGGTTTGGTATGGTTGGTATGTGATGCA
CACAAAGCAGAGACAGCTGCATGTAGAAGGGCAGGGGAGCATGGAGGGCCCCAGTACAGCCAGGAGGGCCCTGGAG
CTTCAGGCAGCAGGACATGGGTCTGGATCTGTAGTCAGAGGGGAGGTCAGGAAAGAGCTTGTACACCAGCAAAAG
ATTGGATCCTGTGGTTCTCAAACCCTTATTAGTCCTGGAGCTGTGTTTCAAGGAAATTCTGCAGAAGAACAGCAG
TTCCCTTGCAAGGATGACCCCAGGGCCCTGGTTCCCAGCAGCTCCAAGATGAGATGGCAGAAAGGGAGAGGGGG
AACCAAGGAGAGGGAAGGAGGAAATATATTAGTGCAGCTGCCCCAACGTCCCTCAAGGACAAGCACAAAGGGGT
GGTGTGGACAAGCATAATGCAATTGGCCCAGGGACAGGCCATAGACCCCCTTCCAAACCCCATTTCTCCTCACA
GCCCAGGGCCTGAAGGGAACCCGCTGGATGCAAAGCCGAGGTACCCAGAGATGGAGGTGGACAGACAGTGTGGG
ATGGCCCTGCACCCTGAAACTCCCAGGCACTACCTTGCAATTGTCAGTTTCTAATTTTACACACACTGGGGAGAGG
TCTGCTGTGGGCCAGGCTGGCCACCAGCGCTGGGTAAGTAGGGACTGGCCTAGCCACAGGCCTCAAGGATGCCGA
AGTCTGGTGGGGGAGACAAGCATGGAGAGAGACAGAGATGGCAGAGGCCAGGACAGGAAGCCTCTGGGCATCCTG
GCTGAGGACAGGGTGGCACACCCAGAGGAGAGTGAATCGTGGAAATGCCGAAAGCTAAAGAGAAGATTCCACCA
GAGATCACAGAGCAGAACATGCAAAGTATAAAATTGCCCAACCACCGTCACTCACGGACCCCTTTGTCCCTTC
TCTTCCCTCCACCCCATAGAAGTTTGGCTGACAACCACGGGTTTCATACCACATTTCCACATATGGGAAGAATCT
GTGGCCAGAGTGGTTACATTAGAGCACCTCCTCCCTGAGAGCCACACAAGGGCCCATACCACCTTCCAGTTCA
TGGCTCCACCTTTGTCTGCTCTCACAACCTTCCAGACCTGGCCTATACCACATGTTATTAAATAATCTTCTA
GATATGCCTTTAGGATTTGCTGCAAAGACACTTGAGATAAAGTATCTGTGAGAACCAACCTGGGATGTAGCCAAA
GCTAAGGAATATGTCTGTTCTGTGGAGAGCAGATGATCAATAGGTGGTTCAGCTAATGGAGTGACTGGAGCA
AGGCTCATAGGCCTTTCAGTTCCATCAAAGGAAGATAAGTCCCCTCATTGTCCCTGGAGGAACTGTGAGGTC
TTCTTATATTTGCATGTATGTGCCAAAGAGAGACATGTAAAAACCAGAGCCCGGAGACATAGAGAAGATCATTCA
AAAGCACATGCCAAGCTAAAGACAATACCAGGGACAGGACCTCATCTTCTGACTCTTGGTCCAGTTCTCCCTCCA
ACTCAGCAAACAGCCTTTGGATTCCACTTGGGAAATATGGAACTGAACAGCCAGAAGAAACCTTCCCTAACACT
GAAACCAGTGGTGAATTTGGTAAACGCCCTGCAGAAGATATGGAAGAGGAACAAGCATTAAAAGATCTAGAAAC
ACTGATGAGATGGTTGAATTACCCATTCTGCTTCAGAGCAAGAATGCTGGAGCAGTGAAGGAGGAGGCAAG
AATATTAAGGCTCTCCATACAGACTACAACGCCAGCATTTTCAGTTCTAGACAGCAGTGGCCCCCAGCATATATTG
CATATCAGTGCTGATATCGAAACAATTGGAGAAATTCTGAAGAAAATCATCACTACCTTGGAAGAGGGCCCGCAG
TTGCCATCACCCACTGCAACCAGCCAGCTCCCGCTCGAATCTGATGCTGTGGAATACTTAAATTACCAACAATAT
AAAGGAAGGGACTTTGACTGCGAGTTGAGGCTGTTGATTTCATCAGAGTCTAGCAGGAGGAATTATTGGGGAATGT
TGTCTCATTTTCACTGATAGAGTTGTTCTTATTGGAGGAAAAACCAATAGGGTTGTAGAGTGATAAAGATCATC
CTTGATCTTATTTCTGAGTCTCCCATCAAAGGACATGCACAGCCTTATGATCCCAATTTTTACGATGAAACCTAT
GATTATGGTGGTTTTTACAATGGTGGTTTGTGACGACCGTGGACGCCAGGGGGAGACCTCATGACCTATAACAGA
AAAGGGAGACCTGGAAACCGTTACGACGGCGTGGTTGATTTTCAGTGCTGATGAACTTGGGGCTCTGCAATAGAT
ACATGGAACGCATCAGAAATGGCAGATGGCTTATGAACCACAGGGTGGCTCCAGATATGATTATTCCTATGCAGGG
TGTATGGCTCATATGGTGTCTTGGTGGACCTATTATTACTACACAAGGAGCTTTGATCAAAATTGATGAGCCT
TTAGAAGGATCCGAAGATCGGATCATTACCATTACAGGAACACAGGACCAGATACAGAATGCACAGTATTTGCCG
CAGAATAGTGTGAAGCAGTATTCTGGAAAGTTTTTCTAA

934/6881
FIGURE 868

MTKKNACMGLVFQIQSRLKAFILFLIAPCTDRARQGFAGLNYFPKIDETPQPPGQQHPTAVFQMDELRRKLQSRQ
GCRQGPAPPAEPAACGFLGRMALQNSALNSINMCLRGVYSHGLVWLVCDHKAETAACRRAGEHGGPSTARRPLE
LQAAGHSGSGSVVRGEVRKELVHQKIGSCGSQTLISPGAVFQGN SAEEQQFPCKDDPRAPGSQQLQDEMAERERG
NQEGERRKYIQCSCPNVPGQAQRGGVDKHNAIGPGTGHRPHFQTPFLLTAQGLKGTRWMQSRGHPHEMEVDRQCG
MALHPETPRHYLALSVSNTHTGERSAVGQAGHQRWVSRDWPSHRPQGCRSLVGETSMERDRDGRGQDRKPLGIL
AEDRVAHP EESWKRKLKRRFPPEITEQNMQKYKIAQPPSLTDPFVPFSSPPPHRSLADNHGFIPHFHIWEES
VAQSGYIRAPPPLRATQGPIPPSSSWLHLCPALTTFPDLAYTHMLLNLLDMPLGFAAKTLEIKYLSEPTWDVAK
AKEYVLCFGEQMINRWFPANGVTGARLIGLSVPSKEDKSPLIVPGGNCEVFLYLHVCAKERHVKTRARRHREDHS
KAHAKLKTIPGTGPHLLTLGPVLPPTQQTAFGFHLGNMETEQPEETFPNTETSGEFGKRP AEDMEEEQAFKRSRN
TDEMVELPILLQSKNAGAVTGKGGKNIKALHTDYNASISVLDSSGPQHILHISADIETIGEILKKIITTL EGPQ
LPSP TATSQLPLESDAVEYLYNYQQYKGRDFDCELRLLIHQSLAGGIIGECPPHFTDRVVLI GGKPNRVVECIKII
LDLISESPIKGHAQPYDPNFYDETYDYGGFTMVFAADDRGRPGGDLMTYNRKGRPGNRYDGVVDFSADETWGS
AIDTWNASEWQMAYEPQGGSRYDYSYAGCHGSYGD LGGPIITTGALIKIDEPLEGSEDRIITITGTQDQIQNAQYLP
QNSVKQYSGKFF

935/6881
FIGURE 869

ATGAAGCAGTTAATTACCCCTGCTAAACAGCAGGAAGCATTTGAGCAAAAACCTCTGCTCACCTTCCTCAATCAGA
GGACATTTCTGCTCATCAGTCAAGCAGGCAGACCACAGGACTCTCAGACAAAGGCTGAGAGGTAGACTGATGAGG
AGGAGACTGTCAGTGAGCACAAAGGCCTTAAGATTAGCGACTGAAGGCTCCTGGAATGAGTATGTGGTTAGAGAC
TGGAAC TACTCAGGAGTTTCCCTAGGTCTGCTCCAAATAGCACAAAGCAATGGATGATGAAGGATCCATGTTAATA
GCAGTGGATCCACAGTGCAGATTTTCAGGTGATCTGCTCCCCCTACGACTCACTAATTGGAGTCCCATTGGCCCCC
CATGTGACCCCTCTTGATAAAAAATCAAAATGGCTCTCGTCTTGTTTGTTTCTCCTGTTTGGCCCCCAGTCAGGGCT
GGCACAGAGTGGCAGCTCTCTGCTCTCCACAGGGCTCCCCGCTCCACCCAGCCCGATAAAGCATGCCGACTGGGC
TACAAAGCCAAGCAAGGTTACATTATATATAGGATTTGTGTTTCGCCGTGAGGAGCAAGCTGGACACCACTGTGGG
GCTCTAAGAGTCCTGAATTCGTACTGGGTTGGTGAAGATTCCACATACAAATTTTTTGGAGTTATCCTCATTGAT
CCATTCCATAAAGCTATCAGAAGAAATCCTGACACCCAGTGGATCACCAAACCAGTCCACAAGCACAGGGAAATG
CGTGGGCTGACATCTGCAGGCTGA

936/6881
FIGURE 870

MKQLITPAKQQEAFEQKLCSPSSIRGHFCSSVKQADHRTLRLRGRLMRRRLSVSTKALRLATEGSWNEYVVRD
WNYSGVSLGLLQIAQAMDDEGSMLIAVDPQCRFSGDLLPYDSLIGVPLAPHVTLLDKNQNGSRLVCFSCLPVRA
GTEWQLSALHRAPRSTQPDKACRLGYKAKQGYIIYRICVRREEQAGHHCGALRVLNSYWVGEDSTYKFFEVLID
PFHKAIRRNPDQTQWITKPVHKKHREMRLTSAG

937/6881
FIGURE 871

ATGTGGGGCGACCTCTGGCTCCTCCCGCCTGCCTCTGCCAATCCGGGCACTGGGACAGAGGCTGAGTTTGAGAAA
GCTGCAGAGGAGGTTAGGCACCTTAAGACCAAGCCATCGGATGAGGAGATGCTGTTCATCTATGGCCACTACAAA
CAAGCAACTGTGGGCGACATAAATACAGAACGGCCCGGGATGTTGGACTTCACGGGCAAGGCCAAGTGGGATGCC
TGGAATGAGCTGAAAGGGACTTCCAAGGAAGATGCCATGAAAGCTTACATCAACAAAGTAGAAGAGCTAAAGAAA
AAATACGGGATATGAGAGACTGGATTTGGTTACTGTGCCATGTGTTTATCCTAAACTGAGACAATGCCTTGTTTT
TTTCTAATACCGTGGATGGTGGGAATTCGGGAAAATAACCAGTTAAACCAGCTACTCAAGGCTGCTCACCATACG
GCTCTAACAGATTAGGGGCTAAAACGATTACTGACTTTCCTTGAGTAGTTTTTATCTGAAATCAATTAAAAGTGT
ATTTGTTACTTT

938/6881
FIGURE 872

MWGDWLWLLPPASANPGTGTEAEFEKAAEEVRHLKTKPSDEEMLFYGHYKQATVGDINTERPGMLDFTGKAKWDA
WNELKGTSKEDAMKAYINKVEELKKKYGI

939/6881
FIGURE 873

GTTTAGGGGCTGGTACAAAGGATGAATTGCACATTGTTGAAGTAGAGGCAATGAATTACAAAGGCAGTCCAATTA
AAGTAACACTGGCAACTTTGAAAATGTCTGTACAGCCAAAGGATTCCCTTGGAGGCTTTGAAATCACACCACCAG
TGGTCTTACGGTTGAAGTGTGGTTCAGGGCCAGTGCATATTAGTGGACAGCACTTAGTAGCTGTGGAGGAAGATG
CAGAGTCAGAAGATGAAGAGGAGGAGGATGTGAACTCTTAAGTGTATCTGGAAAGCGGTCTGGCCCGTGGAGGTG
GTAGCAAGATTCCACAGAAAAAGTAAAAGTTGCTGCTGATGAAGATGAAGATGATGATGATGAGGATTTTGATG
ATGGGGAAGCTGAAGAAAAAGCGCCGGTGAAGAAATCCATACGAGATACTCCAGCCAAAAATGCACAAAAGTCAA
ATCAGAATGGAAAAGACTCAAACCGTCAACACCAAGATCAAAGGACAAGACTCCTTCAAAAAACAGGAAAAA
ACTTCTTAAAACACCGAAAGGACCTAGTTCCATAGAAGACATTAAAGCGAAAATGCAAGCAAGTATAGAAAAAGCG
CATTGAACAGTCCTGGGCACTGCTGGTAAATTAAGCCCAAAGATGGGGAGAAAGGAAAAGGAGAGACAAATATAG
TCCATACTGAG

940/6881
FIGURE 874

MNYKGSP IKVTLATLKMSVQPKDSLGGFEITPPVVLRLKCGSGP VHISGQHLVAVEEDAESEDEEEEDVKLLSVS
GKRSARGGGSKIPQKKVKVAADEDEDDEDDDFDDGEAEEKAPVKKSIRDTPAKNAQKSNQNGKDSKPSTPRSKGQ
DSFKKTGKNF

941/6881
FIGURE 875

AGCGGGTTTGCGGGAGCGCCGCGTGGTTAGCGTCGGCGGCTTTTGGCATGGCGACTTTTTCTGGCCCGGCTGGGC
CAATCCTGTCGCTTAATCCGCAGGAAGATGTCGAGTTTCAAAAGGAGGTGGCGCAGGTTTCGCAAGCGCATAACCC
AGCGAAAAAACAAGAACAACCTTACTCCTGGAGTAGTCTATGTGCGCCACCTACCTAACCTACTTGACGAAACCC
AGATCTTTTCATATTTCTCCCAGTTTGGCACTGTGACACGGTTCAGGCTGTCCAGAAGTAAAAGGACTGGAAATA
GCAAAGGCTATGCATTTGTGGAGTTTGAGTCTGAGGATGTTGCCAAAATAGTTGCTGAAACAATGAACAACCTACC
TGTTTGGTGAAAGACTCTTGGAGTGTCAATTTATGCCACCTGAAAAAGTACATAAAGAACTCTTTAAAGACTGGA
ATATTCCATTTAAGCAGCCATCATATCAATCAGTGAAACGGTATAATCGGAATCGGACACTAACACAAAAGCTAC
GGATGGAGGAGCGATTTTAAAAAGAAAGAAAGATTACTCAGGAAGAAATTAGCTAAAAAAGGAATTGACTATGATT
TTCCTTCTTTGATTTTACAGAAAACGGAAGTATTTCAAAAACCTAATCGTCAGACGTCTACAAAAGGCCAGGTTT
TACGTAAGAAGAAGAAAAAGTTTCAGGTACTCTTGACACTCCTGAGAAGACTGTGGATAGCCAGGGCCCCACAC
CAGTTTGTACACCAACATTTTTGGAGAGGCGAAAATCTCAAGTGGCTGAACTGAATGATGATGATAAAGATGATG
AAATAGTTTTTCAAACAGCCCATATCCTGTGTAAAAGAAGAAATACAAGAGACTCAAACACCTACACATTCACGGA
AAAAAAGACGAAGAAGCAGCAATCAGTGAATTTTCAATGTATTATATTTCTTTTGAAAAATATAATATTTTTATGA
GAGTGGACTTTTGATTTTCACTAGGTACAATGGAATACAACCTTTGACAAGATTTTCAGAGGAAAAATACACTGTT
TGGTCAAGTTAAGGAAAGCAGTGTGTAATTTTGGATTGCCTGCCCTTGGCTGAAATACAGGGGTGCATACCATCT
TGCAGTGGCTTGGCTGACATTGCCTCTTTGTCTGGCCTCTAGTTTTCTTTTGATATTTTCATAGCTCTCCTTAGT
TTACTCTGCCTGGATAGAAAGTTGACCACTAACTGCAGGTTTAAGTACTAACTGCAGCCTTTTCTGTGCGCCAGC
AATTAAAGACCACCAATCTTGTGTGTCATCTACATGGTTTGTGCGGGACATTTAACTCATGGAGGTGCTTTAGA
TTTCAACATCAGATGGTTGAAGCTGGAAGTTTAATTATATGTAGAGTGAGAAGGCAGTTCAGTTTTAGCACAGA
TTTGTTTATGTGTTTCAAGTTTTAATAGAGATTCAAAAATGACTCATTTTTACCAATAATGTTAAATTAGTTTTGG
TTGTGCTAGCATGAATTAATAACCACCATTTTATACCAGTATCATCAGTGAAGAATTGATTTCAAGATTCAAAC
AATAACCAGCAATTAACTTTTTTCTACAATGTATTTGTTTGCAGTAGGACTTGGGAGTCATTGGAAAAA
ATAATAAATTTTCCCCTTCATTAACAAAAA

942/6881
FIGURE 876

MATFSGPAGPILSLNPQEDVEFQKEVAQVRKRITQRKKQEQLTPGVVYVRHLPNLLDETQIFS YFSQFGTVTRFR
LSRSKRTGNSKGYAFVEFESEDVAKIVAETMNNYLFGERLLECHFMPPEKVHKELFKDOWNIPFKQPSYQSVKRYN
RNRILTQKLMEERFKKKERLLRKKLAKKGIDYDFPSLILQKTESISKTNRQTSTKGQVLRKKKKKVSGLDTPE
KTVD SQGTPVCTPTFLERRKSQVAELNDDDKDDEIVFKQPI SCVKEEIQETQTPTHSRKKRRRSSNQ

943/6881
FIGURE 877

CCGCGGCGTCCACACTCGCCGCGCGCGCGGCGCGGCTGGACCTTGCTGGCCCGCGGCGCCATGAGCCGCAGC
CTGGACTCGGCGCGGAGCTTCTTGAGCGGCTGGAAGCGCGGGCGGCGGGAGGGGGCAGTCCTCGCCGGCGAG
TTCAGCGACATCCAGGCCTGCTCGGCCGCTGGAAGGCTGACGGCGTGTGCTCCACCGTGGCCGGCAGTCGGCCA
GAGAACGTGAGGAAGAACCGCTACAAAGACGTGCTGCCTTATGATCAGACGCGAGTAATCCTCTCCCTGCTCCAG
GAAGAGGGACACAGCGACTACATTAATGGCAACTTCATCCGGGGCGTGGATGGAAGCCTGGCCTACATTGCCACG
CAAGGACCCTTGCTCACACCCTGCTAGACTTCTGGAGACTGGTCTGGGAGTTTGGGGTCAAGGTGATCCTGATG
GCCTGTGAGAGATAGAGAATGGGCGGAAAAGGTGTGAGCGGTACTGGGCCCAGGAGCAGGAGCCACTGCAGACT
GGGCTTTTCTGCATCACTCTGATAAAGGAGAAGTGGCTGAATGAGGACATCATGCTCAGGACCCTCAAGGTCACA
TTCCAGAAGGAGTCCCCTTCTGTGTACCAGCTACAGTATATGTCTGGCCAGACCGTGGGGTCCCCAGCAGTCCT
GACCACATGCTCGCCATGGTGGAGGAAGCCCGTCGCTCCAGGGATCTGGCCCTGAACCCCTCTGTGTCCACTGC
AGTGCGGGTTGTGGGCGAACAGGCGTCTGTGCACCGTGGATTATGTGAGGCAGCTGCTCCTGACCCAGATGATC
CCACCTGACTTCAGTCTCTTTGATGTGGTCCCTTAAGATGAGGAAGCAGCGGCCCTGCGGCCGTGCAGACAGAGGAG
CAGTACAGGTTTCTGTACCACACGGTGGCTCAGATGTTCTGCTCCACACTCCAGAATGCCAGCCCCCACTACCAG
AACATCAAAGAGAATTGTGCCCCACTCTACGACGATGCCCTCTTCTCCGGACTCCCCAGGCACTTCTCGCCATA
CCCCGCCCACCAGGAGGGGTCTCAGGAGCATCTCTGTGCCCCGGGTCCCCGGGCCACGCCATGGCTGACACCTAC
GCGGTGGTGCAGAAGCGCGGGGTCCAGCGGGCGCCGGGAGTGGGACGCAGACGGGGACGGGGACGGGGACGGGG
GCGCGCAGCGCGGAGGAGGCGCCGCTCTACAGCAAGGTGACGCCGCGCGCCAGCGACCCGGGGCGCACGCGGAG
GACGCGAGGGGGACGCTGCCTGGCCGCGTTCTGCTGACCAAAGTCTGCCGGATCTGGCGCCTACGAGGACGTG
GCGGGTGGAGCTCAGACCGGTGGGCTAGGTTTCAACCTGCGCATTGGGAGGCCGAAGGGTCCCCGGGACCCGCT
GCTGAGTGGACCCGGGTGTAAGTCTAACGCCAGTTCTGCTGTTGCTCTTGTGAGCTCGGACTGCTGATGCCC
CGGTGCTGCTGAGCGCCGTGCGCAGAATGGAACAGTGGGCTGGATCAAAGTTAAAGTTTCTCAGGGTGGGAAA
TGTGGGGGCTTTGCCCCAATGACTGTAGCATTCAAGGCTTGAGGCTGGAGGAGGTAGCTAGGGTATAGTGGCTGG
TGAGGCTGCACAGAGCAGATTCAAGAAAGAAGATCAGGAAGGGGCATGACCCCTGAGTTATGAAGGGGAGAAGGG
ACAGATGAGCTTCCGGAGACTGCTCTCCTCACCACACAGCACTAGTCCATCCTCAGCACCTGAGCCTCCCTCACT
TGGACACTCAGGGGACCACACAGAGAAGTGGATGGACACTTCGCCATCCAGGCAGAACTAAGCCAGGCATAACCA
CAGCCAAGCAGATTAAACCCAGGCAGACCGATAAAAAGACCTCCAGATAGGCAGACAGACAGATGGACCACCAAC
CTGGACAGACAGCCAAAGCTTCAGAGATACAGTCCACAGGTGGACAAAGGGATCCCCAGCCAGAGAGAGAGAGAC
CAGCCAACAGCTTGATAGACCAGTGCAGCCAGAGAGACCACAAACAGAGCCCCCAAAGACAGACATCTCTGCT
AGCTGGACAGCCAGGTGGACCCCTAAGTTAGATTACTAGACAGATATAAACAGATCCCCTGCTGAACAGATACA
CAGAGTTCTCAGACCCACCCCCACCTCAGGTGGGCTGGCTGGCTGACAGACCTTCTGGCCAGACAGACTCCTA
ACCAACCAGATGGACTGCCAGACAGGCAGACATCAGCCACATGGAATCCTGACATCCCAGCCAGCCGGCCAGACT
CTCATCTTGATGTCTTGATGGATGGACCCAGCTAGTCAGACATGATCCTCCAGATTGACAGACAAGTCCCCAA
ATGAGTACACATCTCCAGCTATTGAGACAGATGGACCCCGAGCAAATCAGGACCTATCTAGGCAGACCCAGCCA
GACCCCGCCAGACAGACTCCCAACCAGACTGACCCCTTACTATTACACAGCCTGCCGAGTAGCTGGGACTACA
GGTCTAATTTTTTTTTTTTTTAAAGAAATGAGTTTTTGCCATGTTGCCAGACTGGTCTTGAACCTCCAACCTCAA
GCAATCCTCCTGCCTCAGCCTCCCAAAGTGCTGAGATTACAGGTGTGAGCCACCAGGCTCAGCCCCCTAAGATTT
GAAACACTTTAAATGGCCCATGGTAGGGTTCCTGCTAGGATAAAACATTAAGCGGCTGTTAAAAGAAATAAAGG
AGGACACGTCTCTGTGC

944/6881
FIGURE 878

TGGAAGCGGCACTCAAGATGCTGCGCCGCGAGGCCCGCCTGCGCCGCGAGTACCTGTACCGCAAGGCCCGGGAGG
AGGCGCAGCGCTCAGCCCAGGAGAGGAAGGAGCGGCTGCGGCGCGCGCTGGAAGAAAACCGCCTGATTCCCCTG
AGTTACGCCGAGAGGCTCTGGCCTTACAGGGGTCCCTGGAGTTTGATGATGCTGGAGGTGAAGGTGTGACCAGCC
ACGTGGATGATGAATACCGATGGGCAGGAGTCGAGGATCCCAAGGTTATGATCACTACCTCCCGAGACCCAGTT
CCCGCCTCAAGATGTTTGCAAAGGAGCTGAAGCTGGTGTTCCTGGGCGCCAGCGAATGAACCGAGGTCGACATG
AAGTGGGGGCACTGGTGCAGCCTGCAAAGCCAACGGCGTCACCGATCTGCTGGTCGTTACGAGCATCGGGGCA
CACCTGTGGGGCTCATCGTCAGCCACCTGCCCTTTGGTCCTACTGCCTACTTCACGCTGTGCAATGTGGTCAATGC
GGCATGACATCCCAGACCTGGGCACCATGTGCGAGGCCAAGCCCCACCTCATCACACACGGCTTCTCCTCCCGCC
TGGGCAAGCGGGTCTCTGACATCCTCCGATACCTATTTCCCGTGCCCAAAGATGACAGCCACCGGGTCATCACCT
TCGCAAACCAGGACGACTACATATCATTCCGGCACCATGTGTATAAGAAGACAGACCACCGCAACGTGGAGCTCA
CTGAGGTGCGGGCCCCGCTTTGAGCTGAAGCTGTACATGATCCGTCTGGGCACGCTGGAGCAGGAGGCCACAGCAG
ACGTGGAGTGGCGCTGGCACCCCTTACACCAATACCGCACGCAAGAGAGTCTTCCTGAGCACCGAGTGAACACACT
CACCCTCAGTCAGGACATGGACTTGGAACCTCAGGATGGGGCTGTCATAGACAGACCCACCAGTAGGAACCTGTCA
CAGAATGGCCTGCTGAACTGGGATGTGGAACCTGTGGCGGGTGGAGAGGTCTGAATAAACCGTCTGTGTCATGGCA
AAAAAAAAAAAAAAAAAAAAAAAAA

945/6881
FIGURE 879

MLRREARLRREYLYRKAREEAQRSAQERKERLRRALEENRLIPTELRREALALQGSLEFDDAGGEGVTSHVDDEY
RWAGVEDPKVMITTSRDPSSRLKMFANELKLVFPGAQRMNRRGRHEVGALVRACKANGVTDLLVVHEHRGTPVGLI
VSHLPFGPTAYFTLCNVVMRHDIPDLGTMSEAKPHLITHGFSSRLGKRVS DILRYLFPVPKDDSHRVITFANQDD
YISFRHHVYKKTIDHRNVELTEVGPRFELKLYMIRLGTLEQEATADVEWRWHPYTN TARKRVFLSTE

946/6881
FIGURE 880

GGCGGCGGCAGCGGGTTTCGGTTGCGCGTGACGCACGGGGTGGGAGCGGAGCCCAGGCCGGGAGCAGGCGCCTCTG
CCAGAGACCATGGGGAACGTGTTGGCCGCCAGGTGCGCGCCCGCAGGGCCGCCACCGCCGCTGCGCCGGCCCTC
GTGGAGCTGCCGCCACCTCCGCCCTCGCCGCCGGGCTTCACGCTGCCGCCGCTGGGAGGCGGCCTGGGCGCCGGC
ACCAGTACGAGTCGAGGTTTCGGAACTGACCCCCGGGGCTGCAACTGCCAGCGCCTCAGGGGCCGCCGAGGATGGG
GCCTGCGGCTGCCTGCCCAACCCGGGCACATTGCGGGAGTGCCACCGGAAGTGCAAGGAGCTGTTTCCCATTTCAG
ATGGAGGGTGTCAAGCTCATAGTCAACAAAGGGTTGAGTAACCATTTCCAGGTGAACCACACAGTAGCCCTCAGC
ACAATCAGGGAGTCCAGCTACCACTTCGGGGTCACGTATGTGGGGACAAAGCAGCTGAGTCCCACAGAGGCGTTC
CTTGATTGGTGGGTGACATGGACAACAGCGGCAGTCTCAACGCTCAGGTCATTACACAGCTGGGCCCCCGCCTC
AGGTCCAAGATGGCCATCCAGACCCAGCAGTCGAAGTTTGTGAACTGGCAGGTGGACGGGGAGTATCGGGGCTCT
GACTCACAGCAGCCGTAAACCTGGGGAAACCCAGACGTCCTCGTGGGTTTCAGGAATCCTCGTAGCCCACTACCTC
CAGAGCATCACGCCTTGCCCTGGCCCTGGGCAGAATGCTGGTCTACCAACCAGCAGCCTGGGGAGGAGGGCACTGTC
ATGTCCTCTAGCTGGGAAATACACATTGAACAACCTGGTTGGCAACGGTAACGTTGGGCCAGGCGGGCATGCACGCA
ACATACTACCACAAAGCCAGTGACCAGCTGCAGGTGGGTGTGGAGTTTGAGGCCAGCACAAAGGATGCAGGACACC
AGCGTCTCCTTCGGGTACCAGCTGGACCTGCCCAAGGCCAAAGGCTCTGTGGATAGCAACTGGATCGTGTGTGCC
ACGTTGGAGAAGAAGCTCCCGCCCCTGCCCCTGACACTGGCCCTTGGGGCCTTCCTGAATCAC

947/6881
FIGURE 881

AAGAACTGGCCTGTACATTTTCAAGGAATTCTTGAGAGGTTCTTGGAGAGATTCTGGGAGCCAAACACTCCATTG
GGATCCTAGCTGTTTTAGAGAACAACCTTGTAATGAGAGCCTTCATCTCTTGAGCTGCCGGCTGACACAGTGCAGCG
CATTGCGGCTGAACTCAAATGCCACCCAACGGATGAGAGGGTGGCTCTCCACCTAGATGAGGAAGATAAGCTGAG
GCACTTCAGGGAGTGCTTTTATATTCCCAAATAACAGGATCTGCCTCCAGTTGATTTATCATTAGTGAATAAAGA
TGAAAATGCCATCTATTTCTTGGGAAATTCTCTTGGCCTTCAACCAAAAATGGTTAAAACATATCTTGAAGAAGA
ACTAGATAAGTGGGCCAAAATAGCAGCCTATGGTCATGAAGTGGGGAAGCGTCCTTGGATTACAGGAGATGAGAG
TATTGTAGGCCTTATGAAGGACATTGTAGGAGCCAATGAGAAAGAAATAGCCCTAATGAATGCTTTGACTGTAAA
TTTACATCTTCTAATGTTATCATTTTTTAAGCCTACGCCAAAACGATATAAAAATTCTTCTAGAAGCCAAAGCCTT
CCCTTCTGATCATTATGCTATTGAGTCACAACCTACAACCTTACGGACTTAACATTGAAGAAAGTATGCGGATGAT
AAAGCCAAGAGAGGGGGGAAGAAACCTTAAGAATAGAGGATATCCTTGAAGTAATTGAGAAGGAAGGAGACTCAAT
TGCAGTGATCCTGTTTCAAGTGGGGTGCATTTTTTACACTGGACAGCACTTTAATATTCCTGCCATCACAAAAGCTGG
ACAAGCGAAGGGTTGTTATGTTGGCTTTGATCTAGCACATGCAGTTGGAAATGTTGAACTCTACTTACATGACTG
GGGAGTTGATTTTGCTGCTGGTGTTCCTACAAGTATTTAAATGCAGGAGCAGGAGGAATTGCTGGTGCCTTCAT
TCATGAAAAGCATGCCCATACGATTAAACCTGCATTAGTGGGATGGTTTGGCCATGAACTCAGCACCAGATTTAA
GATGGATAACAACTGCAGTTAATCCCTGGGGTCTGTGGATTCCGAATTTCAAATCCTCCCATTTTGTGGTCTG
TTCCTTGCACTGCTAGTTTAGAGATCTTTAAGCAAGCGACAATGAAGGCATTGCGGAAAAAATCTGTTTTGCTAAC
TGGCTATCTGGAATACCTGATCAAGCATAACTATGGCAAAGATAAAGCAGCAACCAAGAAACCAGTTGTGAACAT
AATTACTCCGTCTCATGTAGAGGAGCGGGGTGCCAGCTAACAATAACATTTTCTGTTCCAAACAAAGATGTTTT
CCAAGAACTAGAAAAAGAGGAGTGGTTTGTGACAAGCGGAATCCAAATGGCATTGAGTGGCTCCAGTTCCCTCT
CTATAATTCTTTCCATGATGTTTATAAATTTACCAATCTGCTCACTTCTATACTTGAAGTCTGCAGAAACAAAAAA
TTAGCAGTGTCTTCTAGAACAACCTTAAGCAAATTATACTGAAAGCTGCTGTGGTTATTTTCAAGTATTATTTCGATTT
TTAATTATTGAAAGTATGTCACCATTGACCACATGTAACCTAACAATAAATAATATACCTTAC

'948/6881
FIGURE 882

MEPSSLELPADTVQRIAAELKCHPTDERVALHLDEEDKLRHFRECFYIPKIQDLPPVDLSLVNKDENAIYFLGNS
LGLQPKMVKTYLEEEELDKWAKIAAYGHEVGKRPWITGDESIVGLMKDIVGANEKEIALMNALTVNLHLLMLSFFK
PTPKRYKILLEAKAFPSDHYAIESQLQLHGLNIEESMRMIKPREGEETLRIEDILEVIEKEGDSIAVILFSGVHF
YTGQHFNIPAITKAGQAKGCYVGFDLAHAVGNVELYLHDWGVDFACWCSYKYLNAGAGGIAGAFIHEKHAHTIKP
ALVGWFGHELSTRFKMDNKLQLIPGVCGRISNPPILLVCSLHASLEIFKQATMKALRKKSULLTGYLEYLIKHN
YGKDKAATKKPVVNIITPSHVEERGCLTITFSVPNKDVFOELEKRGVCDKRNPNGIRVAPVPLYNFHDVYKF
TNLLTSILDSAETKN

949/6881
FIGURE 883

GTGTACGGTCCGCAGCGGCAGGTGAAGTCTAGCAGAGGACGCGGCCAGGCGATTTCGGTGAAGCGATTTCCTGCAGG
CGTTGGTTCCCCCTCTTTGACCTGGTAAATGCAGGCTTTTATGCGAGAGGATTGAATTTGTTGAAATGAGCAGTC
GTAAATCAAAGAGTAACAGCTTAATTCACACAGAGTGCCTTTACAGGTACAAAGAATTTTACGTGAAAGATTTT
GTCGTCAGAGTCCACATAGTAACCTATTTGGAGTGCAAGTACAATACAAACACTTAAGTGAGCTGCTGAAAAGAA
CTGCTCTCCATGGAGAGAGTAACCTCTGTCCTTATTATCGGACCCCGAGGATCAGGAAAACTATGTTAATAAATC
ATGCTTTGAAAGAACTCATGGAAATAGAAGAAGTGAGTGAAAATGTATTACAAGTTCACTTAAATGGACTGCTGC
AGATCAATGACAAAATCGCCCTAAAGGAAATCACAAGGCAGTTAAATCTGGAAAATGTAGTTGGAGATAAAGTTT
TTGGAAGCTTTGCTGAAAACCTTTTCATTTCTTCTGGAAGCTTTAAAAAAGGTGACCGAACTAGCAGTTGCCAG
TGATCTTCATATTAGATGAATTTGATCTTTTTGCTCATCATAAAAAACCAAACTTCTCTATAATCTTTTTTGACA
TTTCTCAGTCTGCACAGACCCCAATAGCAGTTATTGGTCTTACATGTAGATTGGATATTTTGAACTCTTAGAAA
AAAGAGTGAAGTCAAGATTTTCTCACC GG CAGATACACTTAATGAATTCATTTGGTTTTCCACAGTATGTTAAAA
TATTTAAAGAACAGTTATCTCTACCTGCAGAGTTTCCAGACAAGGTTTTTGCTGAGAAGTGGAATGAAAATGTTT
AGTATCTCTCAGAAGATAGAAGTGTGCAAGAAGTACTACAGAAGCATTTCATATCAGCAAAAACCTGCGGTCAT
TACACATGCTATTGATGCTTGCTTTAAATCGAGTAACAGCATCGCACCCATTTATGACTGCCGTAGATCTAATGG
AAGCAAGCCAACCTGTGTAGCATGGACTCGAAAGCAAATATTGTACATGGTCTATCAGTCTTGGAATCTGTCTTA
TAATAGCAATGAAACATTTAAATGACATCTATGAGGAAGAGCCATTTAATTTTCAAATGGTCTATAATGAGTTTC
AGAAGTTTGTTCAAAGGAAAGCACATTCGGTTTATAATTTTGAAAAACCTGTTGTCATGAAGGCTTTTGAACACT
TGCAGCAATTAGAATTAATAAAGCCCATGGAAAGAACTTCAGGAAATTCACAGAGAGAGTACCAGCTGATGAAAC
TGCTTTTGATAATACTCAAATTATGAATGCTCTGCAGAAATATCCCAACTGTCCTACAGATGTGAGGCAGTGGG
CAACATCCTCACTAAGCTGGTTATGAATATAACCAGTGACTTCAACTTTGGCATTTCATTACACTTCTGTAGAG
AACGGAAAACCTATTGTCCATTAACATGATATGCTAAACATTCTATAAACATTCTTGATTTTATGTGAGACTTGCC
CATCTACTGTCTTGCTGTGCTTGCCTTTTAAATCATGAACAGTTACATGATTTATAATTTCACTGATTGAGATT
ACTTTGTAAGTAGCTGTTTCAAGAATAAAATATGACTGTTTTAGGGACTAGACCATGTGCTTTTTTAAACACTTA
TATATATAATGGTCTATTTGAAGAGCTCACTTCAACCTAACAGCTAGATGTCTTTACAAACCTTAAACCAAAGGA
GTAAAAAACAATGGTAAGCACTGAAGTATAATAAGTAACCTTTGGTACAGCAGGTTTGCTGCAGTGTTTTTTT
CTGTCCACATGCAAATTTTGGATTCTATCCCAGACCCAGGTTTTCTAGTTTCAAGACTAACAGCTTAGTCAGA
AGATGGTTCCATGGAAGAAAAAGGCCAAGGAGTTTGAAGATTTTCTTCTAGACATCTCAAATGTGGTACTCAT
ACCATCCACATCAGAATCCCTTGTAGGATTTTCTAAAATTACAGATTGTTGAGCCTACCATAGGTCAAAGGACT
GGAATTTTCTTCTTAAACAAGTATAGTCATGGCACCACGTAACATTTTGGTCAATGACATTGTATAAAGGGTGGT
CTCATAAGATTATACCATATTTTTACTGTACCTTTTCTATGTCTAAATATACAAATGTTTTACCATTG

950/6881
FIGURE 884

MSSRKSKSNSLIHTECLSQVQRILRERFCRQSPHSNLFQVQVQYKHLSELLKRTALHGESNSVLIIGPRGSGKTM
LINHALKELMEIEEVSENVLQVHLNGLLQINDKIALKEITRQLNLENVVGDKVFGSFAENLSFLEALKKGDRTS
SCPVIFILDEFDLFAHHKNQTLLYNLFDISQSAQTPIAVIGLTCRLDILELLEKRVKSRFSHRQIHLMNSFGFPQ
YVKIFKEQLSLPAEFPDKVFAEKWNENVQYLSEDRSVQEVQKHFNISKNLRLHMLLMALNRVTASHPFMTAV
DLMEASQLCSMDSKANIVHGLSVLEICLI IAMKHLNDIYEEEPFNFQMVYNEFQKFVQRKAHSVYNFEKPVVMKA
FEHLQQLELIKPMERTSGNSQREYQLMKLLLDNTQIMNALQKYPNCPTDVRQWATSSLSWL

951/6881
FIGURE 885

ATTTCGGCACCGCAGCGTAGGTGCTACCACCGCTGCCGTCGCCGCCGCCATTTTGATGGCAGGAAGAGTCCGGTTC
TGGGACAGCTGGAGACAGTGGTGGTGAAGTAACTTTACCAAAGGAAAGCTATTTTGCGAACTATCTTCTCC
AGCGGAGATGGCCAATGTGCTTTGTAAACAGAGCCAGACTGGTTTCCTATCTCCCAGGATTTTGCTCTTTAGTTAA
AAGGGTTGTCAATCCCAAAGCCTTTTCGACTGCAGGATCATCAGGTTCCGATGAGTCTCATGTGGCTGCTGCACC
TCCAGATATATGCTCTCGAACAGTGTGGCCTGATGAACTATGGGACCCTTTGGACCTCAAGATCAGAGGTTCCA
GCTTCCTGGGAACATAGGTTTTGATTGTACCTCAATGGGACTGCTTCACAGAAGAAAAGCCTGGTTCATAAAAC
TTTGCCTGATGTTCTAGCAGAACCTTTATCAAGTGAAAGACATGAGTTTGTGATGGCACAATATGTGAATGAATT
TCAGGGTAATGATGCACCTGTTGAACAAGAAATTAACAGTGCAGAACTTACTTTGAAAGTGCCAGAGTAGAGTG
TGCAATACAAACATGTCCAGAATTGCTGCGAAAAGATTTTGAATCACTGTTTCCAGAAGTAGCTAATGGCAAAC
AATGATTCTGACTGTAACACAAAAAATAAGAATGATATGACTGTTTGGAGTGAAGAAGTAGAAATTGAAAGAGA
AGTGCTCTTAGAAAAGTTCATCAATGGTGCTAAGGAAATTTGCTATGCTCTTCGAGCTGAGGGTTATTGGGCTGA
CTTTATTGACCCATCATCTGGTTTGGCATTTTTTTGGACCATATACAAACAACACTCTTTTTGAAACTGATGAACG
CTACCGACATTTAGGATTCTCTGTTGATGACCTTGGATGCTGTAAAGTGATTTCGTCATAGTCTCTGGGGTACCCA
TGTAAGTTGTAGGGAGTATCTTCACTAATGCAACACCAGACAGCCATATTATGAAGAAATTAAGTGGAAATTAGCA
GAAATATCCATTCAATTTGCTGTACTATTTGTATGTAATATTTGGGTTGATCTATAAACACTGTCAGACTAAAGTT
TTTAAAATATACTTATTTCTAAGTATTTATTTTTCAGCATTTATGAATTTGCAACATTGGCAAGTGATTGTTGGGATT
TAAAATTGCAATGTTCAATTTATTCATATCATTGAATACACGTTGAACACATCCACATTGTATAGGATGTGGTAA
TTAGCTTGTAACCAGGGTATGATCTGCTATTGTTATTTCTCCTCTTTATTGGAAAAAGGCCTCAGTTTTAATTAT
TTTCTTCCCAAATAAATCACACATTTGGTTACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

952/6881
FIGURE 886

MANVLCNRARLVSYLPGFCSLVKRVVNPKAFSTAGSSGSDESHVAAAPPDICSRTVWPDETMGPFPGPDQRFQLP
GNIGFDCHLNGTASQKKS LVHKTLPDVLAEPLSSERHEFVMAQYVNEFQGNDAPVEQEINSAETYFESARVECAI
QTCPELLRKDFESLFPEVANGKLMILTVTQTKNDMTVWSEEVEIEREV LLEKFINGAKEICYALRAEGYWADFI
DPSSGLAFFGPYTNNTLFETDERYRHLGFSVDDLGCCKVIRHSLWGTHVVGSIFTNATPD SHIMKKLSGN

953/6881
FIGURE 887

TATCGCAAGCAGCAGTCTCTGGTCCCAGCCCCACCCCATGGCCCCCTCCCAGTCCCAGCACCCACCAGCAGTAATAAC
AACAGTAGCAGCAGTAGCAACTCAGGATGGGATCAGCTCAGCAAAACGAACCTCTATATCCGAGGACTGCCTCCC
CACACCACCGACCAGGACCTGGTGAAGCTCTGTCAACCATATGGGAAAATAGTCTCCACAAAGGCAATTTTGGAT
AAGACAACGAACAAATGCAAAGGTTATGGTTTTGTGACTTTGACAGCCCTGCAGCAGCTCAAAAAGCTGTGTCT
GCCCTGAAGGCCAGTGGGGTTCAAGCTCAAATGGCAAAGCAACAGGAACAAGATCCTACCAACCTCTACATTTCT
AATTTGCCACTCTCCATGGATGAGCAAGAACTAGAAAATATGCTCAAACCATTGGACAAGTTATTTCTACAAGG
ATACTACGTGATTCCAGTGGTACAAGTCGTGGTGTGGCTTTGCTAGGATGGAATCAACAGAAAAATGTGAAGCT
GTTATTGGTCATTTTAATGGAAAATTTATTAAGACACCACCAGGAGTTTCTGCCCCACAGAACCTTTATTGTGT
AAGTTTGCTGATGGAGGACAGAAAAAGAGACAGAACCCAAACAAATACATCCCTAATGGAAGACCATGGCATAGA
GAAGGAGAGGTGAGACTTGCTGGAATGACACTTACTTACGACCCAACTACAGCTGCTATACAGAACGGATTTTAT
CCTTCACCATACAGTATTGCTACAAACCGAATGATCACTCAAACCTTCTATTACACCCTATATTGCATCTCCTGTA
TCTGCCTACCAGGTGCAAAGTCCTTCGTGGATGCAACCTCAACCATATAATTCTACAGCACCCCTGGTGCCGTGTTA
ACTCCCTCAATGGAGCACACCATGTCACTACAGCCCGCATCAATGATCAGCCCTCTGGCCCAGCAGATGAGTCAT
CTGTCACTAGGCAGCACCGGAACATACATGCCTGCAACGTCAGCTATGCAAGGAGCCTACTTGCCACAGTATGCA
CATATGCAGACGACAGCGGTTCCCTGTTGAGGAGGCAAGTGGTCAACAGCAGGTGGCTGTGAGACGTCTAATGAC
CATTCTCCATATACCTTTCAACCTAATAAGTAACTGTGTGAGATGTACAGAAAGGTGTTCTTACATGAAGAAGGGTG
TGAAGGCTGAACAATCATGGATTTTTCTGATCAATTGTGCTTTAGGAAATTATTGACAGTTTTGCACAGGTTCTT
GAAAACGTTATTTATAATGAAATCAACTAAAACATTTTTTGCTATAAGTTCTATAAGGTGCATAAAACCCTTAAA
TTCATCTAGTAGCTGTTCCCCGAACAGGTTTATTTTAGTAAAAAAAAAAAAA

954/6881
FIGURE 888

MAPPSPTTSSNNNSSSSSSNSGWDQLSKTNLYIRGLPPHTTDQDLVKLCOPYGKIVSTKAILDKTTNKCKGYGFV
DFDSPAAQKAVSALKASGVQAQMAKQQEQDPTNLYISNLPLSMDEQELENMLKPFQVISTRILRDSSGTSRGV
GFARMESTEKCEAVIGHFNGKFIKTPPGVSAPTEPLLCFADGGQKKRQNPKNYIPNGRPWHREGEVRLAGMTLT
YDPTTAAIQNGFYPSYSIATNRMITQTSITPYIASPVSAQVQSPSWMQPPYILQHPGAVLTSPMEHTMSLQP
ASMISPLAQQMSHLSLGSTGYMPATSAMQGAYLPQYAHMQTTAVPVEEASGQQQVAVETSNDHSPYTFQPNK

955/6881
FIGURE 889

AGACTTGGAACCCCAAAGTGTCCGCGACCCTGCACGGCAGCTCCCTTCCAGCTTCATGGGCAAAGTGTGGAAAC
AGCAGATGTACCCTCAGTACGCCACCTACTATTACCCCCAGTATCTGCAAGCCAAGTTTGGAAGGCATTTCGGGAA
TACCAAGTGAAAAGGAAGAGTGAAGAACAGAAAAATGTTAGTGGGATGGCAAACACTGTGAACATTGCTGTTTCT
AGTGGGCCAGAAAAATCAGTCTCTGGTCCCAGCCCACCCCATGGCCCCCTCCCAGTCCCAGCACCCACCAGCAGTAA
TAACAACAGTAGCAGCAGTAGCAACTCAGGATGGGATCAGCTCAGCAAAACGAACCTCTATATCCGAGGACTGCC
TCCCCACACCACCGACCAGGACCTGGTGAAGCTCTGTCAACCATATGGGAAAATAGTCTCCACAAAGGCAATTTT
GGATAAGACAACGAACAAATGCAAAGGTTATGGTTTTGTGCGACTTTGACAGCCCTGCAGCAGCTCAAAAAGCTGT
GTCTGCCCTGAAGGCCAGTGGGGTTCAAGCTCAAATGGCAAAGCAACAGGAACAAGATCCTACCAACCTCTACAT
TTCTAATTTGCCACTCTCCATGGATGAGCAAGAACTAGAAAAATATGCTCAAACCATTTGGACAAGTTATTTCTAC
AAGGATACTACGTGATTCCAGTGGTACAAGTCGTGGTGTGGCTTTGCTAGGATGGAATCAACAGAAAAATGTGA
AGCTGTTATTGGTCATTTTAATGGAAAATTTATTAAGACACCACCAGGAGTTTCTGCCCCACAGAACCTTTATT
GTGTAAGTTTGCTGATGGAGGACAGAAAAAGAGACAGAACCCAAACAAATACATCCCTAATGGAAGACCATGGCA
TAGAGAAGGAGAGGTGAGACTTGCTGGAATGACACTTACTTACGACCCAACTACAGCTGCTATACAGAACGGATT
TTATCCTTCACCATAACAGTATTGCTACAAACCGAATGATCACTCAAACCTTCTATTACACCCTATATTGCATCTCC
TGTATCTGCCTACCAGGTGGCAAAGGAAACCAGAGAAAACAAGTATCGGGGCTCTGCTATCAAGGTGCAAAGTCC
TTCGTGGATGCAACCTCAACCAATATATTCTACAGCACCCCTGGTGCCGTGTTAACTCCCTCAATGGAGCACACCAT
GTCCTACAGCCCGCATCAATGATCAGCCCTCTGGCCCAGCAGATGAGTCATCTGTCACTAGGCAGCACCGGAAC
ATACATGCCTGCAACGTCAGCTATGCAAGGAGCCTACTTGCCACAGTATGCACATATGCAGACGACAGCGGTTCC
TGTTGAGGAGGCAAGTGGTCAACAGCAGGTGGCTGTGAGACGTCTAATGACCATTCTCCATATACCTTTCAACC
TAATAAGTAACTGTGAGATGTACAGAAAGGTGTTCTTACATGAAGAAGGGTGTGAAGGCTGAACAATCATGGATT
TTTCTGATCAATTGTGCTTTAGGAAATTATTGACAGTTTTGCACAGGTTCTTGAAAACGTTATTTATAATGAAAT
CAACTAAAACATTTTTTGCTATAAGTTCTATAAGGTGCATAAAACCCTTAAATTCATCTAGTAGCTGTTCCCCCG
AACAGGTTTATTTTAGTAAAAAAAAAAAAA

956/6881
FIGURE 890

MAPPSPTTSSNNNSSSSSSNSGWDQLSKTNLYIRGLPPHTTDQDLVKLCQPYGKIVSTKAILDKTTNKCKGYGFV
DFDSPAAQKAVSALKASGVQAQMAKQQEQDPTNLYISNLPLSMDEQELENMLKPFQGVISTRILRDSSGTSRGV
GFARMESTEKCEAVIGHFNGKFIKTPPGVSAPTEPLLCKFADGGQKKRQNPKNYIPNGRPWHREGEVRLAGMTLT
YDPTTAAIQNGFYPSPIATNRMITQTSITPYIASPVSAQVAKETRENKYRGSIAKVQSPSWMQPQPYILQHP
GAVLTPSMEHTMSLQPASMISSPLAQQMSHLSLGSTGTYPATSAMQAYLPQYAHMQTTAVPVEEASGQQQVAVE
TSNDHSPYTFQPNK

957/6881
FIGURE 891

GGCTAATGTAACATACTCTACCACTTGGTCTGAAGCCCAGCAGTATCTGATGGATAATCCAACCTTTTGCAGAAGA
TGAGGAGTTACAAAATATGGACAAAGAAGATGCATTAATTTGCTTTGAAGAACACATTCGGGGCTTTAGAAAAGGA
GGAAGAAGAAGAAAAACAGAAGAGTTTGTCTGAGAGAAAAGGAGACGACAGCGAAAAAATAGGGAATCTTTCAGAT
ATTTTTAGATGAATTACATGAACATGGACAACCTGCATTCTATGTCATCTTGGATGGAATTGTATCCAACCTATTAG
TTCTGATATTAGATTCACTAATATGCTTGGTCAGCCTGGATCAACTGCACCTTGATCTTTTTCAAGTTTTATGTTGA
GGATCTTAAAAGCACGTTATCATGACGAGAAGAAGATAATAAAAAGACATTCTAAAGGATAAAGGATTTGTAGTTGA
AGTAAACACTACTTTTTGAAGATTTTTGTGGCGATAATCAGTTCAACTAAAAGATCAACTACATTAGATGCTGGAAA
TATCAAATTTGGCTTTCAATATTACTAGAAAAGGCAGAAGCCCGTGAACGTGAAAGAGAAAAAGAAGAGGCTCGGA
AGATGAAAACGAAAAGAATCTGCATTTAAGAGTATGTTAAAACAAGCTGCTCCTCCGATAGAATTGGATGCTGTCT
GGGAAGATATCCGTGAGAGATTTGTAAAAGAGCCAGCATTTGAGGACATAACTCTAGAATCTGAAAGAAAACGAA
TATTTAAAGATTTTATGCATGTGCTTGAGCATGAATGTCAGCATCATCATTCAAAGAACAAGAAACATTCTAAGA
AATCTAAAAAACATCATAGGAAACGTTCCCGCTCTCGATCGGGGTCAGATTCAGATGATGATGATAGCCATTCAA
AGAAAAAAGACAGCGATCAGAGTCTCGTTCTGCTTCAGAACATTCTTCTAGTGCAGAGTCTGAGAGAAGTTATA
AAAAGTCAAAAAAGCATAAGAAGAAAAGTAAGAAGAGGAGACATAAATCTGACTCTCCAGAATCCGATGCTGAGC
GAGAGAAGGATAAAAAAGAAAAGATCGGGAAAGTGAAAAAGACAGAAGTAGACAAAAGATCAGAATCAAAACACA
AATCGCCTAAGAAAAAGACTGGAAAGGATTCTGGTAATTGGGATACTTCTGGCAGCGAACTGAGTGAAGGGGAAT
TGGAAAAGCGCAGAAGAACCCTTTTGGAGCAACTGGATGATGATCAATTAATTTATACCAAATATATGTTTACAGT
ATGATTTAAAGTCTGATTGAGACCAGGGACTCTATTTTAAAGTTCAACTGAAATAACACTGGGTTTTAATTATATC
ACAGGAAAAAAGTGCATTTAAGTATTGTTATCGTGGACTTTATAAAAGCAAAGGAAATTGAAAGTAACTTTT
GATTCTGTATCAAGAATCATATTTTATACAGTCATAACTGTCTTTCTGTGACCCTTTACAGGGCACTGTAGGA
TGGATTAAAGGTGGCAATTTACTGATAACTGCAGATGTCTCTACTTTGTTCTAAAATCTAAGTCATGAGGTGATT
TGATTTACTTTATAGAAGCTGGATTTTGAAGATCTAATGAAAAATTTTTTGATAATATAGTAGTACAAAAAAGC
ACCAGCAACTGATAAAAATTGCTTTTTTGTGCGCTACCCAACTGGTTAAAGCCAATGTGATCTTTTATGGTGAAA
CTCCTAAGAAACAGGTGGTTTTGCTGGAACTTGGTAGACCCTTAATTATAGTGGTGCTAATGAGCACTACTGTA
ATATAAAGCCACCATTATTTTTTATCAAACATCTGAATACATTTTACAAAGGCTATTGTGAGGGCATTATTTTGA
GCATCTATTTTGGAGGTGATGTTTTAAAAAACTTTAACATCAAATCAAATTGTAAATTAATTTAAATATATTGCCT
TAAGGACCTACTAAAGAATGTGCCACCAGACTTTAAGTGATAGTTGCAATATCCTTGCTCTAAAAAAGGAGGAGG
GTTGACTTAAACATTTTCTTTAACAGTTGTCTTTTTTTTCTAAATTCAGTCTTTCTCTTGCTTTTTTTTCCCTGC
TATTGAGGAAGTATTTTGCCTTCCCTACTCACTGAGAAGTATTGACTTCGTGGTACACATTCTAAAGCATTTCGTG
ATTTGAATATTTTTGTACATTTTTATCAATTATTAAACCTTCTCTCTAGTG

958/6881
FIGURE 892

MLEISNWLSILLEKAEAREREREKEEARKMKRKESAFKSMLKQAAPPIELDAVWEDIRERFVKEPAFEDITLESE
RKRIFKDFMHVLEHECQHHSKNNKHSKKSCKHHRKRSRSGSDSDDDSHSKKKRQRSESRASEHSSSAESE
RSYKKSCKHKKSKKRRHKSDSPESDAEREKDKKEKDRESEKDRTRQRSESKHKSPKKKTGKDSGNWDTSGSELS
EGELEKRRRTLLEQLDDDQ

959/6881
FIGURE 893

CCAGCACGCGGCCGCTCTGGCCCAGGGAAGTCCCTGTCCTTACCTTCAGCAGGAGCCGGTTCCCTGTGTGTGTGT
CCGCTCGCCCTCTGCTCCGTCTGCGGCTGCCCCTGCCCTCCTACGGTCCACCATGGCCCTGCTGCACTCCGGC
CGCGTCTCCCCGGGATCGCCGCCGCTTCCACCCGGGCCTCGCCGCCGCGGCTCTGCCAGAGCCAGCTCCTGG
TGGACCCATGTGGAATGGGACCTCCAGATCCCATTCTGGGAGTCACTGAAGCCTTTAAGAGGGACACCAATAGC
AAAAAGATGAATCTGGGAGTTGGTGCCTACCGGGATGATAACGGAAGCCTTACGTGCTGCCTAGCGTCCGCAAG
GCAGAGGCCCAGATTGCCGCAAAAAATTTGGACAAGGAATACCTGCCCATTTGGGGGACTGGCTGAATTTTGCAAG
GCATCTGCAGAACTAGCCCTGGGTGAGAACAGCGAAGTCTTGAAGAGTGGCCGGTTTGTCACTGTGCAGACCATT
TCTGGAACCTGGAGCCTTAAGGATCGGAGCCAGTTTTCTGCAAAAGATTTTTTAAGTTTCAGCCGAGATGTCTTTCTG
CCCAAACCAACCTGGGGAAACCACACACCCATCTTCAGGGATGCTGGCATGCAGCTACAAGGTTATCGGTATTAT
GACCCCAAGACTTGCGGTTTTGACTTCACAGGCGCTGTGGAGGATATTTCAAAAATACCAGAGCAGAGTGTTCTT
CTTCTGCATGCCTGCGCCACAAATCCCACGGGAGTGGACCCGCGTCCGGAACAGTGGAAGGAAATAGCAACAGTG
GTGAAGAAAAAGGAATCTCTTTGCGTTCTTTGACATGGCCTACCAAGGCTTTGCCAGTGGTGATGGTGATAAGGAT
GCCTGGGCTGTGCGCCACTTCATCGAACAGGGCATTAAATGTTTGTCTCTGCCAATCATATGCCAAGAACATGGGC
TTATATGGTGAGCGTGTAGGAGCCTTCACTATGGTCTGCAAAGATGCGGATGAAGCCAAAAGGGTAGAGTCACAG
TTGAAGATCTTGATCCGTCCCATGTATTCCAACCTCCCTCAATGGGGCCCGGATTGCTGCTGCCATTCTGAAC
ACCCAGATTTGCGAAAACAATGGCTGCAAGAAGTGAAAGGCATGGCTGACCGCATCATTGGCATGCGGACTCAA
CTGGTCTCCAACCTCAAGAAGGAGGGTTCCACCCACAATTGGCAACACATCACCGACCAAATTGGCATGTTCTGT
TTCACAGGGCTAAAGCCTGAACAGGTGGAGCGGCTGATCAAGGAGTTCTCCATCTACATGACAAAAGATGGCCGC
ATCTCTGTGGCAGGGGTACCTCCAGCAACGTGGGCTACCTTGCCCATGCCATTACCAGGTCACCAAGTAATGT
CCCTGGTGCGAGGAAACAGAGACAACCTTTCTGTCTTCAGCCTCTGCTATTGAGAGCTTCACACAGACAATGAGA
GAGGGTGGATGGTGGTGAGTGGATCATTTCTTTTCAGCCACAGTGTGTAACACTCAGCATTTGAATGTTTCTCAGA
AAAGAACATGTAGTGACACAGGGCAGAGGCATCCATGGCTGGCGTCTGGAATATTAAACCAAACCTCTCCCGGTC
CTTTTTTCTCCAACTTTTCTCAAAGAGTTTACATGTGCAAGAAAGTCATCGCACCAAAAAACCTGTCAATTATGC
CATTGCAATATTTCAGAAGCTTTAACTGAAGTGTGAGGTTCTCTGTGAGAAACAGCACACGTTAGAGGCTTTGAG
AGAAGGCCTAGTTCTGTGCATGAGTAGTCGGCCTCGTGTCTGTCTCTCCCATCTTGGAACAACCTTATCAACAGGCC
GCACTGCAGAAATGATGTTTTATGAAAACCAATGAGGCTGCTGCCACTCCAGCAAGGGAAATAATGCAGTTTCCT
GTCTTATTTAAGAAAAAGAGAAGGCTCTCTTTTCTCCCTTGTCATTGCCGTTCTTTTCTTACACGCAAAGATTT
TTTAACTATTGCAGATTTTCATCCCATTTCTACTGCTTGATTGACCATCAACTCCATCCTATCGAGATTTATTTAA
GAATGAAGAACATAATTTTCTGCTGATGCCGTACCTCACCTTTTTTCAGCAAAGAATAGTGGAGAGTAGGAAACT
GTACTTTATCTCGGCATCCTCTTGAATGATAGTGCAAGTTTCTCCAGTTGGGATGTTGTCTCTGCCCGGTTGGAC
CTCCTCCCTTTGTTGAATGTGGTGTGCAGCCTCTCATCTCACACTGTGAGTCCAGCGGCGCAGGGTGGTACCAGG
AAAGAGGATATTCTAGGCTTTGCGTGCTGCTAGCTGGGTTTCAGGCTTCACCCACTGGAAAGAACCACCATCTGCT
CTAACCATGTAGACTTATTGCGGCCTGGTTTCTCTGTTACAATAAAATTACTGTAGACCC

960/6881
FIGURE 894

GAGTGACTCCACCGCCCGGAGCAGCGGTGCAGGACGCGCGTCTCCGCCGCCCGCGGTGACTTCTGCCTGCGCTCC
TTCTCTGAACGCTCACTTCCGAGGAGACGCCGACGATGAAGACACCGTGGAAGGTTCTTCTGGGACTGCTGGGTG
CTGCTGCGCTTGTACCATCATCACCGTGCCCGTGGTTCTGCTGAACAAAGGCACAGATGATGCTACAGCTGACA
GTCGCAAACTTACACTCTAACTGATTACTTAAAAATACTTATAGACTGAAGTTATACTCCTTAAGATGGATTT
CAGATCATGAATATCTCTACAAACAAGAAAATAATATCTTGGTATTCAATGCTGAATATGGAAACAGCTCAGTTT
TCTTGGAGAACAGTACATTTGATGAGTTTGGACATTCTATCAATGATTATTCAATATCTCCTGATGGGCAGTTTA
TTCTCTTAGAATACAACCTACGTGAAGCAATGGAGGCATTCTACACAGCTTCATATGACATTTATGATTTAAATA
AAAGGCAGCTGATTACAGAAGAGAGGATTCCAAACAACACACAGTGGGTCACATGGTCACCAGTGGGTCATAAAT
TGGCATATGTTTGGAAACAATGACATTTATGTTAAAAATTGAACCAAATTTACCAAGTTACAGAATCACATGGACGG
GGAAAGAAGATATAATATATAATGGAATAACTGACTGGGTTTATGAAGAGGAAGTCTTCAGTGCCTACTCTGCTC
TGTGGTGGTCTCCAAACGGCACATTTTTTAGCATATGCCCAATTTAACGACACAGAAGTCCCACTTATTGAATACT
CCTTCTACTCTGATGAGTCACTGCAGTACCCAAAGACTGTACGGGTTCATATCCAAAGGCAGGAGCTGTGAATC
CAACTGTAAAGTTCTTTGTTGTAAATACAGACTCTCTCAGCTCAGTCACCAATGCAACTTCCATACAAATCACTG
CTCCTGCTTCTATGTTGATAGGGGATCACTACTTGTGTGATGTGACATGGGCAACACAAGAAAGAATTTCTTTGC
AGTGGCTCAGGAGGATTGAGAACTATTCCGGTCATGGATATTTGTGACTATGATGAATCCAGTGAAGATGGAAC
GCTTAGTGGCACGGCAACACATTGAAATGAGTACTACTGGCTGGGTTGGAAGATTTAGGCCTTCAGAACCTCATT
TTACCCTTGATGGAATAGCTTCTACAAGATCATCAGCAATGAAGAAGTTACAGACACATTTGCTATTTCCAAA
TAGATAAAAAAGACTGCACATTTATTACAAAAGGCACCTGGGAAGTCATCGGGATAGAAGCTCTAACCACTGATT
ATCTATACTACATTAGTAATGAATATAAAGGAATGCCAGGAGGAAGGAATCTTTATAAAATCCAACCTAGTGACT
ATACAAAAGTGACATGCCTCAGTTGTGAGCTGAATCCGGAAGGTGTCAGTACTATTCTGTGTCATTAGTAAAG
AGGCGAAGTATTATCAGCTGAGATGTTCCGGTCTGGTCTGCCCTCTATACTCTACACAGCAGCGTGAATGATA
AAGGGCTGAGAGTCCTGGAAGACAATTCAGCTTTGGATAAAATGCTGCAGAATGTCCAGATGCCCTCCAAAAAC
TGGACTTCATTATTTTGAATGAAACAAAATTTTGGTATCAGATGATCTTGCCTCCTCATTTTGATAAATCCAAGA
AATATCCTCTACTATTAGATGTGTATGCAGGCCCATGTAGTCAAAAAGCAGACACTGTCTTCAGACTGAACTGGG
CCACTTACCTTGCAAGCACAGAAAACATTATAGTAGCTAGCTTTGATGGCAGAGGAAGTGGTTACCAAGGAGATA
AGATCATGCATGCAATCAACAGAAGACTGGGAACATTTGAAGTTGAAGATCAAATTGAAGCAGCCAGACAATTTT
CAAAAATGGGATTTGTGGACAACAAACGAATTGCAATTTGGGGCTGGTCATATGGAGGGTACGTAACCTCAATGG
TCCTGGGATCGGGAAGTGGCGTGTTCAGTGTGGAATAGCCGTGGCGCCTGTATCCCGGTGGGAGTACTATGACT
CAGTGTACACAGAACGTTACATGGGTCTCCAACTCCAGAAGACAACCTTGACCATTACAGAAATTC AACAGTCA
TGAGCAGAGCTGAAAAATTTAAACAAGTTGAGTACCTCCTTATTTCATGGAACAGCAGATGATAACGTTCACTTTC
AGCAGTCAGCTCAGATCTCCAAAGCCCTGGTCGATGTTGGAGTGGATTTCCAGGCAATGTGGTATACTGATGAAG
ACCATGGAATAGCTAGCAGCACAGCACACCAACATATATATATACCCACATGAGCCACTTCATAAAACAATGTTTCT
CTTTACCTTAGCACCTCAAAAATACCATGCCATTTAAAGCTTATTAATAAACTCATTTTTGTTTTTATTATCTCAAAA
CTGCACTGTCAAGATGATGATGATCTTTAAATACACACTCAAATCAAGAACTTAAGGTTACCTTTGTTCCCAA
ATTTATACCTATCATCTTAAGTAGGGACTTCTGTCTTCAACACAGATTATTACCTTACAGAAGTTTGAATTATC
CGGTCCGGTTTTTATTGTTTAAATCATTCTGCATCAGCTGCTGAAACAACAAATAGGAATTGTTTTTATGGAGG
CTTTGCATAGATTCCCTGAGCAGGATTTTAAATCTTTTCTAACTGGACTGGTTCAAATGTTGTTCTCTCTTTAA
AGGGATGGCAAGATGTGGGCAGTGATGTCACTAGGGCAGGGACAGGATAAGAGGGATTAGGGAGAGAAGATAGCA
GGGCATGGCTGGGAACCCAAGTCCAAGCATAACACAGCAGGCTACTGTCAGCTCCCTCGGAGAAGAGCTG
TTCACAGCCAGACTGGCACAGTTTTCTGAGAAAGACTATTCAAACAGTCTCAGGAAATCAAATATGCAAAGCACT
GACTTCTAAGTAAAACACAGCAGTTGAAAAGACTCCAAAGAAATGTAAGGGAACTGCCAGCAACGCAGGCCCC
CAGGTGCCAGTTATGGCTATAGGTGCTACAAAACACAGCAAGGGTGATGGGAAAGCATTGTAAATGTGCTTTTA
AAAAAATACTGATGTTCTAGTGAAAGAGGCAGCTTGAACTGAGATGTGAACACATCAGCTTGCCTGTGTA
AAGATGAAAATATTTGTATCACAAATCTTAACCTGAAGGAGTCCTTGATCAATTTTTCTTATTTCAATTTCTTG
AGTGTCTTAATTAAGAATATTTTAACTTCCTTGACTCATTTTAAAAATGGAACATAAATACAATGTTATG
TATTATTATCCATTCTACATACTATGGAATTTCTCCAGTCATTTAATAAATGTGCCTTCATTTTTTC

961/6881
FIGURE 895

MKTPWKVLLGLLGAAALVTIITVPVLLNKGTDATADSRKTYTLTDYLNKNTYRLKLYSLRWISDHEYLYKQENN
ILVFNAEYGNSSVFLENSTFDEFGHSINDYSISPDGQFILLEYNVVKQWRHSYTASYDIYDLNKRQLITEERIPN
NTQWVTWSPVGHKLAYVWNNDIYVKIEPNLPSYRITWTGKEDIYNGITDWVYEEEFVSAYSALWWSPNGTFLAY
AQFNDTEVPLIEYSFYSDSLQYPKTVRVPYPKAGAVNPTVKFFVVNTDSLSSVTNATSIQITAPASMLIGDHYL
CDVTWATQERISLQWLRRIQNYSVMDICDYDESSGRWNCILVARQHIEMSTTGWVGRFRPSEPHFTLDGNSFYKII
SNEEGYRHCYFQIDKKDCTFITKGTWEVIGIEALTSYLYYISNEYKGMPGGRNLYKIQLSDYTKVTCLSCELN
PERCQYYSVSFSKEAKYYQLRCSGPGLPLYTLHSSVNDKGLRVLEDNSALDKMLQNVQMPSKKLDFIILNETKFW
YQMILPPHFDKSKKYPLLLDVYAGPCSQKADTVFRLNWATYLASTENIIVASFDGRGSGYQGDKIMHAINRRLGT
FEVEDQIEAARQFSKMGFVDNKRIAIWGWSYGGYVTSMVLGSGSGVFKCGIAVAPVSRWEYYDSVYTERYMGLPT
PEDNLDHYRNSTVMSRAENFKQVEYLLIHGTADDNVHFQQSAQISKALVDVGVDFAQMWYTDHGHASSTAHQH
IYTHMSHFIFKQCFSLP

962/6881
FIGURE 896

GTTTGAAATCGGAAAGTTGGCGGGGCTGCGGGGAGCTGAGCCTAGAGTCCGGCTGTTGGCTAGAGTGGGCGCGGAT
CTGGTGTGGGGAAGGCGGGCGGGACTCAGGCCTGCCTGCGAAGCATTGTCCTACATAATGGTAGAGGACGAAC TGG
CACTTTTCGATAAAAAGCATAAAATGAATTTTGGAAATAAATTCAAAAGTACGGACACCTCCTGTCAGATGGCGGGAC
TAAGAGATACCTACAAGGATTCCATCAAAGCATTTCAGAGAAAAGCTGTCTGTGAAATTAAAGGAAGAAGAACGAA
TGGTTGAGATGTTTCTGGAATATCAAAATCAGATCAGCAGGCAAAATAAGCTCATTCAAGAAAAAAGGATAACT
TGTTAAAATTGATTGCTGAAGTAAAAGGCAAAAAGCAGGAATTGGAAGTACTGACTGCAAATATCCAGGATCTTA
AGGAAGAATATTCTAGGAAGAAGGAAACTATTTCTACTGCTAATAAAGCGAATGCAGAGAGGTTGAAAAGGCTGC
AGAAATCTGCAGACTTGTATAAAGATCGACTTGGACTAGAAATTCGAAAAATTTATGGTGAGAAATTGCAGTTTA
TTTTCACTAATATTGACCCTAAGAATCCTGAGAGCCCATTTATGTTTTCTTACATCTCAATGAAGCAAGGGACT
ATGAAGTGTGAGATAGTGCCCCTCATCTTGAGGGCCTAGCAGAATTTCAAGAGAAATGTAAGGAAGACCAACAATT
TTTCAGCTTTTCTTGCCAATGTTTCGGAAAGCTTTTACTGCCACGGTTTATAATTAACATACAAATAGTGTATATA
AAAACGGTTTATTTTTCTTCTCTATTACATATCTCTTTTTTTTTCTTGTTTTTATTATTACTATACTTTAAGTTTT
AGGGTACATGTGCACAATGTGCAGGTTTGTTACATATGTATACATGTGCCATATTGGTGCTGCACCCATTAAAC
TCGTCATTTTCATTAGGTATATCTCCTAAIGCTATCCCTCCCCCTCCCCCAACCCACAACAGTCCCCGTTGTGTG
ATGTTCCCCTTCCTGTGTCCATGTGTTCTCATTGTTCAATTCACCTAGGAGTGAGAATATGTGGTGTTTGGTT
TTTTGTCTTTTCGATAGTTTGCTGAGAATGATGGTTTCCAGCTTCATCCATGTTCTTACAAAGGACATGAAC TCA
TCCTTTTTTATGGCTGCATAGTATTCCATGGTGTATATGTGCCACATTTTCTTAATCCAGTCTATCATTGTTGGA
CATTTGGGTTGGTTCCAAGTCTTTGCTATTGTGAATAGTGCCGAAATAAACATACGTGTGCATGTGTCTCCAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

963/6881
FIGURE 897

MVEDELALFDKSINEFWNFKSTDTSCQMAGLRDITYKDSIKAFAEKLSVKLKEEERMVEMFLEYQNQISRQNKLI
QEKKNLLKLI AEVKGKKQELEVLTANIQDLKEEYSRKKETISTANKANAERLKRLQKSADLYKDRLGLEIRKIY
GEKLQFIFTNIDPKNPESPFMFSLHLNEARDYEVSDSAPHLEGLAEFQENVRKTNNFSAFLANVRKAFTATVYN

964/6881
FIGURE 898

AAGCACAGGCCACCACTCTGCCCTGGTCCACACAAGCTCCGGTAGCCCATGGAGCCCTGGCCTCTCCTCCTGCTC
TTTAGCCCTTTGCTCAGCTGGCCTCGTCCTGGGCTCCGAACATGAGACCCGTCTGGTGGCAAAGCTATTTAAAGAC
TACAGCAGCGTGGTGCGGCCAGTGGAAGACCACCGCCAGGTCGTGGAGGTCACCGTGGGCCTGCAGCTGATACAG
CTCATCAATGTGGATGAAGTAAATCAGATCGTGACAACCAATGTGCGTCTGAAACAGCAATGGGTGGATTACAAC
CTAAAATGGAATCCAGATGACTATGGCGGTGTGAAAAAAATTCACATTCCTTCAGAAAAGATCTGGCGCCAGAC
CTTGTTCTCTATAACAATGCAGATGGTGACTTTGCTATTGTCAAGTTCACCAAAGTGCTCCTGCAGTACACTGGC
CACATCAGCTGGACACCTCCAGCCATCTTTAAAAGCTACTGTGAGATCATCGTCACCCACTTTCCCTTTGATGAA
CAGAACTGCAGCATGAAGCTGGGCACCTGGACCTACGACGGCTCTGTCTGGCCATCAACCCGGAAAGCGACCAG
CCAGACCTGAGCAACTTCATGGAGAGCGGGGAGTGGGTGATCAAGGAGTCCCAGGGCTGGAAGCACTCCGTGACC
TATTCCTGCTGCCCCGACACCCCTACCTGGACATCACCTACCACTTCGTTCATGCAGCGCCTGCCCCCTCTACTTC
ATCGTCAACGTTCATCATCCCTGCCTGCTCTTCTCCTTCTTAACTGGCCTGGTATTCTACCTGCCCACAGACTCA
GGGAGAAGATGACTCTGAGCATCTCTGTCTTACTGTCTTTGACTGTGTTCTTCTGGTCATCGTGGAGCTGATC
CCCTCCACGTCCAGTGCTGTGCCCTTGATTGGAAAATACATGCTGTTACCATGGTGTTCGTTCATTGCCTCCATC
ATCATCACTGTTCATCGTCATCAACACACACCACCGCTCACCCAGCACCCATGTTCATGCCCAACTGGGTGCGGAAG
GTTTTTATCGACACTATCCCAAATATCATGTTTTTCTCCACAATGAAAAGACCATCCAGAGAAAAGCAAGACAAA
AAGATTTTTTACAGAAGACATTGATATCTCTGACATTTCTGGAAAGCCAGGGCCTCCACCCATGGGCTTCCACTCT
CCCCTGATCAAAACACCCCGAGGTGAAAAGTGCCATCGAGGGCATCAAGTACATCGCAGAGACCATGAAGTCAGAC
CAGGAGTCTAACAATGCGGCGGCAGAGTGGAAGTACGTTGCAATGGTGATGGACCACATACTCCTCGGAGTCTTC
ATGCTTGTTTGCATCATCGGAACCTAGCCGTGTTTGAGGTCGACTCATTGAATTAAATCAGCAAGGATAGCA
GAAAATGAGCTGAGCTTAGCTCTGCCCTGGAACCTACCAGAGCAGAGAAGGGCAGGAGAGGAAGATTTGTCTACT
TGCTCCACTCGCACTTATCAAACGTGTTATATTCCATACTTATTATTGATGATAAGATTTACCTTTATGTAAGTT
TATGGCCTTGAAGTGTTTTCATATTGCTTCTCCCTTTAGTTCTGCTGTCTCCCTGAAGAGTGAACCCTCTTTAGT
AAATGAACTAATCACT

965/6881
FIGURE 899

MEPWPLLLLFSLCSAGLVLGSEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTVGLQLIQLINVDEVNQIVTTNVR
LKQQWVDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTPPAIFKSYCEI
IVTHFFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKESRGWKHSVTYSCCPDTPYLDITYHF
VMQRLPLYFIVNVIIPCLLFSLTGLVFYLPDTSGEKMTLSISVLLSLTVFLLVIVELIPSTSSAVPLIGKMYLF
TMVFVIASIIITVIVINTHHRSPSTHVMPNWRKVFIDTIPNIMFFSTMKRPSREKQDKKIFTEDIDISDISGKP
GPPPMGFHSPLIKHPEVKSAIEGIKYIAETMKSDQESNNAAEWKYVAMVMDHILLGVFMLVCIIGTLAVFAGRL
IELNQQG

966/6881
FIGURE 900

GTTTCGCAGCCGCCGCCGCCGCCGCTCGCTCTCCAACGCCAGCGCCGCCCTCTCGCTCGCCGAGCTCCAGCCGAAG
GAGAAGGGGGGTAAGTAAGGAGGTCTCTGTACCATGGCTCGTACAAAGCAGACTGCCCGCAAATCGACCGGTGGT
AAAGCACCCAGGAAGCAACTGGCTACAAAAGCCGCTCGCAAGAGTGCGCCCTCTACTGGAGGGGTGAAGAAACCT
CATCGTTACAGGCCTGGTACTGTGGCGCTCCGTGAAATTAGACGTTATCAGAAGTCCACTGAACTTCTGATTTCGC
AAACTTCCCTTCCAGCGTCTGGTGCGAGAAATTGCTCAGGACTTTAAACAGATCTGCGCTTCCAGAGCGCAGCT
ATCGGTGCTTTGCAGGAGGCAAGTGAGGCCTATCTGGTTGGCCTTTTTGAAGACACCAACCTGTGTGCTATCCAT
GCCAAACGTGTAACAATTATGCCAAAAGACATCCAGCTAGCACGCCGCATACGTGGAGAACGTGCTTAAGAATCC
ACTATGATGGGAAACATTTTCACTCTCAAAAAAAAAAAAAAAAAAATTTCTCTTCTTCTGTTATTGGTAGTTCTGAAC
GTTAGATATTTTTTTTCCATGGGGTCAAAAGGTACCTAAGTATATGATTGCGAGTGGAAAAATAGGGGACAGAAA
TCAGGTATTGGCAGTTTTTCCATTTTCATTTGTGTGTGAATTTTAAATAAATGCGGAGACGTAAAGCATTAAAT
GCAAGTTAAATGTTTCAGTGAACAAGTTTCAGCGGTCAACTTTATAATAATTATAAATAAACCTGTAAATTT
TTCTGGACAATGCCAGCATTGGATTTTTTTTAAACAAGTAAATTTCTTATTGATGGCAACTAAATGGTGTGTTGT
AGCATTTTTATCATACAGTAGATTCCATCCATTCACTATACTTTTCTAACTGAGTTGTCCTACATGCAAGTACAT
GTTTTTAATGTTGTCTGTCTTCTGTGCTGTTTCTGTAAGTTTGCTATTAAAATACATTAAACTAT

967/6881
FIGURE 901

CGCCGAGCTCCAGCCGAAGGAGAAGGGGGGTAAGTAAGGAGGTCTCTGTACCATGGCTCGTACAAAGCAGACTGC
CCGCAAATCGACCGGTGGTAAAGCACCCAGGAAGCAACTGGCTACAAAAGCCGCTCGCAAGAGTGCGCCCTCTAC
TGGAGGGGTGAAGAAACCTCATCGTTACAGGCCTGGTACTGTGGCGCTCCGTGAAATTAGACGTTATCAGAAGTC
CACTGAACTTCTGATTCGCAAACCTCCCTTCCAGCGTCTGGTGCGAGAAATTGCTCAGGACTTTAAACAGATCT
GCGCTTCCAGAGCGCAGCTATCGGTGCTTTGCAGGAGGCAAGTGAGGCCTATCTGGTTGGCCTTTTTGAAGACAC
CAACCTGTGTGCTATCCATGCCAAACGTGTAACAATTATGCCAAAAGACATCCAGCTAGCACGCCGCATACGTGG
AGAACGTGCTTAAGAATCCACTATGATGGGAAACATTTTCATTCTCTCCATGGGGTCAAAGGTACCTAAGTATAT
GATTGCGAGTGGA

968/6881
FIGURE 902

MARTKQTARKSTGGKAPRKQLATKAARKSAPSTGGVKKPHRYRPGTVALREIRRYQKSTELLIRKLFPQRLVREI
AQDFKTDLRFSAAIGALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA

969/6881
FIGURE 903

CAGCCGTTGAGGGGACGGGCCTGCGTTCTCTCCTCCTTCCCTCCCCGCCTCCAGCTGCCGGCAGGACCTTTCTCTC
GCTGCCGCTGGGACCCCGTGTCTATCGCCAGGCCGAGCACGATGCCCCCTAAAAAGGGAGGTGATGGAATTAAAC
CACCCCCAATCATTTGGAAGATTTGGAACCTCACTGAAAATTGGTATTGTTGGATTGCCAAATGTTGGGAAATCTA
CTTTCTTCAATGTGTTAACCAATAGTCAGGCTTCAGCAGAAAACCTCCCGTTCTGCACTATTGATCCTAATGAGA
GCAGAGTACCTGTGCCAGATGAAAGGTTTGACTTTCTTTGTCAATACCACAAAACCAGCAAGCAAAATTCCTGCCT
TTCTAAATGTGGTGGATATTGCTGGCCTTGTGAAAGGAGCTCACAATGGGCAGGGCCTGGGGAATGCTTTTTTAT
CTCATATTAGTGCCTGTGATGGCATCTTTCATCTAACACGTGCTTTTGAAGATGATGATATCACGCACGTTGAAG
GAAGTGTAGATCCTATTTCGAGATATAGAAATAATACATGAAGAGCTTCAGCTTAAAGATGAGGAAATGATTGGGC
CCATTATAGATAAACTAGAAAAGGTGGCTGTGAGAGGAGGAGATAAAAAACCTAAACCTGAATATGATATAATGT
GCAAAGTAAAATCCTGGGTTATAGATCAAAAGAAACCTGTTTCGCTTCTATCATGATTGGAATGACAAAGAGATTG
AAGTGTGAATAAAACACTTATTTTTGACTTCAAAACCAATGGTCTACTTGGTTAATCTTTCTGAAAAAGACTACA
TTAGAAAGAAAAACAAATGGTTGATAAAAATTAAAGAGTGGGTGGACAAGTATGACCCAGGTGCTTTGGTCATTC
CTTTTAGTGGGGCCTTGGAACCTCAAGTTGCAAGAATTGAGTGCTGAGGAGAGACAGAAGTATCTGGAAGCGAACA
TGACACAAAGTGCTTTGCCAAAGATCATTAAAGGCTGGGTTTGCAGCACTCCAACCTAGAATACTTTTTCACTGCAG
GCCCAGATGAAGTGCGTGCATGGACCATCAGGAAAGGGACTAAGGCTCCTCAGGCTGCAGGAAAGATTACACAG
ATTTTGAAAAGGGATTCAATTATGGCTGAAGTAATGAAATACGAAGATTTTAAAGAGGAAGGTTCTGAAAATGCAG
TCAAGGCTGCTGGAAAGTACAGACAACAAGGCAGAAATTATATTGTTGAAGATGGAGATATTATCTTCTTCAAAT
TTAACACACCTCAACAACCGAAGAAGAAATTAAAATTTAGTTATTGCTCAGATAAACATACAACCTTCCAAAAGGCA
TCTGATTTTTTAAAAAATTAAAAATTTCTGAAAACCAATGCGACAAATAAAGTTGGGGAGATGGGAATCTTTGACAA
ACAAATTATTTTTATTTGTTTTTAAAATTAAAATACTGTGTACCCCCCCCCCCCCATGAAATGCAGGTTCACTAAA
TGTGAACAGCTTTGCTTTTCACGTGATTAAGACCCTACTCCAAATTGTAGAAGCTTTTCAGGAACCATATTACTC
TCATGATACTTCATTAATCTCCATCATGTATGCCAAGCCTGACACATTTGACAGTGAGGACAATGTGGCTTGCTC
CTTTTTGAATCTACAGATAATGCATGTTTTACAGTACTCCAGATGTCTACACTCAATAAAACATTTGACAAAACC
AAAAA

970/6881
FIGURE 904

MPPKKGGDIKPPPIIGRFGTSLKIGIVGLPNVGKSTFFNVLNSQASAENFPFCTIDPNESRVVPDERFDFLC
QYHKPASKIPAFNLNVVDIAGLVKGAHNGOGLGNAFLSHISACDGIFHLTRAFEDDDITHVEGSVDFIRDIEIIE
ELQLKDEEMIGPIIDKLEKVAVRGGDKKLKPEYDIMCKVKSVIDQKKPVRFYHDWNDKEIEVLNKHFLTSKPM
VYLVNLSEKDYIRKKNKWLIKIKEWVDKYDPGALVIPFSGALELKLQELSAEERQKYLEANMTQSALPKIIKAGF
AALQLEYFFTAGPDEVRAWTIRKGTKAPQAAGKIHTDFEKGFI MAEVMKYEDFKEEGSENAVKAAGKYRQQGRNY
IVEDGDIIFFKFNTPPQPKKK

971/6881
FIGURE 905

CTGCCAGCCGCGCTGCTGCTGCTCCTCCTGCTGTGGGACCGCTGACCGCGCGGCTGCTCCGCTCTCCCCGCTCCA
AGCGCCGATCTGGGCACCCGCCACCAGCATGGACGCTCGCCGCGTGCCGCAGAAAGATCTCAGAGTAAAGAAGAA
CTTAAAGAAAATTCAGATATGTGAAGTTGATTTCCATGGAGACCTCGTCAICCTCTGATGACAGTTGTGACAGCTT
TGCTTCTGATAATTTTGCAAACACGAAACCTAAATTCAGGTCAGATATCAGTGAAGAAGTGGCAAGTGTTTTTTA
TGAGGACTCTGATAATGAATCTTTCTGCGGCTTTTCAGAAAAGTGAGGTGCAAGATGTATTAGACCATTGTGGATT
TTTACAGAAAACCAAGGCCAGATGTCACTAACGAAGTGGCCGGTATTTTTTCATGCCGACTCTGACGATGAATCATT
TTGCGGTTTTCTCAGAGAGTGAGATACAAGATGGAATGAGGCTGCAGTCAGTTCGGGAAGGCTGTAGGACCCGCAG
CCAGTGCAGGCACTCTGGACCTCTCAGGGTGGCGATGAAGTTTCCAGCGCGGAGTACCAGGGGAGCAACCAACAA
AAAAGCAGAGTCCCGCCAGCCCTCAGAGAATTCTGTGACTGATTCCAACCTCCGATTGAGAAGATGAAAGTGGAAT
GAATTTTTTGGAGAAAAGGGCTTTAAATATAAAGCAAAACAAAGCAATGCTTGCAAAACTCATGTCTGAATTAGA
AAGCTTCCCTGGCTCGTTCCGTGGAAGACATCCCTCCCAGGCTCCGACTCACAATCAAGGAGACCGCGAAGGCG
TACATTTCCCGGTGTGCTTCCAGGAGAAACCTGAACGGAGAGCTCGTCTCTTACCAGGTCAAGGTCCCGGAT
CCTCGGGTCCCTTGACGCTCTACCCATGGAGGAGGAGGAGGAAGAGGATAAGTACATGTTGGTGAGAAAGAGGAA
GACCGTGGATGGCTACATGAATGAAGATGACCTGCCCAGAAGCCGTCGCTCCAGATCATCCGTGACCTTCCGCA
TATAATTCGCCCAGTGGAAAGAAATTACAGAGGAGGAGTTGGAGAACGTCGTCAGCAATTCTCGAGAGAAGATATA
TAACCGTTCACTGGGCTCTACTTGTTCATCAATGCCGTGAGAAGACTATTGATACCAAAACAACTGCAGAAACCC
AGACTGCTGGGGCGTTCGAGGCCAGTTCTGTGGCCCTGCCTTCGAAACCGTTATGGTGAAGAGGTGAGGGATGC
TCTGCTGGATCCGAACGGCATTGCCCGCCTTGTGCGAGGAATCTGCAACTGCAGTTTCTGCCGGCAGCGAGATGG
ACGGTGTGCGACTGGGGTTCCTTGTGTATTTAGCCAAATATCATGGCTTTGGGAATGTGCATGCCTACTTGAAAA
CCTGAAACAGGAATTTGAAATGCAAGCATAATATCTGGAAAATTTGCTGCCTGCCTTCTACTTCTCAAATCTTTC
TTGTAAAGTTTTCCAAITTTTTCACTGAAACCTGAGTTAAAAATCTTGATGATCAGCCTGTTTCATAAGAAACTC
CAATCAAGTTAATCTTAGCAGACATGTGTTTTCTGGAGCATCACAGAAGGTATATTGCTAGTTACACTTTGCCCTC
CTGCAGTTTCTTCTCTGCTCCCAACCCCATCTCATAGCATCCCCCTCTATTTCCAATGCTCCTCTCCAACCGCT
TAGTTTCTGAATTTCTTTTAAATTACAGTTTTATGAAAGCATATTTTATTTACTTGGTGTGAAATAGCCCTCAT
AAAACCTAAGCACTTGGAACACAATAATAGTATTAATACTAAGTATCTATTGAATTTGAGAGAAGAGCCTTCTA
ACTTGTTTACACAAAAACGAGTATGATTTAGCATTCTACTAGTTGAAATTTTTAATAGAATCAAGGCACAAAAG
TCTTAAACCATGTGGAATAATTAGGTAATTATTGCAGATTGATGTCTCTCAATCCCATGTATTGCGCTTATGTT
ACAAGTTGTTGTACAGTTGAGACTTAATTTCTCCTAATTTCTTCTGCCGAAGGGTAAGTGGTGCCTCCAGCTT
ACACAATCATAATTCAGAGTTGGTGGGCAATGTAATACTTAATTAATAATGATGGAAGAGCTATCTGGAGAT
TATGAGTAAGCTGATTTGAATTTTCAGTATAAACTTTAGTATAATTGATGTTTGCAAAGTTTATTTAGTTTAC
ATGTAAGGTATTGCAAATAAATCTTGGACAATTTGTATGGAACTTGATATTAAAACTAGTCTGTGGTTCTT
TGCAGTTTCTTGTAAATTTATAAACCAGGCACAAGTTCAAGTTTAGATTTTAAGCACTTTTATAACAATGATAA
GTGCCTTTTTGGAGATGTAACTTTAGCAGTTTGTAACTTGACATCTCTGCCAGTCTAGTTTCTGGGCAGGTTT
CCGTGTGTCAGTATTTCCCTCCTCTTGCATTAATCAAGGTATTTGGTAGAGGTGGAATCTAAGTGTGTTGTATGT
CCAATTTACTTGATATGTAAACCATGCTGTGCTATTCAATGTTTGATGCATAATTGGACCTTGAATCGATAAG
TGTAATACAGCTTTTGATCTGTAATGCTTTTATACAAAAGTTTATTTAATAATAAAATGTTTGTCT

972/6881
FIGURE 906

MDARRVPQKDLRVKKNLKKFRYVKLISMETSSSSDDSCDSFASDNFANTKPKFRSDISEELASVFYEDSDNESFC
GFSESEVQDVLHDHCGFLQKPRPDVTNELAGIFHADSDDESFCGFSESEIQDGMRLQSVREGCRTRSQCRHSGPLR
VAMKFPARSTRGATNKKAESRQPSSENSVTDSNSDSEDESGMNFLEKRALNIKQNKAMLAKLMSELESFPGSFRGR
HPLPGSDSQSRPRRRRTFPGVASRRNPERRARPLTRSRILGSLDALPMEEEEEEDKYMLVRKRKTVDGYMNED
DLPRSRRSRSSVTLPHIIRPVEEITEEELENVCSNSREKIYNRSLGSTCHQCRQKTIDTKTNCRNPD CWGVRGQF
CGPCLRNRYGEEVRDALLDPNWHCPPCRGICNCSFCRQRDGRCATGVLVYLAKYHGFGNVHAYLKS LKQEFEMQA

973/6881
FIGURE 907

GCAAGATGGCAGAAGTAGAGCAGAAGAAGAAGCGGACCTTCCGCAAGTTCACCTACCGCGGCGTGGACCTGGACC
AGCTGCTGGACATGTCCTACGAGCAGCTGGAGCAGCCGATGCAGCTGTACAGTGC GCGCCAGCGGCGGCGGCTGA
ACCGGGGCCTGCGGCGGAAGCAGCACTCCCTGCTGAAGCGCCTGCGCAAGGCCAAGAAGGAGGCGCCGCCATGG
AGAAGCAGGAAGTGGTGAAGACGCACCTGCGGGACATGATCATCCTACCCGAGATGGTGGGCAGCATGGTGGGCG
TCTACAACGGCAAGACCTTCACCTACAAGCCCGTAAAGCACGGCCGGCCCGGCATCGGGGCCACCCACTCCTCCC
GCTTCATCCCTCTCAAGTAATGGCTCAGCTAATAAAGGCGCACATGACTCC

974/6881
FIGURE 908

MAEVEQKKKRTFRKFTYRGVDLDQLLDMSYEQLEQPMQLYSARQRRRLNRGLRRKQHSLLKRLRKAKKEAPPMEK
QEVVKTHLRDMIILPEMVGSMVGVYNGKTFTYKPVKHGRPGIGATHSSRFIPLK

975/6881
FIGURE 909

GCTGAAATTAAAAGTACTGAGCTTACCAAGTGTTGATAAGGATGTAGAGGAACTGGAACTTTCATACACTGCTGG
TGGGAATATAAAATGGTATAACCATTTTGAATACAACCTGGCAGTTTATTTGTTTGTITAGGTTGTTTTACTC
ACCACTATGCTAACGAGGAACTTGGCAGTTTCTTTAAAAGATAAACATATATCTCTGGTCCGTGCCTCCAAGATG
ACAAAGAAAAGAAGGAACAACGGTCATGCCAAAAAGGGCCGCGGCCACGTGCATCCTATTTCGCTGCACTAACTGT
ACCCGATGCGTGCCCAAGGACAAGGCCATTAAGAAATTCGTCATTTCGAAACGTAGTGGAGGCCGCAGCAGTCAGG
GACATTTCTGAAGTGAGCGTCTTCAATGCCTATGTGCTTCCCAAGCTGTATGTGAAGCTATATTACTGTGTGAGT
TGTGCAATTCACAGCAAAGTAGTCAGGAATCGATCTCGTGAAGCCACAAAGACCGAACACCCCCACCCTGATTT
AGACCTGTGGGTGCTGCCCCACGTCCCCACCAAAGCCCATGTAAGGAGCTGAGTTCTTAAAGACTGAAGACAGA
CTATTCTCTGGAGAAAAATAAAATGGAAATTGTACTT

976/6881
FIGURE 910

CTTTTATGTTAGATGAGGAAGGGGATACCCAAACAGAGGAAACCCGGCCTTCAGAAACAAAAGAAGTGGAGCCAG
AGCCAACTGAGGACAAAGATTTGGAAGCTGATGAAGAGGACACTAGGAAAAAGATGCTTCTGATGATCTAGATG
ACTTGAACTTCTTTAATCAAAAGAAAAAGAAGAAAAAACTAAAAAGATATTTGATATTGATGAAGCTGAAGAAG
GTGTAAAGGATCTTAAGATTGAAAGTGATGTTCAAGAACCAACTGAACCAGAGGATGACCTTGACATTATGCTTG
GCAATAAAAAGAAGAAAAAGAAGAATGTTAAGTTCCCAGATGAGGATGAAGCTCTAGAAGATGAAGACAACAAAA
AAGATGATGGTATCTCATTTCAGTAATCAGACAGGCCCTGCTTGGGCAGGCTCAGAAAGAGACTACACATACGAGG
AGCTGCTGAATCGAGTGTTCAACATCATGAGGGAAAAGAATCCAGATATGGTTGCTGGGGAGAAAAGGAAATTTG
TCATGAAACCTCCACAAGTCGTCCGAGTAGGAACCAAGAAAACCTTCTTTTGTCAACTTTACAGATATCTGTAAAC
TTGGTTCTATAGATGGTAATAACCAACTTGTAATCAAAGGAAGATTCCAACAGAAACAGATAGAAAATGTCTTGA
GAAGATATATCAAGGAGTATGTCACTTGTCACACATGCCGATCACCGGACACAATCCTGCAGAAGGACATGCGAC
TCTATTTTCCTACAGTGCAGAACTTGTCATTCTAGATGTTCTGTTGCCATTATCAAAATTGGCTTCCAGGCTGTCA
TGGGCAAGCGAGCACAGCTCCGTGCCAAAGCTAACTAATTTGCTAATCACTGATTTTGCAAAGCTTGTTGTGGAG
ATGTGGCTGGACAGGTTTGCCATCAGAGTGGATATACCATTGTATTAAAAACAAGATAAAAAAGCTGCCAAGATT
TTTGGCGAGTGGTTGGTTGGTCTGAAGTCCTTGCAAGACGCTGATGCTCAAGCTGTTGACATACTCATTGCCTAC
TTTAACACCTGTCAGAGAAACGTGATATGGGGTAAGGAGGTGCTTTTTTAAAAATAGTTCATAGACTTCTGTAAAA
TGCAAGATAAATTAAAGTTATTATAACAGTGA

977/6881
FIGURE 911

GGTGGGAGAGGTATCGGCAGGGGCAGCGCTGCCGCCGGGGCCTGGGGCTGACCCGTCTGACTTCCCGTCCGTGCC
GAGCCCACTCGAGCCGCAGCCATGTCTGGGGACGAGATGATTTTTGATCCTACTATGAGCAAGAAGAAAAAGAAG
AAGAAGAAGCCTTTTATGTTAGATGAGGAAGGGGATACCCAAACAGAGGAAACCCGGCCTTCAGAAACAAAAGAA
GTGGAGCCAGAGCCAAC TGAGGACAAAGATTTGGAAGCTGATGAAGAGGACACTAGGAAAAAAGATGCTTCTGAT
GATCTAGATGACTTGAAC TTCTTTAATCAAAGAAAAAGAAGAAAAAACTAAAAAGATATTTGATATTGATGAA
GCTGAAGAAGGTGTAAAGGATCTTAAGATTGAAAGTGATGTTCAAGAACCAACTGAACCAGAGGATGACCTTGAC
ATTATGCTTGGCAATAAAAAGAAGAAAAAGAAGATGTTAAGTTCCCAGATGAGGATGAAGCTCTAGAAGATGAA
GACAACAAAAAAGATGATGGTATCTCATT CAGTAATCAGACAGGCCCTGCTTGGGCAGGCTCAGAAAGAGACTAC
ACATACGAGGAGCTGCTGAATCGAGTGTTCAACATCATGAGGGAAAAAGAATCCAGATATGGTTGCTGGGGAGAAA
AGGAAATTTGTCATGAAACCTCCACAAGTCGTCCGAGTAGGAACCAAGAAAAC TTCTTTTGTCAACTTTACAGAT
ATCTGTAAACTATTACATCGTCAACCCAAACATCTCCTTGCAATTTTTATTGGCTGAATTGGGTACAAGTGGTTCT
ATAGATGGTAATAACCAACTTGTAATCAAAGGAAGATTCCAACAGAAACAGATAGAAAATGTCTTGAGAAGATAT
ATCAAGGAGTATGTCAC TTGTACACATGCCGATCACCGGACACAATCCTGCAGAAGGACATGCGACTCTATTTCT
CTACAGTGCAGAACTTGTCATTCTAGATGTTCTGTTGCCATTATCAAAATTGGCTTCCAGGCTGTCATGGGCAAG
CGAGCACAGCTCCGTGCCAAAGCTAACTAATTTGCTAATCACTGATTTTGCAAAGCTTGTTGTGGAGATGTGGCT
GGACAGGTTTGCCATCAGAGTGGATATACCATTGTATTAAAAACAAGATAAAAAAGCTGCCAAGATTTTGGCGA
GTGGTTGGTTGGTCTGAAGTCCTTGCAAGACGCTGATGCTCAAGCTGTTGACATACTCATTGCCTACTTTAACAC
CTGTCAGAGAAAACGTGATATGGGGTAAGGAGGTGCTTTTTTAAATAGTTCATAGACTTCTGTAAAATGCAAGAT
AAATTAAAGTTATTATAACAGTGA

978/6881
FIGURE 912

CGAGTTGGAAGAGGCGAGTCCGGTCTCAAAATGGAGGTAACACCGCCGCCCGGTGCGCCCCAGCCCCGACTCCGGC
CGTCGCCGTCGCCGCCGGGGGAGGAGGGCCATGATCCAAAGGAACCAGAGCAGTTGAGAAAAGTGTATTGGT
GGTCTGAGCTTTGAAACTACAGATGATAGTTTACGAGAACATTTTGAGAAATGGGGCACACTCACAGATTGTGTG
GTAATGAGAGACCCCCAAACAAAACGTTCCAGGGGCTTTGGTTTTGTGACTTATTCTTGTGTTGAAGAGGTGGAT
GCAGCAATGTGTGCTCGACCACACAAGGTTGATGGGCGTGTAGTGGAACCAAAGAGAGCTGTTTCTAGAGAGGAT
TCTGTAAAGCCTGGTGCCCATC**TAA**CAGTGAAGAAAATTTTGTGGTGGTATTAAAGAAGATACAGAAGAATAT
AATTTGAGAGACTACTTTGAAAAGTATGGCAAGATTGAAACCATAGAAGTTATGGAAGACAGGCAGAGTGAAAA
AAGAGAGGATTTGCTTTTGTAACTTTTGATGATCATGATACAGTTGATAAAATTGTTGTTTCAGAAATACACACT
ATTAATGGGCATAATTGTGAAGTGAAAAAGGCCCTTTCTAAACAAGAGATGCAGTCTGCTGGATCACAGAGAGGT
CGTGGAGGTGGATCTGGCAATTTTATGGGTGCGGGAGGGAACCTTTGGAGGTGGTGGAGGTAATTTTGGCCGTGGT
GGAAACTTTGGTGGAAAGAGGTAGGCTATGGTGGTGGAGGTGGTGGCAGCAGAGGTAGTTATGGAGGAGGTGATGG
TGGATATAATGGATTTGGAGGTGATGGTGGCAACTATGGCGGTGGTCCCTGGTTATAGTAGTAGAGGGGGCTATGG
TGGTGGTGGACCAGGATATGGAACCAAGGTGGTGGATATGGTGGAGGTGGAGGATATGATGGTTACAATGAAGG
AGGAAATTTTGGCGGTGGTAACTATGGTGGTGGTGGGAACATAATGATTTTGGAAATTATAGTGGACAACAGCA
ATCAAATTATGGACCCATGAAAGGGGGCAGTTTTGGTGGGAAGAAGCTCGGGCAGTCCCTATGGTGGTGGTTATGG
ATCTGGTGGTGGAAAGTGGTGGATATGGTAGCAGAAGGTTCTAAAAACAGCAGAAAAGGGCTACAGTTCTTAGCAG
GAGAGAGAGCGAGGAGTTGTCAGGAAAGCTGCAGGTTACTTTGAGACAGTCGTCCCAAATGCATTAGAGGAACTG
TAAAAATCTGCCACAGAAGGAACGATGATCCATAGTCAGAAAAGTTACTGCAGCTTAAACAGGAAACCCCTTCTTG
TTCAGGACTGTCATAGCCACAGTTTGCAAAAAGTGCAGCTATTGATTAATGCAATGTAGTGTCAATTAGATGTAC
ATTCTGAGGTCTTTTATCTGTTGTAGCTTTGTCTTTTTCTTTTTCTTTTCATTACATCAGGTATATTGCCCTGT
AAATTGTGGTAGTGGTACCAGGAATAAAAAATTAAGGAATTTTAACTTTTCAATATTTGTGTAGTTTCAGTTTTT
CTACATTTTAGTACAGAACTTTAACAAAATGCAGTTTCGAAGGTGTTTCCTTGTGAGTTACAAGTAAAGAAGA
TCATTGTTAATTACTATTTTGTATGAATTTTGCTAAAGTTAACTGTAAAGAAACACCTGCTGACTTGCAGTTTAA
GGGAATCTATTCTCCCCATTTCCAAACCATGATATGAATGGGCGCTGACATGTGGAGAGAATAGATAATTTGTG
TGTTTGCAATGTGTGTTTTAGATAAATAGGATTGGGTATTTAAATTAGCATTGTGTAATTTAATAGCATTAAAGAT
TACCTTCAAATGAAAAAAAATCTCAAAATTTCTATTTGGTTTTTGTGCATTTTCTTTTAAATGTAATCATATGA
TTTTAGTGTGTTAGACTTGCTGAGTCCTAGCTGTGTTTAGAACATCTCTATTCTACATTTACCTTGGTCAAATTT
GAACTGCTGCCATAGG

979/6881
FIGURE 913

MEGHDPKEREQLRKPFIFGGLSFETDDGLREHFKEWVTLTDCVVMRDPQTKCSRGFGFVTYSYIEEVDAAMCAPP
HKVDGCVVEPKRAVSREDFVKPGAHLTVKKIFVGGIKIQKNII

980/6881
FIGURE 914

CTTCATCCTGCGACTAGCACCGCGTCCGGCAGCGCCTGCCCTACACTCGCCCCTGCCATGGCCTCCGTCTCCAAG
CTCGCCTGCATCTACTCGGCCCTCATTCTGCACGACGATGAGGTGACAGTCACGGAGGATAAGATCAATGCCCTC
ATTAAAGCAGCCGGTGTAATGTTGAACCTTTTTGGCCTGGCTTGTTTGCAAAGGCCCTGGCCAACGTCAACATT
GGGAGCCTCATCTGCAATGTAGGGGCTGGTGGACCTGCTCCAGCTGAGGAGAAGAAAGTGGGAAGCAAAGAAAGAA
GAATCCAAGGAGTCTGATGATGACATGGGCCTTGCTTTTTGACTAAACCTCTTTTATAACGTGTTCAATAAAA
AGCTGAACTT

981/6881
FIGURE 915

MASVSKLACIYSALILHDDEVTVTEDKINALIKAAGVNVEPFWPGLFAKALANVNIGSLICNVGAGGPAPAEKK
VEAKKEESKESDDDMGLGLFD

982/6881
FIGURE 916

ACGGGGCCTGGGCGGSAGGGGCGGTGGCTGGAGCTCGGTAAAGCTCGTGGGACCCCATTGGGGGAATTTGATCCA
AGGAAGCGGTGATTGCCGGGGGAGGAGAAGCTCCCAGATCCTTGTGTCCACTTGCAGCGGGGGAGGCGGAGACGC
GGAGCGGGCCTTTTGGCGTCCACTGCGCGGCTGCACCCTGCCCCATCCTGCCGGGATC**ATCGT**CTGCGGCAGCCC
GGGAGGGATGCTGCTGCTGCGGGCCGGGCTGCTTGCCCTGGCTGCTCTCTGCCTGCTCCGGGTGCCCCGGGGCTCG
GGCTGCAGCCTGTGAGCCCGTCCGCATCCCCCTGTGCAAGTCCCTGCCCTGGAACATGACTAAGATGCCCAACCA
CCTGCACCACAGCACTCAGGCCAACGCCATCCTGGCCATCGAGCAGTTCGAAGGTCTGCTGGGCACCCACTGCAG
CCCCGATCTGCTCTTCTTCTCTGTGCCATGTACGCGCCCATCTGCACCATTGACTTCCAGCACGAGCCCATCAA
CCCCTGTAAGTCTGTGTGCGAGCGGGCCCGGCAGGGCTGTGAGCCCATACTCATCAAGTACCGCCACTCGTGGCC
GGAGAACCTGGCCTGCGAGGAGCTGCCAGTGTACGACAGGGGCGTGTGCATCTCTCCCGAGGCCATCGTTACTGC
GGACGGAGCTGATTTTCCCTATGGATTCTAGTAACGGAAACTGTAGAGGGGCAAGCAGTGAACGCTGTAAATGTAA
GCCTATTAGAGCTACACAGAAGACCTATTTCCGGAACAATTACAACCTATGTCATTCCGGGCTAAAGTTAAAGAGAT
AAAGACTAAGTGCCATGATGTGACTGCAGTAGTGGAGGTGAAGGAGATTCTAAAGTCCTCTCTGGTAAACATTCC
ACGGGACACTGTCAACCTCTATACCAGCTCTGGCTGCCTCTGCCCTCCACTTAATGTTAATGAGGAATATATCAT
CATGGGCTATGAAGATGAGGAACGTTCCAGATTACTCTTGGTGGAAGGCTCTATAGCTGAGAAGTGAAGGATCG
ACTCGGTAAAAAAGTTAAGCGCTGGGATATGAAGCTTCGTCATCTTGGACTCAGTAAAAGTGATTCTAGCAATAG
TGATTCCACTCAGAGTCAGAAGTCTGGCAGGAACCTCGAACCCCCGGCAAGCACGCAAC**TAAAT**CCCCGAAATACAA
AAAGTAACACAGTGGACTTCCTATTAAGACTTACTTGCATTGCTGGACTAGCAAAGGAAAATTGCACTATTGCAC
ATCATATTCTATTGTTTACTATAAAAATCATGTGATAACTGATTATTACTTCTGTTTCTCTTTTGGTTTCTGCTT
CTCTCTTCTCTCAACCCCTTTGTAATGGTTTGGGGGCAGACTCTTAAGTATATTGTGAGTTTTCTATTTCACTAA
TCATGAGAAAACTGTTCTTTTGCAATAATAATAAATTAAACATGCTGTTA

983/6881
FIGURE 917

MVCGSPGGMLLLRAGLLALAALCLLRVPGARAAACEPVRIPLCKSLPWNMTKMPNHLHHSTQANAILAIEQFEG
LGTHCSPDLLFFLCAMYAPICTIDFQHEPINPCKSV CERARQGCEPILIKYRHSWPENLACEELPVYDRGVCISP
EAIVTADGADFPMDSSNGNCRGASSERCKCKPIRATQKTYFRNNYNYVIRAKVKEIKTKCHDVTAVVEVKEILKS
SLVNIPRDTVNLYTSSGCLCPPLNVNEEYIIMGYEDEERSRLLLVEGSIAEKWKDRLGKKVKRWDMLRHLGLSK
SDSSNSDSTQSQKSGRNSNPRQARN

984/6881
FIGURE 918

ATGTCCATCAGGACGACCCAGAAGTCCTACAGGGTGTCCACTTCTGGCCCCCGGGCCTTCAGCAGCCATTTCTAC
ACAAGTGGGCCTGGTGCCTCCATCAGCTCCTCGAGCTTCTCCCAAGTGGGCAGCAGCAGCTTCCGGGGTGGCCTG
GGAGGAGGCTACGGTGGGGCCAGTGGCATGGGAGGCATCACCACCGTCACTGTCAACCAGAGCCTGCTGAGCCCC
CTTAACCTGGAGGTGGACCCACACATCCAGGCAGTGCACACTCAGAAGAAGGAGCAGATCAAGACCCTCAACACT
AAGTTTGCCACCTTCATATACAAGAGTTACATCAACAACCTTAGGCAGCAGCTGGAGACTCTGGGCCAGGAAAAG
CTGAAGCTGGAGGCGGAGCTTGGCAACATGCAGGGGCTGGTGGAGGACTTCAAGAACAAGTATGAGGATGAGATC
AATAAGCGTACAGAGATGGAGAATGAATTTGTCCTCATCAAGAAGGATGTGGATGAAGCTTACCTGAACAAGGTA
GAGCTGGAGTCTCGCCTGGAAGGGCTGACTGACGAAATCAACTTCCTCAGGCAGCTGTATGAAGAGGATATCCCG
GAGCTGCAGTCCCAGATCTCAGACACGTCTGTGGTGTCTGCCCATGGACAACAGCCACTCCCTGGACATGGACAGC
ATCATCAATGAGGTCAAGCGCAGTACGAGATCACCAACCGCAGCCAGCTGGCTCCAGGCAGAGATTGAGGGTCTC
AAAGGCCAGAGGGCTTCCCTGGAGGCCGCCATCGCAGATGCGGAGCAGCGCGGGGAGTTGGCCGTTAAGGATGCC
AGCGCCAAGCTGTCTGAGCTGGAGGCCGCCCTGCAGCAAACCAAGCAGGACGTGGAGCTGATGAACGACAAGCTG
GCCCTGGACATTGAGATCGCCACCTACAGGCAGCTGCTGGAGGGCGAGGAGAGCTGGCTGGAGTCTGGGATGCAG
AGCATGAGTATCCATACAAAGACCATCAGCAGCTATGCAGGTGGTCTGAGCTCGGCCTATGGGGGCCTCACAAGC
CCCGGCCTCAGCTGTGGACTGGGCTCCAGCTTTGGCTCTGGCGCGGGCTCCAGTTCCTTCAGCTGCATCAGCTAC
ACCAGGGCCGTGGTTGTGAAGAAGATTGAGACCCGTGATGGGACGCTGGTGTCTCAGAGTTCTCTGACGTCTGCCC
AAGTGA

985/6881
FIGURE 919

MSIRTTQKSYRVSTSGPRAFSSHFYTS GPGASISSSSFSQVGSSSF RGGLGGGYGGASGMGGITTTVTVNQSL LSP
LNLEVDPHIQAVHTQKKEQIKTLN TKFATFIYKSYINNLRQQLETLGQEKLKLEAELGNMQGLVEDFKNKYEDEI
NKRTEMENEFVLIKKDVDEAYLNKVELESRL EGLTDEINFLRQLYEEDIPELQSQISDTSVVLPM DN SHSLDMS
IINEVKRSTRSPTAASWLQAEIEGLKGQRASLEAAIADAEQRGELAVKDASAKLSELEAALQQT KDVELMNDKL
ALDIEIATYRQLLEGEESWLESGMQSMSIHTKTISSYAGGLSSAYGGLTSPGLSCGLGSSFGSGAGSSSFSCISY
TRAVVVKKIETRDGTLVSEFSDVLPK

986/6881
FIGURE 920

ACGCAACCCCATAGGTAGCACGCCGTTACCCGTGGGGAGCGTTTCCGCCATTTTGGAAAATTAATTGGGAAGGT
ACTGGTTTTAAGTGTAAGTTGCCGACGCAATGGCAGCCTTTGCAGTGGAACCTCAGGGGCCCCGCGTTAGGATCTGA
ACCAATGATGCTGGGTTACCCACATCTCCAAAGCCAGGAGTTAATGCCAGTTCTTACCTGGATTTTTAATGGG
GGATTTGCCAGCTCCGGTGACTCCACAACCTCGATCAATTAGTGGCCCTTCAGTAGGAGTAATGGAAATGAGATC
ACCTTTACTTGCAGGTGGGTCAACCACACAACCAGTTGTACCAGCTCATAAAGATAAAAGTGGCGCTCCACCAGT
TAGAAGTATATATGATGACATTTCTAGCCCAGGACTTGGATCAACACCTTTAACTTCAAGAAGACAGCCAAACAT
TTCAGTAATGCAGAGTCCTCTTGTTGGAGTTACATCTACTCCTGGAACAGGGCAAAGTATGTTTAGTCCAGCAAG
TATCGGTACAGCCACGAAAGACGACATTATCTCCTGCCAGTTGGATCCTTTTTATACTCAAGGAGATTCTTTGAC
TTCAGAAGATCACCTCGATGACTCTTGGGTGACTGTATTTGGGTTTCCTCAAGCATCTGCTTCTACATATTACT
ACAATTTGCACAGTATGGGAATATCTTAAACATGTGATGTCTAATACAGGAAATTGGATGCATATTCGTTATCA
ATCTAAACTGCAGGCTCGGAAAGCCTTAAGCAAAGATGGGAGGATTTTTGGAGAATCCATCATGATTGGTGTAAA
ACCATGTATTGACAAAAGTGTTATGGAAAGCAGTGACAGATGTGCTTTATCATCTCCATCTTTAGCCTTTACACC
ACCAATCAAACTCTAGGTACACCAACACAACCTGGAAAGTACTCCTAGGATTTCTACCATGAGACCTCTTGCTAC
AGCATACAAAAGCCTCTACTAGTGATTATCAGGTTATTTCTGACAGACAAACGCCAAAAAAGATGAAAGTCTTGT
ATCCAAAGCAATGGAGTACATGTTTGGCTGGTAGTAGAACACCAAGAAGGAGGTTGCTACACTAAAACAGAGTTA
GCAGAGTGCTGCTGGTTCCTTCGGTTAGTTATATAACTGTTCTGTCAGTATTGGATAGCTATCTCATACTTCTTT
TAGAAAGAAGCCTTTTTCATTAAGGATACAACCTATTTGTAGCTCGCACTTTAAAGATGCTTGAGATACATTTT
AAAGAAAACATAAAATCCCTGTAAATAGGATTTTGTGCTTCTGTAAACAGTGCATGCTTCAGCACAGAAAACCTCA
GCATTGATTATTGTAAATTAAATAACTGAAATTGTGGTGAGACGTCATAGTCTTCATGAGAACGTGGGGGTGAAT
TTCATGAAGGGGAACATATAGTTATTTCTACCGACACAAATATTATAATTAGCAATTTGAATTATGGTCTTTTAAT
TTAGATAGTATTTAATATTTTAATTATCCTTGTTTGTATATGTCCTGTCACAGAGTGTCTCTTGGTGTATTCTA
AAACGAGCATTCCTTTAAAAAACCTAAAGTTTCTTGATAATAAACATTGTCAATGAT

987/6881
FIGURE 921A

GGCTGAGTTTTATGACGGGCCCCGGTGCTGAAGGGCAGGGAACAACCTTGATGGTGCTACTTTGAACTGCTTTTCTT
TTCTCCTTTTTGCACAAAGAGTCTCATGTCTGATATTTAGACATGATGAGCTTTGTGCAAAAGGGGAGCTGGCTA
CTTCTCGCTCTGCTTCATCCCCTATTATTTTGGCACAACAGGAAGCTGTTGAAGGAGGATGTTCCCATCTTGGT
CAGTCTATGCGGATAGAGATGTCTGGAAGCCAGAACCATGCCAAATATGTGTCTGTGACTCAGGATCCGTTCTC
TGCGATGACATAATATGTGACGATCAAGAATTAGACTGCCCCAACCCAGAAATTCCATTTGGAGAATGTTGTGCA
GTTTGCCACAGCCTCCAACCTGCTCCTACTCGCCCTCCTAATGGTCAAGGACCTCAAGGCCCAAGGGAGATCCA
GGCCCTCCTGGTATTCTGCGGAGAAATGGTGACCCTGGTATTCCAGGACAACCAGGGTCCCCTGGTTCTCCTGGC
CCCCCTGGAATCTGTGAATCATGCCCTACTGGTCTCAGAACTATTCTCCCCAGTATGATTTCATATGATGTCAAG
TCTGGAGTAGCAGTAGGAGGACTCGCAGGCTATCCTGGACCAGCTGGCCCCCAGGCCCTCCCGGTCCCCCTGGT
ACATCTGGTTCATCCTGGTTCCCCTGGATCTCCAGGATACCAAGGACCCCTGGTGAACCTGGGCAAGCTGGTCCT
TCAGGCCCTCCAGGACCTCCTGGTGCTATAGGTCCATCTGGTCTGCTGGAAGATGGAGAATCAGGTAGACCC
GGACGACCTGGAGAGCGAGGATTGCCTGGACCTCCAGGTATCAAAGGTCCAGCTGGGATACCTGGATTCCCCTGGT
ATGAAAGGACACAGAGGCTTCGATGGACGAAATGGAGAAAAGGGTGAAACAGGTGCTCCTGGATTAAAGGGTGAA
AATGGTCTTCCAGGCGAAAATGGAGCTCCTGGACCCATGGGTCCAAGAGGGGGCTCCTGGTGAGCGAGGACGGCCA
GGACTTCTGGGGCTGCAGGTGCTCGGGGTAATGACGGTGCTCGAGGCAGTGATGGTCAACCAGGCCCTCCTGGT
CCTCCTGGAACCTGCCGGATTCCCCTGGATCCCCTGGTGCTAAGGTGAAGTTGGACCTGCAGGGTCTCCTGGTTCA
AATGGTGCCCCCTGGACAAAGAGGAGAACCTGGACCTCAGGGACACGCTGGTGCTCAAGGTCTCCTGGCCCTCCT
GGGATTAATGGTAGTCTTGGTGGTAAAGGCGAAATGGGTCCCCTGGCATTCTGGAGCTCCTGGACTGATGGGA
GCCCCGGGTCTCCTCAGGACCAGCCGGTGCTAATGGTGCTCCTGGACTGCGAGGTGGTGAGGTGAGCCTGGTAAG
AATGGTGCCAAAGGAGAGCCCGGACCACGTGGTGAAACGCGGTGAGGCTGGTATTCCAGGTGTTCCAGGAGCTAAA
GGCGAAGATGGCAAGGATGGATCACCTGGAGAACCTGGTGCAAATGGGCTTCCAGGAGCTGCAGGAGAAAGGGT
GCCCCCTGGGTTCGAGGACCTGCTGGACCAAATGGCATCCCAGGAGAAAAGGGTCTGCTGGAGAGCGTGCTGCT
CCAGGCCCTGCAGGGCCCAGAGGAGCTGCTGGAGAACCTGGCAGAGATGGCGTCCCTGGAGGTCCAGGAATGAGG
GGCATGCCCCGAAGTCCAGGAGGACCAGGAAGTGATGGGAAACCAGGGCTCCCGGAAGTCAAGGAGAAAGTGGT
CGACCAGGTCTCCTGGGCCATCTGGTCCCCGAGGTACAGCTGGTGTCATGGGCTTCCCCGGTCTAAAGGAAAT
GATGGTGCTCCTGGTAAGAATGGAGAACGAGGTGGCCCTGGAGGACCTGGCCCTCAGGGTCTCCTGGAAAGAAT
GGTGAAACTGGACCTCAAGGACCCCCAGGGCCTACTGGGCTGGTGGTGACAAAGGAGACACAGGACCCCCCTGGT
CCACAAGGATTACAAGGCTTGCTGGTACAGGTGGTCTCCTCAGGAGAAAATGGAAAACCTGGGGAACCAGGTCCA
AAGGGTGATGCCGGTGACCTGGAGCTCCAGGAGGCAAGGGTGATGCTGGTGCCCTGGTGAACGTGGACCTCCT
GGATTGGCAGGGGCCCCAGGACTTAGAGGTGGAGCTGGTCCCCCTGGTCCCGAAGGAGGAAAGGGTGCTGCTGGT
CCTCCTGGGCCACCTGGTGCTGCTGGTACTCCTGGTCTGCAAGGAATGCCTGGAGAAAGAGGAGGTCTTGGAAGT
CCTGGTCCAAAGGGTGACAAGGGTGAACCAGGCGGCCAGGTGCTGATGGTGTCCAGGGAAGATGGCCCAAGG
GGTCTACTGGTCTATTGGTCTCCTGGCCAGCTGGCCAGCCTGGAGATAAGGGTGAAGGTGGTGGCCCCGGA
CTTCCAGGTATAGCTGGACCTCGTGGTAGCCCTGGTGAGAGAGGTGAAACTGGCCCTCCAGGACCTGCTGGTTTC
CCTGGTGCTCCTGGACAGAATGGTGAACCTGGTGGTAAAGGAGAAAAGAGGGGCTCCGGGTGAGAAAGGTGAAGGA
GGCCCTCCTGGAGTTGCAGGACCCCCCTGGAGGTTCTGGACCTGCTGGTCTCCTGGTCCCCAAGGTGTCAAAGGT
GAACGTGGCAGTCTTGGTGGACCTGGTGCTGCTGGCTTCCCTGGTGCTCGTGGTCTTCTGGTCTCCTGGTAGT
AATGGTAACCCAGGACCCCCAGGTCCCAGCGTTCTCCAGGCAAGGATGGGCCCCAGGTCTGCGGGTAACACT
GGTGCTCCTGGCAGCCCTGGAGTGTCTGGACCAAAGGTGATGCTGGCCAACCAGGAGAGAAGGGATCGCCTGGT
GCCAGGGCCCACCAGGAGCTCCAGGCCACTTGGGATTGCTGGGATCACTGGAGCACGGGTCTTGACAGGACCA
CCAGGCATGCCAGGTCTTAGGGGAAGCCCTGGCCCTCAGGGTGTCAGGGTGAAAGTGGGAAACCAGGAGCTAAC
GGTCTCAGTGGAGAACGTGGTCCCCCTGGACCCAGGGTCTTCTGGTCTGGCTGGTACAGCTGGTGAACCTGGA
AGAGATGGAACCCCTGGATCAGATGGTCTTCCAGGCCGAGATGGATCTCCTGGTGGCAAGGGTGATCGTGGTGAA
AATGGCTCTCCTGGTGCCCTGGCGCTCCTGGTCATCCAGGCCACCTGGTCTGCTGGTCCAGCTGGAAGAGT
GGTGACAGAGGAGAAAGTGGCCCTGCTGGCCCTGCTGGTGCTCCCGGTCTGCTGGTTCCTGAGGTGCTCCTGGT
CCTCAAGGCCACGTGGTGACAAAGGTGAAACAGGTGAACGTGGAGCTGCTGGCATCAAAGGACATCGAGGATTC
CCTGGTAATCCAGGTGCCCCAGGTTCTCCAGGCCCTGCTGGTCAGCAGGTGCAATCGGCAGTCCAGGACCTGCA
GGCCCCAGAGGACCTGTTGGACCCAGTGGACCTCCTGGCAAAGATGGAACCAGTGGACATCCAGGTCCCATTGGA

988/6881

FIGURE 921B

CCACCAGGGCCTCGAGGTAACAGAGGTGAAAAGAGGATCTGAGGGCTCCCCAGGCCACCCAGGGCAACCAGGCCCT
CCTGGACCTCCTGGTGCCCCCTGGTCCTTGCTGTGGTGGTGTGGAGCCGCTGCCATTGCTGGGATTGGAGGTGAA
AAAGCTGGCGGTTTTGCCCGTATTATGGAGATGAACCAATGGATTTCAAAATCAACACCGATGAGATTATGACT
TCACTCAAGTCTGTTAATGGACAAATAGAAAAGCCTCATTAGTCCTGATGGTTCTCGTAAAAACCCCGCTAGAAAC
TGCAGAGACCTGAAATTCTGCCATCCTGAACTCAAGAGTGGAGAATACTGGGTTGACCCTAACCAAGGATGCAAA
TTGGATGCTATCAAGGTATTCTGTAATATGGAACTGGGGAAACATGCATAAGTGCCAATCCTTTGAATGTTCCA
CGGAAACACTGGTGGACAGATTCTAGTGCTGAGAAGAAACACGTTTGGTTTGGAGAGTCCATGGATGGTGGTTTT
CAGTTTAGCTACGGCAATCCTGAACTTCCTGAAGATGTCCTTGATGTGCAGCTGGCATTCTTCGACTTCTCTCC
AGCCGAGCTTCCCAGAACATCACATATCACTGCAAAAAATAGCATTGCATACATGGATCAGGCCAGTGGAATGTA
AAGAAGGCCCTGAAGCTGATGGGGTCAAATGAAGGTGAATTCAGGCTGAAGGAAATAGCAAATTCACCTACACA
GTTCTGGAGGATGGTTGCACGAAACACACTGGGGAATGGAGCAAACAGTCTTTGAATATCGAACACGCAAGGCT
GTGAGACTACCTATTGTAGATATTGCACCCCTATGACATTGGTGGTCTGATCAAGAATTTGGTGTGGACGTTGGC
CCTGTTTGCTTTTTATTAACCAAACTCTATCTGAAATCCCAACAAAAAAATTTAACTCCATATGTGTTCCTCTT
GTTCTAATCTTGTCAACCAAGTGCAAGTGACCGACAAAATTCCAGTTATTTATTTCCAAAATGTTTGGAACAGTA
TAATTTGACAAAGAAAAATGATACTTCTCTTTTTTGTCTGTTCCACCAAATACAATTCAAATGCTTTTTGTTTTA
TTTTTTTACCAATTCCAATTTCAAATGTCTCAATGGTGTCTATAATAAATAAACTTCAACACTCTTTATGATAAC
AACACTGTGTTATATTCTTTGAATCCTAGCCCCATCTGCAGAGCAATGACTGTGCTCACCAGTAAAAGATAACCTT
TCTTTCTGAAATAGTCAAATACGAAATTAGAAAAGCCCTCCCTATTTTAACTACCTCAACTGGTCAGAAACACAG
ATTGTATTCTATGAGTCCCAGAAGATGAAAAAATTTTATACGTTGATAAACTTATAAAATTCATTGATTAATC
TCCTGGAAGATTGGTTTAAAAAGAAAAAGTGTAATGCAAGAATTTAAAGAAATATTTTTTAAAGCCACAATTATTTT
AATATTGGATATCAACTGCTTGTAAGGTGCTCCTCTTTTTTCTTGTCATTGCTGGTCAAGATTACTAATATTTG
GGAAGGCTTTAAAGACGCATGTTATGGTGCTAATGTACTTTCACTTTTAACTCTAGATCAGAATTGTTGACTTG
CATTCAGAACATAAATGCACAAAATCTGTACATGTCTCCCATCAGAAAGATTTCATTGGCATGCCACAGGGATTCT
CCTCCTTCATCCTGTAAAGGTCAACAATAAAAACCAAATTATGGGGCTGCTTTTGTACACTAGCATAGAGAATG
TGTTGAAATTTAACTTTGTAAGCTTGTATGTGGTGTGTGATCTTTTTTTTTCTTACAGACACCATAATAAAATA
TCATATTAAAATTC

989/6881
FIGURE 922

MMSFVQKGSWLLLALLHPTIILAQQEAVEGGCSHLGQSYADRDVWKPEPCQICVCDSGSVLCDDIICDDQELDCP
NPEIPFGECCA VCPQPPTAPTRPPNGQGPQGPKGDPGPPGIPGRNGDPGIPGQPGSPGSPGPPGICESCFTGPQN
YSPQYDSYDVKSGVAVGGLAGYFPGAGPPGPPGPPGTSGHPGSPGSPGYQGPPGEPGQAGPSGPPGPPGAIGPSG
PAGKDGESGRPGRPGERGLPGPPGIKGPAGIPGFFPMKGHRGFDGRNGEKGETGAPGLKGENGLPGENGAPGPMG
PRGAPGERGRPGLPGAAGARGNDGARGSDGQPGPPGPPGTAGFPSPGAKGEVGPAGSPGSNGAPGQRGEPGPQG
HAGAQQPPGPPGINGSPGGKGEMGPAGIPGAPGLMGARGPPGPAGANGAPGLRGGAGEPGKNGAKGEPGPRGERG
EAGIPGVPGA KGEDGKD GSPGEPGANGLPAAAGERGAPGFRGPAGPNGIPGEKGPAGERGAPGPAGPRGAAGEPG
RDGVPPGGP GMRGMPGSPGGPGSDGKPGPPGSQGESGRPGPPGPSGPRGQPGVMGFPGPKGNDGAPGKNGERGGPG
GPGPQQPPGKNGETGPQGPPTGPGGDKGDTGPPGPQGLQGLPGTGGPPGENGKPGEPGPKGDAGAPGAPGGKG
DAGAPGERGPPGLAGAPGLRGGAGPPGPEGGKGAAGPPGPPGAAGTPGLQMPGERGGLGSPGPKGDKGEPGGPG
ADGVPPKDGPRGPTGPIGPPGPAGQPGDKGEGGAPGLPGIAGPRGSPGERGETGPPGPAGFPAGPQNGEPGGKG
ERGAPGEKGE GGGPGVAGPPGGSGPAGPPGPQGVKGERGSPGGPGAAGFPGARGLPGPPGSNGNP GPPGPSGSPG
KDGPPGPAGNTGAPGSPGVSGPKGDAGQPGKEKSGPGAQGPFGAPGLGIAGITGARGLAGPPGMPGPRGSPGPQG
VKGESGKPGANGLSGERGPPGPQGLPGLAGTAGEPGRDGNPGSDGLPGRDGSPGGKGDRGENSGPAGPAGHPG
PPGPVGPAGKSGDRGESGPAGPAGPAGPSRGAPGPQGPGRGDKGETGERGAAGIKGHRGFPGNPGAPGSPGPAG
QQGAIGSPGPAGPRGPVGPSPGPPGKDGTSGHPPGPIGPPGPRGNRGERGSESGPHPGQPGPPGPPGAPGPCCGV
GAAAIAGIGGEKAGGFAPYYGDEPMDFKINTDEIMTSLKSVNGQIESLISP DGSRKNPARNCRDLKFCHPELKSG
EYWVDPNQCKLDAIKVFCNMETGETCISANPLNVPRKHWWTDSSAEKKHVWFGESMDGGFQFSYGNPELPEDVL
DVQLAFLRLSSRASQNITYHCKNSIAYMDQASGNVKKALKLMGSNEGEFKAEGNSKFTYTVLEDGCTKHTGEWS
KTVFEYRTRKAVRLPIVDIAPYDIGGPDQEFGVDVGPVCFL

990/6881
FIGURE 923

ACGCGTCCGAGCTGGCTCAGGGCGTCCGCTAGGCTCGGACGACCTGCTGAGCCTCCCAAACCGCTTCCATAAGGC
TTTGCCTTTCCAACCTCAGCTACAGTGTTAGCTAAGTTTGAAAGAAGGAAAAAAGAAAATCCCTGGGCCCTTT
TCTTTTGTCTTTGCCAAAGTCGTCGTTGTAGTCTTTTGCCCAAGGCTGTTGTGTTTTTAGAGGTGCTATCTCC
AGTTCCTTGCACTCCTGTTAACAAGCACCTCAGCGAGAGCAGCAGCAGCGATAGCAGCCGCAGAAGAGCCAGCGG
GGTCGCCTAGTGTCATGACCAGGGCGGGAGATCACAAACGCCAGAGAGGATGCTGTGGATCCTTGGCCGACTACC
TGACCTCTGCAAAATTCCTTCTCTACCTTGGTCATTCTCTCTCTACTTGGGGAGATCGGATGTGGCACTTTGCGG
TGTCTGTGTTTCTGGTAGAGCTCTATGGAAACAGCCTCCTTTTGACAGCAGTCTACGGGCTGGTGGTGCGAGGT
CTGTTCTGGTCTGGGAGCCATCATCGGTGACTGGGTGGACAAGAATGCTAGACTTAAAGTGGCCCAGACCTCGC
TGGTGGTACAGAATGTTTCAGTCATCCTGTGTGGAATCATCCTGATGATGGTTTTCTTACATAAAACATGAGCTTC
TGACCATGTACCATGGATGGGTCTCACTTCTGCTATATCCTGATCATCACTATTGCAAAATATTGCAAAATTTGG
CCAGTACTGCTACTGCAATCACAATCCAAAGGGATTGGATTGTTGTTGTTGCAGGAGAAGACAGAAGCAAACTAG
CAAATATGAATGCCACAATACGAAGGATTGACCAGTTAAACCAACATCTTAGCCCCCATGGCTGTTGGCCAGATTA
TGACATTTGGCTCCCCAGTCATCGGCTGTGGCTTTATTTCTGGGATGGAACCTTGGTATCCATGTGCGTGGAGTACG
TCCTGCTCTGGAAGGTTTACCAGAAAACCCAGCTCTAGCTGTGAAAGCTGGTCTTAAAGAAGAGGAAACTGAAT
TGAAACAGCTGAATTTACACAAAGATACTGAGCCAAAACCCCTGGAGGGAACTCATCTAATGGGTGTGAAAGACT
CTAACATCCATGAGCTTGAACATGAGCAAGAGCCTACTTGTGCCTCCCAGATGGCTGAGCCCTTCCGTACCTTCC
GAGATGGATGGGTCTCCTACTACAACCAGCCTGTGTTTCTGGCTGGCATGGGTCTTGCTTTTCTTTATATGACTG
TCCTGGGCTTTGACTGCATCACCACAGGGTACGCCTACACTCAGGGACTGAGTGGTTCCATCCTCAGTATTTTGA
TGGGAGCATCAGCTATAACTGGAATAATGGGAAGTGTAGCTTTTACTTGGCTACGTCGAAAATGTGGTTTGGTTC
GGACAGGTCTGATCTCAGGATTGGCACAGCTTTCTGTTGATCTTGTGTGTGATCTCTGTATTTCATGCCTGGAA
GCCCCCTGGACTTGTCCGTTTCTCCTTTTGAAGATATCCGATCAAGGTTTCAAGGAGAGTCAATTACACCTA
CCAAGATACCTGAAATTACAAGTGAATATACATGTCTAATGGGTCTAATTCTGCTAATATTGTCCCGGAGACAA
GTCCTGAATCTGTGCCATAATCTCTGTGCTGCTGTTTGCAGGCGTCATTGCTGCTAGAATCGGTCTTTGGT
CCTTTGATTTAACTGTGACACAGTTGCTGCAAGAAAATGTAATTGAATCTGAAAGAGGCATTATAAATGGTGTAC
AGAAGTCCATGAACATCTTCTTGATCTTCTGCATTTTCATCATGGTCATCCTGGCTCCAAATCCTGAAGCTTTTG
GCTTGCTCGTATTGATTTTCACTCTCCTTTGTGGCAATGGGCCACATTATGTATTTCCGATTTGCCCAAAATACTC
TGGGAAACAAGCTCTTTGCTTGGCTCCTGATGCAAAAGAAGTTAGGAAGGAAAATCAAGCAAATACATCTGTTG
TTTGAGACAGTTTAACTGTTGCTATCCTGTTACTAGATTATATAGAGCACATGTGCTTATTTTGTACTGCAGAAAT
TCCAATAAATGGCTGGGTGTTTTGCTCTGTTTTTACCACAGCTGTGCCCTTGAGAACTAAAAGCTGTTTAGGAAAC
CTAAGTCAGCAGAAATTAAGTGAATTTTCCCTTATGTTGAGGCATGGAAAAAAATTGAAAAAGAAAAACTCA
GTTTAAATACGGAGACTATAATGATAACACTGAATTCCCCTATTTCTCATGAGTAGATACAATCTTACGTAAAAAG
AGTGGTTAGTCACGTGAATTCAGTTATCATTTGACAGATTCTTATCTGTACTAGAATTCAGATATGTCAGTTTTTC
TGCAAAACTCACTCTTGTTCAGACTAGCTAATTTATTTTTTTTGCATCTTAGTTATTTTTTAAAAACAAATCTTC
AAGTATGAAGACTAAAATTTTGATAACTAATATTATCCTTATTGATCCTATTGATCTTAAGGTATTTACATGTATG
TGAAAAACAAAAACACTTAAGTGAATTTCTAATAAGGTTTATGGTTTAGCTTAAAGAGCACCTTTGTATTTTTT
ATTATCAGATGGGGCAACATATTGTATGAAGCATATGTAGCACTTCACAGCATGGTTATCATGTAAGCTGCAGGT
AGAAGCAAAGCTGTAAAGTAGATTTATCACACAATGACTGCATACAGACTTCAAATATGTCAATAGTTTGGTCAT
AGAACCTAGAAGCCAAAAGCCACACAGAAGGGCAAGAATCCCAATTTAACTCATGTTATCATCATTAGTGATCTG
TGTTGTAGAACATGAGGGTGTAAGCCTTCAGCCTGGCAAGTTACATGTAGAAAGCCACACTTGTGAAGGTTTTG
TTTTACAAATCACTTGATTTAACACACTCAGGTAGAATATTTTTTATTTTTTACTGTTTTTATACCAGAAGTTATTT
CTACATTGTTCTACAGCAAGAATATTCATAAAAGTATCCCTTTCAAATGCCTTTGAGAAGAATAGAAGAAAAAA
GTTTGTATATATTTTTAAAAAATGTTTTTAAAGTCAGTTTGCAACATGTCTGTACCAAGATGGTACTTTGCCTTA
ACGTTTTATATGCACCTTCATGGAGACTGCAATACGTTGCTATGAGCACTTCTTTATCCTTGGAGTTTAACTCT
TTGCTTCATCTTTCTACAGTATGACATAATGATTGCTATGTTGTAAATCTTTGTAAAAAATTTCTATATAAAA
ATATTTTGAAGTCTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTT

991/6881
FIGURE 924

MTRAGDHNRRQGCCGSLADYLTSAKFLLYLGHSLSTWGDRMWHFAVSFVLVELYGNSLLLLTAVYGLVVAGSVLVL
GAIIGDWVDKNARLKVAQTSLVVQNVSVILCGIILMMVFLHKHELLTMYHGWVLTSCYILIITIANIANLASTAT
AITIQRDWIVVVAGEDRSKLANMNATIRRIDQLTNILAPMAVGQIMTFGSPVIGCGFISGWNLVSMCVEYVLLWK
VYQKTPALAVKAGLKEEETELKQLNLHKDTEPKPLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTRDGVV
SYYNQPVFLAGMGLAFLYMTVLGFDCITTGYAYTQGLSGSILSILMGASAITGIMGTVAFTWLRRKCGLVRTGLI
SGLAQLSCLILCVISVFMPSPLDLSVSPFEDIRSRFIQGESITPTKIPEITTEIYMSNGSNSANIVPETSPEV
PIISVSLLFAGVIAARIGLWSFDLTVTQLLQENVIESERGIINGVQNSMNYLLDLLHFIMVILAPNPEAFGLLVL
ISVSFVAMGHIMYFRFAQNTILGNKLFACGPDKEVRKENQANTSVV

992/6881
FIGURE 925

TTTTGTGAAGAGACGAAGACTGAGCGGTTGCGGCCGCGTTGCCGACCTCCAGCAGCAGTCGGCTTCTCTACGCAG
AACCCGGGAGTAGGAGACTCAGAATCGAATCTCTTCTCCCTCCCCTTCTTGTTTTCGGCTTTGTGAGAAACCTTA
CCATCAAAACACAATGGCCAGCAACGTTACCAACAAGACAGATCCTCGTTCCATGAACTCCCGTGTAATTCATTGGG
AATCTCAACACTCTTGTTGGTCAAGAAATCTGATGTGGAGGCAATCTTTTCGAAGTATGGCAAAATTGTGGGCTGC
TCTGTTCATAAGGGCTTTGCCTTCTTTTCAGTATGTTAATGAGAGAAATGCCCGGGCTGCTGTAGCAGGAGAGGAT
GGCAGAATGATTGCTGGCCAGGTTTTAGATATTAACCTGGCTGCAGAGCCAAAAGTGAACCGAGGAAAAGCAGGT
GTGAAACGATCTGCAGCGGAGATGTACGGCTCCTCTTTTGACTTGGATTGTGACTTTCAACGGGACTATTATGAT
AGGATGTACAGTTACCCAGCACGTGTACCTCCTCCTCCTATTGCTCGGGCTGTAGTGCCCTCGAAACGTCAG
CGTGATATCAGGAAACACTTCACAAAGGGGCATAAGTGGCTTCAATTCTAAGAGTGGACAGCGGGGATCTTCCAAG
TCTGGAAAAGTTGAAAGGAGATGACCTTCAGGCCATTAAGAGGGAGCTGACCCAGATAAAACAAAAAGTGGATTCT
TTCTTGAAAACCTGGAAAAAATTGAAAAGGAACAGAGCAAACAAGCAGTAGAGATGAACAATGTTAAGTCAGAA
GAGGAGCAGAGCAGCAGCTCCGTGAAGAAAGATGAGACTAATGTGAAGATGGAGTCTGAGGGGGGTGCAGATGAC
TCTGCTGAGGAGGGGGACCTACTGGATGATGATGATAATGAAGATGGGGGGATGACCAGCTGGAGTTGATCAAGG
ATGATGAAAAAGAGGCTGAGGAAGGAGAGGATGACAGAGACAGCGCCAATGGCGAGGATGACTCTTAAGCACATA
GTGGGGTTTAGAAATCTTATCCCATTTATTTCTTTACCTAGGCGCTTGTCTAAGATCAAATTTTTTCACCAGATCCT
CTCCCCTAGTATCTTCAGCACATGCTCACTGTTTTCCCCATCCTTGTCCTTCCCATGTTTCATTAATTAATTCATA
TTGCCCCGCGCCTAGTCCCATTTTCACTTCCTTTGACGCTCCTAGTAGTTTTGTAAAGTCTTACCTGTAAATTTT
TGCTTTTAATTTTGATACCTCTTTATGACTTAACAATAAAAAATGATGTATGGTTTTTATCAACTGTCTCCAAAAT
AATCTCTTGTTATGCAGGGAGTACAGTTCTTTTCATTCATACATAAGTTCAGTAGTTGCTTCCCTAACTGCAAAG
GCAATCTCATTTAGTTGAGTAGCTCTTGAAAGCAGCTTTGAGTTAGAAGTATGTGTGTTACACCCCCACATTAGT
GTGCTGTGTGGGGCAGTTCAACACAAATGTAACAATGTATTTTTGTGAATGAGAGTTGGCATGTCAAATGCATCC
TCTAGAAAAATAATTAGTGTTATAGTCTTAAGATTTGTTTTCTAAAGTTGATACTGTGGGTTATTTTTGTGAACA
GCCTGATGTTTGGGACCTTTTTTCTCAAAATAAACAAGTCCTTATTAAACCAGG

993/6881
FIGURE 926

GCCGACCTCCAGCAGCAGTCGGCTTCTCTACGCAGAACCCGGGAGTAGGAGACTCAGAATCGAATCTCTTCTCCC
TCCCCTTCTTGTTTTCGGCTTTGTGAGAAACCTTACCATCAAACACAATGGCCAGCAACGTTACCAACAAGACAG
ATCCTCGTTCCATGAACTCCCGTGTATTTCATTGGGAATCTCAACACTCTTGTGGTCAAGAAATCTGATGTGGAGG
CAATCTTTTCGAAGTATGGCAAAATTGTGGGCTGCTCTGTTTCATAAGGGCTTTGCCTTCTTTTCAGTATGTTAATG
AGAGAAATGCCCCGGGCTGCTGTAGCAGGAGAGGATGGCAGAATGATTGCTGGCCAGGTTTTAGATATTAACCTGG
CTGCAGAGCCAAAAGTGAACCGAGGAAAAGCAGGTGTGAAACGATCTGCAGCGGAGATGACCTTCAGGCCATTAA
GAGGGAGCTGACCCAGATAAAACAAAAGTGGATTCTTTCTGGAAAACCTGGAAAAAATTGAAAAGGAACAGAG
CAAACAAGCAGTAGAGATGAACAATGTTAAGTCAGAAGAGGAGCAGAGCAGCAGCTCCGTGAAGAAAGATGAGAC
TAATGTGAAGATGGAGTCTGAGGGGGGTGCAGATGACTCTGCTGAGGAGGGGGACCTACTGGATGATGATGATAA
TGAAGATGGGGGGATGACCAGCTGGAGTTGATCAAGGATGAGGATGACTCTTAAGCACATAGTGGGGTTTTAGAAA
TCTTATCCCATTTATTTCTTTACCTAGGCGCTTGTCTAAGATCAAATTTTTACCAGATCCTCTCCCCTAGTATCT
TCAGCACATGCTCACTGTTTTCCCCATCCTTGTCCTTCCCATGTTCAATTAATTAATTCATATTGCCCCGCGCCTA
GTCCCATTTTCACTTCCTTTGACGCTCCTAGTAGTTTTGTTAAGT

994/6881
FIGURE 927

GAGACGAAGACTGAGCGGTTGCGGCCGCGTTGCCGACCTCCCCTTCTTGTTTTCGGCTTTGTGAGAAACCTTACC
ATCAAACACAATGGCCAGCAACGTTACCAACAAGACAGATCCTCGTTCCATGAACTCCCGTGTATTTCATTGGGAA
TCTCAACACTCTTGTTGGTCAAGAAATCTGATGTGGAGGCAATCTTTTCGAAGTATGGCAAAATTGTGGGCTGCTC
TGTTTCATAAGGGCTTTGCCTTCTTTTCAGTATGTAAATGAGAGAAATGCCCGGGCTGCTGTAGCAGGAGAGGATGG
CAGAATGATTGCTGGCCAGGTTTTAGATATTAACCTGGCTGCAGAGCCAAAAGTGAACCGAGGAAAAGCAGGTGT
GAAACGATCTGCAGCGGAGATGTACGGCTCCTCTTTTGACTTGGATTGTGACTTTCAACGGGACTATTATGATAG
GATGTACAGTTACCCAGCACGTGTACCTCCTCCTCCTATTGCTCGGGCTGTAGTGCCCTCGAAACGTCAGCG
TGTATCAGGAAACACTTCACAAAGGGGCATAAGTGGCTTCAATTCTAAGAGTGGACAGCGGGGATCTTCCAAGTC
TGGAAAGTTGAAAGGAGATGACCTTCAGGCCATTAAGAGGGAGCTGACCCAGATAAAACAAAAAGTGGATTCTTT
CCTGGAAAACCTGGAAAAAATTGAAAAGGAACAGAGCAAACAAGCACTGGAGTTGATCAAGGATGATGAAAAAGA
GGCTGAGGAAGGAGAGGATGACAGAGACAGCGCCAATGGCGAGGATGACTCTTAAGCACATAGTGGGGTTTAGAA
ATCTTATCCCATTATTTCTTTACCTAGGCGCTTGTCTAAGATCAAATTTTTTACCAGATCCTCTCCCCTAGTATC
TTCAGCACATGCTCACTGTTTTCCCATCCTTGTCCTTCCCATGTTCAATTAATTCATATTGCCCCGCGCCT
AGTCCCATTTTCACTTCCTTTGACGCTCCTAGTAGTTTT

995/6881
FIGURE 928

ATCTTTTATAGAGAAATCTCGGGTTGTTAAACAGCCAAGAGGTGAAAGAACTTCCATGTGTTCTATCAGCTGCTCT
CTGGTGCCCTCTGAAGAGCTCCTCAATAAACTTAAGCTTGAGAGGGATTTTCAGCAGGTATAACTACCTGAGTCTGG
ATTTCGGCCAAAGTGAATGGAGTGGATGATGCAGCAAAATTTAGAACCGTGCGGAATGCCATGCAGATTGTGGGCT
TTATGGATCATGAAGCTGAGTCTGTCTTGGCGGTGGTGGCAGCAGTGTGAACTGGGGAAACATTGAGTTCAAGC
CCGAATCTCGAGTGAATGGTCTAGATGAAAGCAAAATCAAAGATAAAAATGAGTTAAAAGAAATTTGTGAATTGA
CCGGCATTGATCAATCAGTTCTAGAACGAGCATTAGTTTCCGAACAGTTGAGGCCAAACAGGAGAAAAGTTTCAA
CTACACTGAATGTGGCTCAGGCTTATTATGCCCGTGATGCTCTGGCTAAAAACCTCTACAGCAGGTTGTTTTCAT
GGTTGGTAAATCGAATCAATGAAAGCATTAAAGGCACAAAACAAAAGTGAGAAAGAAGGTGATGGGTGTTCTGGACA
TTTATGGCTTTGAGATTTTCGAGGACAACAGCTTTGAGCAGTTCATTATTAATTATTGTAACGAAAAGCTGCAAC
AAATCTTCATTGAACTTACTCTTAAAGAAGAGCAGGAGGAGTATATACGGGAGGATATAGAATGGACTCACATTG
ACTACTTCAATAATGCTATCATTGTGTGACCTAATAGAAAAATAACACAAATGGAATCCTGGCCATGCTGGATGAAG
AGTGCCTCAGACCTGGCACAGTCACTGATGAGACCTTCTTAGAAAAGCTGAACCAAGTATGTGCCACCCACCAGC
ATTTTGAGAGCAGGATGAGCAAGTGCTCTCGGTTTCTCAATGACACGTCTCTGCCTCACAGCTGCTTCAGGATCC
AGCATTATGCTGGAAAAGGTGCTGTACCAGGTGGAAGGATTTCGTTGACAAAAACAATGACCTTCTCTATCGAGACC
TGTCCCAAGCCATGTGGAAGGCCAGCCATGCCCTCATCAAGTCTTTGTTCCCCGAAGGGAATCCCGCCAAGATCA
ACCTGAAAAGGCTTCTACAGCAGGCTCACAGTTCAAGGCATCCGTGGCCACTCTGATGAAAAACCTACAGACCA
AGAACCCAAACTATATTAGGTGTATCAAACCGAATGATAAAAAAGCAGCACACATCTTCAACGAGGCTCTAGTGT
GTCATCAGATCAGGTACCTGGGGCTTTTGGAGAACGTCCGAGTGCGGAGGGCAGGCTACGCCTTCAGGCAGGCCT
ATGAACCTTGCTAGAAAAGATACAAAATGCTTTGTAAACAAACATGGCCTCATTGGAAAGGACCAGCCAGGTCTG
GTGTGGAGGTCTATTTAATGAATTAGAAATTCCCGTGGAAGAATACTCCTTTGGTAGATCAAAGATATTCATCC
GAAACCCAAGAACATTATTCAAATTAGAAGACCTGAGGAAGCAACGCCTGGAGGACTTGGCCACTCTCATTGAGA
AGATATATCGGGGGTGGAATGCCGCACACACTTCTGCTAATGAAAAAAGCCAAATTGTGATTGCCGCCTGGT
ACAGGAGATATGCGCAACAAAAGAGGTACCAGCAGACAAAGAGTTCGCCTTAGTAATTCAGTCTTATATCCGGG
GTTGGAAGGCTCGAAAAATTCTGCGGGAAGTGAAGCATCAAAAGCGCTGTAAGGAAGCAGTCACGACCATTGCTG
CATATTGGCATGGGACCCAGGCTCGAAGGGAATTGAAACGCTTGAAGGAGGAGGCTAGGCGTAAGCATGCAGTTG
CTGTCAATTTGGGCTTACTGGCTTGGACTGAAGGTACGTAGAGAATACAGGAAATTCTTCAGAGCCAATGCTGGAA
AGAAAATCTATGAGTTTACGCTTCAGAGAATTGTGCAAAAATACTTCTTGGAATGAAAAATAAGATGCCTTCCT
TATCTCCAATAGACAAGAATTGGCCCTCAAGACCTTACTTATTCTTGGATTCTACTACAAGGAGCTAAAAAGGA
TTTTCCACTTGTGGAGGTGTAAAAAATACAGGGACCAATTACAGACCAGCAGAACTTATTTATGAAGAGAAAC
TAGAAGCCAGTGAATCTTCAAAGACAAGAAGGCTTTATACCCATCTAGTGTGGGCAACCATTCCAAGGGGCTT
ACCTGGAAATCAACAAGAACCCCAAGTATAAGAACTCAAAGATGCCATTGAAGAAAAGATCATCATTGCTGAAG
TCGTGAACAAAATTAACCGTGCTAATGGGAAGAGTACATCTCGGATTTTCTCTTAACAAACAATAATCTCCTTC
TTGCTGACCAAAAGTCTGGACAAATCAAGTCAGAGGTTCCATTGGTGGATGTGACCAAGGTATCAATGAGCTCAC
AAAATGATGGCTTCTTCGCCGTCCACCTCAAAGAGGGCTCAGAAGCAGCTAGTAAAGGAGACTTCTCTTCAGCA
GTGATCACCTGATTGAAATGGCCACCAAGCTCTATCGCACAACCTCTCAGCCAAACCAACAGAAGCTCAATATTG
AGATTTCCGATGAGTTCTTGGTACAGTTTACAGACAGGACAAAGTATGTGTGAAGTTTATTAGGAACCCTGTAGTAT
GATATTTAACAATATAGGCTTCAAAGAAGGGCTGGTCCTAAGAGGGGGCAGAAATGAATGACCAGGTTAAATCCCT
CTACATGTGGTTTCTGTTTG

996/6881
FIGURE 929

AGGTCAGAAATGTGAATTCCAGGATGCCTATGTTCTGTTGAGTGAAAAGAAAATTTCTAGTATCCAGTCCATTGT
ACCTGCTCTTGAAATTGCCAATGCTCACCGTAAGCCTTTGGTCATAATCGCTGAAGATGTTGATGGAGAAGCTCT
AAGTACACTCGTCTTGAATAGGCTAAAGGTTGGTCTTCAGGTTGTGGCAGTCAAGGCTCCAGGTTTGGTGACAA
TAGAAAAGAACCAGCTTAAAGATATGGCTATTGCTACTGGTGGTGCAGTGTTTGGAGAAGAGGGATTGACCCTGAA
TCTTGAAGACGTTCAGCCTCATGACTTAGGAAAAGTTGGAGAGGTCATTGTGACCAAAGACGATGCCATGCTCTT
AAAAGGAAAAGGTGACAAGGCTCAAATTGAAAAACGTATTCAAGAAATCATTGAGCAGTTAGATGTCACAACTAG
TGAATATGAAAAGGAAAACTGAATGAACGGCTTGCAAACTTTTCAGATGGAGTGGCTGTGCTGAAGGTTGGTGG
GACAAGTGATGTTGAAGTGAATGAAAAGAAAGACAGAGTTACAGATGCCCTTAATGCTACAAGAGCTGCTGTTGA
AGAAGGCATTGTTTTGGGAGGGGGTTGTGCCCTCCTTCGATGCATTCCAGCCTTGGACTCATTGACTCCAGCTAA
TGAAGATCAAAAAATTGGTATAGAAATTATTAAGAAGCACTCAAAATTCAGCAATGACCATTGCTAAGAATGC
AGGTGTTGAAGGATCTTTGATAGTTGAGAAAATTATGCAAAGTTCCTCAGAAGTTGGTTATGATGCTATGGCTGG
AGATTTTGTGAATATGGTGGAAAAAGGAATCATTGACCCAAACAAAGGTTGTGAGAACTGCTTTATTGGATGCTGC
TGGTGTGGCCTCTCTGTAACTACAGCAGAAGTTGTAGTACAGAAATTCCTAAAGAAGAGAAGGACCCTGGAAT
GGGTGCAATGGGTGGAATGGGAGGTGGTATGGGAGGTGGCATGTTCTAACTCCTAGACTAGTGCTTTACCTTTAT
TAATGAACTGTGACAGGAAGCCCAAGGCAGTGTTCCCTACCAATAACTTCAGAGAAGTCAGTTGGAGAAAATGAA
GAAAAAGGCTGGCTGAAAATCACTATAACCATCAGTTACTGGTTTCAGTTGACAAAATATATAATGGTTTACTGC
TGTCAATTGTCCATGCCTACAGATAATTTATTTTGTATTTTGAATAAAAAACATTTGTACATTCCTGATACTGGG
TACAAGAGCCATGTACCAGTGACTGCTTTCAACTTAAATCACTGAGGCATTTTACTACTATTCTGTTAAAATC
AGGATTTTGTAGTGCTTGCCACCACCAGATGAGAAGTTAAGCAGCCTTTCTGTGGAGAGTGAGAATAATTGTGTACA
AAGTAGAGAAGTATCCAATTATGTGACAACCTTTGTGTAATAAAAATTTGTTTAA

997/6881
FIGURE 930

GCTACACTAGAGCAGAGTACGAGTCTGAGGCGGAGGGAGTAATGCCAGGACAAGCGTTTAGAAAAGTTTCTTCCAC
TCTTTGACCGAGTATTGGTTGAAAGGAGTGCTGCTGAAACTGTAACCAAAGGAGGCATTATGCTTCCAGAAAAAT
CTCAAGGAAAAGTATTGCAAGCAACAGTAGTCGCTGTTGGATCGGGTTCTAAAGGAAAGGGTGGAGAGATTCAAC
CAGTTAGCGTGAAAGTTGGAGATAAAGTTCTTCTCCCAGAATATGGAGGCACCAAAGTAGTTCTAGATGACAAGG
ATTATTTCTTATTAGAGATGGTGACATTCTTGGAAGTACGTAGACTTGAAATAAGTCACTATTGAAATGGCATC
AACATGATGCTGCCCATTCCACTGAAGTTCTGAAATCTTTCGTCATGTAAATAATTTCCATATTTCTCTTTTATA
ATAAACTAATGATAACTAATGACATCCAGTGTCTCCAAAATTGTTTCCTTGTACTGATATAAACACTTCCAAATA
AAAATATGTAAAT

998/6881
FIGURE 931

MAGQAFRKFLPLFDRVLVERSAAETVTKGGIMLPEKSQGKVLQATVVAVGSGSKGKGGEIQPVSVKVGDKVLLPE
YGGTKVVLDDKDYFLFRDGDILGKYVD

999/6881
FIGURE 932

GATTTGACCCTTGAGCCGTAGGGAGCGCGGCATTTTCTGGAAAGTTCTGGAACCGAGCGAGGCCCGGGAAC TAGA
CTAAGCCGGCCGGAGAGGGCTGAGCGCGCTAGCACACCCTGCGCGGAAATGCTTCGGTTACCCACAGTCTTTCGC
CAGATGAGACCGGTGTCCAGGGTACTGGCTCCTCATCTCACTCGGGCTTATGCCAAAGATGTAAAATTTGGTGCA
GATGCCCCGAGCCTTAATGCTTCAAGGTGTAGACCTTTTAGCCGATGCTGTGGCCGTTACAATGGGGCCAAAGGGA
AGAACAGTGATTATTGAGCAGAGTTGGGGAAGTCCCAAAGTAACAAAAGATGGTGTGACTGTTGCAAAGTCAATT
GACTTAAAAGATAAATACAAAACATTGGAGCTAAACTTGTTCAAGATGTTGCCAATAACACAAATGAAGAAGCT
GGGGATGGCACTACCACTGCTACTGTACTGGCACGCTCTATAGCCAAGGAAGGCTTCGAGAAGATTAGCAAAGGT
GCTAATCCAGTGGAATCAGGAGAGGTAGGAATGTCTGTTGTCACCACAGTGTTCTAAACTTCAGTGTGCTTTAA
GGCATTGATTCCTTGGACCTAAGGAAAGTGTTAACTTGAGGAAATTAATCCTTCTCTCATTCCCTCCTCTTGGCCT
GGAGAAATCTTAAACTGGGTTTTCTTTAGCAAGCTTGGCTGT

1000/6881
FIGURE 933

TGGAAAGAGTGGAACGAGAAAACCTTTTCAGACTATTGTGTTCTGGGCCAGCGTCCAATGCATTTACCAAATATGA
ACCAGCTGGCATCCCTGGGGAAAACCAACGAACAGTCTCCTCACAGCCAAATTCACCACAGTACTCCAATCCGAA
ACCAAGTGCCCGCATTACAGCCCATCATGAGCCCTGGTCTTCTTTCTCCCCAGCTTAGTCCACAACCTTGTAAGGC
AACAAATAGCCATGGCCCATCTGATAAACCAACAGATTGCCGTTAGCCGGCTCCTGGCTCACCAGCATCCTCAAG
CCATCAACCAGCAGTTCCTGAACCATCCACCCATCCCCAGAGCAGTTAAGCCAGAGCCAACCAACTCTTCCGTGG
AAGTCTCTCCAGATATCTACCAGCAAGTCAGAGATGAGCTGAAGAGGGCCAGTGTGTCCCAAGCTGTCTTTGCAA
GAGTGGCATTCAACCGCACACAGGTACAATTAGCATTAAACACTGTGAATTAACAGTAATACTGGGGACAGAATTG
AGATAGGTTATAATTATTTTTATCTCTTTAAAAAGCTTTATGGATCTCAGGACATAGAATTAGATTAATTAATAA
TCCTTAGTTAATGAAACGCTATTACCATTGATCCATGCATGACCATGATTAATTAATACTAATTGATTAATTTTGAT
GAGGTAATGGACATCTTTGAACCCAACATGCAACTCAGGACCCCAAATGTTACTAATGACTTGGGTATGTACTCT
CTCATCCTCTCCATTTACTGTTTGCAGATGTAACCCCTGATCTTGAATTTTGTGATTATCAGTCTCTTGCCATTTT
TTAAAACAAATTATAAACTATGCATGCCAGACAATCTATTTTTTTCCCTTGGTTTTGAACGTTATAAAAGAAA
TAAAATTATGTTTTATAATTTTATAAGTAAAGTTTTATTTAAAAATTTATAAAAATCCTTCAAAACATAAAAGTT
AGATTTAAGATATTGATAAAATGATAATGGATAGTTTACTTTTATTTTTTAATGTTTGAGAGAATTATATGCCAAT
TATAACACTAAATGTTGAAAATGTAAACAGTTAATTCACACGTCTTATTTTTATTGAGGGTGCTTATATGTAAGA
CATTCTTTTCTGCTAGTAGTTCCTTAACTGGAGTGTGCATCAGAATCACCTGGAGGGCTGTGAAACACAGACTGC
TGGGCCTCATCCCATAGTTTCTGATTGAGTAAGTCTGAGGTTGGACTCAGAAATGGACATTTCTAACAAGATCCC
AGGTGATTATGATGGTACTGATCCGGGGCCGCATGTTGAGAAAACTTACCTAGCCCTTATATGAGTAAGAACAA
AGCAGATGTGCATAATCTCGGGGAGCTAACGATCTAGTGGTGAAGAACAGGTAACCAGATAATTAGAGTAAATG
TGAAGTGGTATGAGTAATGTTGGAGAGTGTAAGCAATAGTTGTGGTGGAGGTTTCATGGTGAGCTGGAGGTGAGGA
ATACTTCCAGGAGAATGAATATGGTAAGCCTTCAAGAAAACAGTAGATTAAAATTTAGCACCCCTCGTAAATGCA
AGGCAGGAAGCTAAGCTCTATGTGGGTGCAAAGAGGAAAAAGATAATGGGCAAGCACATATGTAAACAACACTCT
AGAGTATTAGGTTGTCAATGGGTTAGACCTTGAAGGATTAATAAAGTACAGCAGGCAAAGATGATGAAGAAGAAG
ATTATTATTTTAAGGTAAAGACATTCATAGGAAAGATGTTGAGTTAAAAATGCAGGAATAATTTGAAGACATAA
AACAACTGATTTCTGAGAAAAACCCTGTGAACGTACAGAATGTAGGAATGCTTTTATTTATCTGATACCTGTTCA
GAGACACATGATAACACACGCTGTAGATGGACCTTACAAATGAAAGAAAGCATGCTGGATTGAAACCTCAATAAT
TTGGAATAACAGGAATGTTTCCAAATTTAATGATTACTTCAGAAGTTAAGGGGCTGGGCACAGTGGCTCATGTC
TGTAAGTCTAGCACTTTGGGAGGCCAAGGTGGGCGGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGGCAAG
ATGGTAAACACCATCTCTACTAAAACAGAACAAAAACAAAAAATTAGCTGGGCGTGGTGATGCGTGCCTGTAGT
CTCAGCTACTCAGGAGGCTGAGGCAGAAGAATCCCTTGAACCCAGGAGGCGGAGGCTGCAGTGAGCCGAGATCAT
GCCACTGCACTCCAGCCTGAGTGAGAGTGAACTCCATCTCAAAAAAAAAAAAAAAAAA

1001/6881
FIGURE 934

GAGAGGAGACACCGCCGAGTTGCCGGTACATCGGGGATTTCTGGCTCTTTCTCTTCGCCTTAAATTCGGGTGT
CTTTTATGAATAATCAAAAGCAGCAAAAGCCAACGCTATCAGGCCAGCGTTTTAAACTAGAAAAAGAGATGAAA
AAGAGAGGTTTGACCCTACTCAGTTTCAAGACTGTATTATTCAAGGCTTAACTGAAACCGGTACTGATTGGAAG
CAGTAGCTAAGTTTCTTGATGCTTCTGGAGCAAACTTGATTACCGTCGATATGCAGAAACACTCTTTGACATTCT
TGGTGGCTGGTGGGAATGCTGGCCCCAGGTGGTACACTGGCAGATGACATGATGCGTACAGATGTCTGCGTGTTTG
CAGCCCAAGAAGATCTAGAGACCATGCAAGCATTGCTCAGGTTTTTAACAAGTTAATCAGGCGCTACAAATACC
TGGAGAAAGGTTTTGAAGATGAAGTAAAAAAGCTGCTGCTGTTCTTGAAGGGTTTTTCAGAGTCGGAGAGGAACA
AGCTAGCTATGTTGACTGGTGTCTTCTGGCTAATGGAACACTTAATGCATCCATTCTTAATAGCCTTTATAATG
AAAATTTGGTTAAAGAAGGAGTTTCAGCAGCTTTTGCTGTGAAGCTCTTTAAATCATGGATAAATGAAAAAGATA
TCAATGCAGTAGCTGCAAGTCTTCGGAAGTCAGCATGGATAACAGACTGATGGAACCTTTCTCTGCCAATAAGC
AAAGTGTGTAACACTTCACAAAATATTTTACTGAGGCAGGCTTGAAAGAGCTTTCAGAATATGTTCCGAATCAGC
AAACCATCGGAGCTCGTAAGGAGCTCCAGAAAGAACTTCAAGAACAGATGTCCCGTGGTGATCCATTTAAGGATA
TAATTTTATATGTCAAGGAGGAGATGAAAAAAACAACATCCCAGAGCCAGTTGTCATCGGAATAGTCTGGTCAA
GTGTAATGAGCACTGTGGAATGGAACAAAAAAGAGGAGCTTGTAGCAGAGCAAGCCATCAAGCACTTGAAGCAAT
ACAGCCCTCTACTTGCTGCCTTTACTACTCAAGGTCAGTCTGAGCTGACTCTGTTACTGAAGATTCAGGAGTATT
GCTATGACAACATTCAATTCATGAAAGCCTTCAGAAAATAGTGGTGCTTTTTTATAAAGCTGAAGTCCTGAGCG
AGGAGCCCATTTTGAAGTGCTATAAAGATGCACATGTTGCAAAGGGGAAGAGTGTTTTCTTGAGCAAAATGAAAA
AGTTTGTAGAATGGCTCAAAAATGCTGAAGAAGAATCTGAATCTGAAGCTGAAGAAGGTGACTTGAATTTTGAAC
TACACCCTCAGTAAAGCAAACAGGAGTTGTAGATAAAATGTCATGTCTCATGTGTCCTGGTTCTTACATCTTCCT
ACCTCCCTGTATCAAGCATGATATAAGGGCTTTTCATGGCAAATTTTATTTTAACTGTTTCTATGGTTGCTGGAAA
TGTTGGGTTTAGTTTCTAAAACCATGTTTTAAGTAGCTACAGGAGCTATAGATTTGAATCTAATGTTGCATTAGT
CTTTTCAGTTATCTTCTACCTCCTGTATTTTCTACTGTAATAATGTAATTTAAGGCCTTCACAATGAACAGTTC
ACTTTATTCCCTGGGTTTTCTATAAACAGTTTTAAGGATATGATTTGGTTAAAAAATAATTTGTTATAAAAATTC
TGTTTGCAAATTAAGCTGAAAAAGTATCCAGAGTCTCAAAGGCAATGATTTGTGAGATAATATGGCATGCCCGG
AGCCCTGCTCATCAATGAAAAACCATATGTAATAATCGAATTCATTTAACATGAATCTTGAGTACGTGGACCAT
TGCTTGCAATGTTAACTTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGCAATTTTAACTCCAGATATCCTAAAGCTC
AATTGTTTGGTCTCTGGTTTTTCATCCTTAGAGAAGCCATGGAGAACAGACTTGAAAAGTTTAGGAAATCATAATG
TGGCAGAGGTGGTGGGAAGAAGAAAGTTGAGCTTTTTCCCTTGAGAAACTTCTGCATTTAGTTTCTATCTTTCC
AGGCAAAACAAATGGGTATTCTTTTCATACAACCATTTTCAAATGAACCTTAGAAAAGTCTTAACATTTAAGGTA
TTTTATGCACAGAATACACTTAGATTGATAGGAAAGAAGCTCGTAATGGAGTTTGAGTAAAGAAAATGACTGATGT
ACTAAACCCAGTAAAAATGTTGAAAATGTTAAAGGTCAGCATGTTCTAATTGGGAATCTAGATATAGCTTAGAT
TTCCTATTGGCTTAGAGTATTTGCTATAACAAATGAAGTGCAATGACAATTATATATTCCTACTCGGTCATACTG
GACTGGCTTCGTTCTCTTAATATACTCAGTAATGACTCAAGCCTCTGGCTATTAACATACCCTAGTTGCCGTTTT
TTAATTGCCATGAGCCAAATACTTCTTGGTATACAATTGATCCATTTATTTAATGGCTGCCTTTTCAATTTTCAT
CTTTTCTTGCTGCTACCCATCTATGTATGTAGTCATTGGGGGGAAAATGTAGCCACATTTTTTATGGGAAGACTT
TGTGTTAAAAGTGAACATTTTGAAGGTTTTTAACTGGTGAACTAGCCTGGAATAATGCCACCAGAGACTGAGTG
GAAATCGCCCCCTTTTGAAGGTGCCATTCTTATGAGCCAAAAGTTTGTCAATTTAAAAGTTCAATTTGAGGGAATAA
CATGTAATATAATTTGAAATAAAGGTATAGTAACCTTAAAAAGAACATTATAACTGATTGTTGTGAATGGGGTGA
ATTTGTTAAAATGAGTAACCTTTGATAAAGTTTTTCATGCACAGGCAAAATGTATTCCTAGATTTCTACGTAGTG
ATCTGCTTTTACTTTGTAAATTTGTAGTTCTCAAAGACTTTTTTTTTAAAAAATAAAGTCCATACTTACACTT

1002/6881
FIGURE 935

MNNQKQQKPTLSGQRFKTRKRDEKERFDPTQFQDCIIQGLTETGTDLEAVAKFLDASGAKLDYRRYAETLFDILV
AGGMLAPGGTLADDMMRTDVCVFAAQEDLETMQAFAQVFNKLIRRYKYLEKGFEDDEVKKLLFLKGFSESERNKL
AMLTGVLLANGTLNASILNSLYNENLVKEGVSAFAVKLFKSWINEKDINAVAASLRKVSMDNRLMELFPANKQS
VEHFTKYFTEAGLKELSEYVRNQOTIGARKELQKELQEOMSRGDPFKDIILYVKEEMKKNNIPEPVVIGIVWSSV
MSTVEWNKKEELVAEQAIKHLKQYSPLLAFTTQGOSELTLLLKIQEYCYDNIHFMKAFQKIVVLFYKAEVLSEE
PILKWYKDAHVAKGKSVFLEQMKKFVEWLKNAEESESEAEEGD

1003/6881
FIGURE 936

ACGCAGAGAAGTTTCCGGGACTGAAACTTTGAACTTTACCTGATTTCTGTATGTTGTCATCTTGCGTACGCCCAGT
CCCCACGACAGTCCGGTTTGTAGATTCCCTGATCTGCAATTCTTCCCGTTCCCTTCATGGATTGGAAGGCTCTCCT
TTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAGAGTTGGGACAATGTTGGATTACTGGTGGAACCAAG
CCCACCACATACTGTAAATACACTCTTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAA
GAAGGCAGACCTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAAACACATGGAA
GGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCATAACAGCCTATGATGCTGCGCC
CCAGGGCGTCAACAACCTGGTTGGCTAAAGGGCTTGGAGCTTGACCTCCAGGCCCATAACATCCTTCCAAAGCTCC
CAACTACCTTACAGAGGGAAACCCAGAGTAGAATTCAACGTTAACTACACCCAAGACCTGGACAAAGTCATGTC
TGCAGTGAAAGGAATTGACGGTGTTTCTGTCACTTCTTTTTCTGCTAGGACTGGTAATGAGGAACAAACACGGAT
TAATCTGAATTGTACTCAGAAGGCTTTGATGCAGGTGGTAGATTTTCTTTCCCGGAACAAACAACTTTATCAGAA
GACGAAATTCTGTCACTGGAGAAGCCTTTGCTTCTACATACTGGAATGGGACGGTTATGCACACTGGATGAATC
TGTCTCCCTGGCAACCATGATTGATCGAATAAAAAGACACCTAAACTATCTCATATTTCGCTTAGCCCTTGGGGT
GGGGAGAACCTTAGAGTCTCAAGTCAAAGTCGTGGCCCTGTGTGCTGGTTCTGGGAGCAGCGTTCTGCAGGGTGT
TGAGGCTGACCTTTACCTCACAGGTGAGATGTCCCATCATGATACTTTGGATGCTGCTTCCCAAGGAATAAATGT
CATCCTCTGTGAACACAGCAACACTGAACGAGGCTTTCTTTCTGACCTTCGAGATATGCTGGATTCTCACTTGGA
GAATAAGATAAATATTATCCTATCAGAGACTGACAGGGACCCTCTTCAGGTGGTATTAATTGCAGAAACATCAGGA
TAACACATTCTACAAATCAGCTGGATGCCAACTTAAATTTGTAACATGAGTCAGTGGGACTGGTGTGCTTCCAGA
GAGTGTCTTCGAGGGTATCATCATTTCCGGTTTGTTAATCTTATTCACCAAATGTTCTATCGCTCGTAAGGTAAA
ACTGTAATATAACTACCATATTAAATAACAAATGTTTATTATAAACTCTAGGAAAGATTGAATAAAATCTGTTTA
CTTAACATTCT

1004/6881
FIGURE 937

MLSSCVRPVPTTVRFVDSLICNSSRSFMDLKALLSSLNDFASLSFAESWDNVGLLVEPSPPHTVNTLFLTNDLTE
EVMEEVLQKKADLILSYHPPIFRPMKRITWNTWKERLVIRALENRVGIYSPHTAYDAAPQGVNNWLAKGLGACTS
RPIHPSKAPNYPTTEGNHRVEFNVNYTQDLDKVMSAVKGIDGVSVTSFSARTGNEEQTRINLNCTQKALMQVVDL
SRNKQLYQKTEILSLEKPLLLHTGMGRCTLDESVS LATMIDRIKRHLKLSHIRLALGVGR TLESQVKVVALCAG
SGSSVLQGVEADLYLTGEMSHHDTLDAASQGINVILCEHSNTERGFLSDLRDMLDSHLENKINIILSETDRDPLQ
VV

1005/6881
FIGURE 938

CTCCTTTCTGCCCCGTGGACGCCGCCGAAGAAGCATCGTTAAAGTCTCTCTTCACCCTGCCGTCATGTCTAAGTCA
GAGTCTCCTAAAGAGCCCCGAACAGCTGAGGAAGCTCTTCATTGGAGGGTTGAGCTTTGAAACAACCGATGAGAGC
CTGAGGAGCCATTTTGAAGCAACGGGGAAACGCTCACAGACTGTGTGGTAATGAGAGATCCAAACACCAAGTGCTCC
ACGGGCTTTGGGTTTGTACATATGCCACTGTGAAGGAGGTGGAGGCAGCTATGAATGCAAGGCCACAGAAGGTG
GATGGAAGAGTCGTGGAACCAAAGAGAGCTGTCTCGAGAGAAGATTCTCAAAGACCAGGTGCCCACTTAAGTGTG
AAAAAGATATTTGTTGGTGGCATTAAAGAAGACACTGAAGAACATCACCTAAGAGATTATTTTGAACAGTATGGA
AAAATTGAAGTGATTGAAATCATGACTGACCGAGGCAGTGGGAAGAAAAGGGGCTTTGCCTTTGTAACCTTTGAT
GACCATGACTCCGTGGATAAGATTGTCAATTCAGAAATACCACACTGTGAATGGCCACAACCTGTGAAGTTAGAAAA
GCCCTGTCAAAGCAAGAGATGACTAGTGCTTCATCTAGCCAAAGAGGTGCAAGTGGTTCTGGAAACTTTGGTGGT
GGTCGTGGAGGTGGTTTTCAGTGGGAATGACAACCTTTGGTCATGGAAGAACTTCAGTGGTCATGGTGGCTTTGGT
GGCAGCCGTGGTGGTGGTGGATATGATGGCAGTGGGGATGGCTATAATGGATTTGGTAATGATGGAAGCCATTTT
GGAGGTGGTGGGAAGCTACAATGATTTTGGCAATTACAAAAATCAGTCTTCAAATTTTGGACCCGTGAAGGGAGGA
AATTTTGGAGGCAGAAGCTCTGGCCCCCTATGGCGGTGGAGGCCAATACTTTGCAAAAACACGAAACTAAGGTGGC
TATGGCGGTTCCAGCAGTAGCAGTAGCTATGGCAGTGGCAGAAGATTTTTAAATTAGGAAACAAAGCTTAGCAGGAG
AGGAGAGCCAGAGAAGTGACAGGGAAGCTACAGGTTACAACAGATTTGTGAACTCAGCCAAGCACAGTGGTGGCA
GGGCCTAGCTGCTACAAAGAAGACATGTTTTAGACAAATACTCATGTGTATGGGCAAAAAACTCGAGGACTGTAT
TTGTGACTAATTGTATAACAGGTTATTTTAGTTTCTGTTCTGTGGAAAGTGTAAGCATTCCAACAAAGGGTTTT
AATGTAGATTTTTTTTTTTTGCACCCATGCTGTTGATTGCTAAATGTAATAGTCTGATCGTGACGCTGAATAAATG
TCTTTTTTTTTTAATGTGCTGTGTAAAGTTAGTCTACTCTGAAGCCATCTTGGTAAATTTCCCCAACAGTGTGAAG
TTAGAATTCCTTCAGGGTGATGCCAGGTTCTATTTGGAATTTATATACAACCTGCTTGGGTGGAGAAGCTATTGT
CTTCGGAAACCTTGGTGTAGTTGAACTGATAGTTACTGTTGTGACCTGAAGTTCACCATTAAAAGGGATTACCCA
AGCAAAATCATGGAATTATTGGTTATAAAAGTGATTGTTGGCACATCCTATGCAATATATCTAAATTGAATAATG
GTACCAGATAAAATTATAGATGGGAATGAAGCTTGTSTATCATCCATTATCATGTGTAATCAATAAACGATTTAA
TTCTCTGGAA

1006/6881
FIGURE 939

MSKSESPKEPEQLRKLFIGGLSFETTDESLRSHFEQRTLTDCVVMRDPNTKCSTGFGFVTYATVKEVEAAMNAR
PQKVDGRVVEPKRAVSREDSQRPGAHLTVKKIFVGGIKEDTEEHHLRDYFEQYGKIEVIEIMTDRGSGKKRGFAF
VTFDDHDSVDKIVIQKYHTVNGHNCEVRKALSKQEMTSASSSQRGRSGSGNFGGGRGGGFSGNDNFGHGRNFSGH
GGFGGSRGGGGYDGS GDGYNGFGNDGSHFGGGGSYNDFGNYKNQSSNFGPVGKNFGGRSSGPYGGGGQYFAKPR
NRWLWRFQQVAVAMAVAEDF

1007/6881
FIGURE 940

GAGGCGTAGCGGAAGTTACTGCAGCCGCGGTGTTGTGCTGTGGGGAAGGGAGAAGGATTTGTAAACCCCGGAGCG
AGGTTCTGCTTACCCGAGGCCGCTGCTGTGCGGAGACCCCGGGTGAAGCCACCGTCATCATGTCTGACCAGGAG
GCAAAACCTTCAACTGAGGACTTGGGGGATAAGAAGGAAGGTGAATATATTAAACTCAAAGTCATTGGACAGGAT
AGCAGTGAGATTCACTTCAAAGTGAAAATGACAACACATCTCAAGAACTCAAAGAATCATACTGTCAAAGACAG
GGTGTTCGAATGAATCACTCAGGTTTCTCTTTGAGGGTCAGAGAATTGCTGATAATCATACTCCAAAAGAACTG
GGAAATGGAGGAAGAAGATGTGATTGAAGTTTATCAGGAACAAACGGGGGGTCATTCAACAGTTTAGATATTCTTT
TTATTTTTTTTTCTTTTCCCTCAATCCTTTTTTATTTTTAAAAATAGTTCTTTTGTAATGTGGTGTTCAAACGGA
ATTGTTATTCATTATTGTTTGTTTTCAATTGTGCTGATTTTTGGTGATCAAGCCTCAGTCCCCTTCATATTACC

1008/6881
FIGURE 941

ATGTTGGTGCTGTTTGAAACGTCTGTGGGTTACGCCATCTTTAAGTTCTAAATGAGAAGAACTTCAAGAGGTT
GATAGTTTATGGAAAGAATTTGAAACTCCAGAGAAAGCAAACAAAATAGTAAAGCTAAAACATTTTGAGAAATTT
CAGGATACAGCAGAAGCATTAGCAGCATTACAGCTCTGATGGAGGGCAAAATCAATAAGCAGCTGAAAAAAGTT
CTGAAGAAAATAGTAAAAGAAGCCCATGAACCGCTGGCAGTAGCTGATGCTAAACTAGGAGGGGTCATAAAGGAA
AAGCTGAATCTCAGTTGTATCCATAGTCCTGTTGTTAATGAACTTATGAGAGGAATTCGTTACAAAATGGATGGA
TTAATCCCTGGGGTAGAACCACGTGAAATGGCAGCTATGTGTCCTGGATTGGCTCAAGCCTGTCTCGATATAGA
TTGAAGTTTAGCGCTGATAAAGTAGACACAATGATTGTTTCAGGCAATTCCTTGTTAGATGACTTGGATAAAGAA
CTAAACAACCTACATTATGCGATGTAGAGAATGGTATGGCTGGCATTTCCTGAATTAGGAAAAATTATTTAGAT
AATTTAACATACTGCAAGTGTTCACAGAAAGTTGGCGATAGGAAGAACTATGCCTCTGCCAAGCTTTCTGAGTTG
CTGCCAGAAGAAGTTGAAGCAGAAGTGAAAGCAGCTGCAGAGATATCAATGGGAACAGAGGTTTCAGAAGAAGAT
ATTTGCAATATTCTGCATCTTTGCACCCAGGTGATTGAAATCTCTGAATATCGAACCAGCTCTATGAATATCTA
CAAAATCGAATGATGGCCATTGCACCCAATGTTACAGTCATGGTTGGGGAATTAGTTGGAGCACGGCTTATTGCT
CATGCAGGTTCTCTTTTAAATTTGGCCAAGCATGCAGCTTCTACCGTTTCTGAGATTCTTGGAGCTGAAAAGGCACTT
TTCAGAGCCCTCAAACTAGACGGGATACCCCTAAGTATGGTCTCATTATCATGCTTCACTCGTGGGCCAGACA
AGTCCCAAACACAAAAGGAAAGATTTCTCGAATGCTGGCAGCCAAAACCGTTTTGGCTATCCGTTATGATGCTTTT
GGTGAGGATTCAAGTTCTGCAATGGGAGTTGAGAACAGAGCCAAATTAGAGGCCAGGTTGAGAACTTTGGAAGAC
AGAGGGGATAAGAAAAATAAGTGGAACAGGAAAAGCATTAGCAAAAACAGAAAAATATGAACACAAAAGTGAAGTG
AAGACTTACGATCCTTCTGGTGACTCCACACTTCCAACCTGCTCTAAAAAACGCAAAATAGAACAGGTAGATAAA
GAGGATGAAATTACTGAAAAGAAAGCCAAAAAAGCCAAGATTAAAGTTAAAGTTGAAGAAGAGGAAGAAGAAAAA
GTGGCAGAAGAAGAAGAAACATCTGTGAAGAAGAAGAAGAAAAGGGGTAAAAAGAAACACATTAAGGAAGAACCA
CTTTCTGAGGAAGAACCATGTACCAGCACAGCAATTGCTAGTCCAGAGAAAAAGAAGAAAAAGAAAAAAGAGA
GAGAACGAGGATTAA

1009/6881
FIGURE 942

GGAGGCCAAGGTGCAACTTTCTTCGGTCGTCCCGAATCCGGGTTTCATCCAACACCAGCCGCCTCCACCATGCCGC
CGAAGTTCGACGGTGCCACTTCTGCCCTGGCCCCCAAGATCGGCCCCCTGGGTCTGTCTCCAAAAAAGGTTGGTG
ATGACATTGCCAAGGCAACGGGTGACTGGAAGGGCCTGAGGATTACAGTGAAACTGACCATTCAGAACAGACAGG
CCCAGATTGAGGTGGTGCCTTCTGCCTCTGCCCTGATCATCAAAGCCCTCAAGGAACCACCAAGAGACAGAAAGA
AACAGAAAAACATTAAACACAGTGGGAATATCACTTTTGATGAGATCGTCAACATTGTTGACAGATGCGGCACC
GATCCTTAGCCAGAGAACTCTCTGGAACCATTAAGAGATCCTGGGGACTGCCCAGTCTGTGGGCTGTAATGTTG
ATGGCCGCCATCCTCATGACATCATCGATGACATCAACAGTGGTGCTGTGGAATGCCCAGCCAGTTAAGCACAAA
GGAAAATATTTCATAAAGGATCATTGACAACCTG

1010/6881
FIGURE 943

MPPKFDGATSALAPKIGPLGLSPKKVGDDIAKATGDWKGLRITVKLTIQNRQAQIEVVPSASALI IKALKEPPRD
RKKQKNIKHSGNITFDEIVNIVRQMRHRSLARELSGTIKEILGTAQSVGCNVDGRHPHDIIDDINSGAVECPAS

1011/6881
FIGURE 944

ATGGGAAGATTTGATGGACATGGACATGAGCCTCCTGAGGCCCCAGAACTATCTTTTCGGTTGTGAACTAAAGGCC
GACAAAGATGATCACTTTAAGGTGGATAATGATGAAAATGAGACCATCAGTTTAGGGGCTGGTGCAAGGGATGAA
TTGCACATTGTTGAAGCAGAGGCCATGAATGATGAAGGCAGTCCAATTAAAGTCACACTGGCAACTTTGAAAATG
TCTGTACAGCCAACTGCTTCCCTTGGGGGCTTTGAAATCACACCACCAGTGGTCTTACAGTTGAAGTGTGGTTCA
GGGCCAGTGCATATTAGTAGACAGTGCTTAGTAGCTGTGGAGGAAGATGCAGAGTCAGAAGATGAAGAGGAGGAG
GATGTGAACCTCTTAAGCATATCTGGAAAGCGGTCTGCCTCTGGAGGTGGTAGCAAGGCGCCCAGCTACCGCGCC
CACTGGTCAGAAGTGTGGCCAGCGTCTATGCAGGCCCTGGGAGCTCAGGGTGGCTTGGGGTCCAGGAGCATGGCC
GCAGGTATGGCCGGGGGTCTGGCAGGAATGGGAGGCATCCAGAACGAGAAGGAGACCATGCAAAGCCTGAATGAC
CGCCTGGCCTCCTACCTGGACAGAGTGAGGAGCCTGGAGATGGGAAACTGGAAGCTGGAGAGCAAAATCTGGGAG
CACCTGGAGAAGAAGGGACCCCAGGTGAGAGACTGGGGCCACTACTTCAAGACCATCGAGGAGGACCTGACTCAG
ATCTTCACAAGTACTGTGGACAATACCTGCATCATTCTGCAGATCGACAATGCCATCTTGCTGCTGATGACTTT
AGAGTCAAGTATGAGACAGAGCCGGCCACGTGCCAGTCTGTGGAGAACGACATCCATGGGCTCCACAAGGTCATT
GATGACACCAGTGTCACTCAGCTGCAGCTAGAGACAGAGATCGAGGCTCTCAAGGAGGAGCTGCTCTTCCTGAAG
AAGAACCACGAAGAGGAAGTAAAAGGCCTACAAGCCCAGATTGCCAGCTCTGTTGACCATGGAGGCCTTGGAGAT
CGACCTGGACTGGATGAAAAATCTGGAGGCCAGCTTGGAGAACAGCCTGAAGGGGGGTGGAGGCCTGCTACACC
CTGCAGATGGAACAACCTCAATGGGATCCTGCTGCACCTGGAGTCAGAGCTGGCACAGACCTGGGCAGAGGGACAG
GGCCAGGCCCAGGAGTACCAGGCCCTGCCAAACATCAAGCAGCAACTCCACGCAAACCATCCAAAAGACTCCCCAC
CTGCCAACAGTGGATGGCAAAGTGGTGTCTGAGACCAATGACACCAAAGTTCTGAGACATTAA

1012/6881
FIGURE 945

MEDLMDMDMSLLRPQNYLFGCELKADKDDHFKVDNDENETISLGAGARDELHIVEAEAMNDEGSPIKVTLATLKM
SVQPTASLGGFEITPPVVLQLKCGSGPVHISRQCLVAVEEDAESEDEEEEDVNLLSISGKRSASGGGSKAPSYRA
HWSEVWPASMQUALGAQGGLGSRSMAGGLAGMGGIQNEKETMQSLNDRILASYLDRVRSLEMGNWKLESKIWE
HLEKKGPQVRDWGHYFKTIEEDLTQIFTSTVDNTCIIQLIDNAHLAADD FRVKYETEPATCQSVENDIHGLHKVI
DDTSVTQLQLETEIEALKEELLFLKKNHEEEVKGLQAQIASSVDHGGLGDRPGLDEKSGGQLGEQPEGGVEACYT
LQMEQLNGILLHLESELAQTWAEGQGQAQEQALPNIKQQLHANHPKDSHLPTVDGKVVSETNDTKVLRH

1013/6881
FIGURE 946

GACAGTTTAGCAGAACAGCCTCCGCGGCTCCGGGGAGAAGCAATATGTTAAGGATACCTGTAAGAAAGGCCTTAG
TAGGCCTTTCTAAGTCTCCTAAAGGATGTGTTTGAACAACCTGCCACAGCAGCAAGCAACTTGATTGAAGTATTTG
TTGATGGTCAGTCTGTCTATGGTGGAAACCGGGAACGACCGTCTCCAAGCTTGTGAGAAGGTTGGCATGCAGATCC
CTCGATTCTGTTATCATGAAAGGTTGTCTGTTGCTGGAAACTGCAGGATGTGCCTTGTTGAAATTGAGAAAGCCC
CTAAGGTTGTAGCTGCTTGTGCCATGCCAGTAATGAAGGGTTGGAATATCCTAACAACTCAGAAAAATCCAAAA
AAGCCAGGGAAGGTGTGATGGAGTTCTTATTAGCAAAATCACCCATTGGACTGTCCTATTTGTGACCAGGGAGGTG
AATGTGATCTGCAGGACCAGTCCATGATGTTTGGAAATGATAGGAGCCGATTTTTAGAGGGGAAGCGTGCTGTGG
AAGACAAGAACATTGGGCCATTGGTAAAGACCATCATGACAAGATGTATACAGTGTACTCGCTGCATCAGGTTTG
CAAGTGAGATTGCAGGAGTAGATGATTTGGGAACAACAGGCAGAGGAAATGATATGCAAGTTGGGCACATACATTG
AAAAGATGTTTCATGTCTGAACTGTCTGGGAATATCATTGATATCTGCCCTGTAGGTGCCCTAACCTCTAAGCCCT
ATGCCCTTTACTGCCCGGCCTTGGGAACAAGAAAGACAGAATCCATTGATGTAATGGATGCGGTTGGAAGTAATA
TTGTGGTTAGCACAAGAAGCTGGAGAAGTGATGAGGATTTTGCCACGTATGCATGAGGACATCAATGAAGAGTGGA
TCTCTGATAAAACCAGATTTGCCTATGATGGGCTAAAACGTCAAAGACTTACCGAGCCAATGGTCAGAAATGAAA
AAGGGCTTTTAACCTATACTTCTTGGGAGGATGCGCTCTCTCGCTAGCTGGAATGTTGCAGAGTTTTCAAGGCA
AAGATGTGGCAGCAATTGCAGGTGGCTTGGTGGATGCTGAAGCCCTGGTAGCTCTCAAAGATTTGCTTAATAGAG
TGGACTCTGACACCTTATGCACTGAAGAGGTCTTCCCCACTGCAGGAGCTGGCACAGATTTGCGTTCCAATTATC
TTCTTAATACTACAATTGCTGGTGTGGAAGAGGCAGATGTTGTTCTTCTGTTGGTACAAACCCACGTTTTGAGG
CACCCTGTTTAATGCTAGAATTCGAAAGAGCTGGCTGCATAATGACTTAAAGTGGCCCTTATAGGCAGTCCAG
TGGACCTCACTTACACATATGACCACCTGGGAGACTCCCCAAAATTCTTCAAGACATTGCTTCGGGAAGCCATC
CATTTAGCCAGGTCCTAAAGGAAGCTAAAAAACCAATGGTGGTTTTAGGCAGTTCTGCACTCCAAAGAAATGATG
GAGCAGCAATTCTTGCACTGTTTTCTAGCATTGCACAAAAGATTCCGATGACTAGTGGTGTACTGGTGATTGGA
AAGTTATGAATATCCTTCATAGGATTGCAAGTCAAGTAGCTGCTTTGGACCTTGGCTATAAGCCTGGGGTGGAG
CAATTCGGAAGAACCCTCCCAAGGTGCTGTTTCTCCTGGGAGCAGATGGAGGTTGTATCACACGACAGGATTTGC
CAAAGGATTGTTTCATTATTTATCAAGGACATCATGGTGATGTTGGGGCTCCCATAGCTGATGTTATTCTCCAG
GAGCTGCTTACACAGAGAAGTCTGCTACATATGTCAACACTGAGGGTAGAGCTCAGCAGACTAAGGTAGCAGTGA
CACCTCCTGGCTTGGCAAGAGAAGACTGGAAAAATTATAAGAGCACTCTCTGAGATTGCTGGAATGACTCTTCCAT
ATGATACTCTGGATCAAGTAAGGAACAGATTGGAAGAAGTCTCTCCTAATCTTGTTTCGATATGATGATATTGAAG
GGGCTAATTACTTCCAGCAAGCAAATGAGCTCTCAAAGCTAGTGAACCAGCAGCTTCTTGCTGACCCACTTGTTT
CACCTCAGCTAACTATAAAAGACTTCTACATGACAGATTCAATTAGCAGAGCCTCACAGACAATGGCCAAATGTG
TCAAAGCTGTACAGAGGGTGCCAGGCAGTAGAGGAACCATCCATATGCTGAAGCTTCTACTAGGATCCCAGTT
TTGCCGAGATAATTAATGGACAACCTGTAGTGCAGTGATCCTTTACAGGTTTATTTCTTTGTAAAAAAAATAAT
AATAATTTGAATCATGTAATATTTAAGGTTATACATATGCTTATTTGAAAATGATATTAGTTATCAACTTTGCAGT
TTGAAAAACATGTATTGTGTGTAAAGGTTAAATAACAAAACCTATGCAGATGCTCTTAAAGCATTGATAACCTTT
GTGACGAACATAAAGAGATCCTTAAATT

1014/6881
FIGURE 947

MLRIPVRKALVGLSKSPKGCVRRTTATAASNLIIEVFVDGQSVMEPGTTVLQACEKVGMQIPRFCYHERLSVAGNC
RMCLVEIEKAPKVVAACAMPVMKGWNILTNSEKSKKAREGVMEFLLANHPLDCPICDQGGECDLQDQSMMEFGNDR
SRFLEGKRAVEDKNIGPLVKTIMTRCIQCTRCIRFASEIAGVDDLGTGGRGNDMQVGTYIEKMFMSSELSGNIIDI
CPVGALTSPKYAFTARPWETRKTESIDVMDAVGSNIVVSTRTGEVMRILPRMHEDINEEWISDKTRFAYDGLKRQ
RLTEPMVRNEKGLLTYTSWEDALSRVAGMLQSFQGKDVAIAGGLVDAEALVALKDLLNRVDSDTLCTEEVFPTA
GAGTDLRSNYLLNTTIAGVEEADVLLVGTNPRFEAPLFNARIRKSWLHNDLKVALIGSPVDLTYTYDHLGDSPK
ILQDIASGSHPFSSQVLKEAKKPMVVLGSSALQRNDGAAILAAVSSIAQKIRMTSGVTGDWKVMNILHRIASQVAA
LDLGYKPGVEAIRKNPPKVLFLLGADGGCITRQDLPKDCFIIYQGHGHDVGAPIADVILPGAAYTEKSATYVNT
GRAQQTKVAVTPPGLAREDWKIIIRALSEIAGMTLPYDTLDQVRNRLEEVSFNLVRYDDIEGANYFQQANELSKLV
NQQLLADPLVPPQLTIKDFYMTDSISRASQTMACVKAVTEGAQAVEEPSIC

1015/6881
FIGURE 948

GCCTCGAGGCGGGCGTCTTCGGTCATCTCCGGCGCTTCTAGGGCTGGTTCCCGTCATCTTCGGGAGCCGTGGAGC
TCTCGGATACAGCCGACACCATGGGTTTCGGAGACCTGAAAAGCCCTGCCGGCCTCCAGGTGCTCAACGATTACC
TGGCGGACAAGAGCTACATCGAGGGGTATGTGCCATCACAAAGCAGATGTGGCAGTATTTGAAGCCGTGTCCAGCC
CACCGCCTGCCGACTTGTGTTCATGCCCTACGTTGGTATAATCACATCAAGTCTTACGAAAAGGAAAAGGCCAGCC
TGCCAGGAGTGAAGAAAGCTTTGGGCAAATATGGTCCTGCCGATGTGGAAGACACTACAGGAAGTGGAGCTACAG
ATAGTAAAGATGATGATGACATTGACCTCTTTGGATCTGATGATGAGGAGGAAAGTGAAGAAGCAAAGAGGCTAA
GGGAAGAACGTCTTGCAACAATATGAATCAAAGAAAGCCAAAAAACCTGCACTTGTTGCCAAGTCTTCCATCTTAC
TAGATGTGAAACCTTGGGATGATGAGACAGATATGGCGAAATTAGAGGAGTGCATCAGAAGCATTCAAGCAGACG
GCTTAGTCTGGGGCTCATCTAAACTAGTTCCAGTGGGATACGGAATTAAGAACTTCAAATACAGTGTGTAGTTG
AAGATGATAAAGTTGGAACAGATATGCTGGAGGAGCAGATCACTGCTTTTGAGGACTATGTGCAGTCCATGGATG
TGGCTGCTTTCAACAAGATCTAAAATCCATCCTGGATCATGGCATTTAAATAAAAGATTGAAAGATTAAAA

1016/6881
FIGURE 949

MGFGDLKSPAGLQVLNDYLADKSYIEGYVPSQADVAVFEAVSSPPPADLCHALRWYNHIKSYEKEKASLPGVKKA
LGKYGPADVEDTTGSGATDSKDDDDIDLFGSDDEEESEEAERLREERLAQYESKKAKKPAKSSILLDVKPWD
DETDMAKLEECVRSIQADGLVWGSSKLVPGYGIKKLQIQCVVEDDKVGTDMLEEQITAFEDYVQSM DVAAFNKI

1017/6881
FIGURE 950

GGACAATTTGTGGGCCATTTAATTCAGGGCCCCCAATTCGTACGTGGAGAAGTGGGAATGCAAAAGTACTTTGAC
CTTTAACCTTCGGTCCGGCGCGGTGGAGGGAAACGCCTCCGTCTCTATATAAGGAATTTTCCGGTCTCTTCGGGT
CCTTTTTCTCTCTTCAGCGTGGGGCGCCACAATTTGCGCGCTCTCTTTCTGCTGCTCCCCAGCTCTCGGATAC
AGCCGACACCAATGGGTTTCGGAGACCTGAAAAGCCCTGCCGGCCTCCAGGTGCTCAACGATTACCTGGCGGACAA
GAGCTACATCGAGGGGTATGTGCCATCACAAAGCAGATGTGGCAGTATTTGAAGCCGTGTCCAGCCCACCGCCTGC
CGACTTGTGTCATGCCCTACGTTGGTATAATCACATCAAGTCTTACGAAAAGGAAAAGGCCAGCCTGCCAGGAGT
GAAGAAAGCTTTGGGCAAATATGGTCCTGCCGATGTGGAAGACACTACAGGAAGTGGAGCTACAGATAGTAAAGA
TGATGATGACATTGACCTCTTTGGATCTGATGATGAGGAGGAAAGTGAAGAAGCAAAGAGGCTAAGGGAAGAACG
TCTTGACAAATATGAATCAAAGAAAGCCAAAAAACCTGCACTTGTTGCCAAGTCTTCCATCTTACTAGATGTGAA
ACCTTGGGATGATGAGACAGATATGGCGAAATTAGAGGAGTGCCTCAGAAGCATTCAAGCAGACGGCTTAGTCTG
GGGCTCATCTAAACTAGTTCCAGTGGGATACGGAATTAAGAACTTCAAATACAGTGTGTAGTTGAAGATGATAA
AGTTGGAACAGATATGCTGGAGGAGCAGATCACTGCTTTTGAGGACTATGTGCAGTCCATGGATGTGGCTGCTTT
CAACAAGATCTTAAAATCCATCCTGGATCATGGCATTTAAATAAAAGATTGAAAGATTAAAA

1018/6881
FIGURE 951

MGFGDLKSPAGLQVLNDYLADKSYIEGYVPSQADVAVFEAVSSPPPADLCHALRWYNHIKSYEKEKASLPGVKKA
LGKYGPADVEDTTGSGATDSKDDDDIDLFGSDDEEESEEAERLREERLAQYESKKAKKPAKSSILLDVKPWD
DETDMAKLEECVRSIQADGLVWGSSKLVVGYGIKKLQIQCVVEDDKVGTDMLEEQITAFEDYVQSM DVAAFNKI

1019/6881
FIGURE 952

GAAGGGGCGGGGCCAAAACCTGCGCGCCCAATCGGGGTGACGCTCTAGCCTTGCCGGGGACTCGTGGGTAACCTTGC
TTTTGGGAGCCAGCGGTATGGCGTCGGGCTGCAAGATTGGCCCGTCCATCCTCAACAGCGACCTGGCCAATTTAG
GGGCCGAGTGCTCCGGATGCTAGACTCTGGGGCCGATTATCTGCACCTGGACGTAATGGACGGGCATTTTGTTC
CAACATCACCTTTGGTCCACCCTGTGGTAGAAAGCCTTCGAAAGCAGCTAGGCCAGGACCCCTTCTTTGACATGCA
CATGATGGTGTCCAAGCCAGAACAGTGGGTAAAGCCAATGGCTGTAGCAGGAGCCAATCAGTACACCTTTTCATCT
CGAGGCTACTGAGAAGCCAGGGGCTTTGATTAAAGACATTCTGGGAGAATGGGATGAAGGTGGCCTTGCCATCAA
ACCAGGAACCTCAGTTGAGTATTTGGCACCATGGGCTAATCAGATAGATATGGCCTTGGTTATGACAGTGGAAAC
GGGGTTTGGAGGGCAGAAATTCATGGAAGATATGATGCCAAAGGTTCACTGGTTGAGGACCCAGTTCCTATCTTT
GGATATAGAGGTCGATGGTGGAGTAGGTCTTGACACTGTCCATAAATGTGCAGAGGCAGGAGCTAACATGATTGT
GTCTGGCAGTGCTATTATGAGGAGTGAAGACCCAGATCTGTGATCAATCTATTAAGAAATGTTTGCTCAGAAGC
TGCTCAGAAACGTTCTCTTGATCGGTGAACCATTAAGGAGCCAGTGTTCTCTGTTTCATGAAATCTCCCTTTTACT
GGAAAACAGGAATATTGACTACCAAATCACAATGCAATTGAAGCCGTAAGTCTTTTTTGGAGCAGTTATTCATTCC
AGTGATTAAAACCTGATTGTGAGAATATTCTAAGAGGTCAGAAATTGGTGTGTATAACTACATTTTGTAGTGATGC
AATTTATTGATTAGTGAGTAAGATACTGTTTTTATTGAGAGATTTGATTTTTATAAAGTAAAAATACGGCTGCAT
TAGGGTTACAAACAGAAAAGTGTCTTAATGTCTAAGGAGGGCATATTAGCTACACTACAAAAACAAATTTTGTCT
GTACTTCTGAAAAGAATTTTGTGTCTCTCAGCTGTTTTCCAAAAGCAAAGGAAGTCTTTATGGTTTTTTTCTAT
TTCATGTTATTGTGATTTGTTTATAAGTTTGGGTGGGGTGCATACCATATTCTTGGTTCTTAAATCTATCACTT
TTCACCTTACACTTGATGTGTGAAAACATAAAAAACAATGTGTGAAACCCAGGGGTTCTAAATAACAAGCATAGA
TTTTATCAGGGTGTTTTGTCAAAGCAGGTTATTCAGTGATTCCTCCCAACATTCTTAAGAACGTTAAATAATGC
TGTTGTGTTAGCTCTGAGTAGAAAGGAAAAAGTAAACCTCTGTTTGGAGGTAATATTGGGTTGAATTCTGACTG
CCCCTTTCTAGCTGGACCTTTAACAAATCACCAATCTTTTTTGTGTTTCTCTAAAGTCATTTATACATTAAATG
TAATTATAGCAACTGTGGGGTTCTGTTGAGAATTAAGAGCTAACACTATATATGTAAAGTTTCCAGTACTAGTCC
CAGAAATTTAGAATATGCTCAACACAAAGTAAACAGCATTATATAAGTTTATATTTTGTGAGTTATAAAGTACTT
TGATATATTCTCATTAAATCTGTAAATCACCTCTATAAGTAAGTGGTAATAATAAAGCAGATATTTTGTCCCCA
TTTAAAAAATGAAGAAATTAATGCTTAATAGGGTGGTACCCTGGAAAGGATCTGGGAAGTGGTAGAATTTCTGGT
CTGTACTTTTACAAATGGAGCCCTTGGGAGGTGGGTAGGTAAAAGAAGCTTTTACTTAACGTTGTCTTATTTCT
CAGTCTAATTTTACGCTGTAGCAGAACAGATGGCTGAGAAAATTCTGGAACATATGGATCTTGACCCCAAGGATA
TATTATTTTATTCCAAGAAAGATCAGGTAGGCGAAAAGATGACAGGATACAGAGTCAATCCATAAACTAAATATT
TATAACTGTTCTGAATTATACAGAGTCTAAAAATATGTGTGAGTACTTCAATTCCTGTAAATACTCTTGCTGTGT
TATAAATATGGCAAGAAATAAACATGACCAATATCAATAGACTTCTTGAGGCTACTATAAGTTTTGAGAAATAAG
GTTCAAAAAATAAGAATGCTAACACTTAAGCACAGACTAGAGCTTGCTTGGGTTTCTTCTGCAATTACAAGGTAA
AAATTTGTTAATGTTTGTGTTTTTATTGAGCTTGGGAAAGCTTTGTGCCATGAATACGTCGCATTTAATAACAAGCA
ACACACGGCATATAGAAATAACTTTAATTAAAAAACTTACATAGAAGATTATAATATCAGACGTGACAAAGATTT
GAGTTTATTTGCCTGGACAACCTGGGTTTGTCTGGCTTTTGTGTTTCTTTTCTTTTAAAAATAAATGTACAGTAA
ACTAC

1020/6881
FIGURE 953

MLDSGADYHLVDMDGHFVPNITFGHPVVESLRKQLGQDPFFDMHMMVSKPEQWVKPMAVAGANQYTFHLEATEN
PGALIKDIRENGMKVGLAIKPGTSVEY LAPWANQIDMALVMTVEPGFGGQKFMEDMMPKVHWLRTQFP SLDIEVD
GGVGPDTVHKCAEAGANMIVSGSAIMRSEDPRSVINLLRNVCSEAAQKRSLDR

1021/6881
FIGURE 954A

GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCAAAGCAAGCCCCGGTTG
TTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGGCAATGCGTTGGTTTGTAC
TTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAGAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACAC
TGGGAACACTTACCGAGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG
GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTCTTACAAGATTGGTG
CACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTGTGTGTCTTGGTAATGGAAAAGGAGAATG
GACCTGCAAGCCCATAGCTGAGAAGTGTGTTGATCATGCTGCTGGGACTTCCTATGTGGTTCGGAGAAACGTGGGA
GAAGCCCTACCAAGGCTGGATGATGGTAGATTGTACTTGCCCTGGGAGAAGGCAGCGGACGCATCACTTGCACCTC
TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAATCG
AGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGAAGTGTGAGAGGCACACCTCTGTGCA
GACCACATCGAGCGGATCTGGCCCCCTTACCGATGTTCTGTCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCC
TCTTCCCTATGGCCACTGTGTACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAAGTGGCTGAAGACACAAGG
AAATAAGCAAATGCTTTGCACGTGCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGTAACCCAGACTTACGG
TGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTACCTACAATGGCAGGACGTTCTACTCCTGCACCACAGA
AGGGCGACAGGACGGACATCTTTGGTGCAGCACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCAC
AGACCACACTGTTTTGGTTTCAGACTCGAGGAGGAAATTCGAATGGTGCCTTGTGCCACTTCCCCCTTCTATACAA
CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGGGACCACACAGAACTA
TGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCACGAGGAAATCTGCACAACCAATGAAGGGGTCAT
GTACCGCATTTGGAGATCAGTGGGATAAGCAGCATGACATGGGTTCATGATGAGGTGCACGTGTGTTGGGAATGG
TCGTGGGGAATGGACATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT
GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAAGTGTACATGCTTCGGTCAGGGTCGGGGCAG
GTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTACAGAGACTGGGACGTTTTATCAAATTGGAGATTTCATGGGA
GAAGTATGTGCATGGTGTGATACACAGTGTCTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTT
ACAGACCTATCCAAGCTCAAGTGGTCTGTGCAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC
CATCCAGTGGAAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACCTAAAAATTCTGTAGG
CCGTGGAAGGAAGCTACCATAACAGGCCACTTAACTCCTACACCATCAAAGGCCTGAAGCCTGGTGTGGTATA
CGAGGGCCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGAAGTGAAGTGTGCTTTGACTTCACCACCACCAGCAC
CAGCACACCTGTGACCAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTGTGGCCACTTCTGAATC
TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGTGTGCGGATTCCGGGT
GGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGATCTTCCAAGCACAGCCACTTCTGTGAACAT
CCCTGACCTGCTTCTGGCCGAAAATACATTGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGAT
CCTGTCTACTTCACAAACAACAGCGCCTGATGCCCCCTCTGACACGACTGTGGACCAAGTTGATGACACCTCAAT
TGTTGTTTCGCTGGAGCAGACCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTTCGCCATCAGTAGAAGGTAG
CAGCACAGAACTCAACCTTCTGAAAAGTCAAACTCCGTCACCTCAGTGAAGTGGTGTTCAGTATAA
CATCACTATCTATGCTGTGGAAGAAAATCAAGAAAGTACACCTGTTGTGATTCAACAAGAAACCACTGGCACCCC
ACGCTCAGATACAGTGCCTCTCTCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTACCATCATGTG
GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCCTGGCGAGCACGGGCA
GAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAAGTACCGGGCTGTCCCTGGGGTCACTTATTACTTCAAAGT
CTTTGCAGTGAGCCATGGGAGGGAGAGCAAGCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAA
CCTCCAGTTTGTCAATGAACTGATTCTACTGTCTGCTGGTGGATGGACTCCACCTCGGGCCAGATAACAGGATA
CCGACTGACCGTGGGCTTACCCGAAGAGGACAGCCAGGAGTACAATGTGGGTCCCTCTGTCTCCAAGTACCC
ACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGGCAACCAAGAGAGCCCCAA
AGCCACTGGAGTCTTTACCACTGCAGCCTGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCAC
CATTGTGATCACATGGACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC
ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGAAGTCCAGGAGTAGAATACGTCTACAC
CATCCAAGTCCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTGACACCATTGTCTCCACC
AACAACTTGCATCTGGAGGCAACCCCTGACACTGGAGTGTCTACAGTCTCCTGGGAGAGGAGCACCACCCAGAG
CATTACTGGTTATAGAATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCCTTGGGAAGAGTGGTCCATGC

1022/6881
FIGURE 954B

TGATCAGAGCTCCTGCACTTTTGTATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAAGGA
TGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGTTCCCTCCTCCCACTGACCTGCGATTACACAA
CATTGGTCCAGACACCATGCGTGTACCTGGGCTCCACCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTA
CTCACCTGTGAAAAATGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA
TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCACACCTCTTAGAGG
AAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTGATATTACTGCCAACTCTTTTACTGTGCA
CTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCG
AGAAGATCGGGTGCCCCACTCTCGGAATTCCATCACCCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG
CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCCGAG
GGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCTGGGATGCTCCTGCTGTACAGTGAGATA
TTACAGGATCACTTACGGAGAGACAGGAGGAAATAGCCCTGTCCAGGAGTTCAGTGTGCCTGGGAGCAAGTCTAC
AGCTACCATCAGCGGCCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG
CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACCGA
TGTTTACAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCCTGTACTGGTTACAGAGTAACCACCAC
TCCCAAAAATGGACCAGGACCAACAAAACCTAAACCTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTT
GCAGCCCACAGTGGAGTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAAGCCTCTGGTTTCAGAC
TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTGATTCCATCAAAATTGCTTG
GGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGAGCCCTGAGGATGGAATCCATGAGCTATT
CCCTGCACCTGATGGTGAAGAAGACACTGCAGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCACTGT
GGTTGCCTTGCACGATGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCTGACACCAACTGA
CCTGAAGTTCACTCAGGTACACCCACAAGCCTGAGCGCCAGTGGACACCACCCAATGTTTCAGCTCACTGGATA
TCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGCTCCTGACAGCTCATCCGT
GGTTGTATCAGGACTTATGGTGGCCACCAATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAG
ACCAGCTCAGGGAGTTGTCAACACTCTGGAGAATGTGAGCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA
GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGATGCCGTTCCAGCCAA
TGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCTACACCATCACAGGTTTACAACCAGGCAC
TGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCGGAGCTCCCCTGTGGTTCATCGACGCTCCACTGC
CATTGATGCACCATCCAACCTGCGTTTCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG
TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCAGAGAAGTGGTCCCTCGGCCCCG
CCCTGGTGTACAGAGGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAA
GAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCCTTCCACA
CCCCAATCTTCATGGACCAGAGATCTTGGATGTTCTTCCACAGTTCAAAGACCCCTTTTCGTCACCCACCCTGG
GTATGACACTGGAAATGGTATTTCAGCTTCTGGCACTTCTGGTCAGCAACCCAGTGTGGGCAACAAATGATCTT
TGAGGAACATGGTTTTAGGCGGACCACACCGCCCAACCGGCCACCCCATAGGCATAGGCCAAGACCATAACCC
GCCGAATGTAGGACAAGAAGCTCTCTCTCAGACAACCATCTCATGGGCCCATTCAGGACACTTCTGAGTACAT
CATTTTCATGTCATCCTGTTGGCACTGATGAAGAACCCTTACAGTTTCAGGGTTCTGGAACCTTCTACCAGTGCCAC
TCTGACAGGCCTCACCAGAGGTGCCACCTACAACGTCATAGTGAGGCACTGAAAGACCAGCAGAGGCATAAGGT
TCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATGACTCGTGCTTTGA
CCCCTACACAGTTTCCCATATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAACTGTTGTG
CCAGTGCTTAGGCTTTGGAAGTGGTCATTTTCAGATGTGATTTCATCTAGATGGTGCCATGACAATGGTGTGAAC
CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATGTCTTGGGAACGGAAA
AGGAGAATTCAAGTGTGACCCCTCATGAGGCAACGTGTTATGATGATGGGAAGACATAACCAGTAGGAGAACAGTG
GCAGAAGGAATATCTCGGTGCCATTTGCTCCTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTG
CCGCAGACCTGGGGGTGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCCTACAACAGTATTCTCAGAGATACCA
TCAGAGAACAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACAGGCTGACAGAGAAGA
TTCCCAGAGATAAATCATCTTTCCAATCCAGAGGAACAAGCATGTCTCTCTGCCAAGATCCATCTAACTGGAGT
GATGTTAGCAGACCCAGCTTAGAGTTCTTCTTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCA
GCTCAACTCACAGCTTCTCCAAGCATCACCCCTGGGAGTTTCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT

1023/6881
FIGURE 954C

GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGATTTGGTTTGGGATCA
ATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAATGATATGACCAAATTTTAAGTAGGAAAGTC
ACCCAAACACTTCTGCTTTCACTTAAGTGTCTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGA
TATTTTAAATATCCACAGTACTCACTTTTTCCAAATGATCCTAGTAATTGCCTAGAAATATCTTTCTCTTACCTG
TTATTTATCAATTTTTCCAGTATTTTTATACGGAAAAAATTGTATTGAAAACACTTAGTATGCAGTTGATAAGA
GGAATTTGGTATAATTATGGTGGGTGATTATTTTTTATACTGTATGTGCCAAAGCTTTACTACTGTGGAAAGACA
ACTGTTTTAATAAAAGATTTACATTCC

1024/6881
FIGURE 955

CGGCAGCCCTCCTACCTGCGCACGTGGTGCCGCTGCTGCTGCCTCCCGCTCGCCCTGAACCCAGTGCCTGCAGCC
ATGGCTCCCGGCCAGCTCGCCTTATTTAGTGTCTCTGACAAAACCGGCCTTGTGGAATTTGCAAGAAACCTGACC
GCTCTTGGTTTGAATCTGGTCGCTTCCGGAGGGACTGCAAAAGCTCTCAGGGATGCTGGTCTGGCAGTCAGAGAT
GTCTCTGAGTTGACGGGATTTCTGAAATGTTGGGGGGACGTGTGAAAACCTTGCATCCTGCAGTCCATGCTGGA
ATCCTAGCTCGTAATATTCCAGAAGATAATGCTGACATGGCCAGACTTGATTTCAATCTTATAAGAGTTGTTGCC
TGCAATCTCTATCCCTTTGTAAAGACAGTGGCTTCTCCAGGTGTAAGTGTGAGGAGGCTGTGGAGCAAATTGAC
ATTGGTGGAGTAACCTTACTGAGAGCTGCAGCCAAAAACCGCTCGAGTGACAGTGGTGTGTGAACCAGAGGAC
TATGTGGTGGTGTCCACGGAGATGCAGAGCTCCGAGAGTAAGGACACCTCCTTGGAGACTAGACGCCAGTTAGCC
TTGAAGGCATTCACTCATACGGCACAATATGATGAAGCAATTTTCAGATTATTTTCAGGAAACAGTACAGCAAAGGC
GTATCTCAGATGCCCTTGAGATATGGAATGAACCCACATCAGACCCCTGCCAGCTGTACACACTGCAGCCCAAG
CTTCCCATCACAGTTCTAAATGGAGCCCCCTGGATTTATAAACCTTGTGCGATGCTTTGAACGCCTGGCAGCTGGTG
AAGGAATCAAGGAGGCTTTAGGTATTCCAGCCGCTGCCTCTTTCAAACATGTGAGCCCAGCAGGTGCTGCTGTT
GGAATTCCTACTCAGTGAAGATGAGGCCAAAGTCTGCATGGTTTATGATCTCTATAAAAACCTCACACCCATCTCA
GCGGCATATGCAAGAGCAAGAGGGGCTGATAGGATGTCTTCATTTGGTGATTTTGTGTCATTGTCCGATGTTTGT
GATGTACCAACTGCAAAAATTATTTCCAGAGAAGTATCTGATGGTATAATTGCCCCAGGATATGAAGAAGAAGCC
TTGACAATACTTTCCAAAAAGAAAAATGGAACCTATTGTGTCTTCAGATGGACCAATCTTACAAACCAGATGAA
AATGAAGTTCGAACTCTCTTTGGTCTTCATTTAAGCCAGAAGAGAAATAATGGTGTGCTCGACAAGTCATTATTT
AGCAATGTTGTTACCAAAAATAAAGATTTGCCAGAGTCTGCCCTCCGAGACCTCATCGTAGCCACCATTGCTGTC
AAGTACACTCAGTCTAACTCTGTGTGCTACGCCAAGAACGGGCAGGTTATCGGCATTGGAGCAGGACAGCAGTCT
CGTATACACTGCACTCGCCTTGAGGAGATAAGGCAAACCTATTGGTGGCTTAGACACCATCCACAAGTGCTTTTCG
ATGAAGTTTAAAACAGGAGTGAAGAGAGCAGAAATCTCCAATGCCATCGATCAATATGTGACTGGAACCATTGGC
GAGGATGAAGATTTGATAAAGTGAAGGCACTGTTTGAGGAAGTCCCTGAGTTACTCACTGAGGCAGAGAAGAAG
GAATGGGTTGAGAACTGACTGAAGTTTCTATCAGCTCTGATGCCTTCTTCCCTTTCCGAGATAACGTAGACAGA
GCTAAAAGGAGTGGTGTGGCGTACATTGCGGCTCCCTCCGGTCTGCTGCTGACAAAGTTGTGATTGAGGCCTGC
GACGAACTGGGAATCATCCTCGCTCATACGAACCTTCGGCTCTTCCACCACTGATTTTTACCACACACTGTTTTTT
GGCTTGCTTATGTGTAGGTGAACAGTCACGCCTGAACTTTGAGGATAACTTTTTAAAAAATAAAACAGTATCT
CTTAAAACAATGTTTTGATCTACATAAACATTGTAAAAATTTTCAATCACGCTTTTTAACTTTCTTACCACAAAA
AAATGATAAGTGGGTGAAGTGATGGTTATGTTAATTAGCGTGC

1025/6881
FIGURE 956

MAPGQLALFSVSDKTGLVEFARNLTALGLNLVASGGTAKALRDAGLAVRDVSELTGFPEMLGGRVKTLPVAVHAG
ILARNIPEDNADMARLDFNLIRVVACNLYPFVKTVASPGVTVEEAVEQIDIGGVTLRLRAAAKNHARVTVVCEPED
YVVVSTEMQSSESKDTSLETRRQLALKAFTHTAQYDEAISDYFRKQYSKGVSQMPLRYGMNPHQTPAQLYTLQPK
LPITVLNGAPGFINLCDALNAWQLVKELKEALGIPAAASFKHVSPAGAAVGIPLSEDEAKVCMVYDLYKTLTPIS
AAYARARGADRMSSEFGDFVALSDVCDVPTAKIISREVSDGIIAPGYEEEEALTILSKKKNGNYCVLQMDQSYKPDE
NEVRTLEGLHLSQKRNNGVVDKSLFSNVVTKNKDLPESALRDLIVATIAVKYTQSNVVCYAKNGQVIGIGAGQQS
RIHCTRLAGDKANYWWLRHHPQVLSMKFKTGVKRAEISNAIDQYVTGTIGEDDLIKWKALFEEVPELLTEAEKK
EWVEKLTEVSISSDAFFPFRDNVDRAKRSGVAYIAAPSGSAADKVVEACDELGIILAHTNLRRLFHH

1026/6881
FIGURE 957

GCAGCCAATTAAGCCAACCTGAGTTCCTTTTCCTTGTGGGGGCCAGTGTGCAATGGCTGCACACAGCAGCTTCCTT
GGTAGTGTACACAGCCTGTTGGTTGTATGGGTTGCTCTGAGGGACCTTGGAGACAGGCCTTTCCAATGGATGTTT
ATGTTTCTGACCTTGCGCTACCCCAATGTAGGCTCCAAACAGGCATGCGAGGTGCCTTTGGAATGCCCCAGGGCA
CTGTGGCCAGGGTTCACATTGGCCAAGTTATCATGTCCATCCGCACCAAGCTGCAGAACAAGGAGCATGTGATTG
AGGCCCTGCGCAGGGCCAAGTTCAAGCTTCCTGGCCACCAGAAGATCCACATCTCAAAGAAGTGGGGCTTCACCA
AGTTCAATGCTGATGAATTTGAAGACATGGTGGCTGAGAAGTGGCTCATCCCAGATGGCTGTGGGGTCAAGTACA
TCCCAATCGTGGCCCTCTGGACAAGTGGCGGGCCCTGCACTCATGAGGGCTTCCAATGTGCTGCCCCCTCTTA
ATACTCACCAATAAATTCTACTTCCTGTCAAAAAAATGTCATAATGTACCCTAAATTTTCTTTTTTATTTTTAT
TTTTTATTTATTTATTTATTTTTTTTGGAGATGGTGTCTTGCTCTTTTGCCAGACTGGAGTGAAGTAGCATGATCT
TGGCTTACTGCAACCTCCACCCCCAG

1027/6881
FIGURE 958

GGCGGGCGACCAAAGCGCCTGAGGACCGGCAACATGGTGCGGTGCGGGAATAAGGCAGCTGTTGTGCTGTGTATG
GACGTGGGCTTTACCATGAGTAACTCCATTCTGGTATAGAATCCCCATTTGAACAAGCAAAGAAGGTGATAACC
ATGTTTGTACAGCGACAGGTGTTTGTCTGAGAACAAGGATGAGATTGCTTTAGTCCTGTTTGGTACAGATGGCACT
GACAATCCCCCTTTCTGGTGGGGATCAGTATCAGAACATCACAGTGCACAGACATCTGATGCTACCAGATTTTGAT
TTGCTGGAGGACATTGAAAGCAAAATCCAACCAGGTTCTCAACAGGCTGACTTCCTGGATGCACTAATCGTGAGC
ATGGATGTGATTCAACATGAAACAATAGGAAAGAAGTTTGAGAAGAGGCATATTGAAATATTTACTGACCTCAGC
AGCCGATTGAGCAAAAGTCAGCTGGATAATTATAATTCATAGCTTGAAGAAATGTGACATCTCCCTGCAATTCTTC
TTGCCTTTCTCACTTGGCAAGGAAGATGGAAGTGGGGACAGAGGAGATGGCCCCCTTTCGCTTAGGTGGCCATGGG
CCTTCCTTTCCACTAAAAGGAATTACCGAACAGCAAAAAGAAGTCTTGAGATAGTGAAAATGGTGATGATATCT
TTAGAAGGTGAAGATGGGTGGATGAAATTTATTCATTCACTGAGAGTCTGAGAAAATGTGCGTCTTCAAGAAA
ATTGAGAGGCATTCCATTCACTGGCCCTGCCGACTGACCATTGGCTCCAATTTGTCTATAAGGATTGCAGCCTAT
AAATCGATTCTACAGGAGAGAGTTAAAAAGACTTGGACAGTTGTGGATGCAAAAACCTAAAAAAGAGATATA
CAAAAAGAAACAGTTTATTGCTTAAATGATGATGATGAACTGAAGTTTTAAAGAGGATATTATTCAAGGGTTC
CGCTATGGAAGTGATATAGTTCTTTCTCTAAAGTGGATGAGGAACAAATGAAATATAAATCGGAGGGGAAGTGC
TTCTCTGTTTTGGGATTTTGTAAATCTTCTCAGGTTTCAGAGAAGATTCTTCATGGGAAATCAAGTTCTAAAGGTC
TTTGCAGCAAGAGATGATGAGGCAGCTGCAGTTGCACTTTCCTCCCTGATTTCATGCTTTGGATGACTTAGACATG
GTGGCCATAGTTTCGATATGCTTATGACAAAAGAGCTAATCCTCAAGTCGGCGTGGCTTTTTCCTCATATCAAGCAT
AACTATGAGTGTTTAGTGTATGTGCAGCTGCCTTTTCATGGAAGACTTGCGGCAATACATGTTTTTCATCCTTGAAA
AACAGTAAGAAATATGCTCCACCGAGGCACAGTTGAATGCTGTTGATGCTTTGATTGACTCCATGAGCTTGGCA
AAGAAAGATGAGAAGACAGACACCTTGAAGACTTGTTTCCAACCACCAAATCCCAAATCCTCGATTTTCAGAGA
TTATTTTCAGTGCTGCTGCACAGAGCTTTACATCCCCGGGAGCCTCTACCCCCAATTCAGCAGCATATTTGGAAT
ATGCTGAATCCTCCCGCTGAGGTGACAACAAAAGTCAGATTCTCTCTCTAAATAAAGACCCTTTTCTCTCTG
ATTGAAGCCAAGAAAAAGGATCAAGTGACTGCTCAGGAAATTTTCCAAGACAACCATGAAGATGGACCTACAGCT
AAAAAATTAAAGACTGAGCAAGGGGGAGCCCACTTCAGCGTCTCCAGTCTGGCTGAAGGCAGTGTCACCTCTGTT
GGAAGTGTAATCCTGCTGAAAACCTTCGTTCTAGTGAAACAGAAGAAGGCCAGCTTTGAGGAAGCGAGTAAC
CAGCTCATAAATCACATCGAACAGTTTTTGGATACTAATGAAACACCGTATTTTATGAAGAGCATAGACTGCATC
CGAGCCTTCCGGGAAGAAGCCATTAAAGTTTTCAGAAGAGCAGCGCTTTAACAACCTTCTGAAAGCCCTTCAAGAG
AAAGTGGAATTAACAATTAAATCATTCTGGGAAATTGTTGTCCAGGATGGAATTACTCTGATCACCAAAGAG
GAAGCCTCTGGAAGTTCTGTACAGCTGAGGAAGCCAAAAGTTTCTGGCCCCCAAAGACAAACCAAGTGAGAC
ACAGCAGCTGTATTTGAAGAAGGTGGTGATGTGGACGATTTATTGGACATGATATAGGTCTGTGGATGTATGGGGA
ATCTAAGAGAGCTGCCATCGCTGTGATGCTGGGAGTTCTAACAAAACAAGTTGGATGCGGCCATTCAAGGGGAGC
CAAAATCTCAAGAAATTTCCAGCAGGTTACCTGGAGGCGGATCATCTAATCTCTGTGGAATGAATACACACATA
TATATTACAAGGGATAATTTAGACCCCATACAAGTTTATAAAGAGTCATTGTTATTTTCTGGTTGGTGTATTATT
TTTTCTGTGGTCTTACTGATCTTTGTATATTACATACATGCTTTGAAGTTTCTGGAAAGTAGATCTTTTCTTGAC
CTAGTATATCAGTGACAGTTGCAGCCCTTGTGATGTGATTAGTGTCTCATGTGGAACCATGGCATGGTTATTGAT
GAGTTTCTTAACCCCTTTCCAGAGTCCTCCTTTGCCTGATCCTCCAACAGCTGTCACAACTTGTGTTGAGCAAGCA
GTAGCATTGCTTCTCCCAACAAGCAGCTGGGTTAGGAAAACCATGGGTAAGGACGGACTCACTTCTCTTTTTTA
GTTGAGGCCTTCTAGTTACCACATTACTCTGCCTCTGTATATAGGTGGTTTTCTTTAAGTGGGGTGGGAAGGGGA
GCACAATTTCCCTTCATACTCCTTTTAAGCAGTGAGTTATGGTGGTGGTCTCATGAAGAAAAGACCTTTTGGCCC
AATCTCTGCCATATCAGTGAACCTTTAGAACTCAAAAAGTGAAGAAATTTACTTCAGTAGTTAGAATTATATCAC
TTCAGTGTTCTCTACTTGCAAGCCTCAAAGAGAGAAAGTTTCGTTATATTAAACACTTAGGTAACCTTTTCGGTC
TTTCCATTTCTACCTAAGTCAGCTTTTCATCTTTGTGGATGGTGTCTCCTTTACTAAATAAGAAAATAACAAAGC
CCTTATTCTCTTTTTTCTTGTCTCATTCTTGCCTTGAGTTCCAGTTCCTCTTTGGTGTACAGACTTCTTGGA
CCAGTCACCTCTGTCTTCAGCACCTCATAAGTCGTCATAATACACAGTTTTGTACATGTAACATTAAAGGCA
TAAATGACTC

1028/6881
FIGURE 959

MVRSGNKAADVLCMDVGFTMSNSIPGIESPFEEQAKKVITMFVQRQVFAENKDEIALVLFGTGTDGNPLSGGDQYQ
NITVHRHMLPDPDFDLLEDIESKIQPGSQQADFLDALIVSMDVIQHETIGKKFEKRHIEIFTDLSSRFSKSQLDII
IHSLK¹CDISLQFFLPFSLGKEDGSGDRGDGPFRLGGHGSPFPLKGITEQQKEGLEIVKMVMISLEGEDGLDEIY
SFSESLRKLCVFKKIERHSIHWPCLRTIGSNLSIRIAAYKSILQERVKKTWTVVDAKTLKKEDIQKETVYCLNDD
DETEVLKEDI IQGFRYGS DIVPFSKVDEEQMKYKSEGKCF SVLGFC KSSQVQRRFFMGNQVLKVFAARDDEAAAV
ALSSLIHALDDLDMVAIVRYAYDKRANPQVGVAFP²HIK³NYECLVYVQLPFMEDLRQYMFSSLKNSKKYAPTEAQ
LNAVDALIDSMSLAKKDEKTD⁴TLEDLFPTTKIPNPRFQRL⁵FQCLLHRALHPREPLPPIQQHIWNMLNPPAEVTTK
SQIPLSKIKT⁶LFPLIEAKKKDQVTAQE⁷IFQDNHEDGPTAKKLKTEQGGAHFSVSSLAEGSVTSVGSVNPAENFRV
LVKQKKASFEEASNQLIN⁸HIEQFLDTNETPYFMKSIDCIRAFREEAIKF⁹SEEQRFN¹⁰NFLKALQEKVEIKQLNHF¹¹W
EIVVQDGITLITKEEASGSSVTAE¹²EAKKFLAPKDKPSGDTAAVFEEGGDVDDLDMI

1029/6881
FIGURE 960A

CTTTTGTAGGCAAGTTGGATGAACAGAGAAGGGAAGAGAGGAAGAACGAGAGGAAGAGAAGGGAAGGAAGTGTTT
GTGTAGAAGAGAGAGAGAAAAGACGAATAGAGTTAGGAAAAGGAAGACAAGCAGGTGGGCAGGAAGGACATGCACCGA
GACCAGGCAGGGGCCCAACTTTACGTCCAGCCCTGGCCTGGGGTCGGGAGAGGTGGGCGCTAGAAGATGCAGCC
CAGGATGTGGCAATCAATGACACTATTGGGGTTTCCCAGGATGGATTGGTCAGGGGGAGAAAGGAAAAGGCAAAA
CACTCCAGGACCTCTCCCGATCTGTCTCCTCCTCTAGCCAGCAGTATGGACAGCTGGACCCCTGAACTTCCTCT
CCTCTTACCTGGGCAGAGTGTTGTCTCTCCCAAATTTATAAAAACATAAAATGCATTCCATTCTCTGAAAGCAA
AACAAATTCATAATTGAGTGATATTAAATAGAGAGGTTTTTCGGAAGCAGATCTGTGAATATGAAATACATGTGCA
TATTTTATTCCCCAGGCAGACATTTTTTAGAAATCAATACATGCCCAATATTGGAAAGACTTGTCTTCCACGG
TGACTACAGTACATGCTGAAGCGTGCCGTTTCAGCCCTCATTTAATTCAATTTGTAAGTAGCGCAGCAGCCTCTG
TGGGGGAGGATAGGCTGAAAAAAAAGTGGGCTCGTATTTATCTACAGGACTCCATATAGTCATATATAGGCAT
ATAAATCTATTCTTTTTCTTTGTTTTTTTTCTTTCTTCTTTCTTTCAAAGGTTTGCATTAACTTTTCAAAGTAGT
TCCTATAGGGGCATTGAGGAGCTTCCTCATTTCTGGGAAAACCTGAGAAAACCCATATTCTCCTAATAACAACCCGTA
ATAGCATTTTTTGCCCTGCCTCGAGGCAGAGTTTCCCGTGAGCAATAAACTCAGCTTTTTTGTGGGGCACAGTACTG
GATTTGACAGTGATTCCCCACGTGTGTTTCTGTCACCCACCGAGCCAGGCAGAGGCCAGCCCTCCGTGGTGCAC
ACAGCACGCGCCTCAGTCCATCCCATTTTGTCTTTAAACCCCTCAGGAAGTCACAGTCTCCGGACACCACACCAC
ATGAGCCCAACAGGTCCACGATGGATCCACAGTCCCACCCAGCCTTTTCTTTTCTGTAACAGAATGTGCAT
TTTTTGAAGCCTCCCTCACTCTCCATGCTGGCAGAGCAGGAGGGAGACTGAAGTAAGAGATGGCAGAGGGAGATG
GTGGCAAAAAGGTTTAGATGCAGGAGAACAGTAAGATGGATGGTTCCGGCCAGAGTCGATGTGGGGAGGAACAGA
GGGCTGAAGGGAGAGGGGGCTGACTGTTCCATTCTAGCTTTGGCACAAAGCAGCAGAAAGGGGGAAAAGCCAATA
GAAATTTCTTAGCTTCCCCACCATATGTATTTTCTAGGATTTGAGAGGAAAGAGAGGAAAATGGGGGAATGGGT
TGCAAAATAGAAATGAGCTTAATCCAGGCCGAGAGCCAGGGAAGGTGAGTAACCTTTAGGAGGGTGCTAGACTTT
AGAAGCCAGATAGGAAGAATCAGTCTAACTGGCCATGCTTTGGAAGGGACAAGACTATGTGCTCCGCTGCCCCAC
CTTCAGCCTGCAATGAGGGACTGAGGCCACGAGTCTTTCCAGCTCTTCTCCATTCTGGCCAGTCCCTGCATCC
TCCCTGGGGTGGAGGATGGAAGGAAAGCTGGGACAAGCAGGGAACGCATGATTGAGGGATGCTGTCACTCGGCAG
CCAGATTCCGAAACTCCCATTCTCCAATGACTTCCTCAACCAATGGGTGGCCTTGTGACTGTTCTTTAAGGCTGA
AGATATCCAGGAAAGGGGGCTTGGACACIGGCCAAGGAGACCCCTTCGTGCTGTGGACACAGCTCTCTTCACTCT
TTGCTCATGGCATGACACAGCGGAGACCGCTCCAACAACGAATTTGGGGCTACGAAGAGGAATAGCGAAAAAGC
AAATCTGTTTCAACTGATGGGAACCTATAGCTATAGAACTTGGGGGCTATCTCCTATGCCCTGGACAGGACAG
TTGGCTGGGGACAGGAGAAAGTGCTCAATCTTCATGAGACAAAGGGGCCCCGATAGGGCCAGCAGCCACAAGGCCTT
GACCTGCCGAGTCAGCATGCCCCATCTCTCTGCACAGCTGTCCCTTAAACCCAACTCACGTTTCTGTATGTCTTA
GGCCAGTATCCCAAACCTCTTCCACGTCACTGTTCTTTCCACCCATTCTCCCTTTGCATCTTGAGCAGTTATCCA
ACTAGGATCTGCCAAGTGATACTGGGGTGCCACTCCCTGAGAAAAGACTGAGCCAGGAAGTACAAGCTCCCCC
CACATTCTCCACAGCCTGGACCTAATTCTTGAGAGGGGCTCTCTCTTCACGGACTGTGTCTGGACTTTGAGCAGG
CTTCTGCCCCCTTGCGTTGGCTCTTTGCTGCCAGCCATCAGGTGGGGGATTAGAGCCTGGTGTAAAGTGCGCCAGAC
TCTTCCGGTTTCAAAGTTTCGTGCCCTGCGAACCCAAACCTGTGAGTCTCTTCTGCATGCAGGAGTTTCTCCTGGG
CAGCTGGTCACTCCCAGAGAAGCTGGGCCCTTCATGGACACATGGAACATAAGCCTCCCAAATGGGAGTTCTGGCT
GAGCCCAGGGTGGGGAGATCCTGGGAAGGGAGGCACTGGAGGAAGACGGCACCTCTTCCCCCATGGCAGGGTGTG
AGGGAGGCAGGTTTGAATGGTGCAGTATGGCAATCTAAGCAGGGGTCTGGTCTCTTTGACTCCAGGCTGGCCT
TTGGCCGACTGTCTGCTCACCCAGAGACCTTGACTCCGGACTATCCATGGCTCCGAATCTAAGTGCTGCCACT
CCCATGCTCACACCCACAGAAGGTCTTCCATCCCTTTAGATTCTGTGCTCACTCCACCAGTGAGGAAGATGCC
TCTGTCTTTCCCAGACTGCCAGGAGATAGGGAAGCCCAGCCAGGACTGACCCTCCTTCTCCAGCCTGCCCTGA
CCCACCTGGCAAAGCAGGGCACATGGGGAGGAAGGAGACTGGAACCTTTCTTTGACAGCCAGGCCTAGACAGACAG
GCCTGGGGACACTGGCCCCATGAGGGGAGGAAGGCAGGCGCACGAGGTCCAGGGAGGCCCTTTTCTGATCATGCC
CCTTCTCTCCACCCCATCTCCCCACCAACCTCTGTGGCCTCCATGGTACCCCCACAGGGCTGGCCTCCCCTA
GAGGGTGGGCCCTCAACCACCTGCTCCCGCCACGCACCGGTTAGTGAGACAGGGCTGCCACGGCAACCGCCAAGCC
CCCCTCAAGGTGGGACAGTACCCCGGACCCATCCACTCACTCCTGAGAGGGCTCCGGCCAGAAATGGGAACCTCA
GAGAAGAGCTCTAAGGAGAAGAAACCCCATAGCGTCAGAGAGGATATGTCTGGCTTCCAAGAGAAAGGAGGCTCC
GTTTTGCAAAGTGGAGGAGGGACGAGGGACAGGGGTTTACCAGCCAGCAACCTGGGCCCTTGTACTGTCTGTGTT

1030/6881
FIGURE 960B

TTTAAAACCACTAAAGTGCAAGAATTACATTGCACTGTTTCTCCACTTTTTATTTTCTCTTAGGCTTTTGTTTCT
ATTTCAAACATACTTTCTTGGTTTTCTAATGGAGTATATAGTTTAGTCATTTACAGACTCTGGCCTCCTCTCCT
GAAATCCTTTTGGATGGGGAAAGGGAAGGTGGGGAGGGTCCGAGGGGAAGGGGACCCAGCTTCCCTGTGCCCGC
TCACCCCACTCCACCAGTCCCCGGTCGCCAGCCGGAGTCTCCTCTCTACCGCCACTGTCACACCGTAGCCACAT
GGATAGCACAGTTGTCAGACAAGATTCCCTTCAGATTCCGAGTTGCCTACCGGTTGTTTTCGTTGTTGTTGTTGTT
GTTTTTCTTTTCTTTTTTTTTTTTGAAGACAGCAATAACCACAGTACATATTACTGTAGTTCTCTATAGTTTTAC
ATACATTCATACCATAACTCTGTTCTCTCCTCTTTTTTGTTCCTTAAAAACAAAAATAAACGATGATAAT
CTTTACTGGTGAAAAGGATGGAAAAATAAATCAACAAATGCAACCAGTTTGTGAG

1031/6881
FIGURE 961

MLWKGQDYVLRCPFSACNEGLRPTSLSSSSSILASPCILPGVEDGRKAGTSRERMIQGCCHSAARFRNSHSPMTS
STNGWPCDCSLRLKISRKGGDLTGQGDFVLWTQLSSLFAHGMTQRRPPPTTNLGLRGGIAGKQICFN

1032/6881
FIGURE 962

CCTCTGTGGCCTCCATGGTACCCCCACAGGGCTGGCCTCCCCTAGAGGGTGGGCCTCAACCACCTGCTCCCGCCA
CGCACCGGTTAGTGAGACAGGGCTGCCACGGCAACCGCCAAGCCCCCTCAAGGTGGGACAGTACCCCGGACCCA
TCCACTCACTCCTGAGAGGGCTCCGGCCCAGAATGGGAACCTCAGAGAAGAGCTCTAAGGAGAAGAAACCCATA
GCGTCAGAGAGGATATGTCTGGCTTCCAAGAGAAAGGAGGCTCCGTTTTGCAAAGTGGAGGAGGGACGAGGGACA
GGGGTTTCACCAGCCAGCAACCTGGGCCTTGACTGTCTGTGTTTTTAAAACCACTAAAGTGCAAGAATTACATT
GCACTGTTTCTCCACTTTTTATTTCTCTTAGGCCTTTGTTTCTATTTCAAACATACTTTCTTGTTTTCTAATG
GAGTATATAGTTTAGTCATTTACAGACTCTGGCCTCCTCTCCTGAAATCCTTTTGGATGGGGAAAGGGAAGGTG
GGGAGGGTCCGAGGGGAAGGGGACCCAGCTTCCCTGTGCCCGCTCACCCCACTCCACCAGTCCCGGTGCGCCAG
CCGGAGTCTCCTCTCTACCGCCACTGTGCACACCGTAGCCACATGGATAGCACAGTTGTCAGACAAGATTCCTTC
AGATTCCGAGTTGCCTACCGGTTGTTTTCGTTGTTGTTGTTGTTGTTTTCTTTTCTTTTTTTTTTTGAAGACA
GCAATAACCACAGTACATATTACTGTAGTTCTCTATAGTTTTACATACATTCATACCATAACTCTGTTCTCTCCT
CTTTTTTGTTTTCAACTTTAAAAACAAAAATAAACGATGATAATCTTTACTGGTGAAAAGGATGGAAAAATAAAT
CAACAAATGCAACCAGTTTGTGAGAAAAAAAAAAAAAAAAAGCCGAAAAAAAAAAAAAAAA

1033/6881
FIGURE 963

MVPFQGWPPLEGGPQPPAPATHRLVRQGCHGNRQAPLKVGQYPGPIHSLLRGLRPRMGTSEKSSKEKKPHSVRED
MSGFQEKGGSVLQSGGGTRDRGFTSQQPGPCTVCVFKTTKVQELHCTVSPLFIFS

1034/6881
FIGURE 964

GGCGAGGGAGGAGGAAGAAGCGGAGGAGGCGGCTCCCGCGCTCGCAGGGCCGTGCCACCTGCCCGCCCCGCCCGCT
CGCTCGCTCGCCCGCCGCGCGCTGCCGACCGCCAGCATGCTGCCGAGAGTGGGCTGCCCGCGCTGCCGCTG
CCGCCCGCCGCTGCTGCCGCTGCTGCTGCTACTGGGCGCGAGTGGCGGCGGGCGGGCGCGCGGGAG
GTGCTGTTCCGCTGCCCGCCCTGCACACCCGAGCGCCTGGCCGCTGCGGGCCCCCGCCGGTTGCGCCGCCCGCC
GCGGTGGCCGCAGTGGCCGGAGGCGCCCGCATGCCATGCGCGGAGCTCGTCCGGGAGCCGGGCTGCGGCTGCTGC
TCGGTGTGCGCCCGCTGGAGGGCGAGGCGTGCGGCGTCTACACCCCGCGCTGCGGCCAGGGGCTGCGCTGCTAT
CCCCACCCGGGCTCCGAGCTGCCCCCTGCAGGCGCTGGTTCATGGGCGAGGGCACTTGTGAGAAGCGCCGGGACGCC
GAGTATGGCGCCAGCCCGGAGCAGGTTGCAGACAATGGCGATGACCACTCAGAAGGAGGCCTGGTGGAGAACCAC
GTGGACAGCACCATGAACATGTTGGGCGGGGGAGGCAGTGCTGGCCGGAAGCCCCCTCAAGTCGGGTATGAAGGAG
CTGGCCGTGTTCCGGGAGAAGGTCACTGAGCAGCACCGGCAGATGGGCAAGGGTGGCAAGCATCACCTTGGCCTG
GAGGAGCCCAAGAAGCTGCGACCACCCCTGCCAGGACTCCCTGCCAACAGGAAGTGGACCAGGTCCTGGAGCGG
ATCTCCACCATGCGCCTTCCGGATGAGCGGGGCCCTCTGGAGCACCTCTACTCCCTGCACATCCCCAACTGTGAC
AAGCATGGCCTGTACAACCTCAAACAGTGCAAGATGTCTCTGAACGGGCAGCGTGGGGAGTGCTGGTGTGTGAAC
CCCAACACCGGGAAGCTGATCCAGGGAGCCCCACCATCCGGGGGGACCCCGAGTGTCATCTCTTCTACAATGAG
CAGCAGGAGGCTCGCGGGGTGCACACCCAGCGGATGCAGTAGACCGCAGCCAGCCGGTGCTGGCGCCCCCTGCCC
CCCGCCCTCTCCAAACACCGGCAGAAAACGGAGAGTGCTTGGGTGGTGGGTGCTGGAGGATTTTCCAGTTCTGA
CACACGTATTTATATTTGGAAAGAGACCAGCACCGAGCTCGGCACCTCCCCGGCCTCTCTCTTCCAGCTGCAGA
TGCCACACCTGCTCCTTCTTGCTTTCCCCGGGGGAGGAAGGGGGTTGTGGTCGGGGAGCTGGGGTACAGGTTTGG
GGAGGGGGAAGAGAAATTTTTATTTTTGAACCCCTGTGTCCCTTTTGCATAAGATTAAAGGAAGGAAAAGT

1035/6881
FIGURE 965

AGCGGATCTCCACCATGCGCCTTCCGGATGAGCGGGGCCCTCTGGAGCACCTCTACTCCCTGCACATCCCCAACT
GTGACAAGCATGGCCTGTACAACCTCAAACAGTGCTGGTGTGTGAACCCCAACACCGGGAAGCTGATCCAGGGAG
CCCCACCATCCGGGGGGACCCCGAGTGTCATCTCTTCTACAATGAGCAGCAGGAGGCTCGCGGGGTGCACACCC
AGCGGATGCAGTAGACCGCAGCCAGCCGGTGCCTGGCGCCCCTGCCCCCGCCCCTCTCCAAACACCGGCAGAAA
ACGGAGAGTGCTTGGGTGGTGGGTGCTGGAGGATTTTCCAGTTCTGACACACGTATTTATATTTGGAAAAGAGACC
AGCACCGAGCTCGGCACCTCCCCGGCCTCTCTCTTCCCAGCTGCAGATGCCACACCTGCTCCTTCTTGCTTTCCC
CGGGGAGGAAGGGGGTTGTGGTCGGGGAGCTGGGGTACAGGTTTGGGGAGGGGGAAGAGAAATTTTTATTTTTG
AACCCTGTGTCCCTTTTGCATAAGATTAAAGGAAGG

1036/6881
FIGURE 966

CTTCCTTTCTGGGCTCGGACCTAGGTCGCGGCGACATGGCCAAACGTACCAAGAAAGTCGGGATCGTCGGTAAAT
ACGGGACCCGCTATGGGGCCTCCCTCCGGAAAATGGTGAAGAAAATTGAAATCAGCCAGCACGCCAAGTACTACTT
GCTCTTTCTGTGGCAAAACCAAGATGAAGAGACGAGCTGTGGGGATCTGGCACTGTGGTTTCTGCATGAAGACAG
TGGCTGGCGGTGCCTGGACGTACAATACCACTTCCGCTGTCACGGTAAAGTCCGCCATCAGAAGACTGAAGGAGT
TGAAAGACCAGTAGACGCTCCTCTACTCTTTGAGACATCACTGGCCTATAATAAATGGGTAAATTTATGTAACAA
AAAAAAAAAAAAAAAAAAAA

1037/6881
FIGURE 967

MAKRTKKVGIVGKYGTRYGASLRKMOVKKIEISQHAHYTCSECGKTKMKRRAVGIWHCGSCMKTVAGGAWTYNTTS
AVTVKSAIRRLKELKDQ

1038/6881
FIGURE 968

CCCCCGCCACCTCACACACCCCCATCCGGGAGACCCACGTGCAGCTGGGCCCCGGGCTGGCGCCGCACCTCGGGG
TCTGCGCGTCTCCCCGGCGCGTTCCGGGCGCAGCCCCACGACACGGACCCCTGGCGGGGCGGCATCCGAGAAATC
GCAGGCGGAGAGGGGGCGTCTTGAGGCCGGGGCGGGGACGCTGCGGCCCGCGGCCACACAAAGGAGGCGGCGG
GAAGGCGGGGCAAGGCGGGCCGGGGCGGGGCGGCAGGAAGGGGCGGGGGCCCGCGCGGCGCCGCGGATAAAGC
CCCCGCGCCGCGGCAGCCAGCTTGCGCTGTGGGGCTGCCCGGGCTGCGCGGCGTCTGCAGGCGCCACCGCTGCC
TCTTTCCGGCTGTGACCTCCTCGCCGCGCGCTTGCTGCGTCTCCGACTCCCCGCGCCGCGAGACCAGGC
TCCCGCTCCGGTTGCGGCCGCACCGCCCTCCGCGGCGCGCCCCCTGGGGATCCAGCGAGCGCGGTCTGCTTGGTG
GAAGGAACCATGAACTGGCATCTCCCCCTCTTCTCTTGCCCTCTGTGACGCTGCCTTCCATCTGCTCCCACTTC
AATCCTCTGTCTCTCGAGGAAGTAGGCTCCAACACGGGGATCCAGGTTTTCAATCAGATTGTGAAGTCGAGGCCCT
CATGACAACATCGTGATCTCTCCCCATGGGATTGCGTCGGTCTTGGGGATGCTTCAGCTGGGGGCGGACGGCAGG
ACCAAGAAGCAGCTCGCCATGGTGATGAGATACGGCGTAAATGGAGTTGGTAAATATTAAAGAAGATCAACAAG
GCCATCGTCTCCAAGAAGATAAAGACATTGTGACAGTGGCTAACGCCGTGTTTGTTAAGAATGCCTCTGAAATT
GAAGTGCTTTTGTACAAGGAACAAAGATGTGTTCCAGTGTGAGGTCCGGAATGTGAACTTTGAGGATCCAGCC
TCTGCCTGTGATTCCATCAATGCATGGGTTAAAAATGAAACCAGGGATATGATTGACAATCTGCTGTCCCCAGAT
CTTATTGATGGTGTGCTCACCAGACTGGTCTCGTCAACGCAGTGTATTTCAAGGGTCTGTGGAAATCACGGTTC
CAACCCGAGAACACAAAGAAACGCACCTTCGTGGCAGCCGACGGGAAATCCTATCAAGTGCCAATGCTGGCCAG
CTCTCCGTGTTCCGGTGTGGGTCGACAAGTGCCCCAATGATTTATGGTACAACCTTCATTGAACCTGCCCTACCAC
GGGGAAGCATCAGCATGCTGATTGCACAGCGACTGAGAGCTCCACTCCGCTGTCTGCCATCATCCACACATC
AGCACCAAGACCATAGACAGCTGGATGAGCATCATGGTGCCCAAGAGGGTGCAGGTGATCCTGCCCAAGTTTACA
GCTGTAGCACAAACAGATTTGAAGGAGCCGCTGAAAGTTCTTGGCATTACTGACATGTTTGATTTCATCAAAGGCA
AATTTTGCAAAAATAACAAGGTCAGAAAACCTCCATGTTTCTCATATCTTGCAAAAAGCAAAAATTGAAGTCAGT
GAAGATGGAACCAAGCTTCAGCAGCAACAACCTGCAATTCTCATTGCAAGATCATCGCCTCCCTGGTTTATAGTA
GACAGACCTTTTCTGTTTTTCATCCGACATAATCCTACAGGTGCTGTGTTATTCATGGGGCAGATAAACAACCC
TGAAGAGTATACAAAAGAAACCATGCAAAGCAACGACTACTTTGCTACGAAGAAAGACTCCTTTCTGCATCTTT
CATAGTTCTGTAAATATTTTTGTACATCGCTTCTTTTTCAAACTAGTTCTTAGGAACAGACTCGATGCAAGTG
TTTCTGTTCTGGGAGGTATTGGAGGGAAAAACAAGCAGGATGGCTGGAACACTGTACTGAGGAATGAATAGAAA
GGCTTCCAGATGTCTAAAAGATTCTTTAACTACTGAACGTGTTACCTAGGTAAACAACCCCTGTTGAGTATTTGCT
GTTTGTCCAGTTCAGGAATTTTTGTTTTGTTTTGTCTATATGTGCGGCTTTTCAGAAAGAAATTTAATCAGTGTGA
CAGAAAAAAAATGTTTTATGGTAGCTTTTACTTTTTATGAAAAAAAATTATTTGCCTTTTAAATTCTTTTCCC
CCATCCCCCTCCAAAGTCTTGATAGCAAGCGTTATTTTGGTGGTAGAAACGGTGAAATCTCTAGCCTCTTTGTGT
TTTTGTTGTTGTTGTTGTTGTTTATATAATGCATGTATTCATAAAATAAAATTTAAAAAACTCCTGTCTT
GCTAGACAAGGTTGCTGTTGTGAGTGTGCCTGTCACTACTGGTCTGTACTCCTTGGATTGTCATTTTTGTATTT
TGTACAAAGTAAAAATAAACTGTTATGAGTAGT

1039/6881
FIGURE 969

MNWHLPFLFLASVTLPSICSHFNPLSLEELGSNTGIQVFNQIVKSRPHDNIVISPHGIASVLGMLQLGADGRTKK
QLAMVMRYGVNGVGKILKKINKAIVSKKNKDIVTVANAVFVKNASEIEVPFVTRNKDVFQCEVRNVNFEDPASAC
DSINAWVKNETRDMIDNLLSPDLIDGVLTRLVLVNAVYFKGLWKS RFQ PENTKKRTFVAADGKSYQVPMLAQLSV
FRCGSTSAPNDLWYNFIELPYHGESISMLIALPTESSTPLSAIIPHISTKTIDSWMSIMVPKRVQVILEPKFTAVA
QTDLKEPLKVLGITDMFDSSKANFAKITRSENLVSHILQKAKIEVSEDGTKASAATTAILIARSSPPWFIVDRP
FLFFIRHNPTGAVLFMGQINKP

1040/6881
FIGURE 970

ATGCGTGCTGAAAAGAGAAAAAAGAATGCCCCAGAGGAGGTCAGCAGGCTTAAAAGTATTCTCAAACCTAGACGAT
GACGTTTTTAATGAAAGATGTTCAAGAGATAGCAACTGTGGTGGTACCCAAACCCAAACATTGCCAAGAGAAAATG
CAATGTGAGGTAAAAGATGAAAAAGATGACATGAAAATGGAGACTGATATTAAGAGAAAACAAAAAGACTCTTCTA
GACCAGCATGGACAGTACCCAATATGGATGAACCAAAGGCAAAGAAAAAGGCTAAAGGCAAAGCGAGAGAAAAGA
AAGGAGAAAAACAAAGCAAAGCAGTGAAAAGTGGCAAAGGGTTTGGCCTGTAGTATTGTTTCCATAATAGTCCAT
TTCGCAGAAATAAGAAGGAGAATAAAACTTAGAGAAAAAGAGGAGGCCAAAAGGGGCAAGGTAGTGGCTACTTGC
AGAAAACCTGAAAAATATGTGTGACAAAGCCGCCATAATAAGTGCCAGCCGAGCTGCAGCAGCCCGTCTCAGGGGC
ACCGCAGCCTCCCCGGGCCCTACGGCCGCCCGCCAGCAGGATGGCTGGAATGGCCTTAGTCATGAGGCTTTTAGA
ATTGTTTCAAGGCAGGATTATGCGTCAGAAGCAATCAATGGAGCAGCTGGTGGTGTATTATTTGGGTACTACCAAC
TCCTGTGTGGCCTTTACAGCAGATGTACAGAAAGACATTAAAAATATTCCTTTTAAAATTGTCTGTGCCTCCAATGGT
GATGCCTGGGTTGAGGCTCATGGGAAACTGTATTCTCCAAGTCAGATCGGAGCATTGTGTGTCGATGAAGATGAAA
GAGACTGCAGAAAATTACTTGGGGCACACAGCAAAAAATGCTGTGATCGCAGTCCCAGCTTATTTCAATGACTTG
CAGAGGCAGGCCACTAAAGATGCTGGCCAGATATCTGGACTGAATGTGCTTCGGGTGATTAATGAACCCACAGCT
GCTGCTCTTGCCATATGGTCTAGACAAATCAAAAGACAAAGTCATTGCTGTATATGATTTAGGTGGTGGAACTTTT
GATATTTCTATCCTGGAATTTAGAAAAGGAGTATTCGAGGTGAAATCCACAAATGGGGACACTTTCTTAGGTGGG
GAAGACTTTGACCAGGCCTTGCTACAGCACATTGTGAAGGAGTTCAAGAGAGAGACGGGGGTTGATTTGACCAAA
GACAACGTGGCATTTCAGAGGGTGTGGGAAGCTGCTGAAAAGGCTAAATGTGAACCTCCTCATCTGTGCAGACT
GACATCAATTTGCCCTATCTTACAATGGATTCTTCTGGACCCAAGCATTGGAATACAAAGTTGACCCATGCTCAA
TTTGAAGGGATTGTCACTGATCTAATCAGGAGGACTATCGCTCCATGCCAAAAAGCTATGCAAGATGCAGAAGTC
AGCAAGAGTGATATAGGAGAAGTGATTCTTGTGGAGCCCCCAAGTAAAGCTGTCAATCCTGATGAGGCTGTGGCC
ATTGGAGCTGCCATTACAGGGAGATGTGTTGGCCGGCGATGTACAGATGTGCTGCTCCTTGATGTCATTCCCCTG
TCTCTGGGTATTGAACTCTGCGAGGTGTCTTTACCAAACCTTATTAATAGGAATACCACTATTCCAACCAAGAAG
AGCCAGGTATTCTCAACTGCTGCTGATGGGCAGACACAAGTGGAATTAAGTGTGTCAGGGTGAGAGAGAGATG
GCTGGAGACAACAACTCCTTGGACAGTTTACTTTGATTGGAATTCCACCAGCCCCCTCGTGGAGTTCCTCAGATC
AAAGTTACATTTGACATTGATGCCAATGGGATCATACTGTTTCAGCTAAAGATAAAGGCACAGGACATGAGCAG
CAGATTGTAATCCAGTCTTCTGGTGGGTAAAGCAAAGATGATGTTGAAAATATGGTTAAAAATGCAGAGAAATAT
GCTAAGGAAGACCAGCGAAGGAAGGAATGA

1041/6881
FIGURE 971

CGGAGCTGTCCATCAGCACCAAAGGCCGCGGGCGGGCTCAGGGCATGGGGCCGCGGTTCTGGGGCGGGCCGAGCC
CCGGCTCCTGCGCCTTCCCCTTCCCTCAGGCCCAGCCCGAGTTCCCGGACGCCGCGGGACTGGAGTGCCAGCCGGT
GTTGGACGTGGAGCGGCGCCGCCACCGCGCCGACACCATTCTCTCCGGCCCAGCAGCCCCCTTCCCTCGCACGACG
GACTTTCCTTGGACCCAGTCAGTTGGAGCCTCTGGCGCCCCGCAACCCCGGCCCTCGGGCCTCTGCACAGCCT
CTTTCACCTCAGAAGCTCAGGTGCGCTCCAGCCCAGCACTATGCCGGGACTGTGGCAACACTGCGGTTCCAGCTG
CTGCCCCCTGAGCCAGATGATGCCTTCTGGGGTGCACCTTGTGAACAGCCCCCTGGAGCGCAGGTACCAGGCACTG
CCGGCCCCCTCGTCTGCATCATGTGCTGTTTGGTTGGAGTCGTCTACTGCTTCTTCGGTTACCGCTGCTTCAAGGCA
GTGCTCTTTCTCACTGGGTTGCTGTTTGGCTCGGTGGTCATCTTCCTCCTCTGCTACCGAGAGCGGGTGCTAGAG
ACACAGCTGAGTGCTGGGGCGAGCGCGGGGCATCGCTCTGGGCATCGGGCTGCTCTGCGGGCTGGTGGCCATGCTA
GTGCGCAGCGTGGGCCTCTTCCCTGGTGGGGCTGCTGCTCGGCCTGCTGCTCGCAGCTGCTGCCCTGCTGGGCTCC
GCACCCTACTACCAGCCAGGCTCCGTGTGGGGTCCACTGGGGCTGTTGCTGGGGGGCGGGCTGCTCTGTGCCCTG
CTCACTCTGCGCTGGCCCCGCCCACTCACCACCCTGGCCACCGCCGTGACTGGTGCTGCGCTGATCGCCACTGCC
GCTGACTACTTCGCCGAGCTGCTACTGCTGGGGCGCTACGTGGTGGAGCGACTCCGGGCTGCTCCTGTGCCCCCA
CTCTGCTGGCGAAGCTGGGCCCTGCTGGCACTCTGGCCCCTGCTCAGCCTGATGGGCGTTCTGGTGCAGTGGAGG
GTGACAGCTGAGGGGGACTCCCACACGGAAGTGGTCATCAGCCGGCAGCGCCGACGCGTGCAACTGATGCGGATT
CGGCAGCAGGAAGATCGCAAGGAGAAAAGGCGGAAAAAGAGACCTCCTCGGGCTCCCCCTCAGAGGTCCCCGGGCT
CCTCCCAGGCCTGGGCCACCAGACCCTGCTTATCGGCGCAGGCCAGTGCCCATCAAACGCTTCAATGGAGACGTC
CTCTCCCCGAGCTATATCCAGAGCTTCCGAGACCGGCAGACCGGGAGCTCCCTGAGCTCCTTCATGGCCTCAGCC
ACAGATGCGGACTATGAGTATGGGTCCCGGGGACCTCTGACAGCCTGCTCAGGCCCCCAGTGCGGGTATAGCCA
TATCTGTCTGTCTAGACTCTGCAGTCACCAGCTCTGCCAGCTCGAGGAGGCCTGCTAGGCTGCCACTCAGCCTCC
TGGCTTTGGCTGTCCCTCTCCCCAGCCTGGAGAGGGCTGGCCTGGTCACTAGAAAGGGAGGATTGTCTCAGGCGAG
TCTTGGCCTGAGAGGAAAGCCCCCTCCCAAGCTCCCAAGAGGCTCCTGAGGAACTCGGGGTGTGAACCCCATTTGG
GGTGTGCTCAGGGTTGTGAGTGTGTTGCCCCGTGTGTCTGTGTGTATGTGTGTGGGGGTGGGCAGGCTTGGAGGGG
ACGCTGGGACCCTTGCCTTAGATTTCTGACTGGTAGGGTTTCTCCAGGCTCAGCCCCACCTCTTCACTCCCTGCC
AAGGTCCCATGGGCCACCTCCTGCATGTCTCCGCGGAGGGGCTACCTTCCTTCCCATCGCCCTGCCTCGCAGCCA
GACTCATCTAAGGGTTCTTGTCTTGTCTATGGGGCAAAGTGTAGCATCCCTCACCCTGGTCCCCTGGCCTCTGT
AAAGCCACCAGCCTGAGGGCAGTGGCAGGAGATGGGGGTGGGGGGTGTGCTCTGGGCTGGGTGGGAAGGGAG
TTGGGGAGGGGTTTTAAATGCACGGTGCATGTCTGGTGTCTGTATGCCAACCTAGACACCTCATGCTTCTGTCTC
CCCCACCCCACTCTGTTTTACATCTTTTATAAATGTGCCAACTGTGTGGCCTCTGCCA

1042/6881
FIGURE 972

MPGTVATLRFQLLPPEPDDAFWGAPCEQPLERRYQALPALVCIMCCLFGVVYCFFGYRCFKAVLFLTGLLFGSVV
IFLLCYRERVLETQLSAGASAGIALGIGLLCGLVAMLVRSVGLFLVGLLLGLLLAAAALLGSAPYYQPGSVWGPL
GLLLGGGLLCALLTLRWPRPLTTLATAVTGAALIATAADYFAELLLLGRYVVERLRAAPVPPLCWRSWALLALWP
LLSLMGVLVQWRVTAEGDSHTEVVISRQRRRVQLMRIQQEDRKEKRRKKRPPRAPLRGPRAPPRPGFPDPAYRR
RPVPIKRFNGDVLSPSYIQSFRDRQTGSSLSSFMASTADADYEYGSRGPLTACSGPPVRV

1043/6881
FIGURE 973

CGGAGCACATGCTGAGCGGAGCGGCTGGGGCTGCGCGGCGTGGCGGAGCAGCGCTCGCTCCCTCGCTCACTCGCT
CGCTCGCAGGGACACACGCAGGGGCTGACAGCTGTGCTGGTGTGATAAGGGAAGCCACAAGGAGACGATCGAGG
AGAGAGACAAGCGGCAGCAGAGGCAGCAGCGGCAGAGGCAGCACACAGGGCTGCGGAGCTGCTGGGAGTGGGAGTG
ACTCCCCACCTCGGGCCCCCACCCTGTCCCTGTCTCTTCCCCGCTTGCCCTGAGTTTAGAAGAGCAGCCGCTGC
CACCCTGCCACTCGGGAGGGCACCAGGGCTGCTGGCTAGGGAGGGACAGGGCAGGGAGGCTCTGGCCAGTCCCA
GCAGCCGGGGACAGATGCCGATCGAGATTGTGTGCAAAATCAAATTTGCTGAGGAGGATGCGAAACCCAAGGAGA
AGGAGGCAGGGGATGAGCAGAGCCTCCTCGGGGCTGTTGCCCTGGAGCAGCCCCCGAGACCTGGCCACCTTTG
CCAGCACCAGCACCTGTCATGGACTGGGCCGGGCTGTGGCCCAGGCCCCCAGGACTGCGCAGAACCCTGTGGG
CACTGGCCCTACTCACCTCGCTGGCTGCCTTCTGTACCAGGCGGCTGGCCTGGCCCGGGGCTACCTGACCCGGC
CTCACCTGGTGGCAATGGACCCCGCTGCCCCAGCCCCAGTGGCGGGCTTCCCGGCTGTACCCCTCTGCAATATCA
ACCGCTTCCGGCATTTCGGCACTCAGCGATGCCGACATCTTCCACCTGGCCAATCTGACAGGGCTGCCCCCAAAG
ACCGGGATGGGCACCGTGC GGCTGGCCTGCGCTACCCAGAGCCTGACATGGTAGACATCCTCAACCGCACTGGCC
ACCAGCTCGCCGACATGCTTAAGAGCTGCAACTTCAGTGGGCATCACTGCTCCGCCAGCAACTTCTCTGTGGTCT
ATACTCGCTATGGGAAGTGTTACACCTTCAACGCGGACCCGCGGAGCTCGCTGCCAGCCGGGCAGGGGGCATGG
GCAGTGGCCTGGAGATCATGCTGGACATCCAGCAGGAGGAGTACCTGCCCATCTGGAGGGAGACAAATGAGACGT
CGTTTGAGGCAGGTATTCGGGTGCAGATCCACAGCCAGGAGGAGCCGCCCTACATCCACCAGCTGGGGTTCGGGG
TGTCGCCAGGCTTCAGACCTTTGTGTCTGTCAGGAACAGCGGCTGACCTACCTGCCCCAGCCCTGGGGCAACT
GCCGCGCAGAGAGTGAGCTCAGGGAGCCTGAGCTTCAGGGCTACTCGGCCTACAGTGTGTCTGCCTGCCGGCTGC
GCTGTGAAAAGGAGGCCGTGCTTCAGCGCTGCCACTGCCGGATGGTGCACATGCCAGGCAATGAGACCATCTGCC
CACCAAATATCTACATCGAGTGTGCAGACCACACACTGGACTCCCTGGGTGGGGGCCCTGAGGGCCCGTGCTTCT
GCCCCACCCCTGCAACCTGACACGCTATGGGAAAGAGATCTCCATGGTCAGGATCCCCAACAGGGGCTCAGCCC
GGTACCTGGCGAGGAAGTACAACCGCAACGAGACCTACATACGGGAGAACTTCTGGTCCTAGATGTCTTCTTTG
AGGCCCTGACCTCTGAAGCCATGGAGCAGCGAGCAGCCTATGGCCTGTGAGCCCTGCTGGGAGACCTCGGGGGAC
AGATGGGCCTGTTTATTGGGGCCAGCATCCTCACGTTGCTGGAGATCCTCGACTACATCTATGAGGTGTCTGGG
ATCGACTGAAGCGGGTATGGAGGCGTCCCAAGACCCCCCTGCGGACCTCCACTGGGGGCATCTCCACTTTGGGGC
TTCAGGAGCTGAAGGAACAGAGTCCCTGCCCGAGCCTGGGCCGAGCGGAGGGTGGGGGGGTCAGCAGTCTGCTCC
CCAATCACCACCACCCCCACGGTCCCCCAGGAGGTCTCTTTGAAGATTTTGCTTGCTAGGACGGTGCTGTGACTG
AAAGGACCCAGGAGTCTGGGACCCCTCCTGGGATCCCCAGCACATTCTCCTGCTCCTGGGAGAGGCCTGGGGGCG
GTGCTCACTGGGAGGGCCAGGACTCAGTTCCCTGCTCTCATCCTCCCTGCCCTGATGTCAGCTGCTTTGCACAAA
GGTCTTCTTGTCACACCCCTTATCCCCAGGCTGGTGCCCCGGGAGGGCTGGAGACCAGGCCATGGGCCCTCAC
GGAGAGGAAGGGAAGGAAGGAGAGGGAGGGGGAGGATAGAGCCCATCCAGCCGGGGAGGGGGAGCCCTCTGTAC
ATTTGTAAATATTTAGGGAAAGCCGGGTGGGGGGAGGGGATACAGATGTAGAAGGTGGGTAGGGCTACAGGGGTG
GGTGATTTAGGGACAGCCAGGGTCCCAGCCCCAATGTCAGCAGGATAGGGAGAGCCCCAGGACTCAGGAGTGCTG
GGCTGGTCTACTTCTGCCCCCTCTCCAGGCCAGCTCCCCCTCTTGCCAGGGGGAGAGGATGGCCCAGCAGGCCT
GGCCCAGCTCCCAGTTCCCCCTGCACCAGCCCCACCCCTAGAGTCCCTTCTATAGGGAGGGGGCAGGAGACCTTC
CAGACTTCGGCTGAGCTTGGAGGGTGGGAAGGGAGCCTTCTCAGTCTCTCTCCCTCCAGTCTGATTTTATAAAG
TGCTGACGAG

1044/6881
FIGURE 974

MP I E I V C K I K F A E E D A K P K E K E A G D E Q S L L G A V A P G A A P R D L A T F A S T S T L H G L G R A C G P G P H G L R R T L W A L A L L
T S L A A F L Y Q A A G L A R G Y L T R P H L V A M D P A A P A P V A G F P A V T L C N I N R F R H S A L S D A D I F H L A N L T G L P P K D R D G H
R A A G L R Y P E P D M V D I L N R T G H Q L A D M L K S C N F S G H H C S A S N F S V V Y T R Y G K C Y T F N A D P R S S L P S R A G G M G S G L E
I M L D I Q Q E E Y L P I W R E T N E T S F E A G I R V Q I H S Q E E P P Y I H Q L G F G V S P G F Q T F V S C Q E Q R L T Y L P Q P W G N C R A E S
E L R E P E L Q G Y S A Y S V S A C R L R C E K E A V L Q R C H C R M V H M P G N E T I C P P N I Y I E C A D H T L D S I G G G P E G P C F C P T P C
N L T R Y G K E I S M V R I P N R G S A R Y L A R K Y N R N E T Y I R E N F L V L D V F F E A L T S E A M E Q R A A Y G L S A L L G D L G G Q M G L F
I G A S I L T L L E I L D Y I Y E V S W D R L K R V W R R P K T P L R T S T G G I S T L G L Q E L K E Q S P C P S L G R A E G G V S S L L P N H H H
P H G P P G G L F E D F A C

1045/6881
FIGURE 975

CCTCGCCGCATCCACTCTCCGGCCGGCCGCTGCCCCGCCCTCCTCCGTGCGCCCCGCCAGCCTCGCCCCGCGCCG
TCACCATGAGCCAGGCCTACTCGTCCAGCCAGCGCGTGTCTCCTACCGCCGCACCTTCGGCGGGGGCCCCGGGCT
TCCCCTCGGCTCCCCGCTGAGTTGCGCCGTGTTCCCGCGGGCGGGTTTCGGCTCTAAGGGCTCCTCCAGCTCGG
TGACGTCCCGCTGTACCAGGTGTCGCGCACGTGCGGGCGGGGCCGGGGCCTGGGGTTCGCTGCGGGCCAGCCGGC
TGGGGACCACCCGCACGCCCTCCTCCTACGGCGCAGGCGAGCTGCTGGACTTCTCACTGGCCGACGCGGTGAACC
AGGAGTTTCTGACCACGCGCACCAACGAGAAGGTGGAGCTGCAGGAGCTCAATGACCGCTTCGCCAACTACATCG
AGAAGGTGCGCTTCTGGAGCAGCAGAACGCGGCGCTCGCCGCCGAAGTGAACCGGCTCAAGGGCCGCGAGCCGA
CGCGAGTGGCCGAGCTCTACGAGGAGGAGCTGCGGGAGCTGCGGCGCCAGGTGGAGGTGCTCACTAACCAGCGCG
CGCGCGTGCAGCTCGAGCGCGACAACCTGCTCGACGACCTGCAGCGGCTCAAGGCCAAGCTGCAGGAGGAGATT
AGTTGAAGGAAGAAGCAGAGAACAATTTGGCTGCCTTCCGAGCGGACGTGGATGCAGCTACTCTAGCTCGCATTG
ACCTGGAGCGCAGAATTGAATCTCTCAACGAGGAGATCGCGTTCTTAAGAAAGTGCATGAAGAGGAGATCCGTG
AGTTGCAGGCTCAGCTTCAGGAACAGCAGGTCCAGGTGGAGATGGACATGTCTAAGCCAGACCTCACTGCCGCCC
TCAGGGACATCCGGGCTCAGTATGAGACCATCGCGGCTAAGAACATTTCTGAAGCTGAGGAGTGGTACAAGTCGA
AGGTGTGACACCTGACCCAGGCAGCCAACAAGAACAACGACGCCCTGCGCCAGGCCAAGCAGGAGATGATGGAAT
ACCGACACCAGATCCAGTCTTACACCTGCGAGATTGACGCCCTGAAGGGCACTAACGATTCCCTGATGAGGCAGA
TGCGGGAATTGGAGGACCGATTTGCCAGTGAGGCCAGTGGCTACCAGGACAACATTGCGCGCCTGGAGGAGGAAA
TCCGGCACCTCAAGGATGAGATGGCCCGCCATCTGCGCGAGTACCAGGACCTGCTCAACGTGAAGATGGCCCTGG
ATGTGGAGATTGCCACCTACCGGAAGCTGCTGGAGGGAGAGGAGAGCCGGATCAATCTCCCCATCCAGACCTACT
CTGCCCTCAACTTCCGAGAAACCAGCCCTGAGCAAAGGGTTCTGAGGTCCATACCAAGAAGACGGTGATGATCA
AGACCATCGAGACACGGGATGGGGAGGTGCTCAGTGAGGCCACACAGCAGCAGCATGAAGTGCTCTTAAAGACAGA
GACCCTCTGCCACCAGAGACCGTCTCACCCTGTCTCACTGCTCCCTGAAGCCAGCCTTCTTCCATCCCAGGA
CACCACACCCAGCCTCAGTCTCTCCCTCACAGCCTCTGACCCCTCCTCACTGGCCATCCCTCGTGGTCCCCAACA
GCGACATAGCCCATCCCTGCCTGGTCACAGGGCATGCCCCGGCCACCTCTGCGGACCCAGCTGTGAGCCTTGCC
TGTTGGCAGTGAGTGAGCCTGGCTCTTGCTGCTGGATGGAGCCCAGGCGGGAGCGGTGGCCCTGTCCCTCCACCT
CTGTGACCTCAGGCACTAGCCTTTGGCTCTGGAGACAGCCCCAGAGCAGGGTGTTGGGATACTGCAGGGCCAGGA
CTGAGCCCCGCAGACCTCCCCAGCCCCCTAGCCCAGGAGAGAGAAAGCCAGGCAGGTAGCCAGGGGGACTAGCCCC
TGTGGAGACTGGGGGGCTTGAAATTGTCCCCGTGGTCTCTTACTTTCCCTTCCCCAGCCCAGGGTGGACTTAGAA
AGCAGGGGGCTACAAGAGGGAATCCCCGAAGGTGCTGGAGGTGGGAGCAGGAGATTGAGAAGGAGAGAAAGTGGGT
GAGATGCTGGAGAAGAGAGGAGAGAGAGAGGAGAGAGCGGTCTCAGGCTGGTGGGAGGGGCGCCACCTCCCC
ACGCCCTCCCCTCCCCTGCTGCAGGGGCTCTGGAGAGAAACAATAAAGAGATTCACACACAAGCC

1046/6881
FIGURE 976

MSQAYSSSQRVSSYRRTFGGAPGFPLGSPLSSPVFPFRAGFGSKGSSSSSVTSRVYQVSRTSGGAGGLGSLRASRLG
TTRTPSSYGAGELLDFFSLADAVNQEFLLTTRTNEKVELQELNDRFANYIEKVRFLEQQNAALAAEVNRLKGREPTR
VAELYEEELRELRRQVEVLTNQARVDVERDNLLDDLQRLKAKLQEEIQLKEEAENNLAAFRADVDAATLARIDL
ERRIESLNEEIAFLKKVHEEEIRELQAQLQEQQVQVEMDMSKPDLTAAALRDIRAQYETIAAKNISEAEEWYKSKV
SDLTQAANKNNDALRQAKQEMMEYRHQIQSYTCEIDALKGTNDSLMRQMRELEDRFASEASGYQDNIRLEEEIR
HLKDEMARHLREYQDLLNVKMALDVEIATYRKLLERGEESRINLPIQTYSALNFRETSPEQRGSEVHTKKTVMIKT
IETRDGEVVSEATQQQHEVL

1047/6881
FIGURE 977

GCACGAGGGTGATGAAGGCCTACGAGTGCGGCGCGGCCTGAAGGGGCACGCGGGGGACCTGCAAAGCTAGTGAGG
GGCGGGGCAGGCGGCGCGGTGGGGGCGGGCCGAGCCCGAGGCCAGATGAGCGGACACAGCCCCACGCGCGGGGC
CATGCAGGTGGCCATGAACGGTAAGGCCCCGAAAGAGGCGGTGCAGACTGCGGCTAAGGAACTCCTCAAGTTCGT
GAACCGGAGTCCCTCTCCTTTCCATGCTGTGGCTGAATGCCGCAACCGCCTTCTCCAGGCTGGCTTCAGTGA
CAAGGAGACTGAGAAATGGAATATTAAGCCCGAGAGCAAGTACTTCATGACCAGGAACTCCTCCACCATCATAGC
TTTTGCTGTAGGGGGCCAGTACGTTCTTGGCAATGGCTTCAGCCTCATCGGGGGCCACACGGACAGCCCCTGCCT
CCGGGTGAAACGTCGGTCTCGCCGAGCCAGGTGGGCTTCAGCAAGTCGGTGTGGAGACCTATGGTGGTGGGAT
CTGGAGCACCTGGTTTGACCGTGACCTGACTCTGGCTGGACGCGTCATTGTCAAGTGCCCTACCTCAGGTCGGCT
GGAGCAGCAGCTGGTGCACGTGGAGCGGCCCCATTCTTCGCATCCACACCTGGCCATCCATCTGCAGCGAAATAT
CAACGAGAACTTTGGGCCCCAACACAGAGATGCATCTAGTCCCCATTCTTGCCACAGCCATCCAGGAGGAGCTGGA
GAAGGGGACTCCTGAGCCAGGGCCTCTCAATGCTGTGGATGAGCGGCACCATTCGGTCTCATGTCCCTGCTCTG
TGCCCATCTGGGGCTGAGCCCCAAGGACATAGTGGAGATGGAGCTCTGCCTTGACAGACCCAGCCTGCGGTCTT
GGGTGGTGCCTATGATGAGTTTCATCTTTGCTCCTCGGCTGGACAATCTGCACAGCTGCTTCTGTGCCCTGCAGGC
CTTGATAGATTCTGTGTCAGGCCCTGGCTCCCTGGCCACAGAGCCTCACGTGCGCATGGTCACACTCTATGACAA
CGAAGAGGTGGGGTCTGAGAGTGCACAGGGAGCACAGTCACTGCTGACAGAGCTGGTGTGCGGCGGATCTCAGC
CTCGTGCCAGCACCCGACAGCCTTCGAGGAAGCCATACCCAAGTCCTTCATGATCAGCGCAGACATGGCCCATGC
TGTGCATCCCAACTACCTGGACAAGCATGAGGAGAACCACCGGCCTTTATTCCACAAGGGCCCCGTGATCAAGGT
GAACAGCAAGCAACGCTATGCTTCAAACGCGGTGTGAGAGGCCCTGATCCGAGAGGTGGCCAACAAAGTCAAGGT
CCCCCTGCAGGATCTCATGGTCCGGAATGACACCCCTGTGGAACCACCATTTGGACCTATCTTGGCTTCTCGGCT
GGGGCTGCGGGTGTGATTTAGGCAGCCCCCAACTGGCCATGCACTCTATCCGGGAGATGGCCTGCACCACAGG
AGTCCTCCAGACCCTCACCTCTTCAAGGGCTTCTTTGAGCTGTTCCCTTCTCTAAGCCATAATCTCTTAGTGGA
TTGAGCCCTCTTGAAAGACTTCTCTGCCATCCCTTTGCACCTGAGAGGGGAAGTTCTCAGCTGAGCTGAAGCTG
GATTATTAAAGTGGATTGTCACTCAGAAAAAAAAAAAAAAAAAAAAA

1048/6881
FIGURE 978

MQVAMNGKARKEAVQTAAKELLKFVNRSPSPFHAVAECRNRLQAGFSELKETEKWNIPESKYFMTRNSSTIIA
FAVGGQYVPGNGFSLIGAHTDSPCLRVKRRSRRSQVGFQQVGVETYGGGIWSTWFDRLTLAGRVIVKCPTSGRL
EQQLVHVERPILRIPHLAIHLQRNINENFGPNTEMHLVPILATAIQEELEKGTPEPGPLNAVDERHHSVLMSLLC
AHLGLSPKDIVEMELCLADTQPAVLGGAYDEFIFAPRLDNLHSCFCALQALIDSCAGPGSLATEPHVRMVTLYDN
EEVGSESAQGAQSLLTELVLRRISASCQHPTAFEEAIPKSEFMISADMAHAVHPNYLDKHEENHRPLFHKGPVIKV
NSKQRYASNAVSEALIREVANKVKVPLQDLMVRNDTPCGTTIGPILASRLGLRVLDLGSPQLAMHSIREMACTTG
VLQTLTLFKGFFELFPSLSHNLLVD

1049/6881
FIGURE 979

CTTTGCATTGTTTCCTCATCCGCCTCCTTGCTCGCCGCAGCCGCCTCCGCCGCGCGCCTCCTCCGCCGCCGCGGAC
TCCGGCAGCTTTATCGCCAGAGTCCCTGAACTCTCGCTTTCTTTTTAATCCCCTGCATCGGATCACC GGCGTGCC
CCACCATGTCAGACGCAGCCGTAGACACCAGCTCCGAAATCACCACCAAGGACTTAAAGGAGAAGAAGGAAGTTG
TGGAAGAGGCAGAAAATGGAAGAGACGCCCCGTGCTAACGGGAATGCTAATGAGGAAAATGGGGAGCAGGAGGCTG
ACAATGAGGTAGACGAAGAAGAGGAAGAAGGTGGGGAGGAAGAGGAGGAGGAAGAAGAAGGTGATGGTGAGGAAG
AGGATGGAGATGAAGATGAGGAAGCTGAGTCAGCTACGGGCAAGCGGGCAGCTGAAGATGATGAGGATGACGATG
TCGATACCAAGAAGCAGAAGACCGACGAGGATGACTAGACAGCAAAAAAGGAAAAGTTAAACTAAAAAAAAAAAG
GCCGCCGTGACCTATTCACCCTCCACTTCCCGTCTCAGAATCTAAACGTGGTCACCTTCGAGTAGAGAGGCCCGC
CCGCCACCGTGGGCAGTGCCACCCGCAGATGACACGCGCTCTCCACCACCCAACCCAAACCATGAGAATTTGCA
ACAGGGGAGGAAAAAAGAACCAAACTTCCAAGGCCCTGCTTTTTTTCTTAAAAGTACTTTAAAAGGAAATTTG
TTTGTATTTTTTATTTACATTTTATATTTTTGTACATATTGTTAGGGTCAGCCATTTTTAATGATCTCGGATGAC
CAAACCAGCCTTCGGAGCGTTCTCTGTCCTACTTCTGACTTTACTTGTGGTGTGACCATGTTTATTATAATCTCA
AAGGAGAAAAAAACCTTGTAAGGCAAAAATGACAACAGAAAAACAATCTTATTCGAGCATTCCAGTAAC
TTTTTTGTGTATGTACTTAGCTGTACTATAAGTAGTTGGTTTGTATGAGATGGTTAAAAAGGCCAAAGATAAAAG
GTTTCTTTTTTTTTCTTTTTTGTCTATGAAGTTGCTGTTTATTTTTTTTGGCCTGTTTGATGTATGTGTGAAAC
AATGTTGTCCAACAATAAACAGG

1050/6881
FIGURE 980A

GCGGCAAGCCCCGCCTCAGCCCCTCTGGCAGGCTCCCGCCAGCGTCGCTGCGGCTCCGGCCCCGGGAGCGAGCGCC
CGGAGCTCGGAAAGATGCGGCGCCCCGCGGCGGCCTGGGGGTCTCGGGGGATCCGGGGGTCTCCGGCTGCTCCTCT
GCCTCCTGCTGCTGAGCAGCCGCCGGGGGGCTGCAGCGCCGTTAGTGCCACGGCTGTCTATTTGACCGCAGGC
TCTGCTCTCACCTGGAAGTCTGTATTACAGGATGGCTTGTTTGGGCAGTGCCAGGTGGGAGTGGGGCAGGCCCGGC
CCCTTTTGCAAGTCACCTCCCCAGTTCTCCAACGCTTACAAGGTGTGCTCCGACAACCTCATGTCCCAAGGATTGT
CCTGGCACGATGACCTCACCCAGTATGTGATCTCTCAGGAGATGGAGCGCATCCCCAGGCTTCGCCCCCAGAGC
CCCGTCCAAGGGACAGGTCTGGCTTGGCACCCAAGAGACCTGGTCCTGCTGGAGAGCTGCTTTTACAGGACATCC
CCACTGGCTCCGCCCCCTGCTGCCCAGCATCGGCTTCCACAACCACCACTGGGCAAAGGTGGAGCTGGGGCCAGCT
CCTCTCTGTCCCCCTCTGCAGGCTGAGCTGCTCCCGCCTCTCTTGAGACACCTGCTGCTGCCCCACAGCCTCCCC
ACCCCTTCACTGAGTTACGAACCTGCCTTGCTGCAGCCCTACCTGTTCCACCAGTTTGGCTCCCGTGATGGCTCCA
GGGTCTCAGAGGGCTCCCCAGGATGGTCAGTGTGCGCCCCCTGCCCAAGGCTGAAGCCCCCTGCCCTCTTCAGCA
GAACTGCCTCCAAGGGCATATTTGGGGACCACCCTGGCCACTCCTACGGGGACCTTCCAGGGCCTTCACCTGCCC
AGCTTTTTCAAGACTCTGGGTGCTCTATCTGGCCCAGGAGTTGCCAGCACCCAGCAGGGCCAGGGTGCCAAGGC
TGCCAGAGCAAGGGAGCAGCAGCCGGGCAGAGGACTCCCCAGAGGGCTATGAGAAGGAAGGACTAGGGGATCGTG
GAGAGAAGCCTGCTTCCCCAGCTGTGCAGCCAGATGCGGCTCTGCAGAGGCTGGCCGCTGTGCTGGCGGGCTATG
GGGTAGAGCTGCGTCAGCTGACCCCTGAGCAGCTCTCCACACTCCTGACCCTGCTGCAGCTACTGCCCAAGGGTG
CAGGAAGAAATCCGGGAGGGGTGTAAATGTTGGAGCTGATATCAAGAAAACAATGGAGGGGCCGGTGGAGGGCA
GAGACACAGCAGAGCTTCCAGCCCGCACATCCCCATGCCTGGACACCCCACTGCCAGCCCTACCTCCAGTGAAG
TCCAGCAGGTGCCAAGCCCTGTCTCCTCTGAGCCTCCCAAAGCTGCCAGACCCCTGTGACACCTGTCTCTGCTAG
AGAAGAAAAGCCCACTGGGCCAGAGCCAGCCACGGTGGCAGGACAGCCCTCAGCCCGCCAGCAGCAGAGGAAT
ATGGCTACATCGTCACTGATCAGAAGCCCCCTGAGCCTGGCTGCAGGAGTGAAGCTGCTGGAGATCCTGGCTGAGC
ATGTGCACATGTCTCAGGCAGCTTCATCAACATCAGTGTGGTGGGACCAGCCCTCACCTTCCGCATCCGGCACA
ATGAGCAGAACCTGTCTTTGGCTGATGTGACCCAACAAGCAGGGCTGGTGAAGTCTGAACTGGAAGCACAGACAG
GGCTCCAAATCTTGACAGACAGGAGTGGGACAGAGGGAGGAGGCAGCTGCAGTCCTTCCCCAAACTGCGCACAGCA
CCTCACCCATGCGCTCAGTGCTGCTCACTCTGGTGGCCCTGGCAGGTGTGGCTGGGCTGCTGGTGGCTCTGGCTG
TGGCTCTGTGTGTGCGGCAGCATGCGCGGCAGCAAGACAAGGAGCGCCTGGCAGCCCTGGGGCCTGAGGGGGCCC
ATGGTGACACTACCTTTGAGTACCAGGACCTGTGCCGCCAGCACATGGCCACGAAGTCCTTGTTCAACCGGGCAG
AGGGTCCACCGGAGCCTTCACGGGTGAGCAGTGTGTCTCTCCAGTTACAGCGACGCAGCCCAGGCCAGCCCCAGCT
CCCACAGCAGCACCCCGTCTCTGGTGCAGGAGCCGGCCCCAAGCCAACATGGACATCTCCACGGGACACATGATTC
TGGCATAACATGGAGGATCACCTGCGGAACCGGGACCGCCTTGCCAAGGAGTGGCAGGCCCTCTGTGCCTACCAAG
CAGAGCCAAACACCTGTGCCACCGCGCAGGGGGAGGGCAACATCAAAAAGAACCGGCATCCTGACTTCTTGCCCT
ATGACCATGCCCCGATAAAACTGAAGGTGGAGAGCAGCCCTTCTCGGAGCGATTACATCAACGCCAGCCCCATTA
TTGAGCATGACCCTCGGATGCCAGCCTACATAGCCACGCAGGGCCCCGCTGTCCCATACCATCGCAGACTTCTGGC
AGATGGTGTGGGAGAGCGGCTGCACCGTCATCGTCATGCTGACCCCGCTGGTGGAGGATGGTGTCAAGCAGTGTG
ACCGCTACTGGCCAGATGAGGGTGCCTCCCTCTACCACGTATATGAGGTGAACCTGGTGTGCGGAGCACATCTGGT
GCGAGGACTTTCTGGTGCAGGCTTCTACCTGAAGAACGTGCAGACCCAGGAGACGCGCACGCTCACGCAGTTCC
ACTTCCTCAGCTGGCCGGCAGAGGGCACACCGGCCTCCACGCGGCCCTGCTGGACTTCCGCAGGAAGGTGAACA
AGTGCTACCGGGGCCGCTCCTGCCCCATCATCGTGCAGTGCAGTGTGGTGGGGGAGGACCGGCACCTACATCC
TCATCGACATGGTCTTGAACCGCATGGCAAAAGGAGTGAAGGAGATTGACATCGCTGCCACCCCTGGAGCATGTCC
GTGACCAGCGGCTGGCCTTGTCCGCTCTAAGGACCAGTTTGAATTTGCCCTGACAGCCGTGGCGGAGGAAGTGA
ATGCCATCCTCAAGGCCCTGCCCCAGTGAGACCTGGGGCCCCCTTGGCGGGCAGCCCAGCCTCTGTCCCTCTTTG
CCTGTGTGAGCATCTCTGTGTACCCACTCCTCACTGCCCCACCAGCCACCTCTTGGGCATGCTCAGCCCTTCCTA
GAAGAGTCAGGAAGGGAAAGCCAGAAGGGGACAGCCTGCCAGCCTCGCATGCCAGAGCCTGGGGCATCCCAGAG
CCCAGGGCATCCCATGGGGGTGCTGCAGCCAGGAGGAGAGGAAAGGACATGGGTAGCAATTCTACCCAGAGCCTT
CTCCTGCCTACATTCCTGGCCTGGCTCTCCTGTAGCTCTCCTGGGGTTCTGGGAGTTCCCTGAACATCTGTGTG
TGTCCCCCTATGCTCCAGTATGGAAGAATGGGGTGGAGGGTCGCCACACCCGGCTCCCCCTGCTTCTCAGCCCCG
GGCCTGCCTCTGACTCACACTTGGGCGCTCTGCCCTCCCTGGCCTCACGCCCAGCCTCCTCCCACCACCTCCCA
CCATGCGCTGCTCAACCTCTCTCCTTCTGGCGCAAGAGAACATTTCTAGAAAAAACTACTTTTGTACCAGTGTGA

1051/6881
FIGURE 980B

ATAAAGTTAGTGTGTTGTCTGTGCAGCTGCAAAAAAAAAAAAAAAAAAAAA

1052/6881
FIGURE 981

MRRPRRPGGLGGSGGLRLLLLCLLLLSSRPGGCSAVSAHGCLFDRRLCSHLEVCIQDGLFGQCQVGVGQARPLLQV
TSPVLQRLQGVLRLQMSQGLSWHDDLTQYVISQEMERIPRLRPPEPRPRDRSGLAPKRPGPAGELLLQDIPTGSA
PAAQHRLPQPPVKGKGAGASSLSPLQAELLPPLLEHLLLPQPPHPSLSYEPALLQPYLFHQFGSRDGSRVSEG
SPGMVSVGPLPKAEAPALFSRTASKGIFGDHPGHSYGDLPGPSPAQLFQDSGLLYLAQELPAPSRARVPRLEQ
SSSRAEDSPEGYEKEGLGDRGEKPASPAVQPDAAALQRLAAVLAGYGVELRQLTPEQLSTLLTLLQLLPKGAGRNP
GGVVNVGADIKKTMEGPFVEGRDTAELPARTSPMPGHPTASPTSSEVQQVPSPVSSEPPKAARPPVTPVLLEKKSP
LGQSQPTVAGQPSARPAEEYGYIVTDQKPLSLAAGVKLLEILAEHVMSSGSFINISVVGPAITFRIRHNEQNL
SLADVTQQAGLVKSELEAQTGLQILQTGVGQREEAAVLPQTAHSTSPMRSVLLTLVALAGVAGLLVALAVALCV
RQHARQQDKERLAALGPEGAGDITTFEYQDLCRQHMAKSLFNRAEGPPEPSRVSSVSSQFSDAAQASPSSHSST
PSWCEEPAQANMDISTGHMILAYMEDHLNRNDRDLAKEWQALCAYQAEPNTCATAQGEENIKKNRHPDFLPYDHAR
IKLKVESSPSRSDYINASPIIEHDPMPAYIATQGPLSHTIADFWQMVWESGCTVIVMLTPLVEDGVKQCDRYWP
DEGASLYHVYEVNLVSEHIWCEDFLVRSFYLNKVNQTQETRILTQFHFLSWPAEGTPASTRPLLDFFRRKVNKCYRG
RSCPIIVHCSDGAGRTGTYYILIDMVLNRMAKGVKEIDIAATLEHVRDQRFGLVRSKDQFEFALTAVAEEVNAILK
ALPQ

1053/6881
FIGURE 982

AGTTCTCACTGAGACCTGTCACCCCGACTCAACGTGAGACGCACCGCCCGGACTCACCATGCGTGAATGCATCTC
AGTCCACGTGGGGCAGGCAGGTGTCCAGATGGGCAATGCCTGCTGGGAGCTCTATTGCTTGGAACATGGGATTCA
GCCTGATGGGCAGATGCCCAGTGACAAGACCATTGGTGGAGGGGACGACTCCTTCACCACCTTCTTCTGTGAAAC
TGGTGCTGGAAAACACGTACCCCGGGCAGTTTTTGTGGATCTGGAGCCTACGGTCATTGATGAGATCCGAAATGG
CCCATAACCGACAGCTCTTCCACCCAGAGCAGCTCATCACTGGGAAAGAGGATGCTGCCAACAACTATGCCCCTGG
TCACTATACCATTGGCAAGGAGATCATTTGACCCAGTGTGGATCGGATCCGCAAGCTGTCTGACCAGTGCACAGG
ACTTCAGGGCTTCTCTGGTGTTCACAGCTTTGGTGGGGGCACTGGCTCTGGCTTCACCTCACTCCTGATGGAGCG
GCTCTCTGTTGACTATGGCAAGAAAATCCAAGCTGGAATTCTCCATCTACCCAGCCCCCAGGTGTCTACAGCCGT
GGTCGAGCCCTACAACCTCTATCCTGACCACCCACACCACCCTGGAGCACTCAGACTGTGCCTTCATGGTGGACAA
CGAAGCAATCTATGACATCTGCCGCCGCAACCTAGACATCGAGCGCCCAACCTACACCAACCTCAATCGCCTCAT
TAGCCAAATTGTCTCTCCATCACAGCTTCTCTGCGCTTTGACGGGGCCCTCAATGTGGACCTGACAGAGTTCCA
GACCAACCTGGTGCCCTACCCTCGCATCCACTTCCCCCTGGCCACCTATGCACCAGTCATCTCTGCAGAAAAGGC
ATACCACGAGCAGCTGTGGTGGCAGAGATCACCAATGCCTGCTTTGAGCCTGCCAACCAGATGGTAAAGTGTGA
TCCCCGGCACGGCAAGTACATGGCCTGCTGCCTGCTGTACCGTGGAGATGTGGTGCCCAAGGATGTCAACGCTGC
CATTGCCGCCATCAAGACCAAGCGCAGCATTTCAGTTTGTGGACTGGTGCCCCACAGGCTTCAAGGTTGGTATCAA
CTACCAGCCTCCCACTGTGGTGCCTGGGGGTGACCTGGCCAAGGTGCAGCGTGCCGTGTGCATGCTGAGCAACAC
GACCGCCATCGCCGAGGCCTGGGCCCCGCTGGACCACAAGTTTCGACCTGATGTATGCCAAGAGGGCGTTTTGTGCA
CTGGTATGTGGGTGAGGGCATGGAGGAGGGTGAGTTCTCCGAGGCCCCGTGAGGATATGGCTGCCCTGGAGAAGGA
TTATGAGGAGGTGGGCATCGACTCCTATGAGGACGAGGATGAGGGAGAAGAATAAAGCAGCTGCCTGGAGCCTAT
TCACTATGTTTATTGCAAAATCCTTTTGAAATAAACAGTTTCCTTGACACGGTTAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

1054/6881
FIGURE 983

MRECISVHVGQAGVQMGNACWELYCLEHGIQPDGQMPSDKTIGGGDDSF TTF C ETGAGKHVPRAVFVDLEPTVI
DEIRNGPYRQLFHPEQLITGKEDAANNYARGHYTIGKEIIDPVLDRIKLS DQCTGLQGFLVFH SFGGGTGSGFT
SLLMERLSVDYGKKS KLEFSIYPAPQVSTAVVEPYNSILTHTTLEHSDCAFMVDNEAIYDICRRNLDIERPTYT
NLNRLISQIVSSITASLRFDGALNVDLTEFQTNLVPYPRIHFPLATYAPVISAEKAYHEQLSVAEITNACFEPAN
QMVKCDPRHGKYM ACCLLYRGDVVPKDVNAAIAAIKTKRSIQFVDWCPTGFKVGINYQPPTVVPGGDLAKVQRAV
CMLSNTTAIAEAWARLDHKFDL MYAKRAFVHWYVGEGMEEGEFSEAREDMAALEKDYE EVGIDSYEDEDEGEE

1055/6881
FIGURE 984

GGGCCTGCAGTTGGCAGGAGGGTCCCCGGGCCCAGAGCCAGCGGGGCCGTGCTGAGACGGCGTACGTGCCCTGCGT
GAGTGCCTGGCGGCGGCGCGTGCCTAGGGGAGTGGGCGGTGAGGCCTGGTCCACGTGCGTCCCTTCCCGGGACC
CCCCCAGCTTGGCGCCCAGCGGCTACGTGAGCCAAGGCACCCGGATGTCCGCGCCCCCTCTCCGAGTGACCAGTCC
CGGCCTCCGGTCCCGCAGTGCCCGCAGCCTCGGCCGGCGTCCACGCATTGCCATGGTGACTGTGGGCAACTACTG
CGAGGCCGAAGGGCCCCGTGGGTCCGGCCTGGATGCAGGATGGCCTGAGTCCCTGCTTCTTCTTCACGCTCGTGCC
CTCGACGCGGATGGCTCTGGGGACTCTGGCCTTGGTGCTGGCTCTTCCCTGCAGACGCCGGGAGCGGCCCGCTGG
TGCTGATTGCTGTCTTGGGGGGCCGGCCCTCGCATCTCTCCCTACGTGCTGCAGCTGCTTCTGGCCACACTTCA
GGCGGCGCTGCCCTGGCCGGCCTGGCTGGCCGGGTGGGCACTGCCCGGGGGGGCCCCACTGCCAAGCTATCTACT
TCTGGCCTCCGTGCTGGAGAGTCTGGCCGCGCCTGTGGCCTGTGGCTGCTTGTGCTGGAGCGGAGCCAGGCACG
GCAGCGTCTGGCAATGGGCATCTGGATCAAGTTCAGGCACAGCCCTGGTCTCCTGCTCCTCTGGACTGTGGCGTT
TGCAGCTGAGAACTTGGCCCTGGTGTCTTGGAAACAGCCCACAGTGGTGGTGGGCAAGGGCAGACTTGGGCCAGCA
GGTTCAGTTTAGCCTGTGGGTGCTGCGGTATGTGGTCTCTGGAGGGCTGTTTGTCTGGGTCTCTGGGCCCCCTGG
ACTTCGTCCCCAGTCTATACATTGCAGGTTTCATGAAGAGGACCAAGATGTGGAAAGGAGCCAGGTTCCGTCAGC
AGCCCAACAGTCTACCTGGCGAGATTTTGGCAGGAAGCTCCGCCTCCTGAGTGGCTACCTGTGGCCTCGAGGGAG
TCCAGCTCTGCAGCTGGTGGTGCTCATCTGCCTGGGGCTCATGGGTTTGGAAACGGGCACTCAATGTGTTGGTGCC
TATATTCTATAGGAACATTGTGAACCTGCTGACTGAGAAGGCACCTTGGAACTCTCTGGCCTGGACTGTTACCAG
TTACGTCTTCTCAAGTTCCTCCAGGGGGGTGGCACTGGCAGTACAGGCTTCGTGAGCAACCTGCGCACCTTCTT
GTGGATCCGGGTGCAGCAGTTCACGTCTCGGCGGGTGGAGCTGCTCATCTTCTCCACCTGCACGAGCTCTCACT
GCGCTGGCACCTGGGGCGCCGCACAGGGGAGGTGCTGCGGATCGCGGATCGGGGCACATCCAGTGTCACAGGGCT
GCTCAGCTACCTGGTGTTCATATGTCATCCCCACGCTGGCCGACATCATCATTGGCATCATCTACTTCAGCATGTT
CTTCAACGCCTGGTTTGGCCTCATTGTGTTCTGTGCATGAGTCTTTACCTCACCTGACCATTGTGGTCACTGA
GTGGAGAACCAAGTTTCGTGCTGCTATGAACACACAGGAGAAGCTACCCGGGCACGAGCAGTGGACTCTCTGCT
AACTTCGAGACGGTGAAGTATTACAACGCCGAGAGTTACGAAGTGGAAACGCTATCGAGAGGCCATCATCAAATA
TCAGGGTTTGGAGTGGAAAGTCGAGCGCTTCACTGGTTTTACTAAATCAGACCCAGAACCTGGTGATTGGGCTCGG
GCTCCTCGCCGGCTCCCTGCTTTGCGCATACTTTGTCACTGAGCAGAAGCTACAGGTTGGGGACTATGTGCTCTT
TGGCACCTACATTATCCAGCTGTACATGCCCCCTCAATTGGTTTGGCACCTACTACAGGATGATCCAGACCAACTT
CATTGACATGGAGAACATGTTTGACTTGCTGAAAGAGGAGACAGAAGTGAAGGACCTTCCTGGAGCAGGGCCCCCT
TCGCTTTTCAAGAGGGCCGTATTGAGTTTGAAGAGTGCACCTCAGCTATGCCGATGGGCGGGAGACTCTGCAGGA
CGTGTCTTTCACTGTGATGCCTGGACAGACACTTGGCCTGGTGGGCCCCTCTGGGGCAGGGAAGAGCACAATTTT
GCGCCTGCTGTTTTCGCTTCTACGACATCAGCTCTGGCTGCATCCGAATAGATGGGCAGGACATTTACAGGTGAC
CCAGGCCTCTCTCCGGTCTCACATTGGAGTTGTGCCCCAAGACACTGTCCTCTTTAATGACACCATCGCCGACAA
TATCCGTTACGGCCGTGTCACAGCTGGGAATGATGAGGTGGAGGCTGCTGCTCAGGCTGCAGGCATCCATGATGC
CATTATGGCTTTCCCTGAAGGGTACAGGACACAGGTGGGCGAGCGGGGACTGAAGCTGAGCGGCGGGGAGAAGCA
GCGCGTCGCCATTGCCCGCACCATCCTCAAGGCTCCGGGCATCATTCTGCTGGATGAGGCAACGTCAGCGCTGGA
TACATCTAATGAGAGGGCCATCCAGGCTTCTCTGGCCAAAGTCTGTGCCAACCACACCACCATCGTAGTGGCACA
CAGGCTCTCAACTGTGGTCAATGCTGACCAGATCCTCGTCATCAAGGATGGCTGCATCGTGGAGAGGGGACGACA
CGAGGCTCTGTTGTCCCGAGGTGGGGTGTATGCTGACATGTGGCAGCTGCAGCAGGGACAGGAAGAAACCTCTGA
AGACACTAAGCCTCAGACCATGGAACGGTGACAAAAGTTTGGCCACTTCCCTCTCAAAGACTAACCAGAAAGGA
ATAAGATGTGTCTCCTTTCCCTGGCTTATTTTCATCCTGGTCTTGGGGTATGGTGCTAGCTATGGTAAGGGAAAGG
GACCTTTCCGAAAAACATCTTTTGGGGAATAAAAAATGTGGACTGTG

1056/6881
FIGURE 985

GTGCACTTCAGCTATGCCGATGGGTGAGGCCTTCCTTTTGCTTCCTTTGCTTTTCCGTTTCATTTGCACACTGCCT
TCCTGCTTCTCAGTGCTCTGAATCCCTGCTTTTGAAAAAGAGCCTGGGCAGGGGAGGGGCAGGGCCTACTAGCAG
CTCTGGTGATGGAAGGTGCCTGCTGAGCAACCCACCTTTCCTTGCAAGCGGGAGACTCTGCAGGACGTGTCTTT
CACTGTGATGCCTGGACAGACACTTGCCCTGGTGAGAGGAGACCCAGCCACTTGGCCCAGATGCCTCAAGCTTCC
CTCATTTCAGTGCCCATGGTAGCTTGTGACCCAGGCTGTGGAGTCAGAGAGCCCAGTCACGATAGGCAACCGGATT
GAATGGTGACGCCTCCATGGACACTGGTGACCTCTTGGAGAGGGAACTCAAAGCCAGTGGGCCTCGGCCGGCT
GCGGTGGCACATGCCTGTAATCCCAGCACTTTGGGAGGCTTAGGTGGCCAGATCACCTAAGGTGGGCCCATCTGG
GGCAGGGAAGAGCACAATTTTGCGCCTGCTGTTTCGCTTCTACGACATCAGCTCTGGCTGCATCCGAATAGATGG
G

1057/6881
FIGURE 986

GCTGCCCCGGTATCCCCGTGTGGGGCAGGAAGTGGGCTTCCAGATTCCCAGTATCCCCGGTAGGGTCTGCTTCTG
CTCGCTCGGGAAGGGCGGTGGCCGTCCCATTACTCAACCAACCCTCAACGCACTGGTCCTCCAGTTCCCTCCCC
TCAGTGGGTAAACAAACACACACCAGCGCTTGACTCGACAGACTCGAAAACAACATCTACTCAGAAAAGTTGTTT
CTTTCTATCTCCTTAAACTTTCCCACTTCCACATATCGGAGCTTCTTCCACCTCGGCCTACTCAAGCATGAGA
TCGGAGGCGGGAGGGCGGCGACTGGCGGCGCGATGGACCTGACCGGGCTCCTGCTGGACGAAGAAGGCACCTTCT
CCCTCGCCGGCTTCCAGGACTTCACGTTCCCTCCCAGGACACCAGAAGCTGAGTGCCCGGATCCGAAGGAGGCTCT
ACTATGGCTGGGACTGGGAAGCCGACTGTAGCCTGGAGGAGCTCTCCAGCCCGGTGGCAGACATTGCTGTGCAAC
TGCTCCAGAAGGCAGCCCCCAGCCCTATTGCGCCGACTCCAGAAGAAATATGTAGCTCATGTGTCCCGGGAGGCAT
GCATCTCCCCATGTGCTATGATGCTGGCTCTGGTGTACATTGAACGGCTCCGGCACCGAAACCCAGACTACTTGC
AGCATGTGTATCCTCTGACTTGTTCCTGATCTCCATGATGGTGGCCAGTAAGTACCTCTATGATGAAGGGGAGG
AGGAGGAGGTCTTCAACGACGAATGGGGAGCTGCTGGGGGTGTGGCCGTGCCACTCTCAATGCCTTGGAGAGGG
GCTTCTGAGTGCCATGGATTGGCATCTCTACACTGACCCTCGGGAGATCTTTGAGGTGCTGAGCTGGTTGGAGA
GCTGTGTGGCTGAGCAGCAGGGACGGTGGCGAGGCTGGTACACCTACACAGACCTGTGTGTGCTGCTGGAGCAGC
CGACCTGGCAGTTGGCCCTGGGCTCCCTCTGCCAGCGGCTGGTAAAGCTGTCTTGCCCTGTTAGCTGTGGCATATG
TGAGCAGTGTGGCCCTGGCTGTGGCATCGGTGGCCGTAATACATCAGTCTTTGGGGCTGTCTGTCATCCCTACAC
CTGGGCCCGCTGACCTTGGACTGACCTCCCGTTGCCTCCTGGAGCCCTGCATACCTTCTGTGCCACAATGCCTGC
CGTCTCTCGCTAATGTCTCCAGCTGCCTGGAAGGCAGCATGGGGCTGCGGTCACTCTGGGGCAGTCTTCTGGCCT
CACTGACTCCTCCACCATTGCCTCCCCAGACCCCCCTGCCCTCCCACTCTTCTTCATAACTGCCACCTTTGCC
AGAAGCTCCAGAGAGACTCCCCAACCTGCCATGCCTGCCTCCACCCCAACCGTACAGTCCCCACTGCGCTGTCCA
GCCCCTGGTACCATACCTATGGCCTGGCTCCCCCTGGCCTTGGAGCCCGGTGCTCCTTTCACTTCCTCAGCCTC
AGCAATGTTCCCTTTTTCAGTGTATGGAGCTGGCTCGCCTCAAGTCTTTCGTTTTCCAGGCTAGGTAGGGCTGT
GAGGAATGCATTAAGAGGGTTTGGGAGTTTCTGAGAACCTGGAGGAGCAAAGCTTGATTAGATCCTGTCTGCCT
CGCTGGGTCTTGGCAGGTCCCCTGTCCTCCTGGGTGGGAGCTTATGGGGTGGTGGGGCAGAAGGACTGAAGGTA
ATTACTCCTAGATCGCAGTGGCTGGCTGCTTGGCCAGGACAGTGATGCCGCCAGGGAGAGCTTCCGCTTGGTGA
CCAGGGACATGTCCCAGATGGACATAGAAGCCCCTCTCTGCCTCCCTGGGATTTTTTAGACTTTTACTTTTGATT
TCCCTAGGATGGAAGAGTATAGGTGGGAGATAAGGGAAGTGGGGTGAGAGGAGAAAGGAAATGTTGGCATGGGCC
TGTGTGATGTCCCTGAGGCAGAAGAGC

1058/6881
FIGURE 987

MDLTGLLLDDEEGTFSLAGFQDFTFLPGHQKLSARIRRRRLYYGWDWEADCSLEELSSPVADIABELLQKAAPSPIR
RLQKKYVAHVSREACISPCAMMLALVYIERLRHRNP DYLOHVSSSDLFLISMMVASKYLYDEGEEEEVFNDEWGA
AGGVAVPTLNALERGFLSAMDWHLYTDPREIFEVL SWLESCVAEQQGRWRGWYTYTDL CVLLEQPTWQLALGSLC
QRLVKLSCLLAVAYVSSVALAVASVAVIHQSLGLSC IPTPGPPDLGLTSRCLLEPCIPSV PQCLPSLANVSSCLE
GSMGLRSLWGSLLASLT PPPLPPPDP PAPTLLHNC HLCQKLQRDSPTCHACLHPNRTVPTALSSPWYHTYGLAP
PWPWSPVLLSLFQPQQCSLFSVMELARLKSFVFP G

1059/6881
FIGURE 988

GAAGATATGGCGGCGTCTGCGTCTGCAGCTGCAGGGGAGGAGGACTGGGTCCTTCCCTCTGAAGTTGAAGTATTG
GAGTCCATCTATCTAGATGAACTACAGGTGATTAAAGGAAATGGCAGAACTTCACCATGGGAGATCTACATCACT
TTGCATCCTGCCACTGCAGAGGACCAGGATTCACAGTATGTCTGCTTCACTCTGGTGCTTCAGGTCCCAGCAGAG
TATCCCCATGAGGTGCCACAGATCTCTATCCGAAATCCCCGAGGACTTTCAGATGAACAGATCCACACGATCTTA
CAGGTGCTGGGCCACGTGGCCAAGGCTGGGCTGGGCACTGCCATGCTGTATGAACTCATTGAGAAAGGGAAGGAA
ATTCTCACAGATAACAACATCCCTCATGGCCAGTGTGTTCATCTGCCTCTATGGTTTTCCAGGAGAAGGAGGCCTTT
ACCAAAACACCCTGTTACCACTACTTCCACTGCCACTGCCTTGCTCGGTACATCCAGCACATGGAGCAAGAGCTG
AAGGCACAAGGACAGGAGCAGGAACAGGAACGGCAGCATGCTACAACCAACAGAAGGCAGTCGGTGTGCAGTGT
CCAGTGTGCAGAGAGCCCCCTCGTGTATGATCTTGCCTCACTGAAAGCAGCCCCTGAACCCCAACAGCCCATGGAG
CTGTACCAGCCCCAGTGCAGAGAGCTTGCGCCAGCAAGAAGAACGCAAGCGGCTCTACCAGAGGCAGCAGGAGCGG
GGGGGAATCATTGACCTTGAGGCTGAGCGAAACCGATACTTCATCAGCCTTCAGCAGCCTCCTGCCCCCTGCGGAA
CCTGAGTCAGCTGTAGATGTCTCCAAAGGATCCCAACCCAGCACCTTGCAGCAGAACTATCCACCTCACCA
GCCGTCCAATCCACTTTGCCACCTCCTCTGCCTGTGGCGACCCAGCACATATGTGAGAAGATTCCAGGGACCAGG
TCAAATCAGCAAAGGTTGGGCGAAACCCAGAAAGCTATGCTAGATCCCCCAAGCCAGTCGAGGTCCCTGGCGA
CAGCCCGAACGGAGGCACCCAAAGGGAGGGGAGTGCCACGCCCCCTAAAGGTACCCGTGACACCCAGGAACCTGCCA
CCTCCTGAGGGGGCCCCCTCAAGGAGCCCATGGACCTAAAGCCAGAACCCCATAGCCAAGGAGTTGAAGGTCCTCCA
CAAGAGAAGGGGCTTGGCAGCTGGCAGGGGCCCCCACCCCGCAGGACTCGGGACTGTGTTGCTGGGAGCGCTCT
AAAGGCCGGACACCCGGTTCTTCTACCTCGCCTGCCTCGGGGCCAGTAGCATACCGGCCTGGTACTCGGAGGG
AGTCCCTGGGCCTGGAATCTAAGGATGGTTCCTAGCAGGACTTGGTGGGGGGAACAGGGAATTGGGGATGGGAGG
GAGGCAATAAAGATATTTGGCCTTC

1060/6881
FIGURE 989

MAASASAAAGEEDWVLPSEVEVLESIYLDDELQVIKNGRTSPWEIYITLHPATAEDQDSQYVCFTLVLPVPAEYP
HEVPQISIRNPRGLSDEQIHTILQVLGHVAKAGLTAMLYELIEKGKEILTDNNIPHGQCVICLYGFQEKEAFTK
TPCYHYFHCCLARYIQHMEQELKAQGQEQEQERQHATTKQKAVGVQCPVCREPLVYDLASLKAAPEFQQPMELY
QPSAESLRQQEERKRLYQRQQERGGIIDLEAERNRYFISLQQPPAPAEPESAVDVSKGSQPPSTLAAELSTSPAV
QSTLPPPLPVATQHICEKIPGTRSNQORLGETQKAMLDFFKPSRGPWRQPERRHPKGGECHAPKGTRDTQELPPP
EGPLKEPMDLKPEPHSQGVEGPPQEKGPGSWQGPPPRRTRDCVRWERSKGRTPGSSYPRLPRGQ

1061/6881
FIGURE 990

GGCACGAGGGCCAGCTGCTGTAGAAGAGGGGAGGAAACAAGCCAGTGCAAGGGGAGCAAAAGAGAAAAGGAGCCA
GGCTGGGCTTCCTGATCCCACAGCATCGCAGAGCTCGGGAGGCACAGCTCACAGACACAGGAAACACAGGACTGC
TATTCTGCTCTCCTGCCCACGGTGATCTGGTGCCAGCTGGTGGAACAGTGGGTG**ATGG**CGTCCCTGCTGCAAGAC
CAGCTGACCACTGATCAGGACTTGCTGCTGATGCAGGAAGGCATGCCGATGCGCAAGGTGAGGTCCAAAAGCTGG
AAGAAGCTAAGATACTTCAGACTTCAGAATGACGGCATGACAGTCTGGCATGCACGGCAGGCCAGGGGCGAGTGCC
AAGCCCAGCTTCTCAATCTCTGATGTGGAGACAATACGTAATGGCCATGATTCCGAGTTGCTGCGTAGCCTGGCA
GAGGAGCTCCCCCTGGAGCAGGGCTTACCATTGTCTTCCATGGCCGCCGCTCCAACCTGGACCTGATGGCCAAC
AGTGTTGAGGAGGCCCAGATATGGATGCGAGGGCTCCAGCTGTTGGTGATCTTGTACCAGCATGGACCATCAG
GAGCGCCTGGACCAATGGCTGAGCGATTGGTTTTCAACGTGGAGACAAAAATCAGGATGGTAAGATGAGTTTCCAA
GAAGTTCAGCGGTTATTGCACCTAATGAATGTGGAAATGGACCAAGAATATGCCTTCAGTCTTTTTTCAGGCAGCA
GACACGTCCCAGTCTGGAACCCCTGGAAGGAGAAGAATTTCGTACAGTTCATAAGGCATTGACTAAACGTGCTGAG
GTGCAGGAAGTGTGAAAGTTTTTCAGCTGATGGGCAGAAGCTGACTCTGCTGGAATTTTTGGATTTCTCCAA
GAGGAGCAGAAGGAGAGAGACTGCACCTCTGAGCTTGCTCTGGAACCTATTGACCGCTATGAACCTTCAGACAGT
GGCAAAGTGCAGCATGTGCTGAGTATGGATGGCTTCCTCAGCTACCTCTGCTCTAAGGATGGAGACATCTTCAAC
CCAGCCTGCCTCCCCATCTATCAGGATATGACTCAACCCCTGAACCACTACTTCATCTGCTCTTCTCATAACACC
TACCTAGTGGGGGACCAGCTTTGCGGCCAGAGCAGCGTCGAGGGATATATACGGGCCCTGAAGCGGGGGTGCCGC
TGCGTGAGGTTGGATGTATGGGATGGACCTAGCGGGGAACCTGTGCTTTACCACGGACACACCCTGACCTCCCGC
ATCCTGTTCAAAGATGTGCTGGCCACAGTAGCACAGTATGCCTTCAGACATCAGACTACCCAGTCATCTTGTC
CTGGAGACCCACTGCAGCTGGGAGCAGCAGACCATGGCCCGTCATCTGACTGAGATCCTGGGGGAGCAGCTG
CTGAGCACCACCTTGATGGGGTGCTGCCCACTCAGCTGCCCTCGCCTGAGGAGCTTCGGAGGAAGATCCTGGTG
AAGGGGAAGAAGTTAACACTTGAGGAAGACCTGGAATATGAGGAAGAGGAAGCAGAACCTGAGTTGGAAGAGTCA
GAATTGGCGCTGGAGTCCAGTTTGAGACTGAGCCTGAGCCCCAGGAGCAGAACCTTCAGAATAAGGACAAAAAG
AAGAAATCCAAGCCCATCTTGTTGCCAGCCCTCTCTTCCCTGGTTATCTACTTGAAGTCTGTCTCATTCCGCAGC
TTCACACATTCAAAGGAGCACTACCCTTCTACGAGATATCATCTTTCTCTGAAACCAAGGCCAAGCGCCTCATC
AAGGAGGCTGGCAATGAGTTTGTGCAGCACAATACTTGCGAGTTAAGCCGTGTGTATCCCAGCGCCTGAGGACA
GACTCTTCCAACCTACAACCCCCAGGAACCTCTGGAATGCAGGCTGCCAGATGGTGGCCATGAATATGCAGACTGCA
GGGCTTGAAATGGACATCTGTGATGGGCATTTCCGCCAGAATGGCGGCTGTGGCTATGTGCTGAAGCCAGACTTC
CTGCGTGATATCCAGAGTTCTTTCCACCCTGAGAAGCCCATCAGCCCTTTCAAAGCCCAGACTCTCTTAATCCAG
GTGATCAGCGGTGAGCAACTCCCCAAAGTGGACAAGACCAAAGAGGGGTCCATTGTGGATCCACTGGTGAAAGTG
CAGATCTTTGGCGTTTCGTCTAGACACAGCACGGCAGGAGACCAACTATGTGGAGAACAATGGTTTTAATCCATAC
TGGGGGCAGACACTATGTTTCCGGGTGCTGGTGCTGAACTTGCCATGCTGCGTTTTGTGGTAATGGATTATGAC
TGGAATCCCGAAATGACTTTATTGGTCAGTACACCCTGCCTTGACCTGCATGCAACAAGGTTACCGCCACATT
CACCTGCTGTCCAAAGATGGCATCAGCCTCCGCCAGCTTCCATCTTTGTGTATATCTGCATCCAGGAAGGCCTG
GAGGGGGATGAGTCT**TGAGGT**GGGCATTTACCGGGAAGGGTTGGTATGCTGGCTTTAGACGGGGAGAAACATCTG
GAAGGATGCTCGAGAGAACAAATGGAGGTGGTGAAATCAAGCTTTGGATTGTGCATTCCTAGGCACAAAATTAC
CTCATTCTTCTTAACAAGCAATCTGGGACCTGATTTTCCACCTTTTTCTCTTTTCTTCCCTTCCTTTGTTTTCA
TAAGCCTTTGGTATCTTTCCCTGCCCTTTTCCCTTTGTGTACTCTATACTGGAGTCCCTTCTTCCCTCTTGCTGTAG
GCTCAATCCCATACCGACATCTACAATAATCTTTCCCATCAACTCTGTGTGAAGGCAGGTTGCAACTAGAAATT
CAGAGGGGCTTGGAATAGAGAAACCTAAAGAAGCATCATCCCTCCATCCCCAACTTCTCAAAGCCCCAAAGCCA
AGGGAAGGATAAATCAAGGCTCAAGGCTTCCCCAGCAAAGATTAGGGAAAGAGACTTGACCCAGGACTGTACTA
CGACTCTTAAGAGAACACTGCACAGCACTCAAAGTCCCCCACTGGACTGCTTCCTCCTTAGCCCCACTGGTATAA
ATACATCTCTCTCAATTTGGCAAAAAAAAAAAAAAAAAAAAA

1062/6881
FIGURE 991

MASLLQDQLTTDQDLLLLMQEGMPMRKVRSKSWKKLRYFRLQNDGMTVWHARQARGSAKPSFSISDVETIRNGHDS
ELLRS�AEELPLEQGFTIVFHGRRSNLDLMANSVEEAQIWMRGLQLLDLVTSMQERLDQWLSDFQRGDKNQ
DGKMSFQEVQRLHLMNVEMDQEYAFSLFQAADTSQSGTLEGEFVQFYKALTKRAEVQELFESFSADGQKLTLL
EFLDFLQEEQKERDCTSELALELIDRYEPSDSGKLRHVLSMDGFLSYLCSKDGDIFNPACLPYQDMTQPLNHVF
ICSSHNTYLVGDQLCGQSSVEGYIRALKRGCRCEVDVWDGPSGEPVVYHGHTLTSRILFKDVVATVAQYAFQTS
DYPVILSLETHCSWEQQQTMARHLTEILGEQLLSTTLDGVLPTQLPSPEELRRKILVKGKKLTLEEDLEYEEEEEA
EPELEESELALESQFETEPEPQEONLQNKDKKKKSKPILCPALSSSLVIYKSVSFRSFTHSKEHYHFYEISSFSE
TKAKRLIKEAGNEFVQHNTWQLSRVYPSGLRTDSSNYNPELWNAQCQMVAMNMQTAGLEMDICDGHFRQNGGCG
YVLKPDFLRDIQSSEFHPEKPISPFKAQTLLIQVISGQQLPKVDKTKEGSIVDPLVKVQIFGVRLDTARQETNYVE
NNGFNPHYWGQTLCFRVLVPELAMLRFFVMDYDWKSRNDFIGQYTLPWTCMQQGYRHHLLSKDGISLRPASIFVY
ICIQEGLEGDES

1063/6881
FIGURE 992

TTCTCCCCCAGGCTCACTCACCATGACCAAGCTGAGCGCCCAAGTCAAAGGCTCTCTCAACATCACCACCCCGGG
GCTGCAGATATGGAGGATCGAGGCCATGCAGATGGTGCCTGTTCTTCCAGCACCTTTGGAAGCTTCTTCGATGG
TGACTGCTACATCATCCTGGCTATCCACAAGACAGCCAGCAGCCTGTCCTATGACATCCACTACTGGATTGGCCA
GGACTCATCCCTGGATGAGCAGGGGGCAGCTGCCATCTACACCACACAGATGGATGACTTCCTGAAGGGCCGGGC
TGTGCAGCACCGCGAGGTCCAGGGCAACGAGAGCGAGGCCTTCCGAGGCTACTTCAAGCAAGGCCTTGTGATCCG
GAAAGGGGGCGTGGCTTCTGGCATGAAGCACGTGGAGACCAACTCCTATGACGTCCAGAGGCTGCTGCATGTCAA
GGGCAAGAGGAACGTGGTAGCTGGAGAGGTAGAGATGTCTTGGAAAGAGTTTCAACCGAGGGGATGTTTTCTCTCT
GGACCTTGGGAAGCTTATCATCCAGTGGAAATGGACCGGAAAAGCACCCGTATGGAGAGACTCAGGGGCATGACTCT
GGCCAAGGAGATCCGAGACCAGGAGCGGGGAGGGCGCACCTATGTAGGCGTGGTGGACGGAGAGAATGAATTGGC
ATCCCCGAAGCTGATGGAGGTGATGAACCACGTGCTGGGCAAGCGCAGGGAGCTGAAGGCGGCCGTGCCCCGACAC
GGTGGTGGAGCCGGCACTCAAGGCTGCACTCAAAGTGTACCATGTGTCTGACTCCGAGGGGAATCTGGTGGTGAAG
GGAAGTCGCCACACGGCCACTGACACAGGACCTGCTCAGTCACGAGGACTGTTACATCCTGGACCAGGGGGGCCT
GAAGATCTACGTGTGGAAAGGGAAGAAAGCCAATGAGCAGGAGAAGAAGGGAGCCATGAGCCATGCGCTGAAGTT
CATCAAAGCCAAGCAGTACCCACCAAGCACACAGGTGGAGGTGCAGAATGATGGGGCTGAGTCGGCCGTCTTTCA
GCAGCTCTTCCAGAAGTGGACAGCGTCCAACCGGACCTCAGGCCTAGGCAAAACCCACACTGTGGGCTCCGTGGC
CAAAGTGGAAACAGGTGAAGTTCGATGCCACATCCATGCATGTCAAGCCTCAGGTGGCTGCCAGCAGAAGATGGT
AGATGATGGGAGTGGGGAAGTGCAGGTGTGGCGCATTGAGAACCTAGAGCTGGTACCTGTGGATTCCAAGTGGCT
AGGCCACTTCTATGGGGGCGACTGCTACCTGCTGCTCTACACCTACCTCATCGGCGAGAAGCAGCATTACCTGCT
CTACGTTTGGCAGGGCAGCCAGGCCAGCCAAGATGAAATTACAGCATCAGCTTATCAAGCCGTCATCCTGGACCA
GAAGTACAATGGTGAACCAGTCCAGATCCGGGTCCCAATGGGCAAGGAGCCACCTCATCTTATGTCCATCTTCAA
GGGACGCATGGTGGTCTACCAGGGAGGCACCTCCCGAACTAACAAGTGGAGACCGGGCCCTCCACACGGCTGTT
CCAGGTCCAGGGAAGTGGCGCCAACAACACCAAGGCCTTTGAGGTCCCAGCGCGGGCCAATTTCTCAATTCCAA
TGATGTCTTTGTCTCAAGACCCAGTCTTGCTGCTATCTATGGTGTGGGAAGGGTTGTAGCGGGACGAGCGGGA
GATGGCCAAGATGGTTGCTGACACCATCTCCCGACGGAGAAGCAAGTGGTGGTGAAGGGCAGGAGCCAGCCAA
CTTCTGGATGGCCCTGGGTGGGAAGGCCCCCTATGCCAACACCAAGAGACTACAGGAAGAAAACCTGGTCATCAC
CCCCCGCTCTTTGAGTGTTCACAAGACTGGGCGCTTCTGGCCACAGAGATCCCTGACTTCAATCAGGATGA
CTTGGAAGAGGATGATGTGTTCTACTAGATGTCTGGGACCAGGTCTTCTTCTGGATTGGGAAACATGCCAACGA
GGAGGAGAAGAAGGCCGAGCAACCACTGCACAGGAATACCTCAAGACCCATCCCAGCGGGCGTGACCCTGAGAC
CCCCATCATTGTGGTGAAGCAGGGACACGAGCCCCCACCTTACAGGCTGGTTCCTGGCTTGGGATCCCTTCAA
GTGGAGTAACACCAAATCCTATGAGGACCTGAAGGCGGAGCTTGGCAACTCTAGGGACTGGAGCCAGATCACTGC
TGAGGTCAAGCCCCAAAGTGGACGTGTTCAATGCTAACAGCAACCTCAGTTCTGGGCCTCTGCCCATCTTCCC
CCTGGAGCAGCTAGTGAACAAGCCTGTAGAGGAGCTCCCGAGGGTGTGGACCCAGCAGGAAGGAGGAACACCT
GTCCATTGAAGATTTCACTCAGGCCTTTGGGATGACTCCAGCTGCCTTCTCTGCTCTGCCTCGATGGAAGCAACA
AAACCTCAAGAAAGAAAAAGGACTATTTTGAGAAGAGTAGCTGTGGTTGTAAAGCAGTACCCTACCCTGATTGTA
GGGTCTCATTTTCTACCGATATTAGTCTACACCAATTGAAGTGAATTTTGCAGATGTGCCTATGAGCACAAA
CTTCTGTGGCAAATGCCAGTTTTGTTTAATAATGTACCTATTCTTCAGAAAGATGATACCCC

1064/6881
FIGURE 993

TGCTCCCTTTTCTGTCTCTGTCCATGCTGCCATGTTTCTCTGCTGCCAAATTGGGCCCTTGGCCCCCTCCGGT
TCTGCTTCCTGGGGGCAGGGTTCCTGCCTTGGACCCCCAGTCTGGGAACGGTGGACATCAAGTGCCTTGCATAGA
GCCCCCTCTTCCCCGCCAGCTTTCCAGGGGCACAGCTCTAGGCTGGGAGGGGAGAACCAGCCCCCTCCCCCTGC
CCCACCTCCTCTCCCCAGGGTCTAACGGTTAAGGGGACCCACATACCAGTGCCAAGGGGGATGTCAAGTGGTGAT
GTCGTTGTGCTCCCCTCCCCAGAGCGGGTGGGCGGGGGGTGAATATGGTTGGCCTGCATCAGGTGGCCTTCCCA
TTTAAGTGCCTTCTCTGTGACTGAGAGCCCTAGTGTGATGAGAACTAAAGAGAAAGCCAGACCCCT

1065/6881
FIGURE 994

ATGGA^{CTCT}GGGAGGCGTTTGGGCCCAGAGAAGTGGATCCGCCGCTTGCGCCGCATGGAGTCCGAATCGGAAAGC
GGGGCTGCTGCTGACACCCCCCACTGGAGACCCTAAGCTTCCATGGTGATGAAGAGATTATCGAGGTGGTAGAA
CTTGATCCCGGTCCGCCGGACCCAGATGACCTGGCCCAGGAGATGGAAGATGTGGACTTTGAGGAAGAAGAGGAG
GAAGAGGGCAACGAAGAGGGCTGGGTTCTAGAACCCCAGGAAGGGGTGGTCGGCAGCATGGAGGGCCCCGACGAT
AGCGAGGTCACCTTTGCATTGCACTCAGCATCTGTGTTTTGTGTGAGCCTGGACCCCAAGACCAATACCTTGGCA
GTGACCGGGGGTGAAGATGACAAAGCCTTCGTATGGCGGCTCAGCGATGGGGAGCTGCTCTTTGAGTGTGCAGGC
CATAAAGACTCTGTGACTTGTGCTGGTTTCAGCCATGACTCCACTCTAGTGGCCACAGGGGACATGAGTGGCCTC
TTGAAAGTGTGGCAGGTGGACACTAAGGAGGAGGTCTGGTCCCTTTGAAGCGGGAGACCTGGAGTGGATGGAGTGG
CATCCTCGGGCACCTGTCCCTGTTGGCGGGCACAGCTGACGGCAACACCTGGATGTGGAAAGTCCCGAATGGTGAC
TGCAAGACCTTCCAGGGTCCCAACTGCCCAGCCACCTGTGGCCGAGTCCCTCCCTGATGGGAAGAGAGCTGTGGTA
GGCTATGAAGATGGGACCATCAGGATTGGGACCTGAAGCAGGGAAAGCCCTATCCATGTACTGAAAGGGGACTGAG
GGTCACCAGGGCCCCACTCACCTGTGTTGCTGCCAACCAGGATGGCAGCTTGATCCTAACTGGCTCTGTGGACTGC
CAGGCCAAGCTGGTCAGTGCCACCACCGGCAAGGTGGTGGGTGTTTTTAGACCTGAGACTGTGGCCTCCCAGCCC
AGCCTGGGAGAAGGGGAGGAGAGTGAGTCCAACCTCGGTGGAGTCCCTGGGCTTCTGCAGTGTGATGCCCTGGCA
GCTGTTGGCTACCTGGATGGGACCTTGGCCATCTATGACCTGGCTACGCAGACTCTTAGGCATCAGTGTGAGCAC
CAGTCGGGCATCGTGCAGCTGCTGTGGGAGGCAGGCACTGCCGTGGTATATACCTGCAGCCTGGATGGCATCGTG
CGCCTCTGGGACGCCCCGACCGGCCGCCCTGCTTACTGACTACCGGGGCCACACGGCTGAGATCCTGGACTTTGCC
CTCAGCAAAGATGCCTCCCTGGTGGTGACCACGTCAGGAGACCACAAAGCGAAAGTATTTTGTGTCCAAAGGCCT
GACCGTTAATGGCTGCAGCCCCTGCTGTGTGTCTGGTGTGGAGGGACGAAGGGACCCCTGCCCTGTCTGCCA
GCAGAGGCAGTAGGGCACAGAGGGAAGAGGAGGGTGGGGCCCTGGATGACTTCCAGCCTCTTCAACTGACTTGC
TCCCCTCTCCTTTTCTTCTTTAGAGACCCAGCCAGGGCCCTCCCACCCTTGCCCAGACCTGGTGGGCCCTTC
AGAGGGAGGGGTGGACCTGTTTCTCTTTCACTTTCACTTTGCTGGTGTGAGCCATGGGGTGTGTATTTGTATGTGG
GGAGTAGGTGTTTGGAGTTCCCGTTCTTTCCCTTCCCAAGTCTCTGGGGGTGGAAAGGAGGAAGAGATACTAGTT
AAAGATTTTAAAAATGTAAATAAAATATACTTCCCAG

1066/6881
FIGURE 995

MDSGRRLGPEKWIRRLRMESESESGAAADTPPLETLSFHGDEEIIIEVVELDPGPPDPDDLAQEMEDVDFEEEE
EEGNEEGWVLEPQEGVVGSMEGPDDSEVTFALHSASVFCVSLDPKTNLAVTGGEDDKAFVWRLSDGELLFECAG
HKDSVTCAGFSHDSTLVATGDMGSLKLVQVDTKEEVWSFEAGDLEWMEWHPRAPVLLAGTADGNTWMWKVPNGD
CKTFQGPNCPCATCGRVLPDGKRAVVGIEDGTIRIWDLKQGSPIHVLKGTTEGHQGPLTCVAANQDGSILITGSVDC
QAKLVSATTGKVVGFRPETVASQPSLGESESESNVESLGFCSVMPLAAVGYLDGTLAIYDLATQTLRHQCQH
QSGIVQLLWEAGTAVVYTCSLDGIVRLWDARTGRLLTDYRGHTAEILDFALSKDASLVVTTSGDHHKAKVFCVQRP
DR

1067/6881
FIGURE 996

GGCACGAGCTCTCCCTCCGTCCTTGCCCTCCCTTACCCACCCCTCACCGGCCCTTGTTTCTCCTTCCCCTGGGGGCA
GCCGCCGCCATGATCCTGCTGGAGGTGAACAACCGCATCATCGAGGAGACGCTCGCGCTCAAGTTGAGAACGCG
GCCGCCGGAAACAAACCGGAAGCAGTAGAAGTAACATTTGCAGATTCGATGGGGTCCTCTATCATATTTCAAAT
CCTAATGGAGACAAAACAAAAGTGATGGTCAGTATTTCTTTGAAATTCTACAAGGAACCTCAGGCACATGGTGCT
GATGAGTTATTAAAGAGGGTGTACGGGAGTTTCTTGGTAAATCCAGAATCAGGATACAATGTCTCTTTGCTATAT
GACCTTGAAAATCTTCCGGCATCCAAGGATTCCATTGTGCATCAAGCTGGCATGTTGAAGCGAAATTGTTTTGCC
TCTGTCTTTGAAAAATACTTCCAATTCCAAGAAGAGGGCAAGGAAGGAGAGAACAGGGCAGTTATCCATTATAGG
GATGATGAGACCATGTATGTTGAGTCTAAAAAGGACAGAGTCACAGTAGTCTTCAGCACAGTGTTTAAGGATGAC
GACGATGTGGTCATTGGAAAGGTGTTTCATGCAGGAGTTCAAAGAAGGACGCAGAGCCAGCCACACAGCCCCACAG
GTCCTCTTTAGCCACAGGGAACCTCCTCTGGAGCTGAAAGACACAGACGCCGCTGTGGGTGACAACATTGGCTAC
ATTACCTTTGTGCTGTTCCCTCGTCACACCAATGCCAGTGCTCGAGACAACACCATCAACCTGATCCACACGTTT
CGGGACTACCTGCACTACCACATCAAGTGCTCTAAGGCCTATATTCACACACGTATGCGGGCGAAAACGTCTGAC
TTCCTCAAGGTGCTGAACCGCGCACGCCAGATGCCGAGAAAAAAGAAATGAAAACAATCACGGGGAAGACGTTT
TCATCCCGCTTAATCTTGGAATAAGAGGAGGAAGCGGCTGGCAACTGAAGGCTGGAACACTTGCTACTGGATAAT
CGTAGCTTTTAAATGTTGCGCCTCTTCAGGTTCTTAAGGGATTCTCCGTTTTGGTTCCATTTTGTACACGTTTGGA
AAATAATCTGCAGAAACGAGCTGTGCTTGCAAAGACTTCATAGTTCCAAGAATTAAAAAAAAAAAAAAAAAAAA

1068/6881
FIGURE 997

MILLEVNNRIIEETLALKFENAAAGNKPEAVEVTFADFDGVLYHISNPNGDKTKVMVSI SLKFYKELQAHGADEL
LKRVGSGFLVNPESGYNVSLLYDLENLPASKDSIVHQAGMLKRNCFASVFEKYFQFQEEGKEGENRAVIHYRDDE
TMYVESKKDRVTTVFSTVFKDDDDVVIGKVFMQEFKEGRRASHTAPQVLFSHREPPLELKDTDAAVGDNIGYITF
VLFP RHTNASARDNTINLIHTFRDYLHYHIKCSKAYIHTRMRAKTSDFLKVLNRARPD AEKKEMKTI TGKTFSSR

1069/6881
FIGURE 998

GCGGCGGCGAGAGGATGAACAACAAGTTCGACGCTTTGAAAGATGATGACAGTGGGGACCATGATCAGAAATGAAG
AAAACAGCACACAGAAAGATGGTGAGAAGGAAAAAACGGAACGAGACAAGAATCAGAGCAGTAGCAAGAGAAAGG
CTGTTGTCCCTGGACCGGCAGAGCATCCCCTGCAGTACAACTACACTTTTTGGTACTCCAGGAGAACCCCCGGCC
GTCCACGAGCTCACAGAGCTATGAACAGAATATCAAACAGATTGGCACCTTTGCCTCTGTGGAGCAGTTCTGGA
GGTTTTATAGCCACATGGTACGTCCTGGGGACCTGACAGGCCACAGTGACTTCCATCTCTTCAAAGAAGGAATTA
AACCCATGTGGGAGGATGATGCAAATAAAAAATGGTGGCAAGTGGATTATTCGGCTGCGGAAGGGCTTGGCCTCCC
GTTGCTGGGAGAATCTCATTTTGGCCATGCTGGGGGAACAGTTCATGGTTGGGGAGGAGATCTGTGGGGCTGTGG
TGTCTGTCCGCTTTCAGGAAGACATTATTTCAATATGGAATAAGACTGCCAGTGACCAAGCAACCACAGCCCGAA
TCCGGGACACACTTCGGGCGAGTGCTTAACCTACCTCCCAACACCATTATGGAATACAAAACCTCACACCGACAGCA
TCAAATGCCAGGCAGGCTGGGCCCCCAAAGGCTCCTTTTTCAAACCTCTGGAAGCCGCGGTTGAATGTGCCAT
GACCCTCTCCCTCTCTGGATGGCACCATCATTGAAGCTGGCGTCATCGGAGTCTGTTGTTCTGTTGGCGTGCTAC
CTGGAAGATCCTTCTGTGGTGGACAAGAGGAATTGGAAGAGCATTTTATGTTTTAAGAACAGGCTGACACGCAGC
AGCTACAACAACAGCTGAGATCACTTAATAAATGGTGCTAAACTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

1070/6881
FIGURE 999

MNNKFDALKDDDSGDHDQNEENSTQKDGEKEKTERDKNQSSSKRKAVVPGPAEHPLQYNYTFWYSR RTPGRPTSS
QSYEQNIKQIGTFASVEQFWRFYSHMVRPGDLTGHSDFHLFKEGIKPMWEDDANKNGGKWIIRLRKGLASRCWEN
LILAMLGEQFMVGEEICGAVVSVRFQEDIISIWNKTASDQATTARIRDTLRRVLNLP PNTIMEYKTH TDSIKMPG
RLG PQRLLFQNLWK PRLNVP

1071/6881
FIGURE 1000

GGCACGAGGAGAGCCTCGAGCCTGCGAGGAGCGCGCCGCCAGCTCCCTGCGTCCCGTCCCGCGTCCCGCG
TTCCCGCGTCTTGCATCCGCCGCC**ATG**GCCAGTGAGGAGCTGGCGTGCAAGCTGGAGCGCCGGCTGCGGCGCGA
GGAGGCCGAGGAGAGTGGCCCCAGCTGGCTCCCCTCGGCGCCCCAGCCCCGAGCCCAAGCCCGAGCCCGAGCC
TCCCGCCCGTGCGCCACGGCCAGCGCCGACGCGGAGCTGAGCGCCCAGCTGAGCCGGCGGGCTGGACATCAACGA
GGGCGCTGCGCGGCCCGGCGCTGCAGGGTCTTCAACCCCTACACGGAGTTCCCGGAGTTCAGCCGCCGCTCAT
CAAGGACCTGGAGAGCATGTTCAAACCTGTATGACGCTGGGCGGGATGGCTTCATCGACCTGATGGAGCTGAAGCT
GATGATGGAGAAGCTGGGGGCCCCCAGACCCACCTGGGCCTGAAGAGCATGATCAAGGAGGTGGATGAGGACTT
CGATGGCAAGCTCAGCTTCCGGGAGTTCTGCTCATTTCACAAAGGCCGCGGCAGGGGAGCTGCAGGAGGACAG
TGGGCTGATGGCGCTGGCAAAGCTTTCTGAGATCGATGTGGCCCTGGAGGGTGTCAAAGGTGCCAAGAACTTCTT
TGAAGCCAAGGTCCAAGCCTTGTATCGGCCAGTAAGTTTGAAGCAGAGTTGAAAGCTGAGCAAGATGAGCGGAA
GCGGGAGGAGGAGGAGAGGCGGCTCCGCCAGGCAGCCTTCCAGAACTCAAGGCCAACTTCAATACAT**TAG**TCTTG
CTGACCTTGCCCTCTGCCACAGCTGTGCCTCACAGATGCCCGGAGAAGAGATGACTAGGCATCTTCATCACTGC
TGTCGGTCCCTCCCTGAGCCAGCATCTCCATCCACCACCCGTCGCCAGCTCCCGTGCCAGCCTTCATTCTCC
AGTGTCCAAGCCCTCCAGGAGGGTCTGGGGTGGGCCAGATGCCTGCCACCTCTGTCTCCTGCTCTGTCTCT
CTGCCCTTCTTATAGCCAGAACTTGTATCTTCTCAGCAACCTTCACCTTGTCTCTGTCCCTTTACCATTCCCAT
CAAAGAGTAGTCTGCTATATCAATTTGTGTAGATATGTCTGTCTTTTTGGGTCTCAGAGAAAATGCCATTTTC
TCGGAGAAATCTCTGCACTCCTCTCTGCTTCACATTCAACTTCCCTGTTCTCATCTTTGGTAGGATTCTGCCAGT
TGCTTTTGCATCTTCTGTTCTGTTAATGGTGGGTCTTAATGGAGGCTGGGTGGACCACTGCCCGTCCACTCTT
CAACAGGAGGAACAGCATGCCACCACAGTAACACACATTAGAGAAAGGACAGAGGTCTGCTCCTTCTGCCACCT
TTCTCCTGGCCCCCTTAGCATTCCCCCAGTCCCTCCCTCTTACCTTGCTCCGTCTATGTCTTCCAGCTCAGCCT
TTTCCCCACTCTTAAATACTGTACTACTTCACTGTAAGAACGAAAGAATAGTTAGGATACCAATGAGTAAAGGG
TTCTGTTCACCTCTGACTCTGTGCAAATTGTATTACAGTAGACCGCTGACGTTCCCAAGTGACAGATCCAGGGCC
TTTCAAACATCCCCAAAGTCATGGCCATACTCACCATTAGCCAGTTTCTAACATCTGTTTCAGGGTATCCAGCTG
TAGATGTTCTTATCCCCATACTTGTGAGTTATTGGGGTTGCTCACAAATACTAGGGGTTTTTGTGTATTTTAA
ACAAATATATCCTAATGTCATATTTATTCTCTTTTGTAAGTGTGTCTTTACAATAAAGAAATCATCTGCCTTTC
TAAAAAAAAAAAAAAAAAAAAA

1072/6881
FIGURE 1001

MASEELACKLERRLRREEAEESGPQLAPLGAPAPEPKPEPEPPARAPTASADAELSAQLSRRLDINEGAARPRRC
RVFNPYTEFPFESRRLIKDLESMFKLYDAGRDFIDLMELKLMMEKLGAPQTHLGLKSMIKEVDEDFDGKLSFRE
FLLIFHAAAAGELQEDSGLMALAKLSEIDVALEGVKGAKNFFEAKVQALSSASKFEAELKAEQDERKREEEERRL
RQAAFQKLKANFNT

1073/6881
FIGURE 1002

ATGGTCCCCTGCTGGAACCATGGCAACATCACCCGCTCCAAGGCGGAGGAGCTGCTTTCCAGGACAGGCAAGGAC
GGGAGCTTCCTCGTGCGTGCCAGCGAGTCCATCTCCCGGGCATAACGCGCTCTGCGTGCTGTATCGGAATTGCGTT
TACACTTACAGAATTCTGCCCAATGAAGATGATAAATTCAGTGTTCAGAAATCTGAACCTGACTTCAGCCGATAC
TGGCAGAGAAAAGGGTGTAACGATGAGGAAGGAAGTGCACGCGCAGGATGCAGTAGTAGACAGGGAGCTGGACTC
AAGGTGTGGGGAGACCACAGGCAAGTCCCTGGAGGCAAAAATCCTCCAGAAGTTGTCAAGAGGGAGAGCGTGGTG
AGCAGAACGCCCCCTCAGGAAGACAGCTTATGAGGATGGAAGGAATTGCTTCGAGGAGCGATGTGATTGA

1074/6881
FIGURE 1003

MVPCWNHGNI TRSKAEELLSRTGKDG SFLVRASESISRAYALCVLYRNCVYTYRILPNEDDKFTVQKSEPDFSRY
WQRKGVNDEEGSARAGCSSRQGAGLKVWGDHRQVPGGKNPPEVVKRESVVSRTPLRKTAYEDGRNCFEERCD

1075/6881
FIGURE 1004

CTTCGGGTGTACGTGCTCCGGGATCTTCAGCACCCGCGGCCCATCGCCGTCGCTTGGCTTCTTCTGGACTCAT
CTGCGCCACTTGTCCGCTTCACACTCCGCGGCCATCATGGTGAAAGCTCGCGAAGGCAGGTAAAAATCAAGGTGAC
CCCAAGAAAATGGCTCCTCCTCCAAAGGAGGTAGAAGAAGATAGTGAAGATGAGGAAATGTCAGAAAGATGAAGAA
GATGATAGCAGTGGAGAAGAGGTCTGTCATACCTCAGAAGAAAGGCAAGAAGGCTGCTGCAACCTCAGCAAAGAAG
GTGGTCGTTTCCCCAACAAAAAGGTTGCAGTTGCCACACCAGCCAAAGCAGTTACCACACCTGGCAAGAAGGGAGCCACA
GCAGCAGCAACACCTGCCAAGAAGACAGTTACACCAGCCAAAGCAGTTACCACACCTGGCAAGAAGGGAGCCACA
CCAGGCAAAGCATTGGTAGCAACTCCTGGTAAGAAGGGTGTGCCATCCCAGCCAAGGGGGCAAAGAATGGCAAG
AATGCCAAGAAGGAAGACAGTGATGAAGAGGAGGATGATGACAGTGAGGAGGATGAGGAGGATGACGAGGACGAG
GATGAGGATGAAGATGAAATTGAACCAGCAGCGATGAAAGCAGCAGCTGCTGCCCCCTGCCTCAGAGGATGAGGAC
GATGAGGATGACGAAGATGATGAGGATGACGATGACGATGAGGAAGATGACTCTGAAGAAGAAGCTATGGAGACT
ACACCAGCCAAAGGAAAGAAAGCTGCAAAAGTTGTTCCCTGTGAAAGCCAAGAACGTGGCTGAGGATGAAGATGAA
GAAGAGGATGATGAGGACGAGGATGACGACGACGACGAAGATGATGAAGATGATGATGATGAAGATGATGAGGAG
GAGGAAGAAGAGGAGGAGGAAGAGCCTGTCAAAGAAGCACCTGGAAAACGAAAGAAGGAAATGGCCAAACAGAAA
GCAGCTCCTGAAGCCAAGAAACAGAAAGTGAAGGCACAGAACCAGCTACGGCTTTCAATCTCTTTGTTGGAAC
CTAAACTTTAACAAATCTGCTCCTGAATTAATAAACTGGTATCAGCGATGTTTTTGTCTAAAAATGATCTTGCTGTT
GTGGATGTCAGAATTGGTATGACTAGGAAATTTGGTTATGTGGATTTTGAATCTGCTGAAGACCTGGAGAAAGCG
TTGGAACCTCACTGGTTTGAAAGTCTTTGGCAATGAAATTAACTAGAGAAACCAAAGGAAAAGACAGTAAGAAA
GAGCGAGATGCGAGAACACTTTTGGCTAAAAATCTCCCTTACAAAGTCACTCAGGATGAATTGAAAGAAGTGTTT
GAAGATGCTGCGGAGATCAGATTAGTCAGCAAGGATGGGAAAAGTAAAGGGATTGCTTATATTGAATTTAAGACA
GAAGCTGATGCAGAGAAAACCTTTGAAGAAAAGCAGGGAACAGAGATCGATGGGCGATCTATTTCCCTGTACTAT
ACTGGAGAGAAAAGGTCAAAATCAAGACTATAGAGGTGGAAAAGATAGCACTTGGAGTGGTGAATCAAAAACTCTG
GTTTTAAGCAACCTCTCCTACAGTGCAACAGAAGAACTCTTCAGGAAGTATTTGAGAAAGCAACTTTTATCAAA
GTACCCCAAGAACCAAAATGGCAAATCTAAAGGGTATGCATTTATAGAGTTTGCTTCATTGCAAGACGCTAAAGAA
GCTTTAAATTCCTGTAATAAAAAGGGAAATTGAGGGCAGAGCAATCAGGCTGGAGTTGCAAGGACCCAGGGGATCA
CCTAATGCCAGAAGCCAGCCATCCAAAACCTCTGTTTGTCAAAGGCCGTCTGAGGATACCACTGAAGAGACATTA
AAGGAGTCATTTGACGGCTCCGTTCCGGCAAGGATAGTTACTGACCGGGAAACTGGGTCTCCAAAGGGTTTGGT
TTTGTAGACTTCAACAGTGAGGAGGATGCCAAAGCTGCCAAGGAGGCCATGGAAGACGGTGAAATTGATGGAAAT
AAAGTTACCTTGGACTGGGCCAAACCTAAGGGTGAAGGTGGCTTCGGGGGTCGTGGTGGAGGCAGAGGCGGCTTT
GGAGGACGAGGTGGTGGTAGAGGAGGCCGAGGAGGATTTGGTGGCAGAGGCCGGGGAGGCTTTGGAGGGCGAGGA
GGCTTCCGAGGAGGCAGAGGAGGAGGAGGTGACCACAAGCCACAAGGAAAGAAGACGAAGTTTGAATTAGCTTCTG
TCCCTCTGCTTTCCCTTTTCCATTTGAAAGAAAGGACTCTGGGGTTTTTACTGTTACCTGATCAATGACAGAGCC
TTCTGAGGACATTCCAAGACAGTATACAGTCCTGTGGTCTCCTTGGAATCCGTCTAGTTAACATTTCAAGGGCA
ATACCGTGTTGGTTTTGACTGGATATTCATATAAACTTTTTAAAGAGTTGAGTGATAGAGCTAACCCCTATCTGT
AAGTTTTGAATTTATATTGTTTCATCCCATGTACAAAACCATTTTTTCCTAC

1076/6881
FIGURE 1005

MVKLAKAGKNQGDPPKKMAPPPKEVEEDSEDEEMSEDEEDDSSGEEVVIPQKKGKKAATSAAKVVVSPTKKVAVA
TPAKKAAVTPGKKAAATPAKKTVTPAKAVTTPGKKGATPGKALVATPGKKGAAIPAKGAKNGKNAKKEDSDEEDD
DDSEDEDEDDDEDEDEDEDEIEPAAMKAAAAAPASEDEDDDEDDDEDDDDDDDEEDDSEEEAMETTPAKGKKAACVV
PVKAKNVAEDEDEEEDDEDEDDDDDDEDDDDDEDEEEEEEEEEEEEPVKEAPGKRKKEMAKQKAAPKAKQKVEG
TEPTTAFNLFVGNLNFNKSAPELKTGISDVFAKNDLAVVDVRIGMTRKFGYVDFESAEDLEKALELTGLKVFGNE
IKLEKPKGKDSKKERDARTLLAKNLPHYVTQDELKEVFEDAAEIRLVSKDGKSKGIAYIEFKTEADA EKTFEEKQ
GTEIDGRSISLYYTGEKGQNQDYRGKNSTWSGESKTLVLNLSYSATEETLQEVFEKATFIKVPQNQNGKSKGY
AFIEFASFEDAKEALNSCNKREIEGRAIRLELQGPRGSPNARSQPSKTLFVKGLSED TTEETLKESFDGSVRARI
VTDRETGSSKGFVFDFNSEEDAKAAKEAMEDGEIDGNKVTLDWAKPKGEGGFGGRGGGRGGFGGRGGGRGGRG
FGGRGRGGFGGRGGFRGGRGGGGDHKPKQKKTKFE

1077/6881
FIGURE 1006

TGAACTGAGCGGCCCTGAGCTGACAGATACACTGCGCAGCTGGAACGGCGAGCGAGCCGACGGGCGAGTGAGGG
GCGCAGCCATGATCACCTCGGCCGCTGGAATTATTTCTCTTCTGGATGAAGATGAACCACAGCTTAAGGAATTTG
CACTACACAAATTGAATGCAGTTGTTAATGACTTCTGGGCAGAAATTTCCGAGTCCGTAGACAAAATAGAGGTTT
TATACGAAGATGAAGGTTTCCGGAGTCGGCAGTTTGCAGCCTTAGTGGCATCTAAAGTATTTTATCACCTGGGGG
CTTTTGAGGAGTCTCTGAATTATGCTCTTGGAGCAGGGGACCTCTTCAATGTCAATGATAACTCTGAATATGTGG
AACTATTATAGCAAAATGCATTGATCACTACACCAAAACAATGTGTGGAATGCAGATTTGCCTGAAGGAGAAA
AAAAACCAATTGACCAGAGATTGGAAGGCATCGTAAATAAAATGTTCCAGCGATGTCTAGATGATCACAAGTATA
AACAGGCTATTGGCATTGCTCTGGAGACACGAAGACTGGACGCTTTGAAAAGACCATACTGGAGTCGAATGATG
TCCCAGGAATGTTAGCTTATAGCCTTAAGCTCTGCATGTCTTTAATGCAGAATAAACAGTTTTCGGAATAAAGTAC
TAAGAGTTCTAGTTAAAACTACATGAACTTGGAGAAACCTGATTTTCATCAATGTTTGTGAGTGCTTAATTTTCT
TAGATGATCCTCAGGCTGTGAGTGATATCTTAGAGAAACTGGTAAAGGAAGACAACCTCCTGATGGCATATCAGA
TTTGTGTTTGATTTGTATGAAAGTGCTAGCCAGCAGTTTTTGTGATCTGTAATCCAGAATCTTCGAAGTGTGGCA
CCCCTATTGCTTCTGTGCTGGATCCACTAATACGGGTACTGTTCCGGGATCAGAGAAAGACAGTGACTCGATGG
AAACAGAAGAAAAGACAAGCAGTGCATTTGTAGGAAAGACACCAGAAGCCAGTCCAGAGCCTAAGGACCAGACTT
TGAAATGATTAAAAATTTAAGTGGTGAAATGGCTATTGAGTTACATCTGCAGTTCTTAATACGAAACAATAATA
CAGACCTCATGATTCTAAAAAACACAAAGGATGCAGTACGGAATTTCTGTATGTCATACTGCAACCGTTATAGCAA
ACTCTTTTATGCACTGTGGGACAACCAGTGACCAAGTTTCTTAGAGATAATTTGGAATGGTTAGCCAGAGCCACTA
ACTGGGCAAAATTTACTGCTACAGCCAGTTTGGGTGTAATTCATAAGGGTCATGAAAAAGAAGCATTACAGTTAA
TGGCAACATACCTTCCCAAGGATACTTCTCCAGGATCAGCCTATCAGGAAGGTGGAGGTCTCTATGCACTAGGTC
TTATTTCATGCCAATCATGGTGGTGATATAATTGACTATCTGCTTAATCAGCTTAAGAACGCCAGCAATGATATCG
TTAGACACGGTGGCAGTCTGGGCCTTGGTTTGGCAGCCATGGGAACTGCACGTCAAGATGTTTATGATTTGCTAA
AAACAAACCTTTATCAGGATGATGCAGTAACAGGGGAAGCAGCTGGCCTGGCCCTAGGTTTGGTTATGTTGGGCT
CTAAAAATGCTCAGGCTATTGAGGACATGGTTGGTTATGCACAAGAACTCAACATGAGAAGATTCTGCGTGGTC
TTGCAGTTGGCATAGCTTTAGTAATGTAIGGGAGGATGGAAGAGGCTGATGCTCTCATTGAATCTCTCTGTGCTG
ACAAGGACCCAATTCTTCGAAGGTCTGGAATGTATACTGTAGCCATGGCTTATTGTGGCTCTGGTAACAACAAAG
CAATTCGACGCCTGCTACATGTTGCTGTAAGTGATGTTAATGATGATGTCAGGAGGGCAGCAGTAGAATCACTTG
GGTTCATTCTATTTCAGAACCCCTGAACAGTGCCCAAGTGTGTCTCTTTGTTGTGTCAGAGAGTTACAACCCCTCATG
TGCGCTACGGAGCTGCAATGGCCTTGGGGATATGCTGTGCTGGTACAGGAAAACAAGGAAGCCATTAATTTGCTAG
AACCAATGACAAACGACCCCGTGAACACTACGTGAGGCAAGGGGCACTCATAGCTTCAGCTCTCATCATGATCCAGC
AGACTGAAATCACTTGTCCAAAGGTGAATCAGTTTCAGACAGCTGTATTCCAAAGTCATCAATGATAAGCATGATG
ATGTCATGGCCAAGTTTGGCGCTATTCTGGCCCAGGGCATACTGGATGCAGGTGGTCATAATGTCACAATCTCCT
TGCAGTCCAGGACTGGGCATACTCATATGCCTTCTGTGGTTGGCGTCCTTGTAATTTACCCAGTTTTGGTTCTGGT
TTCTCTTTTACACTTCTGTGTCATTGGCTTATACCCCTACCTGTGTGTCATTGGCCTTAACAAGGACTTAAAGATGC
CGAAAGTTTCAGTATAAATCGAACTGTAAACCATCCACATTTGCATATCCTGCCCTCTGGAAGTACCAAAAGAAA
AAGAAAAGGAAAAGGTTTTCTACTGCTGTATTATCTATAACTGCCAAGGCTAAAAAGAAGGAAAAAGAAAAGGAAA
AAAAAGGAGGAGGAGAAAATGGAAGTGGATGAGGCAGAGAAAAAGGAGGAAAAAGAGAAGAAAAAGAACCTGAGC
CAAACCTCCAGTTATTGGATAACCCAGCCCGAGTTATGCCTGCCAGCTTAAGGTCCTAACCATGCCGGAGACCT
GTAGATACCAGCCTTTCAAACCACTCTCTATTGGAGGCATCATCTTCTGAAGGATACCAGTGAAGACATTGAGG
AGCTGGTGGAAACCTGTGGCAGCACATGGCCCAAAATCGAGGAGGAGGAACAAGAGCCAGAACCCCGAGAACCAT
TTGAGTATATTGATGATTAAAGGGCCAGAGGATCTCACTTGCTTATCTGAAGAAGATTGTCCAGGCTCATATTGGG
AATGCTTATGAGGAAATTCATGCCGAGACCTGCTATTCAATGCATGTATCGTTGCCTCTGCACTGACCTGAAGAA
CCCTGTCTCCAAGTCTTTGGTTGAAGAGAAGATATATGACTGTTGAGTGTGCTCTTTACAGAACTTGGTTTTCA
AATAAATATAAGATCTCCAGATGGACAAG

1078/6881
FIGURE 1007

CTGCAAGCCGCGGAGCCGGGCAACCAGTGGAAAGGAGCCTGGGAGAGGCCAGGCCTCCCCGGACTGCTAGCCTGC
TTTTCTGGGGTCCCTGGAGCCGGAGGAAGAACCAGGATGTTGCTGCCTGCAGAAGCTCAGCTCAGGAAGACTTC
CAGGAACCTGAGGAGGAGCTGCCACTAACAGCCATATTTCCCAATGGAGACTGTGATGACCTTGGAAGGGGGTCA
AAAGCCTGTGATGGAGTCGTACACACTCCTGCTGAGCCCCACCGGAGACTCAAGATGAAGGCTGGACCCCTTGCCT
GTCCCTGGCTCTAACCTACAGACTGGGGCCTGGCTCCGTCTTACTGGCCCCCAGGTCTCCATGGAGACTGCAGAA
ACCCCCGCCTGCTGGAGGCCTGCCACACTCACAGTTACCAGCTAGACAGTGGGGCTTACTAAGACAAGCAGGACC
TAAAACAGTGTCTCCCCCTGGGAACCTACTCCCCACCCAGCATTTGCTAAGTCTGATCACAGGGAGGTTATTTTGT
CTCTCTGTCTCGGTTTTCTCTGAGCCACTGAGACAGATGGCTGTCCGCTTTGAGGCTCTGCAGAGCTGTGGCAGCC
CATGGTGTGTCTGCAGTGTCTGAGGCACATGCATGGGCACCCATCGTTGAGAGTGCAGCTGGGAAGAACTCTGAA
CCAGAAGTCATCAGAGCTGAGGCATGGCCTTGAACATGTCACTCAGTCTCTGGGGCTTCTGTTTTCAAAATGCAT
GAGGGGGCCACCAGCCCAGTGGCTTTAAACCAGGGGCAGGTTGTCCCTCCAGGCAGCATTGGAAATGTGTGTGTG
TTGAGGGGGTCAAGTGAAGTGTGGGGGCACCCCTGGCATCTAGTGGGCATCCCACAATGTGCAGAACAGTCTCTG
ACAGCAAAGAATTGGTCCATTCAATGCCAATTGTAGTACCTTTGAGACATTCTGGCTGAGCCAATGCCTTCTCCC
TGTCAGAGTCCCCCAGAGCAGAGAGGGTTCAGGCTTCCCTGGACCTTGGCTCCCAGAGCAAGCCAAAATAAAGACT
ACACTGTTGCCTTGGGGGCTTGTGCGGCCAGGGCCAAGACGGTCTGCGTGCTGCAGGGCCAGGACAGAAATAGCC
ACACATGCCGGTGAGAACAAAGAGCCTCTTTCTTTCTCATGTTGACATCGACTTTCTGTGCCAAGTCCTTTGGGT
ATAAGGATGCTAGGGAATTCCCTATAGGCACCAAACAGAAGGAAAGCTAGGGGCTTGGACTACTGGGTATAGGACT
TGCTCTAGCTCTCAGGTCCTAGCCCAAGCTCAATGCAAACACAGCCCCTCCGGGCTCTCTGTTTTCTGTGAGGTTT
TGGAATCCCTTCCCTCTGTGTCCGTGAGTCTGACAGAATCGATGATGTTCCCTTAGAGCTGGGAAATCCATGTGTT
TATTCACGGAGGGAACTACCAATTACCTCCCTTGTCTTCTTTGCCTGCCTTGGAGAAATCCAGAGTCTTCGGAAT
GGCAAAGGCAGCTCCTGGATTTCCCTGGAGGGGAGGCACTAGCTGAGGGAAGTAGCTCCCTTCATTCATGATGCA
CAGTTTACGCAGCAGACACACAAGTGCCTACTATTTGCTCGGTGCCCTGCAAGGTGCTGCCTAACTTTGATTT
GTTATTTTACGCTCTCTCCAGGATAGTGCCAAATGGTGCAATGGGAAACCTGTTTTGCTGGGGGGCTCTAGATCAC
TGGCTCCAGAACTCCCGGCTGCCAGGGTAGCCCCCTACCCCCAGCCCCTTGTCTCTGGACAGCAGTGGGTCTCACC
TTTAGCCTCTGCCCCCAGTTCTGGTCTGACCCAACAGAGGGGCTCTATGATATTAAGAAGGGGCCCTTCCTGCTC
TGTGCCTCAACCTATTCTCCATAATAGGGAGTCTAATCCTATTCCCTTCCCTGCCTGATGAGGATGGTGTGAGGAT
GAGGAGGACGGCATCTCATTTGGGGCTTTTTTGGCAGTGGGCCTCATTTTAATCCTGCAGGGCTGCCTGCCAGTGG
ATCTATCCAGCTGCTTCCCTTGTAGCCAAGAATGAGTTCAATGAATTGTGATTCACTGATTTTATTGATTTTGT
TAAAACAGGGAGACTGGTATTTTTGAAGCTGCTATCATTTTCTATTTCTTTATTAATTTCTTTGTAATCATCTTA
TTAAAGTTTTCTTATTTAGTGGG

1079/6881
FIGURE 1008

METVMTLEGGQKPVME SYTLLLSP PETQDEGWTIALSLALTYRLGPGSVLLAPRSPWRLQKPPPAGGLPHSQLPA
RQWGLLRQAGPKTVSPLGTYSPPSIC

1080/6881
FIGURE 1009

GGGACGCGAGCGGGATCCAACTTCCGGTGCCTGCAGAGCTCGGAGCGGCGGAGGCAGAGACCGAGGCTGCACCG
GCAGAGGCTGCGGGGCGGACGCGCGGGCCGGCGCAGCCATGGTGAAAGATTAGCTTCCAGCCCCGCGTGGCTGGCA
TCAAGGGCGACAAGGCTGACAAGGCGTCGGCGTCGGCCCTGCGCCGGCCTCGGCCACCGAGATCCTGCTGACGC
CGGCTAGGGAGGAGCAGCCCCCACAAATCGATCCAAGAGGGGGGGCTCAGTGGGCGGCGTGTGCTACCTGTCTGA
TGGGCATGGTTCGTGCTGCTCATGGGCTCGTGTTCGCCTCTGTCTACATCTACAGATACTTCTTCCTTGCGCAGC
TGGCCCGAGATAACTTCTTCCGCTGTGGTGTGCTGTATGAGGACTCCCTGTCCTCCCAGGTCCGGACTCAGATGG
AGCTGGAAGAGGATGTGAAAATCTACCTCGACGAGAACTACGAGCGCATCAACGTGCCTGTGCCCCAGTTTGGCG
GCGGTGACCTTGCAGACATCATCCATGACTTCCAGCGGGGTCTGACTGCGTACCATGATATCTCCCTGGACAAGT
GCTATGTCTATCGAACTCAACACCACCATTGTGCTGCCCCCTCGCAACTTCTGGGAGCTCCTCATGAACGTGAAGA
GGGGGACCTACCTGCCGCAGACGTACATCATCCAGGAGGAGATGGTGGTACGGAGCATGTGAGTGACAAGGAGG
CCCTGGGGTTCCTTACCTACCACTGTGCAACGGGAAAGACACCTACCGGCTCCGGCGCCGGGCAACGCGGAGGC
GGATCAACAAGCGTGGGGCCAAGAACTGCAATGCCATCCGCCACTTTCGAGAACACCTTCGTGGTGGAGACGCTCA
TCTGCGGGGTGGTGTTGAGGGCCCTCCTCCCCCAGAACCCCTGCCGTGTTCTCTTTTCTTCTTCCGGCTGCTCT
CTGGCCCTCCTTCCTTCCCCCTGCTTAGCTTGTACTTTGGACGCGTTTCTATAGAGGTGACATGTCTCTCCATTCC
TCTCCAACCCTGCCCACCTCCCTGTACCAGAGCTGTGATCTCTCGGTGGGGGGCCCATCTCTGCTGACCTGGGTG
TGGCGGAGGGAGAGGCGATGCTGCAAAGTGTTTTCTGTGTCCCACTGTCTTGAAGCTGGGCCTGCCAAAGCCTGG
GCCCCAGCTGCACCGGCAGCCCAAGGGGAAGGACCGGTTGGGGGAGCCGGGCATGTGAGGCCCTGGGCAAGGGG
ATGGGGCTGTGGGGGCGGGGCGGCATGGGCTTCAGAAGTATCTGCACAATTAGAAAAGTCCTCAGAAGCTTTTTTC
TTGGAGGGTACACTTTTCTTCACTGTCCCTATTCTTAGACCTGGGGCTTGAGCTGAGGATGGGACGATGTGCCCAG
GGAGGGACCCACCAGAGCACAAAGAGAAGGTGGCTACCTGGGGGTGTCCCAGGGACTCTGTGAGTGCCTTCAGCCC
ACCAGCAGGAGCTTGGAGTTTGGGGAGTGGGGATGAGTCCGTCAAGCACAACTGTTCTCTGAGTGAACCAAAGA
AGCAAGGAGCTAGGACCCCCAGTCTGCCCCCAGGAGCACAAAGCAGGGTCCCCTCAGTCAAGGCAGTGGGATGG
GCGGCTGAGGAACGGGGCAGGCAAGGTCACTGCTCAGTCACGTCCACGGGGACGAGCCGTGGGTTCGTGCTGAGT
AGGTGGAGCTCATTGCTTTCTCCAAGCTTGGAAGTGTGTTTGAAGATAACACAGAGGGAAAGGGAGAGCCACCTG
GTACTTGTCCACCCTGCCTCCTCTGTTCTGAAATTCATCCCCCTCAGCTTAGGGGAATGCACCTTTTTCCCTTT
CCTTCTCACTTTTGCATGTTTTTACTGATCATTCGATATGCTAACCGTTCTCAGCCCTGAGCCTTGAGAGAGGAGG
GCTGTAACGCCTTCAGTCAGTCTCTGGGGATGAAACTCTTAAATGCTTTGTATATTTCTCAATTAGATCTCTTT
TCAGAAGTGTCTATAGAACAATAAAAAATCTTTTACTTCTG

1081/6881
FIGURE 1010

MVKISFQPAVAGIKGDKADKASASAPAPASATEILLTPAREEQPPQHRSKRGGSVGGVCYLSMGMVVLLMGLVFA
SVYIYRYFFLAQLARDNFFRCGVLYEDSLSSQVRTQMELEEDVKIYLDENYERINVPVPQFGGGDPADIIHDFQR
GLTAYHDISLDKCYVIELNTTIVLPPRNFWEELLMNVKRGTYLPQTYIIQEEMVVTEHVSDKEALGSFIYHLCNGK
DTYRLRRRATRRRINKRGAKNCNAIRHFENTFVVETLICGVV

1082/6881
FIGURE 1011

GATCACCACCATCGAGGCAGTGAAGTGCAAGATCCAGGTTCTGCAGCAGCAGGCAGATGATGCAGAGGAGCGAGC
TGAGCACCTCCAGCGAGAAGTTGAGGGAGAAAGGCAGGCCCGGGAAGAGAGGTATGAAGGTTGTTGAAAATCGGG
CCTTAAAAGATGAAGAAAAGATGGAACCTCAGGAAATCTAACTCCAAGAAGCTAAGCACATTGCAGAAGAGGCAG
ATAGGAAGTATGAAGAGGTGGCTCATAAGTTGGTGATCATTGAAGGAGACTTGGAAGGCACGGAGGAACGAGCTG
AGCTGGGAGAGTCCCGTTGCCAAGAGATGGATGAGCAGATTAGACTGATGGACCAGAACCTGAAGTGTCTGAGTG
CTGCTGAAGAAATGTACTCTCAAAAAGAAGACAAATATGAGGAAGAGATCAAGATTCTTACTGATAAACTCAAGG
AGGCAGAGACCAGTGCTGAGTTTGCTGAGAGATCGGTAGCCAAGCTGGAAAAGACAATTGATGACTTGGAAGATA
AACTGAAACGCACCAAAGAGGAGCACCTCTGTACACAAAGGATGCTGGACCAGACTCTGATTGACCTGAATGAGA
TGTAGAACGCCCCAGTCCCACCCTGCTGCTGCTCCTCCCTCTTCTCAGAGAATCCAGCTGGGCTAGAGGCTGAGC
ACCTTTGGAAACAACATTTAAGGGAATGTGAGCACAATGCATAATGTCTTTAAAAGCATGTTGTGATG

1083/6881
FIGURE 1012

GTTTTGCCTGCTAGCATCTCCCTGTAACCTCTCCCAATCTTGAGGAGTGATCCCTGTCCCAGCCCCCTGGAAAGGGG
CAGGAACGACAAACTCAAAGTCCAGGATGTTACCATGACAAGAGCCATGGAAGAGGCTCTTTTTTCAGCACTTCA
TGCACCAGAAGCTGGGGATCGCCTATGCCATACACAAGCCATTTCCCTTCTTTGAAGGCCTCCTAGACAACCTCCA
TCATCACTAAGAGAAATGTACATGGAATCTCTGGAAGCCTGTAGAAATTTGATCCCTGTATCCAGAGTGGTGCACA
ACATTCTCACCCAACTGGAGAGGACTTTTAACTGTCTCTTCTGGTGACATTGTTCAGTCAAATTAACCTGCGTG
AATATCCCAATCTGGTGACGATTTACAGAAGCTTCAAACGTGTTGGTGCTTCCTATGAACGGCAGAGCAGAGACA
CACCAATCCTACTTGAAGCCCCAACTGGCCTAGCAGAAGGAAGCTCCCTCCATACCCCACTGGCGCTGCCCCAC
CACAACCCCCCTCAACCAAGCTGTTACCCCTGTGCGCCAAGAGTCAGTGAGCCTGGAACATCCTCCCAGCAAAGCG
ATGAGATCCTGAGTGAGTCGCCCAGCCCATCTGACCCTGTCTGCCTCTCCCTGCACTCATCCAGGAAGGAAGAA
GCACTTCAGTGACCAATGACAAGTTAACATCCAAAATGAATGCGGAAGAAGACTCAGAAGAGATGCCAGCCTCC
TCACTAGCACTGTGCAAGTGGCCAGTGACAACCTGATCCCCCAAATAAGAGATAAAGAAGACCCTCAAGAGATGC
CCCCTCTCCCTTGGGCTCTATGCCAGAGATAAGAGATAATTCCTCCAGAACCAAATGACCCAGAAGAGCCCCAGG
AGGTGTCCAGCACACCTTCAGACAAGAAAGGAAAGAAAAAGAAAGATGTATCTGGTCAACTCCAAAAAGGAGAC
ATAAGAAAAAAGCCTCCCAAGAGGGACAGCCTCATCTAGACACGGAATCCAAAAGAAGCTCAAAAGGGTGGATC
AGGTTCTCAAAAAGAAAGATGACTCAACTTGTAACCTCCACGGTAGAGACAAGGGCCCCAAAAGGCGAGAAGTGAAT
GTGCCCCGAAAGTCGAGATCAGAGGAGATCATTGATGGCACTTCAGAAATGAATGAAGGAAAGAGGTCCCAGAAGA
CGCCTAGTACACCACGAAGGGTCACACAAGGGGCAGCCTCACCTGGGCATGGCATCCAAGAGAAGCTCCAAGTGG
TGGATAAGGTGACTCAAAGGAAAGACGACTCAACCTGGAACCTCAGAGGTCATGATGAGGGTCCAAAAGGCAAGAA
CTAAATGTGCCCGAAAGTCCAGATCGAAAGAAAAGAAAAAGGAGAAAGATATCTGTTCAAGCTCAAAAAGGAGAT
TTCAGAAAAATATTACCGAAGAGGAAAACCCAAAAGTGACACTGTGGATTTTCACTGTTCTAAGCTCCCCGTGA
CCTGTGGTGAGGCGAAAGGGATTTTATATAAGAAGAAAATGAAACACGGATCCTCAGTGAAGTGCATTTCGGAATG
AGGATGGAACCTTGTTAACACCAAATGAATTTGAAGTCGAAGGAAAAGGAAGGAACGCAAAGAAGTGGAAACGGA
ATATACGTTGTGAAGGAATGACCCTAGGAGAGCTGCTGAAGCGGAAAACTCGGATGAATGCGAGGTGTGCTGTC
AAGGGGGACAACCTTCTCTGCTGCGGTACTTGTCCACGAGTCTTCCATGAGGACTGTCACATCCCCCTGTGGAAG
CCAAGAGGATGCTGTGGAGTTGCACCTTCTGCAGGATGAAGAGGTCTTCAGGAAGCCAACAGTGCCATCATGTAT
CTAAGACCCTGGAGAGGCAGATGCAGCCTCAGGACCAGCTGATTCGAGATTACGGTGAGCCCTTTCAGGAAGCAA
TGTGGTTGGACCTGTTAAGGAAAGGCTGATTACGGAATGTACACGGTGGCATGGTTTGTGCGAGACATGCGCC
TGATGTTTCGCAACCATAAAACATTTTACAAGCCTTCTGACTTTGGCCAGGTAGGACTTGACTTAGAGGCAGAAT
TTGAAAAAGATCTCAAAGACGTGCTCGGTTTTTCATGAAGCCAATGACGGCGGTTTTCTGGACTCTTCTCTGACCCT
GTTCTGTAAAGACTGAAGCATCCCCACCTCAGGATTCAGCTGATGGGACCCTGGCTTGGACTGTTGATTGCCAGT
GAGTCTGGGATGTAATTGGCTGCCCTCAGGACCCAAACCCAGACACTTCATAGGATTATCACACCCTCCATCTTT
ATTCTTTCTTTTACCTTTAAAAGTCTATATCTA

1084/6881
FIGURE 1013

MFTMTRAMEEALFQHFMHQKLGIAAYAIHKPFPFFEGLLDNSIITKRMYESLEACRNLI PVSRVVHNILTQLERT
FNLSLLVTLFSQINLREYPNLVTIYRSFKRVGASYERQSRDTPILLEAPTGLAEGSSLHTPLALPPPQPPQPPSCS
PCAPRVSEPGTSSQQSDEILSESPSPSDPVLPLPALIQEGRSTSVTNDKLTSKMNAEEDSEEMPSLLTSTVQVAS
DNLIPQIRDKEDPQEMPHSPLGSMPEIRDNSPEPNDPEEPQEVSSTPSDKKGKKRKRRCIWSTPKRRHKKKSLPRG
TASSRHGIQKKLKRVDQVPQKKDDSTCNSTVETRAQKARTECARKSRSEEIIDGTSEMNEGKRSQKTPSTPRRVT
QGAASPGHGIQEKLQVVDKVTQRKDDSTWNSEVMMRVQKARTKCARKSRSEKKEKKEDICSSSKRRFQKNIHRRG
KPKSDTVDFHCSKLPVTCGEAKGILYKKMKMHGSSVKCIRNEDGTWLT PNEFEVEGKGRNAKNWKRNI RCEGMTL
GELLKRKNSDECEVCCQGGQLLCCGTCPRVFHEDCHIPPVEAKRMLWSCTFCRMKRSSGSQQCHHVSKTLERQMQ
PQDQLIRDYGEFPQEAMWLDLVKERLITEMYTVAWFVRDMRLMFRNHKTFYKASDFGQVGLDLEAEFEKDLKDVL
GFHEANDGGFWTLP

1085/6881
FIGURE 1014

GTTTTGCCTGCTAGCATCTCCCTGTAACCTCTCCCAATCTTGAGGAGTGATCCCTGTCCCAGCCCCCTGGAAAGGGG
CAGGAACGACAAACTCAAAGTCCAGGATGTTACCATGACAAGAGCCATGGAAGAGGCTCTTTTTTCAGCACTTCA
TGCACCAGAAGCTGGGGATCGCCTATGCCATACACAAGCCATTTCCCTTCTTTGAAGGCCTCCTAGACAACCTCCA
TCATCACTAAGAGAATGTACATGGAATCTCTGGAAGCCTGTAGAAATTTGATCCCTGTATCCAGAGTGTTGCACA
ACATTCTCACCCAACTGGAGAGGACTTTTAACTGTCTCTTCTGGTGACATTGTTTCAGTCAAATTAACCTGCGTG
AATATCCCAATCTGGTGACGATTTACAGAAGCTTCAAACGTGTTGGTGCTTCCCTATGAACGGCAGAGCAGAGACA
CACCAATCCTACTTGAAGCCCCAACTGGCCTAGCAGAAGGAAGCTCCCTCCATACCCCACTGGCGCTGCCCCAC
CACAACCCCTCAACCAAGCTGTTACCCCTGTGCGCCAAGAGTCAGTGAGCCTGGAACATCCTCCCAGCAAAGCG
ATGAGATCCTGAGTGAGTCGCCCAGCCCCTGTGACCCTGTCTGCCTCTCCCTGCACTCATCCAGGAAGGAAGAA
GCACTTCAGTGACCAATGACAAGTTAACATCCAAATGAATGCGGAAGAAGACTCAGAAGAGATGCCAGCCTCC
TCACTAGCACTGTGCAAGTGGCCAGTGACAACCTGATCCCCCAAATAAGAGATAAAGAAGACCCTCAAGAGATGC
CCCCTCTCCCTTGGGCTCTATGCCAGAGATAAGAGATAATTCTCCAGAACCAAATGACCCAGAAGAGCCCCAGG
AGGTGTCCAGCACACCTTCAGACAAGAAAGGAAAGAAAAAGAAAGATGTATCTGGTCAACTCCAAAAAGGAGAC
ATAAGAAAAAAGCCTCCCAAGAGGGACAGCCTCATCTAGACACGGAATCCAAAAGAAGCTCAAAAGGGTGGATC
AGGTTCTCAAAAGAAAGATGACTCAACTTGTAACCTCCACGGTAGAGACAAGGGCCCCAAAGGCGAGAAGTGAAT
GTGCCCCGAAAGTCGAGATCAGAGGAGATCATTGATGGCACTTCAGAAATGAATGAAGGAAAGAGGTCCCAGAAGA
CGCCTAGTACACCACGAAGGGTCACACAAGGGGCAGCCTCACCTGGGCATGGCATCCAAGAGAAGCTCCAAGTGG
TGGATAAGGTGACTCAAAGGAAAGACGACTCAACCTGGAACCTCAGAGGTCATGATGAGGGTCCAAAAGGCAAGAA
CTAAATGTGCCCGAAAGTCCAGATCGAAAGAAAAAGAAAGGAGAAAGATATCTGTTCAAGCTCAAAAAGGAGAT
TTCAGAAAAATATTACCCGAAGAGGAAAAACCCAAAAGTGACACTGTGGATTTTCACTGTTCTAAGCTCCCCGTGA
CCTGTGGTGAGGCGAAAGGGATTTTATATAAGAAGAAAAATGAAACACGGATCCTCAGTGAAGTGCATTTCGGAATG
AGGATGGAACCTTGGTTAACACCAAATGAATTTGAAGTCGAAGGAAAGGAAGGAACGCAAAGAAGTGGAAACGGA
ATATACGTTGTGAAGGAATGACCCTAGGAGAGCTGCTGAAGAGTGGAATTTTGCTCTGTCTCCAAGAATAAATC
TCAAGAGAGAGTTAAATAGCAAGTGAATTTCTACTACCTCTCAGTCACCATGTTGCAGACTTTCCCTGTCTGGA
GGCTCACCTTAGAGCTTCTGAGTTTCCAAGCTCTGAGTCACCTCCACATTTGGGCATGGCATCTTCAAACAATT
AATTTGCATAGTTAATTTGGGATGGGGAAGCAAATGACTCTAAAATAAAAATTAAATGAAAAGCTCAAAAAAA
AAAAAAAAAAAA

1086/6881
FIGURE 1015

MFTMTRAMEEALFQHFMHQKLGIAYAIHKPFPFFEGLLDNSIITKRMYESLEACRNLI PVSRVVHNILTQLERT
FNLSLLVTLFSQINLREYPNLVTIYRSFKRVGASYERQSRDTPILLEAPTGLAEGSSLHTPLALPPPQPPQPPSCS
PCAPRVSEPGTSSQQSDEILSESPSPSDPVLPLPALIQEGRSTSVTNDKLT SKMNAEEDSEEMPSSLTSTVQVAS
DNLIPQIRDKEDPQEMPHSPLGSMPEIRDNSPEPNDPEEPQEVSSTPSDKKGKKRKRRCIWSTPKRRHKKKSLPRG
TASSRHGIQKKLKRVDQVPQKKDDSTCNSTVETRAQKARTECARKSRSEEIIDGTSEMNEGKRSQKTPSTPRRVT
QGAASPGHGIQEKLQVVDKVTQRKDDSTWNSEVMMRVQKARTKCARKSRSEKKEKKEKD ICSSSKRRFQKNIHRRG
KPKSDTVDFHCSKLPVTCGEAKGILYKKKMKHGSSVKCIRNEDGTWLT PNEFEVEGKGRNAKNWKRNI RCEGMTL
GELLKSGLLLCPPRINLKRELNSK

1087/6881
FIGURE 1016

GTTTTGCCTGCTAGCATCTCCCTGTAACCTCTCCCAATCTTGAGGAGTGATCCCTGTCCCAGCCCCCTGGAAAGGGG
CAGGAACGACAAACTCAAAGTCCAGGATGTTTACCATTGACAAGAGCCATGGAAGAGGCTCTTTTTTCAGCACTTCA
TGCACCAGAAGCTGGGGATCGCCTATGCCATACACAAGCCATTTCCCTTCTTTGAAGGCCTCCTAGACAACCTCCA
TCATCACTAAGAGAATGTACATGGAATCTCTGGAAGCCTGTAGAAATTTGATCCCTGTATCCAGAGTGGTGCACA
ACATTCTCACCCAACTGGAGAGGACTTTTAACCTGTCTCTTCTGGTGACATTGTTTCAGTCAAATTAACCTGCGTG
AATATCCCAATCTGGTGACGATTTACAGAAGCTTCAAACGTGTTGGTGCTTCCCTATGAACGGCAGAGCAGAGACA
CACCAATCCTACTTGAAGCCCCAACTGGCCTAGCAGAAGGAAGCTCCCTCCATACCCCACTGGCGCTGCCCCCAC
CACAACCCCCCTCAACCAAGCTGTTACCCCTGTGCGCCAAGAGTCAGTGAGCCTGGAACATCCTCCAGCAAAGCG
ATGAGATCCTGAGTGAGTCGCCCAGCCCATCTGACCCCTGTCCTGCCTCTCCCTGCACTCATCCAGGAAGGAAGAA
GCACTTCAGTGACCAATGACAAGTTAACATCCAAAATGAATGCGGAAGAAGACTCAGAAGAGATGCCAGCCTCC
TCACTAGCACTGTGCAAGTGGCCAGTGACAACCTGATCCCCCAAATAAGAGATAAAGAAGACCCTCAAGAGATGC
CCCCTCTCCCTTGGGCTCTATGCCAGAGATAAGAGATAATTCTCCAGAACCAAATGACCCAGAAGAGCCCCAGG
AGGTGTCCAGCACACCTTCAGACAAGAAAGGAAAGAAAAAGAAAGATGTATCTGGTCAACTCCAAAAAGGAGAC
ATAAGAAAAAAGCCTCCCAAGAGGGACAGCCTCATCTAGACACGGAATCCAAAAGAAGCTCAAAAGGGTGGATC
AGGTTCTCAAAAGAAAGATGACTCAACTTGTAACCTCCACGGTAGAGACAAGGGCCCCAAAAGGCGAGAACTGAAT
GTGCCCCGAAAGTCGAGATCAGAGGAGATCATTGATGGCACTTCAGAAATGAATGAAGGAAAGAGGTCCCAGAAGA
CGCCTAGTACACCACGAAGGGTCACACAAGGGGCAGCCTCACCTGGGCATGGCATCCAAGAGAAAGCTCCAAGTGG
TGGATAAGGTGACTCAAAGGAAAGACGACTCAACCTGGAACCTCAGAGGTCATGATGAGGGTCCAAAAGGCAAGAA
CTAAATGTGCCCGAAAGTCCAGATCGAAAGAAAAAGAAAAAGGAGAAAGATATCTGTTCAAGCTCAAAAAGGAGAT
TTCAGAAAAATATTCACCGAAGAGGAAAAACCCAAAAGTGACACTGTGGATTTTCACTGTTCTAAGCTCCCCGTGA
CCTGTGGTGAGGCGAAAGGGATTTTATATAAGAAGAAAAATGAAACACGGATCCTCAGTGAAGTGCAATTCGGAATG
AGGATGGAACCTTGGTTAACACCAAATGAATTTGAAGTCGAAGGAAAAGGAAGGAACGCAAGAAGTGGAAACGGA
ATATACGTTGTGAAGGAATGACCCTAGGAGAGCTGCTGAAGCGGAAAACTCGGATGAATGCGAGGTGTGCTGTC
AAGGGGGACAACCTTCTCTGCTGCGGTACTTGTCCACGAGTCTTCCATGAGGACTGTCACATCCCCCTGTGGAAG
CCAAGAGGATGCTGTGGAGTTGCACCTTCTGCAGGATGAAGAGGTCTTCAGGAAGCCAACAGTGCCATCATGTAT
CTAAGACCCTGGAGAGGCAGATGCAGCCTCAGGACCAGCTGAAATGTGAGTTCTCCTCTTGAAGGCCTACTGTC
ATCCACAAAGCTCCTTTTTTACGGGCATCCCATTTAATATTCGAGATTACGGTGAGCCCTTTCAGGAAGCAATGT
GGTTGGACCTGTTAAGGAAAGGCTGATTACGGAATGTACACGGTGGCATGTTTTGTGCGAGACATGCGCCTGA
TGTTTCGCAACCATAAAACATTTTACAAGGCTTCTGACTTTGGCCAGGTAGGACTTGACTTAGAGGCAGAAATTTG
AAAAAGATCTCAAAGACGTGCTCGGTTTTTATGAAGCCAATGACGGCGGTTTTCTGGACTCTTCCTTGAACCTGTT
CTGTAAAGACTGAAGCATCCCCACCTCAGGATTAGCTGATGGGACCCTGGCTTGGACTGTTGATTGCCAGTGAG
TCTGGGATGTAATTGGCTGCCCTCAGGACCCAAACCCAGACACTTCATAGGATTATCACACCCTCCATCTTTATT
CTTTCTTTTTTACCTTTAAAAGTCTATATCTA

1088/6881
FIGURE 1017

MFTMTRAMEEALFQHFMHQKLGIAAYAIHKPFPFFEGLLDNSIITKRMYESLEACRNLI PVSRVVHNILTQLERT
FNLSLLVTLFSQINLREYPNLVTIYRSFKRVGASYERQSRDTPILLEAPTGLAEGSSLHTPLALPPPQPPQPSCS
PCAPRVSEPGTSSQQSDEILSESPSPSDPVLPLPALIQEGRSTSVTNDKLTSKMNAEEDSEEMPSLLTSTVQVAS
DNLIPQIRDKEDPQEMPHSPLGSMPEIRDNSPEPNDPEEPQEVSSTPSDKKGKKRRCI WSTPKRRHKKKSLPRG
TASSRHGIQKKLKRVDQVPQKKDDSTCNSTVETRAQKARTECARKSRSEEIIDGTSEMNEGKRSQKTPSTPRRVT
QGAASPGHGIQEKLQVVDKVTQRKDDSTWNSEVMMRVQKARTKCARKSRSEKKKEKD ICSSSKRRFQKNIHRRG
KPKSDTVDFHCSKLPVTCGEAKGILYKKMKKHGSSVKIRNEDGTWLT PNEFEVEGKGRNAKNWKRNI RCEGMTL
GELLKRKNSDECEVCCQGGQLCCGTCPRVFHEDCHIPPVEAKRMLWSCTFCRMKRSSGSQQCHHVSKTLERQMQ
PQDQLKCEFLLLKAYCHPQSSFFTGIPFNIRDYGEFFQEAMWLDLVKERLITEMYTVAWFVRDMRLMFRNHKTFY
KASDFGQVGLDLEAEFEKDLKDVLGFHEANDGGFWTLF

1089/6881
FIGURE 1018

ATGCTGGGTACGCTGCGGCCATGGAGGGCGAGGACGTGGAAGACGACCAGCTGCTGCAGAAGCTCAGGGCCAGT
CGCCGCCGCTTCCAGAGGGCGCATGCAGCGGCTGATAGAGAAGTACAACCAGCCCTTCGAGGACACCCCGGTGGTG
CAAATGGCCACGCTGACCTACGAGACGCCACAGGGATTGAGAATTTGGGGTGGAAGACTAATAAAGGAAAGAAAC
AAAGGAGAGATCCAGGACTCCTCCATGAAGCCCGCGGACAGGACAGATGGCTCCGTGCAAGCTGCAGCCTGGGGT
CCTGAGCTTCCCTCGCACCGCACAGTCCTGGGAGCCGATTCAAAAAGCGGTGAGGTGATGCCACGTCAGACCAG
GAAGAGTCAGTTGCTTGGGCCTTAGCACCTGCAGTGCCTCAAAGCCCTTTGAAAAATGAATTAAGAAGGAAATAC
TTGACCCAAGTGGATATACTGCTACAAGGTGCAGAGTATTTTGAGTGTGCAGGTAACAGAGCTGGAAGGGATGTA
CGTGTGACTCCGCTGCCTTCACTGGCCTCACCTGCCGTGCCTGCCCCGGATACTGCAGTCGTATCTCCGGAAAG
AGTCTTGGTGACCCAGCGAAACCAGCTTCATCTCCCAGAGAATGGGATCCTTTGCATCCTTCTCCACAGACATG
GCCTTAGTACCTAGAAATGACAGCCTCTCCCTACAAGAGACCAGTAGCAGCAGCTTCTTAAGCAGCCAGCCCTTT
GAAGATGATGACATTTGCAATGTGACCATCAGTGACCTGTACGCAGGGATGCTGCACTCCATGAGCCGGCTGTTG
AGCACAAAAGCCATCAAGCATCATCTCCACCAAAACGTTTCATCATGCAAACTGGAACTGCAGGAGGAGGCACAGA
TATAAGAGCAGGATGAACAAAACATATTGCAAAGGAGCCAGACGTTCTCAGAGGAGCTCCAAGGAGAACTTCATA
CCCTGCTCTGAGCCTGTGAAAGGGACAGGGGCATTAAGAGATTGCAAGAACGTATTAGATGTTTCTTGCCGTAAG
ACAGGTTTAAAATTGGAAGGAGCTTTTCTTGAAAGTCAACAGACCCCAAATCCATAAGTTAGATCCAAGTTGGAAG
GAGCGCAAAGTGACACCCTCGAAGTATTCTTCCCTTGATTTACTTCGACTCCAGTGCAACATATAATCTTGATGAG
GAAAAATAGATTTAGGACATTAATAATGGTTAATTTCTCCTGTAAAAATAGTTTCCAGACCAACAATACGACAGGGC
CATGGAGAGAACCGTCAGAGGGAGATTGAAATCCGATTTGATCAGCTTCATCGGGAATATTGCCTGAGTCCCAGG
AACCAGCCTCGCCGGATGTGCCTCCCGGACTCCTGGGCCATGAACATGTACAGAGGGGGTCTGCGAGTCTTGGT
GGCCTTCAGGGCTTAGAAACCCGCAGGCTGAGTTTACCTTCCAGCAAAGCAAAGCAAAAAGTTTAAAGTGAGGCT
TTTGAAAACCTAGGCAAAGATCTCTGGAAGCAGGTAGGTGCCTGCCAAGAGCGATTTCATCTTCATCACTTCCA
AAGACCAACCCACACACAGCGCAACTCGCCCGCAGCAGACATCTGACCTTCACGTTACAGGAAATAGTTCTGGA
ATATTTAGAAAGTCAGTGTACCCAGCAAACCTCTTTCAGTCCAGATAAAGAAGTGCCAGGCCACGGAAGGAAT
CGTTACGATGAAATTAAAGAAGAATTTGACAAGCTTCATCAAAGTATTGCCTCAAATCTCCTGGGCAGATGACA
GTGCCTTTATGTATTGGAGTGTCTACAGATAAAGCAAGTATGGAAGTTGATATCAAACAGAAGGCTTCTTAGGA
AAATTAAATCCAGACCCTCACTTCCAGGGTTTCCAGAAGTTGCCATCATCACCCCTGGGGTGCAGAAAAAGTCTA
CTGGGCTCAACTGCAATTGAGGCTCCTTCATCTACATGTGTGCTCGTGCCATCACGAGGGATGGCACGAGGGAC
CATCAGTTCCTTGCAAAAAGACCCAGGCTATCAGAACCCAGGGCTCCGGACGCCAGGGCAATTCCTGGGTGCC
TCAGATGGGGTGGACAACACCGTCAGACCGGGAGACCAGGGCAGCTCTTCAGCCCCAACTCAGAAGAGAGAGGA
GAGAACACGCTTTACAGGATGGAAGAGAAAAAGTGATTTTCATGCTAGAAAAATTGGAACTAAAAGTGTGTAGCTA
GGTTATTTTCGGAGTGTATTTATCTTCCCACTTGCTCTCTGTTTGTATTTTTGTTTTGTTTTGATTCTTGAGAC
TGTGAGGACTTGTTGACTTCTCTGCCCTTAAAGTAAATATTAGTGAAATTGGTTCCATCAGAGATAACCTCGAG
TTCTTGGTGTAGAAATTATGTGAATAAAGTTGCTCAATTAGAAAAAAAAAAAAAAAAAAAAA

1090/6881
FIGURE 1019

MLHSMRLLSTKPSSIIISTKTFIMQNWNCRRRHRYKSRMNKTYCKGARRSQRSSKENFIPCSEFVKGTGALRDCK
NVLDVSCRKTGLKLEKAFLEVNRPQIHKLDPWKERKVTPSKYSSLIYFDSSATYNLDEENRFRTLKWLISPVKI
VSRETIRQGHGENRQREIEIRFDQLHREYCLSPRNQPRRMCLPDSWAMNMYRGGPASPGGLQGLETRRLSLPSSK
AKAKSLSEAFENLGKRSLEAGRCLPKSDSSSSLPKTNPTHSATRPQQTSDLHVQGNSSGIFRKSVSPSKTLSVPD
KEVPGHGRNRYDEIKEEFDKLHQKYCLKSPGQMTVPLCIGVSTDKASMEVRYQTEGFLGKLNPDPHFQGFQKLPS
SPLGCRKSLLGSTAIEAPSSTCVARAITRDGTRDHQFPAKRPRLSEPQSGRQGNSLGASDGVNDTVRPGDQGSS
SQPNSEERGENTSYRMEEKSDFMLEKLETKSV

1091/6881
FIGURE 1020

AAGACCGTCCCGGATGGCCTCGGGGACTGCCAGTGTGTGGAGGTGAGCTCCGGGATTGCCGGCATTCCCGCTTCT
GCTGGTTGCTTCATGCTGCAGGCTGCGGCCGTGAGCCCTCGCTCGCATTGGTGGCGCTGAGGTGCCGGGCGAGCA
AGTGACATGTCGTCGGGCCTCCGCGCCGCTGACTTCCCCCGCTGGAAGCGCCACATCTCGGAGCAACTGAGGCGC
CGGGACCGGCTGCAGAGACAGGCGTTTCGAGGAGATCATCCTGCAGTATAACAAATTGCTGGAAAAGTCAGATCTT
CATTGAGTGTGGCCCAGAACTACAGGCTGAAAAGCATGACGTACCAAACAGGCACGAGATAAGTCCCGGACAT
GATGGCACATGGAATGACAATCAGCTACAAGAAATGGCCCAACTGAGGATTAAGCACCAAGAGGAACTGACTGAA
TTACACAAGAAACGTGGGGAGTTAGCTCAACTGGTGATTGACCTGAATAACCAAATGCAGCGGAAGGACAGGGAG
ATGCAGAAAGAGCTTGCAGAAGCAGCAAAGGAACCTCTACCAGTCGAACAGGATGATGACATTGAGGTGATTGTG
GATGAAACTTCTGATCACACAGAAGAGACCTCTCCTGTGCGAGCCATCAGCAGAGCAGCCACTAAGCGACTCTCG
CAGCCTGCTGGAGGCCTTCTGGATTCTGTCTACTAATATCTTTGGGAGACGCTCTGTCTCTTCTTCCAGTCCCC
CAGGACAATGTGGATACTCATCCTGGTTCTGGTAAAGAAGTGAGGGTACCAGCTACTGCCTTGTGTGCTTCGAT
GCACATGATGGGGAAGTCAACGCTGTGCAGTTCAGTCCAGGTTCCCGGTTACTGGCCACTGGAGGCATGGACCGC
AGGGTTAAGCTTTGGGAAGTATTTGGAGAAAAATGTGAGTTCAAGGGTTCCTATCTGGCAGTAATGCAGGAATT
ACAAGCATTGAATTTGATAGTGCTGGATCTTACCTCTTAGCAGCTTCAAATGATTTTGCAAGCCGAATCTGGACT
GTGGATGATTATCGATTACGGGTAAGACCCAGTTAAGAAAGTTAGTGCAATCTCCAAACTTCATGTGGTGTATC
AAGGCACAACTGGCAGGTGCTTAATTAGGGGACTTTGTTTTCCCAAAAATCATGCTTGATTACCCCTGCCCTTC
CTTTCCTCCTTGGGGAAATCTGTGTTTCCACTTTATACTCTTTGTCCAAAACCTCAGTTTCAAATATTTGCAATG
GGACCCTCACATTTGCATGAAAACCTTGAATACTCTTCATAAGGACTAAATACCTTGGTAGATAGCAATTTTGG
CTTAATGGCACAGAACTTAGCAACAGCATGTGAATTGTGATTCTGTGGGCTCTAAAACCTAATTACCTAAAGTG
GGATATAGAAGTACAAATGGATGTATCATAGGGATAAGACAATTCTGAAACAAAACTCCAAGCTGAGAAAGAGG
GGACAGGTGTGAGAGCAGGGAGAAATGATTGGATGTTGAGGAAAGCTGCATTTGAACCAAACTTGCCAAGAATT
CTCTTGGCATCTGACAGAGAGACCAAACTTGGTTGTATCATTTTTGATTGGGGCAGGGGGCGGAGGCGCAAGCA
TGTAACCTAATTTGCAGACATTTTTTTTCCCATAGCCTGAAGGAATCATCACATAAGCTTATTAAATACAAGC
TATTGAAAGATATAATGGAGGATGAATTTGGCATTAGTAGGCATTTTACT

1092/6881
FIGURE 1021

MSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIILQYNKLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDG
TWNDNQLQEMAQLRIKHQEELTELHKKRGELAQLVIDLNNQMQRKDREMQELAEAAKEPLPVEQDDIEVIVDE
TSDHTEETSPVRAISRAATKRLSQPAGGLLDVTNIFGRRSVSSFPVPQDNVDTHPGSGKEVRVPATALCVFDAH
DGEVNAVQFSPGSRLLATGGMDRRVKLWEVFGKCEFKGSLSGSNAGITSIEFDSAGSYLLAASNDFASRIWTV
DYRLRVRPS

1093/6881
FIGURE 1022A

AAGAGAGAAGGCTTCTGCCAGCTCCTGCAGCAGATGAAGAACAAGCACTCAGAGCAGCCGGAGCCCGACATGATC
ACCATCTTCATCGGCACCTGGAACATGGGTAACGCCCCCCTCCCAAGAAGATCACGTCTGGTTTCTCTCCAAG
GGGCAGGGAAAGACGCGGGACGACTCTGCGGACTACATCCCCCATGACATTTACGTGATCGGCACCCAAGAGGAC
CCCCTGAGTGAGAAGGAGTGGCTGGAGATCCTCAAACACTCCCTGCAAGAAATCACCAGTGTGACTTTTAAACA
GTCGCCATCCACACGCTCTGGAACATCCGCATCGTGGTGCTGGCCAAGCCTGAGCACGAGAACCGGATCAGCCAC
ATCTGTACTGACAACGTGAAGACAGGCATTGCAAACACACTGGGGAACAAGGGAGCCGTGGGGGTGTCGTTTCATG
TTCAATGGAACCTCCTTAGGGTTCGTCAACAGCCACTTGACTTCAGGAAGTGAAAAGAACTCAGGCGAAACCAA
AACTATATGAACATTCTCCGGTTCCTGGCCCTGGGCGACAAGAAGCTGAGTCCCTTTAACATCACTCACCCTTC
ACGCACCTCTTCTGGTTTGGGGATCTTAACCTACCGTGTGGATCTGCCTACCTGGGAGGCAGAAACCATCATCCAG
AAAATCAAGCAGCAGCAGTACGCAGACCTCCTGTCCACGACCAGCTGCTCACAGAGAGGAGGGAGCAGAAGGTC
TTCTACACTTCGAGGAGGAAGAAATCACGTTTGCCCCAACCTACCGTTTTGAGAGACTGACTCGGGACAAATAC
GCCTACACCAAGCAGAAAGCGACAGGGATGAAGTACAACCTTGCCCTTCTGGTGTGACCGAGTCCCTCTGGAAGTCT
TATCCCCTGGTGCACGTGGTGTGTCAGTCTTATGGCAGTACCAGCGACATCATGACGAGTGACCACAGCCCTGTC
TTTGCCACATTTGAGGCAGGAGTCACTTCCAGTTTGTCTCCAAGAACGGTCCCAGGACTGTTGACAGCCAAGGA
CAGATTGAGTTTCTCAGGTGCTATGCCACATTGAAGACCAAGTCCCAGACCAAATTTCTACCTGGAGTTCCACTCG
AGCTGCTTGGAGAGTTTTGTCAAGAGTCAGGAAGGAGAAAATGAAGAAGGAAGTGAGGGGGAGCTGGTGGTGAAG
TTTGGTGAGACTCTTCCAAAGCTGAAGCCCATTATCTCTGACCCTGAGTACCTGCTAGACCAGCACATCCTCATC
AGCATCAAGTCTCTGACAGCGCAGGAATCCTATGGCGAGGGCTGCATTGCCCTTCGGTTAGAGGCCACAGAAACG
CAGCTGCCCATCTACACGCCTCTCACCCACCATGGGGAGTTGACAGGCCACTTCCAGGGGGAGATCAAGCTGCAG
ACCTCTCAGGGCAAGACGAGGGAGAAGCTCTATGACTTTGTGAAGACGGAGCGTGATGAATCCAGTGGGCCAAAG
ACCTGAAGAGCCTCACCAGCCACGACCCCATGAAGCAGTGGGAAGTCACTAGCAGGGCCCCCTCCGTGCAGTGGC
TCCAGCATCACTGAAATCATCAACCCCACTACATGGGAGTGGGGCCCTTTGGGCCACCAATGCCCTGCACGTG
AAGCAGACCTTGTCCCTGACCAGCAGCCACAGCCTGGAGCTACGACCAGCCGCCAAGGACTCCCCGCTGGGG
CCCTGCAGGGGAGAAAGTCTCCGACACCTCCCGGCCAGCCGCCCATATCACCCAAGAAGTTTTTACCCTCAACA
GCAAACCGGGGTCTCCCTCCCAGGACACAGGAGTCAAGGCCAGTGACCTGGGGAAGAACGCAGGGGACACGCTG
CCTCAGGAGGACCTGCCGCTGACGAAGCCCGAGATGTTTGAGAACCCCTGTATGGGTCCCTGAGTTCCTTCCCT
AAGCCTGCTCCCAGGAAGGACCAGGAATCCCCCAAATGCCGCGGAAGGAACCCCGCCCTGCCCGGAACCCGGC
ATCTTGTGCGCCAGCATCGTGCTCACCAAAGCCCAGGAGGCTGATCGCGGCGAGGGGCCCGGCAAGCAGGTGCCC
GCGCCCCGGCTGCGCTCCTTACGTGCTCATCCTCTGCCGAGGGCAGGGCGGCCGGCGGGGACAAGAGCCAAGGG
AAGCCCAAGACCCCGGTGAGCTCCCAGGCCCGGTGCCGCGCAAGAGGCCCATCAAGCCTTCCAGATCGGAAATC
AACCAGCAGACCCCGCCACCCCGACGCGCGGCCGCGCTGCCAGTCAAGAGCCCGCGGTGCTGCACCTCCAG
CACTCCAAGGGCCGCGACTACCGCGACAACACCGAGCTCCCGCATCACGGCAAGCACCGGCCGGAGGAGGGCCA
CCAGGGCCTCTAGGCAGGACTGCCATGCAGTGAAGCCCTCAGTGAGCTGCCACTGAGTCGGGAGCCCAGAGGAAC
GGCGTGAAGCCACTGGACCCTCTCCCGGGACCTCCTGCTGGCTCCTCTGCCAGCTTCCTATGCAAGGCTTTGT
GTTTTAGGAAAGGGCCTAGCTTCTGTGTGGCCACAGAGTTCACTGCCTGTGAGACTTAGCACCAAGTGCTGAG
GCTGGAAGAAAAACGCACACCAGACGGGCAACAAACAGTCTGGGTCCCCAGCTCGCTCTTGGTACTTGGGACCCC
AGTGCTCGTTGAGGGCGCCATTCTGAAGAAAGGAAGTGCAGCGCCGATTTGAGGGTGGAGATATAGATAATAAT
AATATTAATAATAATAATGGCCACATGGATCGAACACTCATGATGTGCCAAGTGCTGTGCTAAGTGCTTTACGAA
CATTCGTATATCAGGATGACCTCGAGAGCTGAGGCTCTAGCCACCTAAAACCACGTGCCCAAACCCACCAGTTT
AAAACGGTGTGTGTTTCGGAGGGGTGAAAGCATTAGAAGCCCAGTGCCCTCCTGGAGTGAGACAAGGGCTCGGCC
TTAAGGAGCTGAAGAGTCTGGGTAGCTTGTTTAGGGTACAAGAAGCCTGTTCTGTCCAGCTTCAGTGACACAAGC
TGCTTTAGCTAAAGTCCCGCGGGTTCGGCATGGCTAGGCTGAGAGCAGGGATCTACCTGGCTTCTCAGTTCTTT
GGTTGGAAGGAGCAGGAAATCAGCTCCTATTCTCCAGTGGAGAGATCTGGCCTCAGCTTGGGCTAGAGATGCCAA
GGCCTGTGCCAGGTTCCCTGTGCCCTCCTCGAGGTGGGCAGCCATCACAGCCACAGTTAAGCCAAGCCCCCAA
CATGTATTCCATCGTGCTGGTAGAAGAGTCTTTGCTGTTGCTCCCGAAAGCCGTGCTCTCCAGCCTGGCTGCCAG
GGAGGGTGGGCCTCTTGGTTCCAGGCTCTTGAAATAGTGCAGCCTTTTCTTCTATCTCTGTGGCTTTTACGCTCT
GCTTCTTGGTTATTAGGAGAATAGATGGGTGATGCTTTTCTTATGTTGCTTTTTCAACATAGCAGAATTAATG
TAGGGAGCTAAATCCAGTGGTGTGTGTAATGCAGAAGGAATGCACCCACATCCCATGATGGAAGTCTGCGT

1094/6881
FIGURE 1022B

AACCAATAAATTGTGCCTTTCTCACTCA

1095/6881
FIGURE 1023

MKNKHSEQPEPDMITIFIGTWNMGNA PPPKKITSWFLSKGQGKTRDDSDADYIPHDIIYVIGTQEDPLSEKEWLEIL
KHSLQEITSVTFKTVAIHTLWNIRIVVLAKPEHENRISHICTDNVKTGIAN TLGNKGAVGV SFMNGTSLGFVNS
HLTSGSEKKLRRNQNYMNILRFLALGDKKLS PFNITHRFTHLFWFGDLN YRVDLPTWEAETIIQKIKQQQYADLL
SHDQLLTERREQKVFLHFEEEEITFAPTYR FERLTRDKYAYTKQKATGMKYNLPSWCDRVLWKSYP LVHVVCQSY
GSTSDIMTSDHSPVFATFEAGVTSQFVSKNGPGTVDSQGQIEFLRCYATLKT KSQTKFYLEFHSSCLESFVKSQE
GENEEGSEGELVVKFGETLPKLKPIISDPEYLLDQHILISIKSSDSDESYGEGCIALRLEATETQLPIYTPLTHH
GELTGHFQGEIKLQTSQGKTREKLYDFVKTERDESSGPKTLKSLTSHDPMKQWEVTSRAPP CSGSSITEIINPNY
MGVGPFPGPPMPLHVKQTLSPDQOPTAWSYDQPPKDSPLGPCRGESPTTPPGQPPISP KKFLLPSTANRGLPPRTQE
SRPSDLGKNAGDTLPQEDLPLTKPEMFENPLYGSLSSFPKPAPRKDQESPKMPRKEPPPCPEPGILSPSIVLTKA
QEADRGE GPGKQVPAPRLRSFTCSSSAEGRAAGDKSQGKPKTPVSSQAPVPAKRP IKPSRSEINQQTPTPTPTPR
PPLPVKSPAVLHLQHSGKGRDYRDNTELP HHGKHRPEEGPPGPLGRTAMQ

1096/6881
FIGURE 1024

CGAGCGGACTCGACTCGGCACCGCTGTGCACCAATGCGCCCGGGCCCTGTGCCGCCTCCCGCGGCGCGGCCTCTGGC
TGCTCCTGGCCCATCACCTCTTCATGACCACTGCCTGCCAGGAGGCTAACTACGGTGCCCTCCTCCGGGAGCTCT
GCCTCACCCAGTTCCAGGTAGACATGGAGGCCGTCGGGGAGACGCTGTGGTGTGACTGGGGCAGGACCATCAGGA
GCTACAGGGAGCTGGCCGACTGCACCTGGCACATGGCGGAGAAGCTGGGCTGCTTCTGGCCCAATGCAGAGGTGG
ACAGGTTCTTCCTGGCAGTGCATGGCCGCTACTTCAGGAGCTGCCCCATCTCAGGCAGGGCCGTGCGGGACCCGC
CCGGCAGCATCCTCTACCCCTTCATCGTGCTCCCCATCACGGTGACCCTGCTGGTGACGGCACTGGTGGTCTGGC
AGAGCAAGCGCACTGAGGGCATTGTGTAGCGGGGGCCCAGGCTGCCCGGGGTGCACCCAGGCTGCAGGGTGAGG
CCAGGCAGGCCTGGGTAGGGGCAGCTTCTGGAGCCTTGGGACAGAGCAGGCCCAATGCCCCCTTCTTCCAGC
CAAGAAGAGCTCACAGGAGTCCAGAGTAGCCGAGGCTCTGGTATTAACCTGGAAGCCCCCTGGCTGGAGGCCAC
CGCCACCCTAGGAAGGGGGCAGGGACGTGACCTTGACTTACCTCTGGAAAGGGTCCCAGCCTAGACTGCTTACCC
CATAGCCACATTTGTGGATGAGTGGTTTGTGATTAAAAGGGATGTTCTTG

1097/6881
FIGURE 1025

MARALCRLPRRGLWLLLAHHLFMTTACQEANYGALLRELCLTQFQVDMEAVGETLWCDWGRITIRSYRELADCTWH
MAEKLGCFWPNAEVD RFFLAVHG RYFRSCPISGRAVRDPPGSILYPFIVVPITVTLLVTALVVWQSKRTEGIV

1098/6881
FIGURE 1026A

GGCACGAGGCCGCTCCCCGGCGGGCTGGCTCCTGGCCCCGGAAGCGCGAGCGTTCACTTAGCGGCGAGTGGCTCC
GTCTCCGCGGACAGAGCGCGCGCCCCCTGGCCCCGGCCGCGAGGGGCTCCCGGCGCGGTCCCCGAGCATTTCCCG
CCGGGTGGAGCGGGCCGAGCCCGGCAGGATGACCAGCCCCGCGGCCGCTCAAAGCCGGGAGATCGACTGTTTGAG
CCCGGAAGCGCAGAAGCTGGCGGAAGCCCGGCTCGCTGCAAAACGGGCGGCCCGCGCGGAGGCTCGCGAGATCCG
CATGAAGGAGCTGGAGCGGCAGCAGAAGGAGGAAGACAGTGAGCGCTACTCTCGTAGATCCAGAAGAAACACATC
GGCTTCTGATGAAGACGAGCGCATGTCACTGGGTAGTCTGGAAGCCTGAGGGTAGAAGAGAGACCAGAAAAAGA
TTTTACTGAGAAGGGGTCTCGTAACATGCCGGGCTGTCTGCAGCCACGCTGGCCTCTCTGGGTGGGACTTCCTC
TCGGAGAGGCAGCGGAGACACCTCCTTCTCCATCGACACCGAGGCATCCATCAGGGAAATCAAGGACTCTCTAGC
AGAAGTTGAAGAGAAATATAAGAAGGCTATGGTTTTCCAATGCTCAGCTAGACAATGAAAAGACAAACTTCATGTA
CCAGGTTGATACCTAAAAGATATGTTGCTGGAGCTTGAAGAACAGCTGGCTGAATCTAGGCGGCAGTACGAAGA
GAAAAACAAAGAATTTGAAAGGGAAAAACACGCCCACAGTATACTGCAATTTAGTTTGTGTAAGTCAAGGAGGC
CCTGAAGCAAAGAGAGGAAATGCTCGAGAAACATGGAATAATCCTAAATTCAGAAATAGCTACCAATGGAGAGAC
TTCCGACACCCCTCAATAATGTTGGATACCAAGGTCCTACCAAGATGACAAAAGAAGAGTTAAATGCCCTCAAGTC
TACAGGGGATGGGACCCTAGGAAGAGCCAGTGAAGTGGAGGTGAAAAATGAAATCGTGGCGAATGTGGGGAAAAAG
AGAAATCTTGACAATACTGAGAAAGAACAACACACAGAGGACACAGTGAAGGACTGTGTGGACATAGAGGTATT
CCCTGCTGGTGAGAATACCGAGGACCAGAAATCCTCTGAAGACACTGCCCCATTCTAGGAACCTTAGCAGGTGC
TACCTATGAAGAACAGGTTCAAAGCCAAATTTCTTGAGAGCAGTTCTCTCCCTGAAAACACAGTACAGGTTGAGTC
AAATGAGGTGATGGGTGCACCAGATGACAGGACCAGAACTCCCCTTGAGCCATCCAAGTGTGGAGTGACTTAGA
TGGTGGGAACACACAGAGAATGTGGGAGAGGCAGCAGTGAAGTGAAGAGCAGGCAGGCACAGTGGCCTC
GTGTCCTTTAGGGCATAGTGATGACACAGTTTATCATGATGACAAATGTATGGTAGAGGTCCCCAAGAGTTAGA
GACAAGCACAGGGCATAGTTTAGAGAAAGAATTCACCAACCAGGAAGCAGCTGAGCCCAAGGAGGTTCCAGCGCA
CAGTACAGAAGTAGGTAGGGATCACAACGAAGAAGAGGGTGAAGAAAACAGGATTAAGGGACGAGAAACCAATCAA
GACAGAAGTTCTGTTCTCCAGCAGGAAGTGAAGGCAACTGTGAGGAAGCGACAGGTCCAAGTACAGTAGACAC
TCAAATGAACCCTTAGATATGAAAGAGCCCGATGAAGAAAAGAGTGACCAACAGGGAGAGGCATTGGACTCATC
GCAGAAGAAGACAAAGAACAAGAAAAAGAAAAACAAGAAGAAAAAATCCCCAGTACCCGTAGAAACCTTAAAGA
TGTTAAAAAAGAGTTAACGTATCAGAACACAGATTTAAGTGAAATTAAGGAAGAAGAGCAGGTAAAGTCTACTGA
CAGAAAGTCAGCAGTGGAAGCCCCAAAACGAGGTGACTGAAAATCCAAAACAGAAAATTGCAGCAGAAAGCAGTGA
AAATGTTGATTGTCCGGAGAATCCTAAAATTAAGTTGGATGGAAGAACTTGACCAAGAAGGTGATGATGTACAAAC
AGCAGCTGAGGAGGTACTAGCTGATGGAGACACATTAGATTTTGGAGATGACACCGTTCAATCATCAGGCCCCGAG
GGCTGGTGGTGAAGAATTAGATGAAGGTGTTGCAAAAGATAATGCTAAAATAGATGGTGCCACTCAAAGCAGTCC
TGCAGAACCAAAGAGCGAAGACGCAGATCGCTGCACCCTGCCCGAACATGAAAGTCCCTCACAGGACATTAGTGA
TGCCTGTGAAGCAGAAAGTACAGAGAGGTGTGAGATGTCAGAACATCCAAGTCAGACCGTCAGGAAAGCTTTAGA
CAGCAATAGCCTAGAGAACGATGACTTGTGCGCACCAGGAAGAGAGCCAGGGCACTTCAATCCAGAAAGCAGAGA
AGATACCAGAGGAGGGAATGAGAAGGGCAAAGCAAAGAAGACTGTACCATGTCCTAAGCTGAGGCAGGCGGCAG
GCGCGGTGCACAGGAAGTCTCAGTGTGAAGGGGTCTTTCTCTCCACTGCCAATGTAAGTAGAATGTTCTAAATT
CATAGAGAGGCACTGTATGACAATTACCAGGTGCTCTACTGCTTTAAGTTATAGACTGTTACTTGTAGATTTCCA
TGTAATCATTGAGGTTATCACCCAGATTAGAAAGACATATTTGTTATCAGTGTACGTTCTAATTGAGAGCATTCC
AGTAGTATCAAACAATAATGTCTACTGTTTATAGTCCACTTAATAAAAAATAGAGGCATTACTATTGCTTAGG
CTGATAGGAATGTGGGTTTTCTTGACCAATATATCAGCATCTAATTGAAATGACCAATAGCATTCTTAGACTT
CTGTATTATGAATATAATTGATATTTAAATTAATGTCTTGTTACATATGTGTACTTTCATATTTGATTTTAAAA
TGTACATTATAACCTGTATGGTATTTTATTTAAAGGAGATAAACAGCCAAATAGCAAATAGGTCAGTGAATGATA
AGATTTGCACCTTAGAACAATAATCATTTTAAAGGATAACAAGTAAATGTCTGAAAAGCATGAGGGGCTTTATTTGC
CTTTACCTCATATGAGTCTTTGATCTTGAACCGATACTTTTGGATCTCATTGTTGATATACCTGAATTTACTTTG
TAAGAGATTTTAACTTCACTTCACTGCTGATGATGATCAAATTCATTTTATAGAAAAGATTTAAAGTTTTTTTCTG
GAAGTGATATATGTCAAATTACATTTCTACTGCAGTATTTGAGCAGGGACAGTCATTTTAAATGTTTTTGGC
CGGGCGTGGTGGCTCATGCCTGTAATCTCAGTACATTTGGGAGGCCAAGGCAGGTGGATCACCTGAGGTCAAGAGT
TCGAGGCCAGCCTGGCCAACATGGTGAAACCTGTCTCTACTAAAAATACAAAAAATGGCCGGGCGTGATGGTG
GGCGCCTGTAATCCCAGCCACTCCAGAGGCTGAGGCAGGAGAATCGCTTGAACCTGCGAGGCAGAGATTGCAGTG

1099/6881
FIGURE 1026B

AGCCAAGATCAAGCCATTGTACTCCAGCCTGGACAACAAGAGCGAAACTCTGTCTA

1100/6881
FIGURE 1027

MTSPAAAQSREIDCLSPEAQKLAEARLAAKRAARAEAREIRMKELERQQKEEDSERYSRRSRRNTSASDEDERMS
VGSRGSLRVEERPEKDFTEKGSRNMPGLSAATLASLGGTSSRRGSGDTSFSIDTEASIREIKDSLAEVEEKYKKA
MVSNAQLDNEKTNFMYQVDTLKDMLLELEEQLAESRRQYEEKNKEFEREKHAHSILQFQFAEVKEALKQREEMLE
KHGIILNSEIATNGETSDTLNNVG YQGPTKMTKEELNALKSTGDGTLGRASEVEVKNEIVANVGKREILHNTEKE
QHTEDTVKDCVDIEVFPAGENTEDQKSSSED TAPFLGTLAGATYEEQVQSQILESSSLPENTVQVESNEVMGAPDD
RTRTPLEPSNCWSDLDGGNHTENVGEAAVTQVEEQAGTVASCPLGHSDDTVYHDDKCMVEVPQELETSTGHSLEK
EFTNQEAAEPKEVPAHSTEVGRDHNEEEGEETGLRDEKPIKTEVPGSPAGTEGNCQEATGPSTVDTQNEPLDMKE
PDEEKSDQQGEALDSSQKKTNNKKKKNNKKKSPVPVETLKDVKKELTYQNTDLSEIKEEEQVKSTDRKSAVEAQN
EVTENPKQKIAAESSENVDPCPENPKIKLDGKLDQEGDDVQTAAEEVLADGDTLDFEDDTVQSSGPRAGGEELDEG
VAKDNAKIDGATQSSPAEPKSEAD RCTLPEHESPSQDISDACEAESTERCEMSEHPSQTVRKALDSNSLENDL
SAPGREPGHFNPE SREDTRGGNEKGKSKEDCTMS

1101/6881
FIGURE 1028A

CAGTTTGGAGCTCAGTCTTCCACCAAAGGCCGTTTCAGTTCTCCTGGGCTCCAGCCTCCTGCAAGGACTGCAAGAG
TTTTCTCCGCAGCTCTGAGTCTCCACTTTTTTGGTGGAGAAAGGCTGCAAAAAGAAAAAGAGACGCAGTGAGTG
GGAAAAGTATGCATCCTATTCAAACCTAATTGAATCGAGGAGCCAGGGACACACGCCTTCAGGTTTGCTCAGGG
GTTTCATATTTGGTGCTTAGACAAATTCAAATGAGGAAACATCGGCACTTGCCCTTAGTGCCCGTCTTTTGCCTC
TTTCTCTCAGGCTTTCCTACAACCTCATGCCCAGCAGCAGCAAGCAGATGTCAAAAATGGTGCCGCTGCTGATATA
ATATTTCTAGTGATTCTCTTGGACCATTGGAGAGGAACATTTCCAACCTGTTTCGAGAGTTTCTATATGATGTT
GTAAAATCCTTAGCTGTGGGAGAAAATGATTTCCATTTTGCTCTGGTCCAGTTCAACGGAAACCCACATACCGAG
TTCCTGTAAATACGTATCGTACTAAACAAGAAGTCCTTTCTCATATTTCCAACATGTCTTATATTGGGGGAACC
AATCAGACTGGAAAAGGATTAGAATACATAATGCAAAGCCACCTCACCAAGGCTGCTGGAAGCCGGGCCGGTGAC
GGAGTCCCTCAGGTTATCGTAGTGTTAACTGATGGACACTCGAAGGATGGCCTTGCTCTGCCCTCAGCGGAACTT
AAGTCTGCTGATGTTAACGTGTTTGCAATTGGAGTTGAGGATGCAGATGAAGGAGCGTTAAAAGAAAATAGCAAGT
GAACCGCTCAATATGCATATGTTCAACCTAGAGAATTTTACCTCACTTCATGACATAGTAGGAACTTAGTGTC
TGTGTGCATTTCATCCGTGAGTCCAGAAAGGGCTGGGGACACGGAAACCCCTAAAGACATCACAGCACAAAGACTCT
GCTGACATTATTTTCTTATTGATGGATCAAACAACACCGGAAGTGTCATTTTCGCAGTCATTCTCGACTTCCTT
GTAAATCTCCTTGAGAACTCCCAATTGGAACCTCAGCAGATCCGAGTGGGGGTGGTCCAGTTTAGCGATGAGCCC
AGAACCATGTTCTCCTTGGACACCTACTCCACCAAGGCCAGGTTCTGGGTGCAGTGAAAGCCCTCGGGTTTGCT
GGTGGGGAGTTGGCCAATATCGGCCTCGCCCTTGATTTTCGTGGTGGAGAACCCTTCACCCGGGCAGGGGGCAGC
CGCGTGGAGGAAGGGGTTCGCCAGGTGCTGGTCCCTATAAGTGCCGGGCCTTCTAGTGACGAGATTCGCTACGGG
GTGGTAGCACTGAAGCAGGCTAGCGTGTTCTCATTGCGCCTTGAGAGCCAGGCCGCCTCCAGGGCAGAGCTTCAG
CACATAGCTACCGATGACAACCTTGGTGTTTACTGTCCCGGAATTCGCTAGCTTTGGGGACCTCCAGGAGAAATTA
CTGCCGTACATTGTTGGCGTGGCCCAAAGGCACATTGTCTTGAAACCGCCAACCTTGTACACAAGTCATTGAA
GTCAACAAGAGAGACATAGTCTTCTGGTGGATGGCTCATCTGCACTGGGACTGGCCAACCTTCAATGCCATCCGA
GACTTCATTGCTAAAGTCATCCAGAGGCTGGAATCGGACAGGATCTTATCCAGGTGGCAGTGGCCAGTATGCA
GACACTGTGAGGCCTGAATTTTATTTCAATACCCATCCAACAAAAGGGAAGTCATAACCGCTGTGCGGAAAATG
AAGCCCCTGGACGGCTCGGCCCTGTACACGGGCTCTGCTCTAGACTTTGTTTCGTAACAACCTATTACAGAGTTCA
GCCGGCTACCGGGCTGCCGAGGGGATTCTAAGCTTTTGGTGTGATCACAGGTGGTAAGTCCCTAGATGAAATC
AGCCAGCCTGCCCAGGAGCTGAAGAGAAGCAGCATAATGGCCTTTGCCATTGGGAACAAGGGTGCCGATCAGGCT
GAGCTGGAAGAGATCGCTTTGACTCCTCCCTGGTGTTCATCCAGCTGAGTTCCGAGCCGCCCATTCAGAGGC
ATGCTGCCTGGCTTGCTGGCACCTCTCAGGACCCTCTCTGGAACCCCTGAAGTTCACTCAAACAAAAGGGATATC
ATCTTTCTTTTGGATGGATCAGCCAACGTTGGAAAAACCAATTTCCCTTATGTGCGCGACTTTGTAATGAACCTA
GTTAACAGCCTTGATATTGGAAATGACAATATTCGTGTTGGTTTAGTGCAATTTAGTGACACTCCTGTAACGGAG
TTCTCTTTAAACACATAACCAGACCAAGTCAGATATCCTTGGTCACTTGAGGCAGCTGCAGCTCCAGGGAGGTTTCG
GGCCTGAACACAGGCTCAGCCCTAAGCTATGTCTATGCCAACCACTTCACGGAAGCTGGCGGCAGCAGGATCCGT
GAACACGTGCCGCGAGCTCCTGCTTCTGCTCACAGCTGGGCAGTCTGAGGACTCCTATTTGCAAGCTGCCAACGCC
TTGACACGCGCGGGCATCCTGACTTTTTTGTGTGGGAGCTAGCCAGGCCGAATAAGGCAGAGCTTGAGCAGATTGCT
TTTAACCCAAGCCTGGTGTATCTCATGGATGATTTTCAGCTCCCTGCCAGCTTTGCCTCAGCAGCTGATTTCAGCCC
CTAACACATATGTTAGTGAGGTGTGGAGGAAGTACCCTCGCTCAGCCAGAGAGCAAGCGAGACATTCTGTTC
CTCTTTGACGGCTCAGCCAATCTTGTGGGCCAGTTCCCTGTTGTCCGTGACTTTCTCTACAAGATTATCGATGAG
CTCAATGTGAAGCCAGAGGGGACCCGAATTGCGGTGGCTCAGTACAGCGATGATGTCAAGGTGGAGTCCCGTTTT
GATGAGCACCAGAGTAAGCCTGAGATCCTGAATCTTGTGAAGAGAATGAAGATCAAGACGGGCAAGCCCTCAAC
CTGGGCTACGCGCTGGACTATGCACAGAGGTACATTTTTGTGAAGTCTGCTGGCAGCCGGATCGAGGATGGAGTG
CTTCAGTTCTTGGTGTCTGGTTCGAGGAAGGTATCTGACCGTGTGGATGGGCCAGCAAGTAACCTGAAGCAG
AGTGGGGTTGTGCCTTTTCATCTTCCAAGCCAAGAAGCAGACCCCTGCTGAGTTAGAGCAGATCGTGTCTGTCTCA
GCGTTTATCCTGGCTGCAGAGTCGCTTCCCAAGATTGGAGATCTTCATCCACAGATAGTGAATCTCTTAAATCA
GTGCACAACGGAGCACCAGCACCAGTTTCAGGTGAAAAGGACGTGGTGTCTGCTTGATGGCTCTGAGGGCGTC
AGGAGCGGTTTTCCCTCTGTTGAAAGAGTTTGTCCAGAGAGTGGTGGAAAGCCTGGATGTGGGCCAGGACCGGGTC
CGCGTGGCCGTGGTGCAGTACAGCGACCGGACCAGGCCGAGTTCTACCTGAATTCATACATGAACAAGCAGGAC
GTCGTCAACGCTGTCCGCCAGCTGACCTGCTGGGAGGGCCGACCCCCAACACCGGGGCCGCCCTGGAGTTTGTC

1102/6881
FIGURE 1028B

CTGAGGAACATCCTGGTCAGCTCTGCGGGAAGCAGGATAACAGAAGGTGTGCCCCAGCTGCTGATCGTCTCACC
GCCGACAGGTCTGGGGATGATGTGCGGAACCCCTCCGTGGTCTGTGAAGAGGGGTGGGGCTGTGCCCATTTGGCATT
GGCATCGGGAACGCTGACATCACAGAGATGCAGACCATCTCCTTCATCCCGGACTTTGCCGTGGCCATTTCCACC
TTTCGCCAGCTGGGGACCGTCCAACAGGTCATCTCTGAGAGGGTGACCCAGCTCACCCGCGAGGAGCTGAGCAGG
CTGCAGCCGGTGTTCAGCCTCTACCGAGCCAGGTGTTGGTGGCAAGAGGGACGTGGTCTTTCTCATCGATGGG
TCCCAAAGTGCCGGGCTGAGTTCCAGTACGTTTCGCACCCCTCATAGAGAGGCTGGTTGACTACCTGGACGTGGGC
TTTGACACCACCCGGGTGGCTGTCATCCAGTTCAGCGATGACCCCAAGGTGGAGTTCCTGCTGAACGCCCATTTCC
AGCAAGGATGAAGTGCAGAACGCGGTGCAGCGGCTGAGGCCCAAGGGAGGGCGGCAGATCAACGTGGGCAATGCC
CTGGAGTACGTGTCCAGGAACATCTTCAAGAGGCCCCCTGGGGAGCCGCATTGAAGAGGGCGTCCCGCAGTTTCTG
GTCCTCATCTCGTCTGGAAGTCTGACGATGAGGTGGACGACCCGGCGGTGGAGCTCAAGCAGTTTGGCGTGGCC
CCTTTCACGATCGCCAGGAACGCAGACCAGGAGGAGCTGGTGAAGATCTCGCTGAGCCCCGAATATGTGTTCTCG
GTGAGCACCTTCCGGGAGCTGCCAGCCTGGAGCAGAAACTGCTGACGCCCATCACGACCCCTGACCTCAGAGCAG
ATCCAGAAGCTCTTAGCCAGCACTCGCTATCCACCTCCAGCAGTTGAGAGTGATGCTGCAGACATCGTCTTTCTG
ATCGACAGCTCTGAGGGAGTTAGGCCAGATGGCTTTGCACATATTCGAGATTTTGTAGCAGGATTGTTTGAAGA
CTCAACATCGGCCCCAGTAAAGTGAGAGTTGGGGTCTGTCAGTTCAGCAATGATGTCTTCCAGAATTCTATCTG
AAAACCTACAGATCCCAGGCCCGGTGCTGGACGCCATACGGCGCCTGAGGCTCAGAGGGGGTTCCCCACTGAAC
ACTGGCAAGGCTCTCGAATTTGTGGCAAGAACTCTTTGTTAAGTCTGCGGGGAGTCGCATAGAAGACGGGGTG
CCCCAACACCTGGTCTTGGTCTGGGTGGAAATCCCAGGACGATGTGTCCAGGTTGCGCCAGGTGATCCGTTC
TCGGGCATTGTGAGTTTAGGGGTAGGAGACCGGAACATCGACAGAACAGAGCTGCAGACCATACCAATGACCCC
AGACTGGTCTTCACAGTGCAGAGTTTCCAGAGCTTCCCAACATAGAAGAAAGAAATCATGAACCTCGTTTGGACCC
TCCGCAGCCACTCCTGCACCTCCAGGGGTGGACACCCCTCCTCCTTCACGGCCAGAGAAGAAGAAAGCAGACATT
GTGTTCTGTGTTGGATGGTTCCATCAACTTCAGGAGGGACAGTTTCCAGGAAGTGCTTCGTTTTGTGTCTGAAATA
GTGGACACAGTTTATGAAGATGGCGACTCCATCCAAGTGGGGCTTGTCCAGTACAACCTCTGACCCCACTGACGAA
TTCTTCTGAAGGACTTCTCTACCAAGAGGCAGATTATTGACGCCATCAACAAAGTGGTCTACAAAGGGGGAAGA
CACGCCAACACTAAGGTGGGCCTTGAGCACCTGCGGGTAAACCACTTTGTGCCTGAGGCAGGCAGCCGCTGGAC
CAGCGGGTCCCTCAGATTGCCTTTGTGATCACGGGAGGAAAGTCGGTGGAAAGATGCACAGGATGTGAGCCTGGCC
CTCACCCAGAGGGGGGTCAAAGTGTTTGTGCTGTTGGAGTGAGGAATATCGACTCGGAGGAGGTGGAAAGATAGCG
TCCAACAGCGCCACAGCGTTCCGCGTGGGCAACGTCCAGGAGCTGTCCGAACTGAGCGAGCAAGTTTTGGAAACT
TTGATGATGCGATGCATGAAACCTTTGCCCTGGTGTAACTGATGCTGCCAAAGCTTGTAATCTGGATGTGATT
CTGGGGTTTTGATGGTTCTAGAGACCAGAATGTTTTTGTGGCCAGAAAGGGCTTCGAGTCCAAGGTGGACGCCATC
TTGAACAGAATCAGCCAGATGCACAGGGTCAGCTGCAGCGGTGGCCGCTCGCCACCGTGCCTGTGTGCTAGTGGTG
GCCAACACGCCCTCGGGCCCCGTGGAGGCCTTTGACTTTGACGAGTACCAGCCAGAGATGCTCGAGAAGTTCCGG
AACATGCGCAGCCAGCACCCCTACGTCTCACGGAGGACACCCCTGAAGGTCTACCTGAACAAGTTTACAGACAGTCC
TCGCCGGACAGCGTGAAAGGTGGTCATTATTTTACTGATGGAGCAGACGGAGATCTGGCTGATTTACACAGAGCA
TCTGAGAACCTCCGCCAAGAAGGAGTCCGTGCCTTGATCCTGGTGGGCCCTGAACGAGTGGTCAACTTGGAGCGG
CTAATGCATCTGGAGTTTGGGCGAGGGTTTATGTATGACAGGCCCTGAGGCTTAACCTTGCTGGACTTGGATTAT
GAACTAGCGGAGCAGCTTGACAACATTGCCGAGAAAGCTTGCTGTGGGGTTCCCTGCAAGTGCTCTGGGCAGAGG
GGAGACCGCGGGCCATCGGCAGCATCGGGCCAAAGGGTATTCTTGAGAGAAGACGGCTACCGAGGCTATCCTGGT
GATGAGGGTGGACCCGGTGAAGCTGGTCCGCTGGTGTGAACGGCACTCAAGGTTTCCAGGGCTGCCCGGGCCAG
AGAGGAGTAAAGGGCTCTCGGGGATCCCAGGAGAGAAGGGCGAAGTAGGAGAAATTGGACTGGATGGTCTGGAT
GGTGAAGATGGAGACAAAGGATTACCTGGTTCTTCTGGAGAGAAAGGGAACTCTGGAAGAAGGGGTGATAAAGGA
CCTCGAGGAGAGAAAGGAGAAAGAGGAGATGTTGGGATTCGAGGGGACCCGGGTAAACCAGGACAAGACAGCCAG
GAGAGAGGACCCAAAGGAGAAACCGGTGACCTCGGCCCATGGGTGTCCAGGGGAGAGATGGAGTACCTGGAGGA
CCTGGAGAACTGGGAAGAATGGTGGCTTTGGCCGAAGGGGACCCCCGGAGCTAAGGGCAACAAGGGCGGTCTCT
GGCCAGCCGGGCTTTGAGGGAGAGCAGGGGACCAGAGGTGCACAGGGCCAGCTGGTCTGCTGGTCTCCAGGG
CTGATAGGAGAAACAAGGCATTTCTGGACCTCGGGGAAGCGGAGGTGCCGCTGGTGCTCTGGAGAACGAGGCAGA
ACCGGTCCACTGGGAAGAAAGGGTGAGCCCGGAGAGCCAGGACCAAAAGGAGGAATCGGGGAACCGGGGCCCTCGT
GGGGAGACGGGAGATGACGGGAGAGACGGAGTTGGCAGTGAAGGACGCAGAGGCCAAAAAGGAGAAAGAGGATTT

1103/6881
FIGURE 1028C

CCTGGATACCCAGGACCAAAGGGTAACCCAGGTGAACCTGGGCTAAATGGAACAACAGGACCCAAAGGCATCAGA
GGCCGAAGGGGAAAATTTCGGGACCTCCAGGGATAGTTGGACAGAAGGGAGACCCTGGCTACCCAGGACCAGCTXXX
XXXXXXXXGGCAACAGGGGCGACTCCATCGATCAATGTGCCCTCATCCAAAGCATCAAAGATAAATGCCCTTGCTGT
TACGGGGCCCTGGAGTGCCCGTCTTCCCAACAGAACTAGCCTTTGCTTTAGACACCTCTGAGGGAGTCAACCAA
GACACTTTTCGGCCGGATGCGAGATGTGGTCTTGAGTATTGTGAATGACCTGACCATTGCTGAGAGCAACTGCCCA
CGGGGGGGCCCGGGTGGCTGTGGTCACCTACAACAACGAGGTGACCACGGAGATCCGGTTTGCTGACTCCAAGAGG
AAGTCGGTCCCTCCTGGACAAGATTAAGAACCTTCAGGTGGCTCTGACATCCAAACAGCAGAGTCTGGAGACTGCC
ATGTCGTTTGTGGCCAGGAACACATTTAAGCGTGTGAGGAATGGATTCCCTAATGAGGAAAGTGGCTGTTTTCTTC
AGCAACACACCCACAAGAGCATCCCCACAGCTCAGAGAGGCTGTGCTCAAGCTCTCAGATGCGGGGATCACCCCC
TTGTTTCCTTACAAGGCAGGAAGACCGGCAGCTCATCAACGCTTTGCAGATCAATAACACAGCAGTGGGGCATGCG
CTTGTCCTGCCTGCAGGGAGAGACCTCACAGACTTCCTGGAGAATGTCTCAGTGTGATGTTTGCTTGGACATC
TGCAACATCGACCCATCCTGTGGATTGTGGCAGTTGGAGGCCTTCCTTCAGGGACAGGAGAGCGGCAGGGAGCGAT
GTGGACATCGACATGGCTTTCATCTTAGACAGCGCTGAGACCACCACCTGTTCCAGTTCAATGAGATGAAGAAG
TACATAGCGTACCTGGTCAGACAACCTGGACATGAGCCCAGATCCCAAGGCCTCCAGCACTTCGCCAGAGTGGCA
GTTGTGCAGCACGCGCCCTCTGAGTCCGTGGACAATGCCAGCATGCCACCTGTGAAGGTGGAATTCTCCCTGACT
GACTATGGCTCCAAGGAGAAGCTGGTGGACTTCCTCAGCAGGGGAATGACACAGTTGCAGGGAACCAGGGCCTTA
GGCAGTGCCATTGAATACACCATAGAGAATGTCTTTGAAAAGTGCCCCAAACCCACGGGACCTGAAAATTGTGGTC
CTGATGCTGACGGGCGAGGTGCCGGAGCAGCAGCTGGAGGAGGCCAGAGAGTCACTCTGCAGGCCAAATGCAAG
GGCTACTTCTTCGTGGTCCCTGGGCATTGGCAGGAAGGTGAACATCAAGGAGGTATACACCTTCGCCAGTGAGCCA
AACGACGTCTTCTTCAAATTAGTGGACAAGTCCACCGAGCTCAACGAGGAGCCTTTGATGCGCTTCGGGAGGCTG
TTGCCATCCTTCGTACAGAGTGAATGCTTTTTACTTGTCCCCAGATATCAGGAAACAGTGTGATTGGTTCCAA
GGGGACCAACCCACAAAGAACCTTGTGAAGTTTGGTCACAAACAAGTAAATGTTCCGAATAACGTTACTTCAAGT
CCTACATCCAACCCAGTGACGACAACGAAGCCGGTGACTACGACGAAGCCGGTGACCACCACAACAAAGCCTGTA
ACCACCACAACAAAGCCTGTGACTATTATAAATCAGCCATCTGTGAAGCCAGCCGCTGCAAGCCGGCCCCCTGCG
AAACCTGTGGCTGCCAAGCCTGTGGCCACAAGACGGCCACTGTTAGACCCCCAGTGGCGGTGAAGCCAGCAACG
GCAGCGAAGCCTGTAGCAGCAAAGCCAGCAGCTGTAAGACCCCCCGCTGCTGCTGCAAAACCAGTGGCGACCAAG
CCTGAGGTCCCTAGGCCACAGGCAGCCAAACCAGCTGCCACCAAGCCAGCCACCACTAAGCCCATGGTTAAGATG
TCCCGTGAAGTCCAGGTGTTTGAGATAACAGAGAACAGCGCCAAACTCCACTGGGAGAGGCCTGAGCCCCCGGT
CCTTATTTTTATGACCTCACCGTCACCTCAGCCCATGATCAGTCCCTGGTTCTGAAGCAGAACCTCACGGTCACG
GACCGCGTCATTGGAGGCCTGCTCGCTGGGCAGACATAACCATGTGGCTGTGGTCTGCTACCTGAGGTCTCAGGTC
AGAGCCACCTACCATGGAAGTTTCAGTACAAAGAAATCTCAGCCCCCACCTCCACAGCCAGCAAGGTGAGCTTCT
AGTTCAACCATCAATCTAATGGTGAGCACAGAACCATTGGCTCTCACTGAAACAGATATATGCAAGTTGCCGAAA
GACGAAGGAACCTGCAGGGATTTCATATTAAATGGTACTATGATCCAAACACCAAAAGCTGTGCAAGATTCTGG
TATGGAGGTTGTGGTGGAACGAAAACAAATTTGGATCACAGAAAAGTGTGAAAAGGTTTGCCTCCTGTGCTC
GCCAAACCCGGAGTCATCAGTGTGATGGGAACCTAAGCGTGGGTGGCCAACATCATATACCTCTTGAAGAAGAAG
GAGTCAGCCATCGCCAACCTTGTCTCTGTAGAAGCTCCGGGTGTAGATTCCCTTGCACTGTATCATTTTCATGCTTT
GATTTACACTCGAACTCGGGAGGGAACATCCTGCTGCATGACCTATCAGTATGGTGCTAATGTGTCTGTGGACCC
TCGCTCTCTGTCTCCAGGCAGTTCTCTCGAATACTTTGAATGTTGTGTAACAGTTAGCCACTGCTGGTGTTTATG
TGAACATTCCATCAATCCAAATTCCCTCTGGAGTTTCATGTTATGCCGTGTGAGGCÁAATGTAAAGTCTAGAA
AATAATGCAATGTACGGCTACTCTATATACTTTTGCTTGGTTTCATTTTTTTTCCCTTTTAGTTAAGCATGACT
TTAGATGGGAAGCCTGTGTATCGTGGAGAAACAAGAGACCAACTTTTTCATTCCCTGCCCCCAATTTCCAGACT
AGATTTCAAGCTAATTTCTTTTTCTGAAGCCTCTAACAATGATCTAGTTCAGAAGGAAGCAAAATCCCTTAAT
CTATGTGCACCGTTGGGACCAATGCCTTAATTAAAGAATTTAAAAAGTTGTAATAGAGAATATTTTTGGCATTC
CTCTAATGTTGTGTGTTTTTTTTTTTTTGTGTGCTGGAGGGAGGGGATTAATTTTAAATTTTAAATGTTTAGGAA
ATTTATACAAAGAACTTTTTAATAAAGTATATTGAAAGTTT

1104/6881
FIGURE 1029

AGCCCAGCGAGGCCTGTGCTGTGAGGGGCTGTGCTGTGCCAGGGGAGGCCCGCACCCGGAAGCCCAGAGGAGA
GTGTGCACTCACGGAGCCCTCCTGGCAGGGCCGCGTCTCTGGAGCAGCAGACCCGTGTCCCTCTGGGAGGTCAAC
TGCGGCCTCACAGCTGGGCCTGTCCAGCACAGCCCTTGTGTGGAGGGCGCACCCCGTGTCTCAGCACCCCACT
GTTGAGTGCCCTTGACCTGCAGAGGGGAGCCTGTGCTGGTCCCGGGCGTCTGTGTGGCTCCTGGGTGCCCATCTGC
ACCCCTGGCCCTGCTCTGGGCTTCAGTGGAGCCGTGCCACCGTGGGAGTGTCCAGGGTCCCTGACGTAGCCCTGAG
ACGTGGCCAGCTCCCTGGCCTGTGCGCCGACAGTGGGCCCTTGTCTCTGCTCTGGGTGAGGCGAGGCAGCCACC
CATGATGAGCTCTGCAGCCTTCCAAGGTGGCTGAGCATGGGGGTCCCTCGTACCCCTTCACGGACAGTGCTCTT
CGAGCGGGAGAGGACGGGCCTGACCTACCGCGTGCCCTCGTTGCTCCCCGTGCCCCCGGGGCCACCCCTGCTGGC
CTTTGTGGAGCAGCGGCTCAGCCCTGACGACTCCACGCCCACCGCCTGGTGCTGAGGAGGGGCACGCTGGCCGG
GGGCTCCGTGCGGTGGGGTGCCCTGCACGTGCTGGGGACAGCAGCCCTGGCGGAGCACCGGTCCATGAACCCCTG
CCCTGTGCACGATGCTGGCACGGGCACCGTCTTCCTCTTCTTCATCGCGGTGCTGGGCCACACGCTGAGGCCGT
GCAGATCGCCACGGGAAGGAACGCCGCGCGCCTCTGCTGTGTGGCCAGCCGTGACGCCGGCCTCTCGTGGGGCAG
CGCCCGGGACCTCACCGAGGAGGCCATCGGTGGTGCGGTGCAGGACTGGGCCACATTGCTGTGGGTCCCGGCCA
CGGCGTGCAGCTGCCCTCAGGCCGCTGCTGGTACCCGCCTACACCTACCGCGTGGACCGCCGAGAGTGTTTTGG
CAAGATCTGCCGGACCAGCCCTCACTCCTTCGCCTTCTACAGCGATGACCACGGCCGCACCTGGCGCTGTGGAGG
CCTCGTGCCCAACCTGCGCTCAGGCGAGTGCCAGCTGGCGGGCGGTGGACGGTGGGCAGGCCGGCAGCTTCCTCTA
CTGCAATGCCCGGAGCCCACTGGGCAGCCGTGTGCAGGCGCTCAGCACTGACGAGGGCACCTCCTTCCTGCCCGC
AGAGCGCGTGGCTTCCCTGCCCCGAGACTGCCTGGGGCTGCCAGGGCAGCATCGTGGGCTTCCAGCCCCCGCCCC

1105/6881
FIGURE 1030

GAATTGGCAGCCAACATGGCGGCGGAACGCGGCGCGGGGCAGCAACAGTCGCAGGAGATGATGGAGGTTGACAGG
CGGGTCGAGTCTGAAGAATCCGGCGATGAAGAAGGGAAGAAACACAGCAGTGGCATCGTGGCCGACCTCAGTGAA
CAGAGCCTGAAGGATGGGGAGGAGCGGGGGAGGAGGCCAGAAAGAAGACATGAGCTGCCTGTGGACATGGAA
ACCATCAACCTGGACAGAGATGCAGAGGATGTTGATTTGAATCACTATCGCATAGGGAAGATTGAAGGATTTGAG
GTACTGAAGAAAGTGAAGACTCTCTGCCTCCGCCAAAATTTAATTAAATGCATTGAGAATCTGGAGGAGCTACAG
AGTCTTCGAGAGCTGGATCTTTACGACAACCAGATCAAGAAGATTGAGAATCTGGAGGCGCTAACAGAGCTGGAG
ATTCTAGATATTTCTTTTAATCTGCTGAGAAACATCGAAGGGGTTGACAAGTTGACACGACTGAAAAAATCTTTC
TTGGTCAACAATAAAATCAGTAAATTGAGAACTTAAGCAACTTACATCAACTACAGATGCTAGAGCTGGGATCT
AACCGCATCCGGGCAATCGAAAATATCGACACCTTAACCAACCTGGAGAGTTTGTTTTTGGGGAAAAACAAAATT
ACTAACTTCAGAACCTGGATGCGCTCACCAACCTGACAGTCCTCAGTATGCAGAGCAACCGGCTGACCAAGATC
GAGGGTCTGCAGAACCTGGTGAACCTGCGGGAGCTGTACCTTAGCCACAATGGCATCGAGGTCATCGAGGGCCTG
GAGAACATAACAACTCACGATGTTGGACATTGCATCAAAATAGAATCAAAAAGATTGAAAATATCAGCCATCTA
ACAGAGCTGCAAGAGTTCTGGATGAACGACAATCTCCTTGAGAGCTGGAGCGACCTCGACGAGCTGAAGGGAGCC
AGGAGCCTGGAGACAGTGTACCTGGAGCGGAACCCCTTGAGAAAGGACCCCAAGTACCGGCGGAAGGTCATGCTC
GCCCTCCCCTCCGTGCGGCAGATCGATGCCACGTTTCGTCAGGTTCTTGAGTCCTTCTTGGCTCCTCATGTGGTCCC
TCTCCTCGGAAGAACTGCCCAGCCACGGGTTTTTAACCCACCTGTTGCTCCTGAGGTCGTCACCTATATCAACAGT
CACAAACCCAATGGCAATAAAGGCACTGACGATAGCTGGCGCGCGACGCCACACACCATTTTCAGATGCCGTT
GCAATTAAATCTTGCCACACTGTC

1106/6881
FIGURE 1031

MAAERGAGQQQSQEMMEVDRRVESEESGDEEGKKHSSGIVADLSEQSLKDGEERGEEDPEEEHELPVDMETINLD
RDAEDVDLNHYRIGKIEGFVLKKVKTLCRQNLKCIENLEELQSLRELDLYDNQIKKIEENLEALTELEILDIS
FNLLRNIEGVDKLTRKKLFLVNNKISKIENLSNLHQLMLELGSNRIRAIENIDTLTNLESFLGKNKITKLQN
LDALTNLTVLSMQSNRLTKIEGLQNLVNLRELYLSHNGIEVIEGLENNNKLTMLDIASNRIKKIENISHLTELQE
FWMNDNLLESWSDLDELKGARSLETVYLERNPLQKDPQYRRKVMLALPSVRQIDATFVRF

1107/6881
FIGURE 1032A

CAAAAGCTGGCAGGCTGACAGAGGCGGCCCTCAGGACGGACCTTCTGGCTACTGACCGTTTTGCTGTGGTTTTCCCG
GGATTGTGTGTAGGTGTGAGATCAACCATGAGTTCCGTTGCAGTTTTGACCCAAGAGAGTTTTGCTGAACACCGA
AGTGGGCTGGTTCCGCAACAAATCAAAGTTGCCACTCTAAATTCAGAAGAGGAGAGCGACCCCTCCAACCTACAAG
GATGCCCTTCCCTCCACTTCCCTGAGAAAGCTGCTTGCCCTGGAAAGTGCCAGGAACCCCTCTGGAGCCTGGGGGAAC
AAGATCCGACCCATCAAGGCTTCTGTCACTCACTCAGGTGTTCCATGTACCCCTGGAGGAGAGAAAATACAAGGAT
ATGAACCAGTTTGGAGAAGGTGAACAAGCAAAAATCTGCCTTGAGATCATGCAGAGAACTGGTGCTCACTTGGAG
CTGTCTTTGGCCAAAGACCAAGGCCTCTCCATCATGGTGTGAGGAAAGCTGGATGCTGTATGAAAGCTCGGAAG
GACATTGTTGCTAGACTGCAGACTCAGGCCTCAGCAACTGTTGCCATTCCCAAAGAACCCATCGCTTTGTTATT
GGCAAAAATGGAGAGAACTGCAAGACTTGGAGCTAAAACTGCAACCAAAAATCCAGATCCCACGCCCCAGATGAC
CCCAGCAATCAGATCAAGATCACTGGCACCAAGAGGGCATCGAGAAAGCTCGCCATGAAGTCTTACTCATCTCT
GCCGAGCAGGACAAACGTGCTGTGGAGAGGCTAGAAGTAGAAAAGGCATTCCACCCCTTCATCGCTGGGCCGTAT
AATAGACTGGTTGGCGAGATCATGCAGGAGACAGGCACGCGCATCAACATCCCCCACCAGCGTGAACCGGACA
GAGATTGTCTTCACTGGAGAGAAGGAACAGTTGGCTCAGGCTGTGGCTCGCATCAAGAAGATTTATGAGGAGAAG
AAAAAGAAGACTACAACCATTGCAGTGGAAGTGAAGAAAATCCCAACACAAGTATGTCAATTGGGCCCCAAGGCAAT
TCATTGCAGGAGATCCTTGAGAGAACTGGAGTTTCCGTTGAGATCCACCCCTCAGACAGCATCTCTGAGACTGTA
ATACTTCGAGGCGAACCTGAAAAGTTAGGTGAGGCGTTGACTGAAGTCTATGCCAAGGCCAATAGCTTCACCGTC
TCCTCTGTGCGCCGCCCTTCCTGGCTTCACCGTTTCATCATTTGGCAAGAAAGGGCAGAACCTGGCCAAAATCACT
CAGCAGATGCCAAAGGTTACATCGAGTTCACAGAGGGCGAAGACAAGATCACCTGGAGGGCCCTACAGAGGAT
GTCAATGTGGCCAGGAACAGATAGAAGGCATGGTCAAAGATTTGATTAACCGGATGGACTATGTGGAGATCAAC
ATCGACCACAAGTTCACAGGCACCTCATTGGGAAGAGCGGTGCCAACATAAACAGAATCAAAGACCAGTACAAG
GTGTCCGTGCGCATCCCTCCTGACAGTGAGAAGAGCAATTTGATCCGCATCGAGGGGGACCCACAGGGCGTGCAG
CAGGCCAAGCGAGAGCTGCTGGAGCTTGATCTCGCATGGAATAAGAGCTACCAAGGATCTAATCATTGAGCAA
AGATTTTCATCGCACAATCATTGGGCAGAAGGGTGAACGGATCCGTGAAATTCGTGACAAATTCAGAGGTCATC
ATTAACCTTTCAGACCCAGCACAAAAAAGTGACATTGTCCAGCTCAGAGGACCTAAGAATGAGGTGGAATAATGC
ACAAAATACATGCAGAAGATGGTGGCAGATCTGGTGGAAAATAGCTATTCAATTTCTGTTCCGATCTTCAAACAG
TTTCACAAGAATATCATTGGGAAAGGAGGCGCAAACATTAATAAGATTTCGTGAAGAAAGCAACACCAAAAATCGAC
CTTCCAGCAGAGAATAGCAATTCAGAGACCATTATCATCACAGGCAAGCGAGCCAACTGCGAAGCTGCCCGGAGC
AGGATTCTGTCTATTTCAGAAAGACCTGGCCAACATAGCCGAGGTAGAGGTCTCCATCCCTGCCAAGCTGCACAAC
TCCCTCATTGGCACCAAGGGCCGTCTGATCCGCTCCATCATGGAGGAGTGCAGCGGGGTCCACATTCACTTTCCC
GTGGAAGGTTTCAGGAAGCGACACCGTTGTTATCAGGGGCCCTTCCTCGGATGTGGAGAAGGCCAAGAAGCAGCTC
CTGCATCTGGCGGAGGAGAAGCAAACCAAGAGTTTCACTGTTGACATCCGCGCCAAGCCAGAATACCACAAAATTC
CTCATCGGCAAGGGGGGCGGCAAAAATTCGCAAGGTGCGCGACAGCACTGGAGCACGTGTCTCTTCCCTGCGGCT
GAGGACAAGGACCAGGACCTGATCACCATCATTGGAAGGAGGACGCCGTCCGAGAGGCACAGAAGGAGCTGGAG
GCCTTGATCCAAAACCTGGATAATGTGGTGAAGACTCCATGCTGGTGGACCCCAAGCACCACCGCCACTTCGTC
ATCCGCAGAGGCCAGGTCTTGCGGGAGATTGCTGAAGAGTATGGCGGGGTGATGGTCAGCTTCCCACGCTCTGGC
ACACAGAGCGACAAAGTCACCCCTCAAGGGCGCCAAGGACTGTGTGGAGGCAGCCAAGAAACGCATTTCAGGAGATC
ATTGAGGACCTGGAAGCTCAGGTGACATTAGAATGTGCTATACCCAGAAATTCCATCGATCTGTCTATGGGCCCC
AAAGGTTCCAGAATCCAGCAGATTACTCGGGATTTAGTGTTCAAATTAAATTCAGACAGAGAGGAGAACGCA
GTTACAGTACAGAGCCAGTTGTCCAGGAGAATGGGGACGAAGCTGGGGAGGGGAGAGAGGCTAAAGATTGTGAC
CCCGGCTCTCCAAGGAGGTGTGACATCATCATCTCTGGCCGAAAGAAAAGTGTGAGGCTGCCAAGGAAGCT
CTGGAGGCATTGGTTCTCTCACCATTGAAGTAGAGGTGCCCTTTGACCTTCACCGTTACGTTATTGGGCAGAAA
GGAAGTGGGATCCGCAAGATGATGGATGAGTTTGAGGTGAACATACATGTCCCGGCACCTGAGCTGCAGTCTGAC
ATCATCGCCATCACGGGCCTCGCTGCAAAATTTGGACGGGGCCAAGGCTGGACTGCTGGAGCGTGTGAAGGAGCTA
CAGGCCGAGCAGGAGGACCGGGCTTTAAGGAGTTTTAAGCTGAGTGTCACTGTAGACCCCAAATACCATCCCAAG
ATTATCGGGAGAAAGGGGGCAGTAATTACCCAAATCCGGTTGGAGCATGACGTGAACATCCAGTTTCTTGATAAG
GACGATGGGAACCAGCCCCAGGACCAAAATTACCATCACAGGGTACGAAAAGAACACAGAAGCTGCCAGGGATGCT
ATACTGAGAATTGTGGGTGAACTTGAGCAGATGGTTTCTGAGGACGTCCCGCTGGACCACCGCGTTACGCCCCG
ATCATTGGTGGCCGCGGCAAGGCCATTGCAAAAATCATGGACGAATTCAAGGTGGACATTGCTTCCCACAGAGC

1108/6881
FIGURE 1032B

GGAGCCCCAGACCCCAACTGCGTCACTGTGACGGGGCTCCCAGAGAATGTGGAGGAAGCCATCGACCACATCCTC
AATCTGGAGGAGGAATACCTAGCTGACGTGGTGGACAGTGAGGCGCTGCAGGTATACATGAAACCCCCAGCACAC
GAAGAGGCCAAGGCACCTTCCAGAGGCTTTGTGGTGCGGGACGCACCCTGGACCGCCAGCAGCAGTGAGAAGGCT
CCTGACATGAGCAGCTCTGAGGAATTTCCAGCTTTGGGGCTCAGGTGGCTCCCAAGACCCTCCCTTGGGGCCCC
AAACGA**TAA**TGATCAAAAAGAACAGAACCCCTCTCCAGCCTGCTGACCCAAACCCAAACCACACAATGGTTTGTCTC
AATCTGACCCAGCGGCTGGACCCTCCGTAAATTGTTGACGCTCTTCCCCCTTCCCGAGGTCCCGCAGGGAGCCTA
GCGCCTGGCTGTGTGTGCGGCCGCTCCTCCAGGCCTGGCCGTGCCCGCTCAGGACCTGCTCCACTGTTTAACT
AAACCAAGGTCATGAGCATTCTGTGCTAAGATAACAGACTCCAGCTCCTGGTCCACCCGGCATGTCAGTCAGCACT
CTGGCCTTCATCACGAGAGCTCCGCAGCCGTGGCTAGGATTCCACTTCCTGTGTCATGACCTCAGGAAATAAACG
TCCTTGACTTTATAAAAGCC

1109/6881
FIGURE 1033

MSSVAVLTQESFAEHRSGLVPQQIKVATLNSEEEEDPPTYKDAFPPLPEKAACLES AQEPAGAWGNKIRPIKASV
ITQVFHVPLEERKYKDMNQFGEQAKICLEIMQRTGAHLELSLAKDQGLSIMVSGKLDVAMKARKDIVARLQTQ
ASATVAIPKEHHRFVIGKNGEKLQDLELKTATKIQIPRPDDPSNQIKITGTKEGIEKARHEVLLISAEQDKRAVE
RLEVEKAFHPFIAGPYNRLVGEIMQETGTRINIPPPSVNRTEIVFTGEKEQLAQAVARIKKIYEEKKKKTTTIAV
EVKKSQHKYVIGPKGNSLQEILERTGVSVEIPPSDSISSETVILRGEPEKLGQALTEVYAKANSFTVSSVAAPSWL
HRFIIIGKKGQNLAKITQQMPKVHIEFTEGEDKITLEGPTEDVNVAQEQIEGMVKDLINRMDYVEINIDHKFHRHL
IGKSGANINRIKDQYKVSVRIPPDSEKSNLIRIEGDPQGVQQA KRELLELASRMENERTKD LII EQRFHRTIIGQ
KGERIREIRDKFPEVIINFPDPAQKSDIVQLRGPKNEVEKCTKYMQKMVADLVENSYSISVPIFKQFHKNIIIGKG
GANIKKIREESNTKIDLPAENSNETIIITGKRANCEAARSRLSIQKDLANIAEVEVSIPAKLHNSLIGTKGRL
IRSIMEECGGVHIHFPVEGSGSDTVVIRGPSSDVEKAKKQLLHLAEEKQTKSFTVDIRAKPEYHKFLIGKGGKI
RKVRDSTGARVIFPAAEDKDQDLITIIIGKEDAVREAQKELEALIQNLDNVVEDSMLVDPKHHRHFVIRRGQVLRE
IAEEYGGVMVSFPRSGTQSDKVT LKGAKDCVEAAKKRIQEIIEDLEAQVTLECAIPQKFHRSVMGPKGSRIQQIT
RDFSVQIKFPDREENAVHSTEPVVQENGDEAGEGREAKDCD PGSPRRCDIIIIISGRKEKCEAAKEALEALVPVTI
EVEVPFDLHRYVIGQKSGIRKMMDEFEVNIHVPAPELQSDIIAITGLAANLDRAKAGLLERVKELQAEQEDRAL
RSFKLSVTVDPKYHPKIIIGRKGAVITQIRLEHDVNIQFPDKDDGNQPDQITITGYEKNTEAARDAILRIVGELE
QMVSEDVPLDHRVHARIIGARGKAIRKIMDEFKVDIRFPQSGAPDPNCVTVTGLPENVEEAIDHILNLEEEYLAD
VVDSEALQVYMKPPAHEEAKAPSRGFVVRDAPWTASSEKAPDMSSSEEFPSFGAQVAPKTLPWGPKR

1110/6881
FIGURE 1034

CCCAGCTCGGTGCTGCCGCCATCTTCTTGGAGGACAGGAGGAGAGGCCGAAGGCTCCCCCTCCCCGTGATCGCTCC
GCACTCCCCGCCACCACCTGCCCTCCCGCGACCGCCTCTCTCCTCCTCAGTGGGCACTTGTCTCCTTCTAACAAC
GGCCTTCCCCCCTCCAGTTACCCACCGCAAGGCGAAGATTCTCATTACCTGTTCCACTCTTATAAGCATAAGA
AAACCGAGCTCATAAGACGAAGCTTCACAAAAGATGTCTAAGCAACAGCCAACTCAGTTTATAAATCCAGAAACA
CCTGGCTATGTTGGATTTGCAAACCTCCCCAATCAAGTTCACCGAAAATCAGTGAAAAAAGGTTTTGAGTTCACA
CTGATGGTGGTGGTGAATCAGGTCTAGGAAAATCGACTCTCATAAACAGCCTATTCCCTAACTGATCTGTACCCA
GAAAGAGTCATACCTGGAGCAGCAGAAAAAATTGAAAGAACTGTCCAGATTGAGGCTTCAACTGTTGAAATTGAA
GAGCGAGGGGTCAAGCTACGCCTGACAGTGGTAGATACCCCTGGCTATGGTGACGCTATCAACTGCAGAGATTGT
TTTAAGACAATTATCTCCTATATTGATGAGCAATTTGAGAGGTACCTGCATGACGAGAGCGGCTTGAACAGGCGG
CACATCATTGATAATAGGGTGCATTGTTGCTTTTACTTTATTTACCTTTTGGACATGGACTTAAGCCCTTAGAT
GTGGCGTTTATGAAGGCAATACACAACAAGGTGAATATTGTGCCTGTCATTGCAAAAGCTGACACTCTCACCCCTG
AAGGAACGGGAGCGGCTGAAGAAAAGGATTCTGGATGAAATTGAAGAACATAACATCAAAATCTATCACTTACCT
GATGCAGAATCAGATGAAGATGAAGATTTTAAAGAGCAGACTAGACTTCTCAAGGCTAGCATCCCATTTCTCTGTG
GTTGGATCCAATCAGTTGATTGAAGCCAAAGGAAAGAAGGTCAGAGGCCGCTCTACCCCTGGGGTGTGTGGAA
GTGGAGAACCCAGAGCACAATGACTTTCTGAAGCTGAGAACCATGCTCATCACCCACATGCAGGATCTCCAGGAG
GTGACCCAGGACCTTCATTATGAAAACCTCCGTTCTGAGAGACTCAAGAGAGGCGGCAGGAAAGTGGAGAATGAG
GACATGAATAAAGACCAGATCTTGCTGGAAAAAGAAGCTGAGCTCCGCCGATGCAAGAGATGATTGCAAGGATG
CAGGCGCAGATGCAGATGCAGATGCAGGGCGGGGATGGCGATGGCGGGGCTCTCGGGCACCACGTGTAAAGGTGAT
GTGCACATATCAAGAAGTCAGAGAAAACACTTTCTGGATAAAAAAGAAAACATTCCAGATGCATGATCCAGCTG
TGTGTTTTCAATCCTTGGGAGGGTGCCATCCACATTTTAACAGTACCTGTGCCTGAGAATTTAATTTTTAAAGA
CTTTGATGTGTTTTTGTATGAAGTACTTTTAACGTATGTATTTTATTGCTGTGTGCACACTCTGTGTTTTGTGAGG
TGAATGTCTTCTTTTCTTTCTCCCTAACCACTAATGTTAGAAATTGATTTCCAAGAATCGGCATGTATACTTAAT
ACTGAATTTCTTTGATTTAACTGACTTAACAACCTGACTAACCATTGATGAGCACTCCTGATTTTTATCTAGAACA
TTCAGATTTACCATAATGTTTCCTTAGTGGTAGAGGTGTGTGCCTAGTGATGTAGAAAGATACACTGACTTGGTGC
AAGGCCATCTGCTTACCACATCACACCACTTGGAGATCTTTGCTTCTTGCTTTTATGTTTGTACACAACACCTA
AAACCAGTTTTGCTGCTATAATTTCTATACTGTTGATTCGTCTGCGATTTTATCTGTTAACCATAAATAACATAAT
AGAATTTCTTAATGAGATATATCTTTATACTTAAACAGCTTTTTTTAGAGGTGAGTTTTAAAGAAGTCTCTTAATT
CTGATGCTAGGTTGTTTTTAAACCCTATGCAAAGAACTCACCACAAGCCACCTTTTGTAGTGTCTCCACTAA
TACTGGTTATCCTGTGCTACAGAGAAAATCAAAGCAGTCATAAGCTCCAGTTTTCCGTATTGCAAAATAAGACTCT
TACCTACAAAATGAGATTCCAGTGAACATAATTTGGTTTTTACTCAACCAATTAATAATTTTTTAAAGGAAAATT
AGCAGTTGGTCTATTTCAGAAATCAAACCTTTTTATATTTTATACTGCACCTTTAGTGTATTTTCTGTCACTGTAGGT
ATAGAAGATCTGCCTCCCCCTGTGGAATTGGGGTCTGTTGGTGGGCTTGCCCCCTGAAGCCTGGCTTGGGTTGAAA
AGTGTTCGCCGCCCTAAGGCCTTGGTGCCCTGAACCTCTGATGCCTACCGGTTCTCCTGATTTGAGTTTCTTTA
AATACTCCCTTTTTGAGTAATTTTCTGATGGGAGGAAAGTAGCAGTCATCATCTTTTTGTGTGCAGGCTGTCTCA
TTTATTTTTTAGCCATTGTGCTTTTATTCAATTTTGTGTAATATAAACCCTGTGTGATGTCAAAGTGAAAGACATTT
CAAATCTGTAGCATAGGCTAGTGGGCAGGTCCGCACAGTCGAAGCCACACCTGGTCTGTTTTCTGTGCACTGTAG
CCTTAGTGTACCTTTCTTCTTGTGTCTCCTTATGGTACACTCCAGCGGTTGCCTTTTTTATCATTCTACTGAA
GTTGGGAAATTCAACCCAGAAATTGACAGATGAAAGGAGACAATGGTTGTGTAGGGAGATGGAGAAAATGCTTA
ATCTGAGGATGAGACAGGGTTTTTTTCAATTTTGTGGGGGCTAGAAAAACATAAAATGAGGCAGTTAAATAATAA
TAGTTAATGAAGGTGTGCTACAGAAAATAATCTGGTGTCTTGCTAACTTTGCCCTTCACTGTTGCTTAATTGTG
AACAGCCAAAAGCTATATGTTATGGCTTATTGTGTGAAGGTAACATAAGAAGTGGTGTTCATGACTTCAGAGTAC
ATCCATGCGGAGTCCATTATTTGAGTTTGACATTTAATAACTTTGCTGGAAAATCTGTAAAAAAGAAAAACAAGT
TTGCTAGTGACTAAGCCCCGCATATGTGAGTGAAAGTACTTCAGGCACGCTGCCTCCTGGTAACAGCTATGCAGG
GAGGGAGGACCCACACTGCTACACTTCTGATCCCTTTGGTTTTACTACCCAAATCTAAATAGATACTTTTGATA
ATAGATAACTGCTCTTTTACTAAGACATAGTCTCTACCTATAGAAATGTATTTTGAAAACACTTATTTTACACAG
CAATTTTGTATCCATTTAAACTAACCTTTTATCAATAAAGCACTATTGTTTAGATATT

1111/6881
FIGURE 1035

MSKQQPTQFINPETPGYVGFANLPNQVHRKSVKKGFETLMVVGESGLGKSTLINSFLTDLYPERVIPGAAEKI
ERTVQIEASTVEIEERGVLRLTVVDTPGYGDAINCRDCFKTII SYIDEQFERYLHDESGLNRRHIIDNRVHCCF
YFISPFHGHLKPLDVAFMKAIHNKVNI PVIAKADTLTLKERERLKKRILDEIEEHNIKIYHLPDAESDEDEDFK
EQTRLLKASIPFSVVGSNQLIEAKGKKVRGRLYPWGVVEVENPEHNDFLKLRTMLITHMQDLQEVTDLHYENFR
SERLKRGGGRKVENEDMNKDQILLEKEAELRRMQEMIARMQAQMOMQMQGGDGDGGALGHHV

1112/6881
FIGURE 1036

CACCGAGCGCCCCTGGTGTCCCTCGCAGTGGACTGACGCCGAGGGGCGAGCTAGCCGGCTCCGCGCCTCTCCGC
GGGATCCAGACGCCTCCTGGGGCTGCTGGCGGAGGGTCTGAGGCGGCGCGGCCATGGCTCACCTCCGGGGATTG
CCAACCAGCACTCTCGAGTGGACCCTGAGGAGCTCTTCACCAAGCTCGACCGCATTGGCAAGGGCTCGTTTGGGG
AGGTCTACAAGGGCATCGATAACCACACAAAGGAGGTGGTGGCCATCAAGATCATCGACCTGGAGGAGGCCGAGG
ATGAGATCGAGGACATCCAGCAGGAGATCACTGTCCTCAGTCAGTGGCGACAGCCCCTACATCACCCGCTACTTTG
GCTCCTACCTAAAGAGCACCAAGCTATGGATCATCATGGAGTACCTGGGCGGCGGCTCAGCACTGGACTTGCTTA
AACCAGGTCCCCTGGAGGAGACATACATTGCCACGATCCTGCGGGAGATTCTGAAGGGCCTGGATTATCTGCACT
CCGAACGCAAGATCCACCGAGACATCAAAGCTGCCAACGTGCTACTCTCGGAGCAGGGTGACGTGAAGCTGGCGG
ACTTTGGGGTAGCAGGGCAGCTCACAGACACGCAGATTAAGAGGAACACATTCTGTTGGGCACCCCCCTTCTGGATGG
CACCTGAGGTTCATCAAGCAGTCGGCCTACGACTTCAAGGCTGACATCTGGTCCCTGGGGATCACAGCCATCGAGC
TGGCCAAGGGGGAGCCTCCAACTCTGACCTCCACCCCATGCGCGTCTGTTCCTGATTCCCAAGAACAGCCAC
CCACACTGGAGGGCCAGCACAGCAAGCCCTTCAAGGAGTTCTGTTGGAGGCCTGCCTCAACAAAGACCCCCGATTCC
GGCCACGGCCAAGGAGCTCCTGAAGCACAAAGTTTCATCACACGCTACACCAAGAAGACCTCCTTCTCACGGAGC
TCATCGACCGCTATAAGCGCTGGAAGTCAGAGGGGCATGGCGAGGAGTCCAGCTCTGAGGACTCTGACATTGATG
GCGAGGCGGAGGACGGGGAGCAGGGCCCCATCTGGACGTTCCCCCTACCATCCGGCCGAGTCCACACAGCAAGC
TTCACAAGGGGACGGCCCTGCACAGTTTCAGAGAAGCCTGCGGAGCCCGTCAAGAGGCAGCCGAGGTCCAGTGCC
TGTCACGCTGGTCCGGCCCCGTCTTCGGAGAGCTCAAAGAGAAGCACAAAGCAGAGCGGCGGGAGCGTGGGTGCGC
TGGAGGAGCTGGAGAACGCCTTCAGCCTGGCCGAGGAGTCTGCCCCGGCATCTCAGACAAGCTGATGGTGCACC
TGGTGGAGCGAGTGCAGAGGTTTTACACAACAGAAACCACCTGACATCCACCCGCTGAAGCGCACTGCTGTTCA
GATAGGGGACGGAAGGTCGTTTGTGTTTTGTTCTGAGCTCCATAAGAACTGTGCTGACTTGGAAGGTGCCCTGTGC
TATGTCGTGCCTGCAGGGACACGTCGGATCCCGTGGGCCTCACATGCCAGGTACCAGGTACCGTCTCCTTCCA
CCCCTGCAGTGTGCTGTTGTGCACGTCAGGGACGCTGTTCTCTATGCCCACTGCCCTCCTCCTCTCCTGGCCCA
GCAGTATTGCTCACGGGGGCTCCAGCCGCCGGCGTGGCCCTCATGAGCTACGCCTGGGTCTTCTGCAGACTCATG
CAGCCCTATGGCCGCTCAGACCAAGGCGCAGAGCAACTATCAGGGCAGCTCTGCCTCCTCCTCCCATGAGGTGGG
GAGAGGCAACAGGGCAGCCCCAGAGGAGTGTCTGGCCGCTGTCTCCCGGGGCCCATGATGGCCATAGATTG
CCTTGTTGGTGTGGATCAGGTACTGTGTCTGCTCATAAGTACTTGTGTCATCCAGAATGTTTTGTTTTTAAGAA
AATTGAATTACTTGTTCCTGAAA

1113/6881
FIGURE 1037

GGCACGAGGCCAATCCCATGCCTGGGGGAGAGACAGCGGCTCAGGAGTGGGGGAGCACGGGCCTTCTACACCACA
TGGGAAGGCTCTGGCATGAGGTTTTCTTTGGGAAGGTTGTTTGGGCCCTGAAGTTCCATCTCCGAGAGTGGTG
TGCAGGGCAGGCCAGGGCCCATGCTGGCTGCAGTCTTTGTGGCTGCCTGCCTGGGCCAGCCTGTTTGGGAGCTGG
GACTGTGGGCTCGCCTTTTCGTACCTGGGCTCAGGTGCGGTGTGGCCACCGCCACCCTCATCCCCCTGCCTGGGAG
GCTCTCCCAGGGGCTGATGGGGGGGTTCTGTGAGGGAGAATCAGGGCTCGGGAAGCCACGCCTGGGAAGGCAGGA
CACAGGACACAGCAGCTTTCTTTGGAAATCTCCCAGGTGAGGATTCACATCCCAAATAAAATTCAGAAGCCAGG
TGGCCTGTGCTCCCCATGGGTGACCTCTGGAGGCAGTGGACCAAGATGCAGCAAGGAGAGGATGCAGAACAGCTT
CTTGCAAGACACCTGCTCCGGCATCCAGCGCTGCCTGGAGGCAGGAAGGAGAGGCAGGGCAGGACACGCTGGTC
TGAGATGAGGGGGAGCCCCATGGGCCCCAGGCAGGCTAGAGGAGGCACAGGCCCTGCCACGGCCAACTCAGGTCA
GCCAGCCTGAGGCTGTGGCCTCCAAAGGTCTGGGCGCACCCCCCAGGTGCGAGGTGTCTGAGGCCAGCCAACT
GCAGAGCACTCGCGCGTGGGTGGGCTGAGTGGAGGTGCCTGGGAGCTGCCTAAATTCAGAAGCCTCCACTGCCA
TGGAGACTGCCTGGCTGTGTCTCTCAGCCAGGTGCCGTGTTGGCCTTGGCTAGGACCCAGAGCCACACTGCAGC
CTCCGCCGACTCCCTCCTTCGGGCCTGCTCTAGTGAGGAGTGCTAAGCCAGGACCCAGAAACTCAGAGTTGAT
GGTGAGAGGAGGCCGCTGAGTCAGGACACCTGGCTTCTTGAAAAGTTCGCTCTGCCAGAAACCACCTAGGGACC
ACGTTAGCTGCCTTCCTTGAGCTCCCCAGGAGTCGGTTTTCCACATCTGTGAGGTGGAGGGCTGGTGTGGAGGTGC
TCATGGGGTGCGGTGCTTGGGAGACAGCCAGGCCCAGGGTGGCTGCTGCTTCCTGCTAAGTGGGGGAGGTGAGAC
AGATCTGGAAGCCGTCTCCCTCAGATGGTTTTATTAAATGCTTTATACTGCCGAGTCTGGGGGCTTGTTTTGGT
TTGGGGGCAGCCATCCTCCACCAGAAAGGGGGAGCTCCTTCCGCTGCGGCTCCAGATAGATGGGGATGCCGGGCT
CCAGGCCGACCAGCACTTGGGATCTGATGGGACACGGCCAGTGCTAGGGGTGCCAAGTCCAAGGCCTCCCACTG
GGAGTCATCGCTGAGAAGATGCCAATGTTTCATCCACCGGCTGCACAGGCACAACTCCCCACCCAGGACGGCT
GTGATGAGGTGGCCCTCCCTGTCAACCCTGGTCCCTGGAGTCCCAGCACCTGGGGCCCTGGTGGGGCTGATGTC
ACAGGTGTTTACTGTGCTGCTGCACTGGTCCATGCCAGCCTCACCCATGTGGGGACCACGGAAGGCACACTCCC
TTACCCCCGGTGCCGGGCCGTGCGGTCCCCCAGACGGACAGCAGCTGTGGCGACCTGCGTTTTCTCCCTGGGCCTG
TGCTTCCTGTAGTTAGTCCGTCCCCTGGTTCCCCTGTGGCTCAGAGGCCGCGTCCCTGGCTTGTACATATGTGAT
TGCTGTGGGCACACCCAGACCCCATGTCATAGCTGCCGTCCCGACGTCACGACGCCTGTCCCGATGTCTTACAC
CCGAGTGTTAGCCCTAGGCTCCTGTACTGTGCGTGCACTTGAGGCTCTGTCCAATTAAGAAATAAATGTGGCTCT
TACTCAACACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

1114/6881
FIGURE 1038

MRWPSLSLTVPGVPSTWGPGGADVTGVYCAAALVLCQPHPCGDHGRHTPLPPVPGRAVPQTDSSCGDLRFSLGLC
FL

1115/6881
FIGURE 1039

ATGGAGGAACGGCGGGCTCCGAGCCGCGCCCCGGAGTCCGCGAACTTCCGAGCGGGCGCCCCCTGAAGGACCTG
ACCCGCTTCGTGGATTTCAACATCAAAGGGCGCGACGTGATCGTGTTCTCCACATCCAGAAGACGGGGGGCACC
ACTTTCGGCCGGCACCTGGTGAAGAACATCCGGCTGGAGCAGCCTTGTAAGCTGCAAAGCGGGTCAGAAGAAGTGC
ACCTGCCACCGGCCTGGCAAGAAGGAGACGTGGCTCTTCTCCCGCTTCTCCACCGGCTGGAGCTGCGGGCTGCAC
GCCGACTGGACGGAGCTCACCAACTGCGTGCCGGCCATCATGGAGAAGAAGGACTGTCCCGCAACCACAGCCAC
ACCAAGTCTGACCCAGAGCGACCCCGCGCTCCCTGCCCCCTGCCGATGGTTTCCTGGCGTCTTCAGCGGTTGGCGC
CGTGGCTTTGGGGAGGGATGA

1116/6881
FIGURE 1040

ATGCTAACTAGTTACGCGACCCCCGAGCGGTCGGCGTCCCCCAACTTCTTAGAGGGACAAGTGGCGTTCAGCCAC
CCGAGATTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCGGGGCTGCACGCGCGCTACACTGACTGGCTCA
GCGTGTGCCTACCCTACGCCGGCAGGCGCGGGTAACCCGTTGAACCCATTTCGTGATGGGGATCGGGGATTGCAA
TTATTCCCCATGAACGAGGAATTCCCAGTAAGTGCGGGTCATAAGCTTGC GTTGATTAAAGTCCCTGCCCTTTGTA
CACACCGCCCGTCGCTACTACCGATTGGATGGTTTAGTGAGGCCCTCGGATCGGCCCCGCCGGGGTCGGCCCACG
GCCCTGGCGGAGCGCTGA

1117/6881
FIGURE 1041

GCGGCAACAGCGGGGCCGATGTGTAGTTGGTGA CTGCCTCTCCAGATGCTGAGGTGCCTGTATCATTGGCACAGG
CCAGTGCTGAACCGTAGGTGGAGTAGGCTGTGCCTTCGGAAGCAGTATCTATTACAAATGAAGTTGCAGTCTCCC
GAATTCAGTCACTTTTCACAGAAGGACTGAAGAGTCTGACAGAATTATTTGTCAAAGAGAATCACGAATTAAGA
ATAGCAGGAGGAGCAGTGAGGGATTTATTAAATGGAGTAAAGCCTCAGGATATAGATTTTGCCACCACTGCTACC
CCTACTCAAATGAAGGAGATGTTTCAGTCGGCTGGGATTCGGATGATAAACACAGAGGAGAAAAGCACGGAACA
ATTACTGCCAGGCTTCATGAAGAAAATTTTGAGATTACTACACTACGGATTGATGTCACCACTGATGGAAGACAT
GCTGAGGTAGAATTTACAAC TGA CTGGCAGAAAGATGCGGAACGCAGAGATCTCACTATAAATTCTATGTTTTTA
GGTTTTGATGGCACTTTATTTGACTACTTTAATGGTTATGAAGATTTAAAAAATAAGAAAGTTAGATTTGTTGGA
CATGCTAAACAGAGAATACAAGAGGATTATCTTAGAATTTTAAGATACTTCAGGTTTTATGGGAGAATTGTAGAC
AAACCTGGTGACCATGATCCTGAGACTTTTGAAGCAATTGCAGAAAATGCAAAGGCTTGGCTGGAATATCAGGA
GAAAGGATTTGGGTGGA CTGAAAAAAATTCTTGTTGGTAACCATGTAAATCATTGATTACCTTATCTATGAT
CTTGATGTGGCTCCTTATATAGGTTTACCTGCTAATGCAAGTTTAGAAGAATTTGACAAAGTCAGTAAAAATGTT
GATGGTTTTTTCACCAAAGCCAGTGACTCTTTTGGCCTCATTATTCAAAGTACAAGATGATGTCACAAAATTGGAT
TTGAGGTTGAAGATCGCAAAAGAGGAGAAAAACCTTGGCTTATTTATAGTTAAAAATAGGAAAGATTTAATTAAA
GCAACAGATAGTTCAGACCCATTGAAACCTTATCAAGACTTCATTATAGATTCTAGGGAACCTGATGCAACTACT
CGTGTATGTGA ACTACTGAAGTACCAAGGAGAGCACTGTCTCCTAAAGGAAATGCAGCAGTGGTCCATTCTCTCA
TTTCCTGTAAGTGGCCATGACATCAGAAAAGTGGGCATTTCTTCAGGAAAAGAAATTGGGGCTCTATTACAACAG
TTGCGAGAACAGTGGA AAAAAAGTGGTTACCAAATGGAAAAAGATGA ACTTCTGAGTTACATAAAGAAGACCTAA
AACTGATGGCTACTAAAAAGCAGAGCATT

FIGURE 1042

[illegible]

1119/6881
FIGURE 1043

CGGGCTTCCGGCGGCGTGACCTGACCGCAAGAGGCCAATGGAGTGTGGGAGCTGAAAGGGTCTTCGCTGGCGGCC
GGTAACTGGCGGCGGTTGGGAACGGCCGAGTGTGGCTCTTCTGGTGTTCAGCTTGGGGAGAGAGGGGTGGCCTT
CCTCTTGACAGTTGAGGCCGGCGCCGAGCCGGACTTCAGGCGGATCTCGTGGCGGAGCCCATCTTGCTCCCTCTCC
CAGGCCTTTACCCGCTCCCTAGGATTCCCGGGCCCTGTAGGTGGGAGTTGGGAGACGACAGTACTGCTTTTAAAG
AGACAGTGTTAGGGATCTTGGAAGCACAGCCAACATGTGTGACATTGAAGAAGCCACTAACCAACTCCTAGATGT
GAACCTTCATGAGAACCAGAAGTCTGTACAAGTGACAGAAAAGTGACCTCGGAAGTGAATCTGAGCTTCTAGTCAC
TATTGGAGCCACTGTACCTACTGGCTTTGAGCAAACAGCTGCAGATGAAGTCAGAGAGAACTTGGGTCTCATG
CAAAATCAGCAGAGACCGTGGCAAGATATATTTTGTCAATTCAGTGGAAAGTCTGGCACAGGTTTATTGTCTGAG
ATCAGTTGATAACTTATTTGTGGTGGTTTCAAGATTACCAGTTCAAACAAACAAAGGAAGAAGTTCT
AAAGGATTTTGAAGACTTGGCTGGAAAACCTCCCATGGTCAAACCCCTTAAAGTGTGGAAAATTAATGCCAGTTT
TAAAAAGAAAAAAGCAAAGCGCAAAAAGATAAATCAGAATTCAGTAAAGAGAAGATTAATAATGGACAAGAAGT
CAAAATCGATCAGAGAAATGTTAAAAAAGAGTTCACTAGCCATGCTTTAGATTCTCATATCTTAGATTATTATGA
AAATCCAGCCATCAAAGAGGATGTATCAACATTAATAGGTGATGATTTGGCATCTTGCAAAGATGAGACTGATGA
AAGCTCAAAAAGAAGAACTGAGCCTCAAGTGCTGAAGTTTAGAGTCACATGCAACAGGGCAGGAGAGAAACATTG
CTTTACCTCAAATGAGGCTGCAAGAGATTTTGGGGGTGCTGTTCAAGATTATTTAAGTGAAGGCCGACATGAC
CAACTTTGATGTGGAGGTTCTTTTGAACATCCATGATAATGAAGTCATTGTGGGCATTGCATTGACTGAAGAGAG
TCTCCACCGAAGAAATATAACACATTTTGGACCTACAACCTCTTAGATCAACTCTTGCCTATGGGATGCTCAGGCT
CTGTGATCCTCTACCTTATGATATAATAGTCGATCCAATGTGTGGAAGTGGGGCAATACCAATAGAGGGGGCCAC
TGAATGGTCTGACTGTTTCCATATTGCTGGTGATAATAATCCACTGGCTGTGAATAGAGCAGCAAATAACATTGC
ATCTTTATTGACCAAGAGCCAAATTAAGAAGGCAAACCCCTCCTGGGGCTTGCCCATAGATGCTGTTTCAAGTGGGA
TATCTGCAATCTGCCGTTGAGAAGTGGCTCTGTGGATATTATTGTAACAGATTGTCATTTGGAAAAAGGATGGG
ATCCAAGAAGAGAACTGGAACCTTTATCCAGCTTGCCTACGCGAGATGAGCCGTGTCTGCACACCTACCACAGG
CCGAGCTGTACTACTTACTCAAGACACAAAATGCTTTACCAAGGCGTTATCTGGAATGCAACACGTATGGCGAAA
GGTGGATACAGTCTGGGTGAACGTTGGTGGTCTTCGTGCTGCAGTTTACGTTCTGATACGTACACCTCAAGCTTT
TGTTTCATCCTTCAGAACAAAGACGGAGAAAGAGGAACTCTTTGGCAATGCAAAGAAATGAAGATGACTAATAGTACT
TGTACTTCCCACCACTGGAAATGTTAGCATAAAAGAACTTGGAGAGGAAAAAAGTATTAACAAAACCTGCAGTCTG
CACTCTTTAAACCTGTTTAAAGGCTCTTCATCCTGGTTAGCAAAAAGGTGTGAATGTAATGTGATGGAATTTAAAG
TTTTATGAGACCAGGCACAGTGGCTCACGACTGTAATTCCAGCAGTTTAGGAAGCCGAAGTGTGCAGATCACCTG
AGGTCCGGAGACCAGCCTGGCCAACATGGTGAAACCCCTGTCTCTACTAGAAATACAAAAATTAGCCAGGTGTGGT
GGCGGGCGCCTGTAATCCCAACTACTCAGGAGGCTGAGGCTAGAGAATCACTTGAACCCAGCAGGCGGAGGTGTC
GGTGAGTCGAGATCACGCCATTGCACTCCAGCCTGTGCGACAAGAGCGAAACTCTGTCTCAAAAAGATTTTATAA
GAAAGCAGAGCTTTTCCCTGAAGCTCTTTTGAAGTGGTAGCTTAATTAGTATTTTGTGAAAATACTTTAAAGAT
GCCTAGTGAAAAGCCTACTAAAGTGCTGTGAGATTGGGGTTTGAACATTTTATTTTTCAGGCTTTATGGCCTATT
TTCCATTGTGTCAAGTGCAAAAACCTACCCTGGCCCAAAGGAAGGGCAGAGAACATAATTACATCTTAGGCCACATT
TCATTCTTTGCAGCTTTGCTAATCCAGTTGCTCAAGTTCTTTACCTCAACCTGAAGGAATGAAGCATTATTACAT
TTTGTGAATGGTGTTCAGCCTATAAGACGAAGTCTCACAAGACCTATAGGAAAGTTTACCATCTGCCTAAATATT
AAAATATCCATCTGTTATTACATTAATACACAGAATGAAAATAGAGGTCTAGGAATTATCAAAGGTACTGCAAA
AATACTGTATAGAAGCTTATTTGTAAATAGCACATACATTGATAGATGGGGTGTGGGACCAACAACCAAATTAAG
AGAAATTGTTTTTCTTTCAGTACACTAAGGTGTGTGTTTTCAAAACC

1120/6881
FIGURE 1044

MCDIEEATNQLLDVNLHENQKSVQVTESDLGSESELLVTIGATVPTGFEQTAADEVREKLGSSCKISRDRGKIYF
VISVESLAQVHCLRSVDNLFVVVQEFQDYQFKQTKEEVLKDFEDLAGKLPWSNPLKVWKINASFKKKKAKRKKIN
QNSSKEKINNGQEVKIDQRNVKKEFTSHALDSHILDYYENPAIKEDVSTLIGDDLASCKDETDSSKEETEPQVL
KFRVTCNRAGEKHCFTSNEAARDFGGAVQDYFKWKADMTNFDVEVLLNIHDNEVIVGIALTEESLHRRNITHFGP
TTLRSTLAYGMLRLCDPLPYDIIIVDPMC GTGAIP IEGATEWSDCFHIAGDNNPLAVNRAANNIASLLTKSQIKEG
KPSWGLPIDAVQWDICNLPLRTGSVDIIVTDLPFGKRMGSKKRNNLYPACLRMSRVCTPTTGRAVLLTQDTKC
FTKALSGMQHVWRKVDTVWVNVGGLRAAVYVLIRTPQAFVHPSEQDGERGTLWQCKE

1121/6881
FIGURE 1045

GCAGGCAGGTGCCATGGGCCCGCTTGAGGCACACTGAGGGGACGCGGGGCTGGGCCATGGCCGGCGCTCGGGCCG
CCGCCGCCGCTGCCTCGGCGGGGTCTCGGCCTCTTCAGGCAACCAGCCGCCTCAGGAGCTGGGGCTTGGGGAGC
TGCTGGAGGAGTTCTCCCGGACTCAGTACCGGGCCAAGGATGGCAGCGGGACCGGCGGCTCTAAGGTTGAGCGCA
TTGAGAAGAGATGTCTGGAGCTGTTTGGCCGAGACTACTGTTTCAGCGTGATTCCAAACACGAATGGGGATATCT
GTGGCCACTATCCCCGGCACATCGTGTTCTTGGAGTATGAGAGTTCTGAGAAGGAGAAAGACACGTTTGAGAGTA
CCGTACAGGTGAGCAAGTTGCAAGACCTCATCCACCGCAGCAAGATGGCCCCGGTGCAGAGGACGGTTTGTCTGCC
CAGTAATCCTGTTCAAGGGCAAGCACATTTGCAGGTGCGCCACACTGGCTGGATGGGGAGAGCTGTATGGACGCT
CAGGCTACAACATATTTTTTCTCAGGGGGTGCAGATGATGCCTGGGCAGATGTGGAGGACGTCACGGAGGAGGACT
GTGCTCTTCGAAGTGGTGACACGCATCTTTTTGATAAGGTCAGAGGCTATGACATCAAGCTGCTTCGATACCTGT
CAGTCAAATACATCTGTGACCTGATGGTGGAGAACAAGAAGGTGAAGTTTGGCATGAATGTAACTCCTCTGAGA
AGGTGGACAAAGCCGAGCGCTATGCCGACTTCACTCTCCTCTCCATCCCGTATCCAGGCTGTGAATTTTTCAAGG
AATATAAAGATCGGGATTACATGGCAGAAGGGCTCATATTTAACTGGAAGCAGGACTACGTTGATGCCCCATTGA
GCATCCCCGACTTCCTGACTCACTCTCTGAACATTGACTGGAGCCAGTATCAGTGTTGGGATCTGGTGCAACAAA
CACAAAACCTACCTGAAGCTGCTGCTTTCTTAGTTAACAGTGATGATGACAGCGGGCTGCTGGTACACTGTATCT
CAGGCTGGGATCGGACCCCCCTCTTCATCTCCCTCCTGCGCCTTTCCTTGTGGGCTGATGGGCTCATCCACACGT
CCCTGAAGCCCACTGAGATCCTCTACCTCACTGTGGCCTATGACTGGTTCCCTCTTCGGGCACATGTTGGTAGATC
GGCTCAGCAAAGGGGAGGAGATTTTCTTCTTCTGCTTCAATTTTTTGAAGCATATTACCTCCGAGGAGTTCTCTG
CTCTGAAGACCCAGAGGAGGAAGAGTTTGCCAGCCCGGGATGGAGGCTTCACCCTGGAAGACATCTGCATGCTGA
GACGAAAGGACCGTGGCAGCACCACCAGCCTTGGCAGCGACTTCTCCCTGGTCATGGAGAGTTCCCCAGGAGCCA
CTGGGAGCTTCACCTATGAGGCCGTGGAGCTGGTCCCAGCAGGAGCGCCAACTCAGGCAGCTTGGCTTGCAGCCC
TGAGTGATCGAGAGACTCGGCTGCAGGAGGTGCGCTCAGCCTTCTTGGCTGCGTACAGCAGCACAGTGGGGCTTC
GGGCAGTAGCCCCCAGTCCTTCCGGTGCCATCGGGGGCCTGCTGGAGCAATTTGCCCGTGGTGTGGACTCCGGA
GCATCAGCAGCAATGCCTTGGAAGAAGCCAGCCCATGACATTTTCTGCTCCTCTCTCAGCTGAGCCCTTAGCA
GAGAATCAAAGCCATGCCTGGCCGAAGGGGTACTTCCAGGTCAGGGGAAATTTTCAGTCCCCCATCTCCATCATGA
ACATGGCAGCCCCAAAGCTGAGCAAGGCCAAAGACAGGGTTTTTCCAACCCCCAGCCTCTTGAAGGTGACCACCA
CCCCTTCTTGTCACTGTCTCCACCCACCCCATCTTTGCTGGGATTCCCATCAACTCTCAGAACTGTGTGGGGTT
TCCCTGGGGCCTTGTGGAAGCCATGACTTCACAAAGACCCTACCTGTCAGTTCTTGTCTTGGGGAGGAGGGATC
ACCTGCACTGAGAATGAGGCAGTTTGACACAGATCACAAAATAAAATCAAAGTCTTTTTTGAAAAAAAAAAAAAA
AAA

1122/6881
FIGURE 1046

MARCRGRFVCPVILFKGKHICRSATLAGWGELYGRSGYNYFFSGGADDAWADVEDVTEEDCALRSGDTHLFDKVR
GYDIKLLRYLSVKYICDLMVENKKVKFGMNVTSSEKVDKAQRYADFTLLSIPYPGCEFFKEYKDRDYMAEGLIFN
WKQDYVDAPLSIPDFLTHSLNIDWSQYQCWDLVQQTQNYLKLLSLVNSDDDSGLLVHCISGWDRTPLFISLLRL
SLWADGLIHTSLKPTIILYLTVAIDWFLFGHMLVDRLSKGEEIFFFCFNFLKHITSEEFSAKLTQRRKSLPARDG
GFTLEDICMLRRKDRGSTTSLGSDFLVMESSPGATGSFTYEAVELVPAGAPTQAAWLAALSDRETRLQEVRSF
LAAYSSTVGLRAVAPSPSGAIGGLLEQFARGVGLRSSNAL

1123/6881
FIGURE 1047A

CCGGACTCGAGGTGGCCGATGTGACAGCATCGGGGTGGACTTTGATGTGAAGACTTTCTGCCACAACCTTGCGGGC
GACTAAGCCACCATACGAGTGCCCGGTGGAGACCTGCCGAAAGGTCTACAAGAGTTACAGTGGTATTGAGTACCA
CCTGTACCCTATGACCACGACAACCCACCACCCCAACAACAACTCCACTCCGCAAGCACAAGAAAAAGGGGCG
CCAGTCACGCCCAGCCAACAAGCAGTCACCCAGCCCCTCAGAGGTCTCACAGTCACCAGGCCGTGAGGTGATGAG
CTATGCACAGGCCAGCGCATGGTGGAGGTGGACTTGCATGGCCGCGTCCACCGCATCAGCATCTTTGACAACCT
GGATGTGGTGTGAGAGGATGAGGAAGCCCCGAGGAGGCCCTGAGAATGGCAGCAACAAGGAGAACAACACTGAGAC
ACCAGCTGCTACTCCCAAGTCAGGCACAACATAAGAACAAGGAGAAGCGCAAGGACTCCAACCATCACCACCACCA
CAATGTTTTCTGCGAGCACCCTCCCAAGCTGCCAGAGGTGGTCTATCGGGAGCTGGAACAGGACACCCCTGATGC
CCCACCCCGGCCAACTTCCTATTACCGGTACATCGAGAAGTCTGCAGAGGAGCTGGACGAGGAAGTAGAGTATGA
CATGGACGAGGAGGACTACATCTGGCTGGATATCATGAATGAGCGTCGGAAGACAGAGGTGTAAGTCCCATCCC
GCAGGAGATCTTTGAGTACCTAATGGACCGACTGGAGAAGGAGTCGTACTTTGAGAGTCATAATAAAGGCGACCC
TAATGCGCTAGTGGACGAGGATGCTGTTTTGCTGTATCTGCAATGATGGTGAGTGCCAGAACAGCAATGTCATCCT
CTTCTGTGACATGTGCAACCTGGCCGTGCACCAGGAGTGCTACGGTGTCCCCTATATCCCCTGAGGGCCAGTGGCT
GTGCCGCCGTTGCTGTCAGTCACCCCTCTCGTGCTGTGGATTGTGCCCTGTGCCCCAACAAGGGCGGTGCCTTCAA
GCAGACAGATGACGGGCGCTGGGCCCATGTGGTGTGTGCCTTGTGGATCCCTGAGGTCTGCTTCGCCAACACGGT
CTTCCTAGAGCCTATTGACAGCATTGAGCACATCCCACCAGCTCGCTGGAAGCTCACCTGCTACATTTGCAAACA
ACGGGGCTCAGGGGCTGTCATCCAGTGCCACAAGGCCAACTGTTACACAGCTTTCCATGTGACATGCGCCAGCA
GGCTGGCCTTTACATGAAGATGGAGCCTGTGCGGGAGACAGGCGCCAACGGCACCTCTTTAGTGTCCGCAAGAC
AGCCTACTGCGACATCCACACGCCTCCAGGTTTACGACGCGGACTGCCTGCCCTGTCCACAGCGAGGGTGAGGA
GGATGAAGATGAGGAGGAGGATGAGGGTAAGGGCTGGAGCTCAGAGAAAGTCAAGAAGGCCAAGGCCAAGTCCCCG
GATCAAAATGAAGAAGGCACGGAAGATCCTGGCAGAGAAGCGGGCAGCAGCACCTGTGGTGTGAGTGCCCTGCAT
CCCACCACACAGGCTTAGTAAAATCACCAACCGCTGACCATCCAAAGGAAGAGCCAGTTTCATGCAGAGGCTGCA
CAGCTACTGGACACTGAAGCGGCAGTCACGGAATGGGGTCCCATTTGCTACGTGCGCTGCAGACACACCTGCAATC
TCAGAGGAAGTGTGACCAAGTTGGGAGAGATTCTGAGGATAAGAACTGGGCCCTTAAAGAACAGCTCAAGTCCCTG
GCAGCGGCTCCGGCATGACTTGGAGCGAGCTCGGCTGCTCGTGGAATTGATCCGCAAGCGGGAAAAACTCAAAAG
GGAGACGATCAAGGTTTACGAGATTGCCATGGAGATGCAGCTGACTCCTTTCTCATCCTCCTTCGCAAAACCTT
GGAGCAGCTCCAAGAGAAGGACACAGGCAACATCTTACGCGAGCCGGTCCCTCTGTCTGAGGTACCTGACTACCT
AGACCACATCAAAAAGCCCATGGACTTTTTTACCATGAAGCAGAACTTGGAGGCTTACCGCTACCTGAATTTTGA
TGATTTTGGAGGAGACTTCAACCTCATCGTCAGCAACTGCCTCAAGTATAACGCCAAGGACACCATCTTCTACCG
GGCAGCAGTGCGGCTTCGTGAGCAGGTTGGTGTGTGCTCCGCCAGGCCCGGCCAGGCAGAAAAAATGGGCAT
TGACTTTGAGACGGGCATGCATATCCCCACAGCCTGGCTGGAGATGAGGCCACACACCACACTGAAGATGCAGC
CGAGGAAGAGCGGCTGGTCTTGCTGGAGAACCAGAAGCACCTGCCAGTGGAAGAACAGCTAAAGCTGCTTCTGGA
GCGGCTGGACGAAGTGAATGCCAGCAAGCAGAGTGTGGGCCGCTCACGGCGTGCAAAGATGATCAAGAAAGAGAT
GACGGCACTGCGGCGGAAGCTTGCCCATCAGCGAGAGACGGGACGTGATGGCCCTGAGCGGCATGGCCCCCTCGAG
CCGGGGTAGTCTGACACCCACCCGGCAGCCTGTGACAAGGATGGGCAGACAGATAGTGCGGCAGAGGAGAGCAG
CAGCCAGGAGACAAGCAAAGGCCTGGGTCCCAACATGTCTCAACCCCCGCACATGAGGTGGGCAGGAGAACCCTC
AGTTCTGTTCTCAAAAAGAACCAGAAGACAGCTGGACCGCCCAAGAGGCCGGGCCGGCCCCCAAAAACCGGGA
GAGCCAGATGACCCCAAGCCACGGAGGCAGTCTGTGGGGCCCCCAGCTCCCCATCATGAGTTCCCTGCGTCA
GCGCAAGCGGGGTAGGAGCCCCCGGCCAGTTTCGAGCTCAGACAGCGACAGTGATAAGTCCACAGAAGACCCCCC
AATGGACTTACCAGCCAATGGCTTACGCGGTGGAACCAACCAGTGAAGAAGAGTTTCTTGGTATACCGTAATGA
CTGCAGCCTTCCCCGAGCAGCTCAGACTCTGAGTCCAGCAGCAGTAGCAGTAGCAGCGCTGCTTCAGACCGGAC
CAGCACAACGCCCTCAAAACAAGGCCGGGGCAAACCTCCTTCTCGGGGCACTTTCCCAGAGGACAGCAGTGA
GGATACCTCAGGCACTGAGAATGAGGCCTACTCCGTGGGCACTGGCCGCGGCGTGGGCCACAGCATGGTAAGGAA
GAGTCTGGGCCGGGAGCTGGCTGGCTGTGAGGATGAGGACTCCCCGCTGGATGCTCTGGACCTCGTGTGGGC
CAAATGCCGAGGCTATCCATCATACCCAGCTCTGATCATTGATCCAAAGATGCCCCGAGAAGGTATGTTCCACCA
TGGGGTTCCCATCCCTGTGCCCCACTGGAGGTGCTGAACTTGGGGAGCAGATGACCCAGGAAGCCCCGAGAGCA
TCTCTACCTCGTCTCTTCTTTGACAACAAACGAACCTGGCAGTGGCTGCCCAGGACCAAGCTGGTTCTCTGGG
TGTGAACCAGGACCTAGACAAGGAGAAGATGCTGGAGGGCCGCAAGTCCAACATCCGCAAGTCAGTACAGATCGC

1124/6881
FIGURE 1047B

CTACCACAGGGCTCTGCAGCACCGCAGCAAGGTGCAAGGCGAGCAGAGCAGTGAGACCAGCGATAGTGATTGATA
CTGCTCAACACAGCCCAACCTATAGTGCCCTGTGACTTCTCTCCTCCCCTTTGCTCACTGTCCTGGAGTGGCACC
GGCCTCTGCACTGACTCATTTCTGGTCTTGGGGCCAGTCTCAGGGGAAGCTGGGTGGGGGAGGTCCCTCCTGCCC
TAAGTGCAGCTGGACTGTACAGAACACTCCAAGGGCCAATGGCAGTTCAGCGCAAGGAGAGGGAGGGCCCACAGG
TCAGAAAAAGCTCCAGAGACCTCACAGCATTGTAGGGCGGGGTGGTGGGCCAAAGTTAGGACACTGCGTAAAACA
GGCCATCCCACCACCTCTACCTGCTCATGCCAGGAGAATCCATAACTGCCTAGAGGCCTGGGGCCCCCTACCGGTC
GTGAGGTGAGTGGGCATCTGTCCAGCCTGGAAGAGGGGCACTAGGTGACTCCCTCCCCTGCTGTTGTAAATACTG
TAATTATCGGAGAATTTAAATTATTCTCATTTGTAAGTTCGTTTCCGGGTCGCGCCAGAGTCATTTGGTACTAAA
AAAAAAAAAAAAAAAAAGACTGGGGGCTGTCCCCATTTCCCTTCTCTTCCCATAGATTCCCCCACCTTTCAAACCTG
GTTTGTATTTATTTCAAAGGAAGAAAATATATTGATTCTTAGAAAATAAA

1125/6881
FIGURE 1048

MGVDFDVKTFCHNLRATKPPYECPVETCRKVYKSYSGIEYHLYHYDHDNPPPPQQTPLRKHKKKGRQSRPANKQS
PSPSEVSQSPGREVMSYAQAQRMVEVDLHGRVHRISIFDNLDVSEDEEAPEEAPENGSNKENTETPAATPKSGK
HKNKEKRKDSNHHHHHNVSASTTPKLPEVVYRELEQDTPDAPPRPTSYYRYIEKSAEELDEEVEYDMDEEDYIWL
DIMNERRKTEGVSPIPQEIFEYLMRLEKESYFESHNGDPNALVDEDAVCCICNDGECQNSNVILFCDMCNLAV
HQECYGVPIYIEGQWLCRRCLQSPSRAVDCALCPNKGGAFFKQTDGGRWAHVVCALWIPEVCFANTVFLEPIDSIE
HIPPARWKLTICYICKQRGSGACIQCHKANCYTAHFVTCAQQAGLYMKMEPVRETGANGTSFSVRKTAYCDIHTPP
GSARRLPALSHSEGEDEDEDEDEDEGKGWSSEKVKKAKAKSRIKMKKARKILAEKRAAAPVVSVP CIPPHRLSKIT
NRLTIQRKSQFMQRLHSYWT LKRQSRNGVPLLRRLQTHLQSQRNCDQVGRDSEDKNWALKEQLKSWQRLRHDLER
ARLLVELIRKREKLKRETIKVQQIAMEMQLTPFLIILLRKTLEQLQEKDTGNIFSEPVPLSEVPDYLDHIKKPMDF
FTMKQNL EAYRYLNFDDFEEDFNLI VSNCLKYNKDTIFYRAAVRLREQGGAVLRQARRQAEKMGIDFETGMHIP
HSLAGDEATHHTEDAAEEERLVLL ENQKHLPVEEQLKLLLERLDEVNASKQSVGRSRRAKMIKKEMTALRRKLAH
QRETGRDGP ERHGPSSRGS LTPHPAACDKDGQTD SAAEESSSQETSKGLGPNMSSTPAHEVGRRTSVLF SKKNPK
TAGPPKRPGRP PKNRESQMTPSHGGSPVGPPQLPIMSSLRQRKGRSPRPSSSSSDSDSDKSTEDPPMDLPANGFS
GGNQPVKKSFLVYRNDCSLPRSSSDSESSSSSSSSAASDRTSTTPSKQGRGKPSFSRGTFPEDSSSEDTSGTENE A
YSVGTGRGVGHSMVRKSLGRGAGWLSEDEDSPLDALDLVWAKCRGYPSYPALI IDPKMPREGMFHHGVPIPVPL
EVLKLGEQMTQEAREHLYLVLF FDNKRTWQWLPRTKLVPLGVNQDIDKEKMLEGRKSNIRKSVQIAYHRALQHRS
KVQGEQSSETS DSD

1126/6881
FIGURE 1049

GTACCCCCATCCTTTCTCTCGCCCCCTCCTACCCGCAGCTCCTGGCGCTCGGCGGGGCTAACTGCAGCGCGGAGAT
CTCGGCCGCCAAGCTCCGCCTCCCGCCCCGGGCTGTGCCCCGGGGCTCGCCTGAGGCCGACCACCCGCACCCAC
CTCTAGCGGCTTTGCTCGAGGGCCACCTTCTTCCCACCCCGGCAAACTCCAGTAGGCTCGCCCTCGCTGACTCC
CCGCCCCCGCGTCAACTGCAAGGGGCCCCGCCATAGCCAGTTCGGGGCGGTTGCTCACATCGACCGAACTCCC
CGCCCCCTCCCGCGGCCCTTGGGGCCGTAGGAGGCCGCAGCGAGGAGGTAGAGGGGGCGGGGTGCGACTAGGGT
GTCCCTAGAGAACGAGGACTCTGAAGGCGGGACATTTGGGCGACCCCGGGCGGGGCCAGCCATTAAACAGTCCC
ACTTCTGTGCCAGACACTGAACTGGGCTCTTGACGGGCATCATCTCTTAATCCTCAGAACATCCAGGGAGCTCC
ACAGGATCCCCATATCCTGGGCCATGAGTGTGAAAGACTGCCCTTGAGTTCCACGACTTCAAGTCTGTGG
ATCACCTGAAGGTCTGTCCCCGCTACACGGCAGTGTGGCACGCTCTGAGGATGATGGCATCGGCATCGAGGAGC
TGGACACCCTGCAGCTGGAGCTGGAGACCCTGCTGTCTTCTGCCAGCCGGCGCCTGCGTGTGCTTGAGGCCGAAA
CCCAGATCCTCACCGACTGGCAGGATAAGAAAGGTGACAGACGATTCTGAAGCTGGGTGCGAGACCATGAACTTG
GAGTCCCCCCCCAAACATGGGAAGCCCAAGAAGCAGAACTGGAAGGGAAGGCAGGACATGGGCCGGGCCCTGGCC
CAGGACGGCCCCAAATCCAAAAACCTTCAGCCCAAGATCCAGGAATATGAATTCAGTGATGACCCTATCGACGTGC
CACGGATCCCCAAAAATGATGCCCCAACAGGTTCTGGGCTTCAGTGGAGCCCTACTGTGCTGACATCACCAGCG
AGGAGGTCCGCACACTTGAGGAGTTACTGAAGCCCCCAGAAGATGAGGCTGAGCATTACAAGATCCCACCCCTGG
GGAAGCACTACTCCAGCGCTGGGCCCAGGAGGACCTGCTGGAGGAGCAGAAGGATGGGGCCCGGGCAGCGGCTG
TGGCTGACAAGAAGAAAGGCCTCATGGGGCCACTGACCGAACTGGACACTAAAGATGTGGATGCCCTGCTGAAGA
AGTCTGAGGCCCAGCATGAACAGCCGGAAGATGGATGCCCTTTGGTGCCCTGACGCAGCGCCTCCTGCAGGCCC
TGGTGGAGGAAAATATTATTTCCCTATGGAGGATTCTCCTATTCTGACATGTCTGGGAAAGAATCAGGGGCTG
ACGGGGCAAGCACCTCCCCTCGCAATCAGAACAAGCCCTTCAGTGTGCCGATACTAAGTCCCTGGAGAGCCGCA
TCAAGGAGGAGCTAATTGCCCAGGGCCTTTTGGAGTCTGAGGACCGCCCCGCAGAGGACTCCGAGGATGAGGTCC
TTGCTGAGCTTCGCAAACGGCAGGCTGAGCTGAAGGCACTTAGTGCCACAACCGCACCAAGAAGCACGACCTGC
TGAGGCTGGCAAAGGAGGAGGTGAGCCGGCAGGAGCTGAGGCAGCGGGTGCGCATGGCTGACAACGAGGTCATGG
ACGCCTTTCGCAAGATCATGGCTGCCCGGCAGAAGAAGCGGACTCCCACCAAGAAAGAAAAGGACCAGGCCTGGA
AGACTCTGAAGGAGCGTGAGAGCATCCTGAAGCTGCTGGATGGGTAGCCCTCACCCTGCCTCAGGCTGATTATC
TGGCCTAGGGGAGGGGAAGGGAGGCCACTTCCTTCTTTGGGCACAGGAAACATTGGCCTGTGGCTGTCCCTCAA
ATGGCGGCAGTCTCTAGAGGGCCGTGGCCCTTCCCCTGAGGTCTTTTGGCCTAGCTCTGTACAACAGGACACAG
GAAGCCCTGCTGGGCTAGCCTGAGGCCTAGTCTCTGCTTGGTCCCCGAGATGGGGTTGGAGGGGACTTCGTTTCT
GGGTCTTCTCTTCCCCTCTTTACCATCCCCACTCCCTAATCCCCTACCCCTGTCTCCCCTTCAAGGACTTCTC
CCTTGTGGTTTTTGTAAAGTGCAAACCTTAAGAATAAAGTGAAGTGTGCTGTGGTTTTTCAAAAAAAAAAAAAA

1127/6881
FIGURE 1050

MSELKDCPLQFHDFKSVDHLKVCPRYTAVLARSEDDGIGIEELDTLQLELETLLSSASRRLRVLEAETQILTDWQ
DKKGDRRFLKLGRDHELGAAPPKHGKPKKQKLEGKAGHGPGPGPRPKSKNLQPKIQEYEFTDDPIDVPRIPKND
PNRFWASVEPYCADITSEEVRTLEELLKPPPEDEAEHYKIPPLGKHYSQRWAQEDLLEEQKDGARAAAVADKKKGL
MGPLTELDTKDVDALLKKSEAQHEQPEDGCPFGALTQRLLQALVEENIISPMEDSPIPDMSGKESGADGASTSPR
NQNKPFVSPHTKSLESRIKEELIAQGILLESEDRPAEDSEDEVLAELRKRQAEKALSAHNRTKKHDLRLAKEEV
SRQELRQVRMADNEVMDAFRKIMAAARQKKRTPTKKEKDQAWKTLKERESILKLLDG

1128/6881
FIGURE 1051

GTACCCCCATCCTTTCTCTCGCCCTCCTACCCGCAGCTCCTGGCGCTCGGCGGGGCTAACTGCAGCGCGGAGAT
CTCGGCCGCCAAGCTCCGCCTCCCGCCCCGGGCTGTGCCCCGGGGCTCGCCTGAGGCCGACCACCCGCACCCAC
CTCTAGCGGCTTTGCTCGAGGCCACCTTCTTCCCACCCCGGCAAACTCCAGTAGGCTCGCCCTCGCTGACTCC
CCGCCCCCGCGTCAACTGCAAGGGGCCCGCCCATAGCCAGTTCCGGGGCGGTTGCTCACATCGACCGGAACCTCC
CGCCCCCTCCCGCGGCCCTTGGGGCCGTAGGAGGCCGCAGCGAGGAGGTAGAGGGGGCGGGGTTCGCACTAGGGT
GTCCCTAGAGAACGAGGACTCTGAAGGCGGGACATTTGGGCGACCCCCGGGCGGGGCCAGCCATTAAACAGTCCC
ACTTCTGTGCCAGACACTGAACTGGGCTCTTGACGGGCATCATCTCTTAATCCTCAGAACATCCCAGGGAGCTCC
ACAGGATCCCCATATCCTGGGGC**ATG**AGTGAGTTGAAAGACTGCCCTTGCAGTTCCACGACTTCAAGTCTGTGG
ATCACCTGAAGGTCTGTCCCGCTACACGGCAGTGCTGGCACGCTCTGAGGATGATGGCATCGGCATCGAGGAGC
TGGACACCCTGCAGCTGGAGCTGGAGACCCTGCTGTCTTCTGCCAGCCGGCGCTGCGTGTGCTTGAGGCCGAAA
CCCAGATCCTCACCGACTGGCAGGATAAGAAAGGTGACAGACGATTCTGAAGCTGGGTTCGAGACCATGAACTTG
GAGCTCCCCCAAAACATGGGAAGCCCAAGAAGCAGAACTGGAAAGGGAAGGCAGGACATGGGCCGGGCCCTGGCC
CAGGACGGCCCAAAATCCAAAAACCTTCAGCCCAAGATCCAGGAATATGAATTCAGTGATGACCCTATCGACGTGC
CACGGATCCCCAAAAATGATGCCCCAACAGGTTCTGGGCTTCAGTGGAGCCCTACTGTGCTGACATCACCAGCG
AGGAGGTCCGCACACTTGAGGAGTTACTGAAGCCCCCAGAAGATGAGGCTGAGCATTACAAGATCCCACCCCTGG
GGAAGCACTACTCCAGCGCTGGGCCCAGGAGGACCTGCTGGAGGAGCAGAAGGATGGGGCCCGGGCAGCGGCTG
TGGCTGACAAGAAGAAAGGCCTCATGGGGCCACTGACCGAACTGGACACTAAAGATGTGGATGCCCTGCTGAAGA
AGTCTGAGGCCCAGCATGAACAGCCGGAAGATGGATGCCCCCTTGGTGCCCTGACGCAGCGCCTCCTGCAGGCC
TGGTGGAGGAAAATATTATTTCCCTATGGAGGATTCTCCTATTCTGACATGTCTGGGAAAGAATCAGGGGCTG
ACGGGGCAAGCACCTCCCTCGCAATCAGAACAAGCCCTTCAGTGTGCCGCATACTAAGTCCCTGGAGAGCCGCA
TCAAGGAGGAGCTAATTGCCCAGGGCCTTTTGGAGTCTGAGGACCGCCCGCAGAGGACTCCGAGGATGAGGTCC
TTGCTGAGCTTCGCAAACGGCAGGCTGAGCTGAAGGCACTTAGTGCCACAACCGCACCAAGAAGCACGACCTGC
TGAGG**TGA**CGTTAGCAGGATGCACAGTCCCGGGGGTGGCCTTGGAGGCTGTGGCCACGGCTAGTCACCTTTCAG
GGTTTTTACAACAGGCTTTCCAATCCTGGCTGGCCTCTAAATCACCTGGAGAGCCTCGAAAAAACAGCAGTGGC
CAGTCCACCGGGTATGTCCCAAACAAATTCTGATTCCACAGAGTGGGGCTCAGGCATCTGTGACTGACCGATTGA
TTTGATTTGTTTTTGTGTTTTTTTTTTTGGAGAGGGAGTCTCGCACTGTCACCCAGGCTGGAGTGCAGTGGCATG
ATCTCGGCTCACTGCAAGCTCCGCCCTCCAGGTTTCATGCCATTCTCCTGCCTCAGCCTCCTGAGTAGCTGATACT
ACAGGCACCCACCACCGCCAGCTAATTTTTTTTGTATTTTTTAGTAGAGACGGGGTTTACCCTGTGTAGCCAGG
ATGGTCTCGATCTCCTGACCTCGTGATCCACCCGCCTCGGCCTCCCAAAGTGCCGGGATTACAGGCGTGAGCCAC
TGCGCCTGGCCTAGTTTGGTTTTTTAATTATGGTAAAGGCATAATATAAAATGTATCTCCATGGGAGGCTGAGGC
AGGAGAATCAGTTGAACCTGGGAGGCGGAGGTTGCAGTGAGCTGAGACTGCACCATTGCATTCCAGCCTGGGCAA
CAAGAGTGAACTGCATCTCAAAAAAAAAAAGAAAAAAAAATTTACGCTTCTTAACCATTTTTTAAGTGTACAGTTT
AGTAGTGTTACCCATATTCACATTGTTGTGTGATTTATTTTTTGTCTTTTCATGCTTCTTTTCTTTTATCCCCA
AAGTTTTGTTATTAATAAATTTGATACACACAGAAAATCTGAAAGAATCATACAATAAACATCAGTATATTCTCCA
CCTAAAAAAAAAAAAAAAAAAAA

1129/6881
FIGURE 1052

MSELKDCPLQFHDFKSVDHLKVCPRYTAVLARSEDDGIGIEELDTLQLELETLLSSASRRLRVLEAETQILTDWQ
DKKGDRRFLKLGRDHELGAPPKHGKPKKQKLEGKAGHGPGPGPRPKSKNLQPKIQEYEFTDDPIDVPRIPKND
PNRFWASVEPYCADITSEEVRTLEELLKPPEDAEHYKIPPLGKHYSQRWAQEDLLEEQKDGARAAAVADKKKGL
MGPLTELDTKDVDALLKKSEAQHEQPEDGCPFGALTQRLQALVEENIISP MEDSPIPDMSGKESGADGASTSPR
NQNKPFVSPHTKSLESRIKEELIAQGLLESEDRPAEDSEDEVLAELRKRQAEKALSAHNRTKKHDLR

1130/6881
FIGURE 1053

GTACCCCCATCCTTTCTCTCGCCCCCTCCTACCCGCAGCTCCTGGCGCTCGGCGGGGCTAACTGCAGCGCGGAGAT
CTCGGCCGCCAAGCTCCGCCTCCCGCCCCGGGCTGTGCCCCGGGGCTCGCCTGAGGCCGACCACCCGCACCCAC
CTCTAGCGGCTTTGCTCGAGGCCACCTTCTTCCCACCCCGGCAAACTCCAGTAGGCTCGCCCTCGCTGACTCC
CCGCCCCCGCGTCAACTGCAAGGGGCCCCGCCATAGCCAGTTCCGGGGCGGTTGCTCACATCGACCGGAACTCCC
CGCCCCCTCCCGCGGCCCTTGGGGCCGTAGGAGGCCGCAGCGAGGAGGTAGAGGGGGCGGGGGTTCGCACTAGGGT
GTCCCTAGAGAACGAGGACTCTGAAGGCGGGACATTTGGGCGACCCCCGGGCGGGGCCAGCCATTAAACAGTCCC
ACTTCTGTGCCAGACACTGAACTGGGCTCTTGACGGGCATCATCTCTTAATCCTCAGAACATCCCAGGGAGTCC
ACAGGATCCCCATATCCTGGGCCATGAGTGAGTTGAAAGACTGCCCCCTTGCAGTTCCACGACTTCAAGTCTGTGG
ATCACCTGAAGGTCTGTCCCCGCTACACGGCAGTGCTGGCACGCTCTGAGGATGATGGCATCGGCATCGAGGAGC
TGGACACCCTGCAGCTGGAGCTGGAGACCCTGCTGTCTTCTGCCAGCCGGCGCCTGCGTGTGCTTGAGGCCGAAA
CCCAGATCCTCACCGACTGGCAGGATAAGAAAGGTGACAGACGATTCTGAAGCTGGGTGAGACCATGAACTTG
GAGCTCCCCCAAACATGGGAAGCCCAAGAAGCAGAAACTGGAAGGGAAGGCAGGACATGGGCCGGGCCCTGGCC
CAGGACGGCCCAAATCCAAAAACCTTCAGCCCAAGATCCAGGAATATGAATTCAGTGATGACCCTATCGACGTGC
CACGGATCCCCAAAAATGATGCCCCAACAGGTTCTGGGCTTCAGTGAGGCCCTACTGTGCTGACATCACCAGCG
AGGAGGTCCGCACACTTGAGGAGTTACTGAAGCCCCCAGAAGATGAGGCTGAGCATTACAAGATCCCACCCCTGG
GGAAGCACTACTCCAGCGCTGGGCCCAGGAGGACCTGCTGGAGGAGCAGAAGGATGGGGCCCGGGCAGCGGCTG
TGGCTGACAAGAAGAAAGGCCTCATGGGGCCACTGACCGAACTGGACACTAAAGATGTGGATGCCCTGCTGAAGA
AGTCTGAGGCCCAGCATGAACAGCCGGAAGATGGATGCCCCCTTGGTGCCCTGACGCAGCGCCTCCTGCAGGCCC
TGGTGGAGGAAAATATTATTTCCCTATGGAGGATTCTCCTATTCTGACATGTCTGGGAAAGAATCAGGGGCTG
ACGGGGCAAGCACCTCCCCTCGCAATCAGAACAAGCCCTTCAGTGTGCCGCATACTAAGTCCCTGGAGAGCCGCA
TCAAGGAGGAGCTAATTGCCCAGGGCCTTTTGGAGTCTGAGGACCGCCCCGCAGAGGACTCCGAGGATGAGGTCC
TTGCTGAGCTTCGCAAACGGCAGGCTGAGCTGAAGGCACTTAGTGCCACAACCGCACCAAGAAGCACGACCTGC
TGAGGTGAGCGTTAGCAGGATGCACAGTCCCGGGGGTGGCCTTGGAGGCTGTGGCCACGGCTAGTCACCTTTCAG
GGGTTTTACAACAGGCTTTCCAATCCTGGCTGGCCTCTAAATCACCTGGAGAGCCTCGAAAAAACAGCAGTGGC
CAGTCCACCGGTATGTCCCAAACAAATTCTGATTCCACAGAGTGGGGCTCAGGCATCTGTGACTGACCGATTGA
TTTGATTTGTTTTTGTGTTTTTGTGTTTTTTTGGAGAGGGAGTCTCGCCTGGGCAACAAGAGTGAACTGCATCTCAA
AAAAAAGAAAAAAATTTACGCTTCTTAACCATTTTTAAGTGTACAGTTTAGTAGTGTTACCCATATTCACAT
TGTGTGTGATTTATTTTTTGTCTTTTCATGCTTCTTTTCTTTTATCCCCAAAGTTTTGTTATTAATAATTTGA
TACACACAGAAAATCTGAAAGAATCATACAATAACATCAGTATATTCTCCACCTAAAAA

1131/6881
FIGURE 1054

MSELKDCPLQFHDFKSVDHLKVCPRYTAVLARSEDDGIGIEELDTLQLELETLLSSASRRLRVLEAETQILTDWQ
DKKGDRRFLKLGRDHELGAAPPKHGKPKKQKLEGKAGHGPGPGPRPKSKNLQPKIQEYEFTDDPIDVPRIPKND
PNRFWASVEPYCADITSEEVRTLEELLKPPPEDEAEHYKIPPLGKHYSQRWAQEDLLEEQKDGARAAAVADKKKGL
MGPLTELDTKDVDALLKKSEAQHEQPEDGCPFGALTQRLQALVEENIISPMEDSPIPDMSGKESGADGASTSPR
NQNKPFVPHTKSLESRIKEELIAQGILLESEDRPAEDSEDEVLAELRKRQAELKALSAHNRTKKHDLLR

1132/6881
FIGURE 1055

CAGCCAGCGCCCGCGATGACTGCCACTCTCCGCCCCCTACCTGAGTGCCGTGCGGGCCACATTGCAGGCTGCCCTC
TGCCTGGAGAACTTCTCCTCCAGGTTGTGGAACGACACAACAAGCCGGAAGTGGAAGTCAGGAGTAGCAAAGAG
CTCCTGTTACAACCTGTGACCATCAGCAGGAATGAGAAGGAAAAGGTTCTGATTGAGGGCTCCATCAACTCTGTC
CGGGTCAGCATTGCTGTGAAACAGGCTGATGAGATCGAGAAGATTTTGTGCCACAAGTTCATGCGCTTCATGATG
ATGCGAGCAGAGAACTTCTTTATCCTTCGAAGGAAGCCTGTGGAGGGGTATGATATCAGCTTTCTGATCACCAAC
TTCCACACAGAGCAGATGTACAAACACAAGTTGGTGGACTTTGTGATCCACTTCATGGAGGAGATTGACAAGGAG
ATCAGTGAGATGAAGCTGTCAGTCAATGCCCCGTGCCCGCATTGTGGCTGAAGAGTTCCTTAAGAATTTTTAAACC
ATCTGGCTGGATCTCGTGGCCTTCCCCCTCAGACTACCCATGTCTCCACGAAGGCGTCCTGGAGTCACTCCCCGA
GCAGCGCGGCGGCGGCAGGGAGTTGGGTTGGGGTGGGCATTTGATGCGGGAGGTGGGTGGTGTGCTTGCTAGCTG
GGCAAGAAAGCAGCAGTGGACCTGCCCCAAGGCCACACGTGCCTGGTCAGGCTGGCTTCTGATGTTTCAGTCCCCT
GGGCCGGGACAGATTTTTTTTAACTCTTGAAACTTAACTCTGTGCTTGTAACAAAAAAAAAAAAAAAAAAAAA

1133/6881
FIGURE 1056

MTATLRPYLSAVRATLQAALCLENFSSQVVERHNKPEVEVRSSKELLLOPVTISRNEKEKVLIEGSINSVRVSIA
VKQADEIEKILCHKFMRFMMRAENFFILRRKPVEGYDISFLITNFHTEQMYKHKLVDFVIHFMEEDKEISEMK
LSVNARARIVAEFFLKNF

1134/6881
FIGURE 1057

GCCTGCCTCTTCCAGAGAGACTCCCCATTGCTGTCTCTTGTGTGTGTGCATGCACAAGGAAGGCTTGTTGTGTG
CCAGGATAAGGGGCACAAGGGCCTCGGGTGTGGCCAGAGACCCCATGCTTAAGCTTTTATGGTATAGGTCAGGCT
GCAGGGGTTTGAGGGCCTCAGTTGTATATCAGAATCTTCAGAGCACTGCGATGTTTCAGGGGTGAGTCAGGTCTGT
AGATGTGCACGGGTCTTCTGAAGGGTCAGTTTCTGTAATCACTTTCAGGTGTGTTCAGGGCCTTGTGCAGTAACA
GTGCACACAGAAGTTAGTGTCTTCTGTGGGCTAAGGGTTGTAGCTCTGTATCAGGATTCTGGGAGTGGGTCTGGAT
TTCTGGTGTGTGGACTTAAGAAGCTGTGTTCAGACTTGGGGGAGGGGCGTTCATGTATAACTGGGTTCACATAGGC
CAAGACTCCCAGGTGCATTTTAGGCAGAGCCTCAGGTGTGTTAGAGGTCCCAGGGGCAGAGAGGCTATAGGTGCT
GTCAGAGGCCTTGGGGACATTTAGGGCAGAGCCTCGAGTGACAGGTCCCTGGGACAGTGGGAGCCAAGGGCAAGTG
CTAGAGTTGCAGTGAATTTAGAGCAAAGCCTCAGCTAAGTGACACATCCAGGGCAGTAGGGGATCTATCTAGGT
TCGTGCTGGGCCTCAGGTAAGTGACAGGCCTTAGGACAATGGGGGCTGTGGCATGCGTCAGGTTACCTGCCTTGA
TATGGGATCGTGACAGGCCCCCTCCCTATGTGCAGGAGACAAGCAGCCCAAGAAACAGGAGAAAAACCCAGTGTG
GTGTCCCCAGAGTTTGTGGATGAAGCTCTGTGTGCGTGCGAGGAGTACCTTAGCAACTTGGCCCACATGGACATC
GACAAGGACCTGGAGGCCCCGCTGTACCTCACCCCGAGGGCTGGTCCCTCTTCCTCCAGCGCTACTACCAAGTG
GTCCACGAAGGGGCAGAACTCAGGCACCTCGACACTCAGGTCCAGCGCTGTGAGGACATCCTGCAGCAGCTGCAG
GCCGTGGTACCCAGATAGACATGGAAGGGGATCGCAACATCTGGATCGTGAAGCCAGGAGCCAAGTCCCGCGGA
CGAGGCATCATGTGCATGGACCACCTGGAGGAGATGCTGAAGCTGGTGAACGGCAACCCCGTGGTGATGAAGGAC
GGCAAGTGGGTGGTGCAGAAGTATATTGAGCGGCCCCCTCCTCATCTTTGGCACCAAGTTTGACCTCAGACAGTGG
TTCTTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT
TTCCTGGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT
CATCGGCATCCACTGCTTCCGCCAGACAACATGTGGTCTAGCCAGAGGTTCCAGGCCCACCTGCAGGAGATGGGT
GCCCCAATGCTTGGTCCACCATCATCGTGCCTGGCATGAAGGATGCTGTGATCCACGCACTTCAGACCTCCAG
GACACCGTGCAGTGTGCGAAGGCCAGCTTTGAGCTCTATGGCGCTGACTTCGTGTTCCGGGAGGACTTCAGCCC
TGGCTGATTGAGATCAACGCCAGCCCCACGATGGCACCCCTCCACAGCAGTCACTGCCCGGCTCTGTGCTGGCGTG
CAAGCTGACACCCTGCGCGTGGTCATTGACCGGATGCTGGACCGCAACTGTGACACAGGAGCCTTTGAGCTCATC
TATAAGCAGCCCGTCAACACTTCCCCAGCCTCCACACCAAGGCCAGCTGCCTTCTCCCCATGTACTCCGACACC
AGGGCCAGGTCTCAGACGACAGCACAGCAAGCTGGTGGGCACTAAGGCCCTGTGACACAGGCAAGGCCTTGA

GGACTCTACCCACGGCTAAGGTCTTCATTTCCCTCCCACCGAACCTTGATTTCAAGGTGGCACCCAGCATCCTGA
AGCCAAGAAAGGTGGGCCTCGACCTGTGACTCACACCCAGTGGACAGTGCTGAGCACGGGGTCAGGGCTGGAGGG
CACAGGCAGAGGGCAGCTCCCAGGCTGGCTGGCACCCCAAGGGAAGAGCTGGTCTCCCTCAGAAGCCCCCTTCCTC
CACAGACTTCTGATCATCTCCCTCTTCTCCCCCTCTTTACACCGAGGCTCCTGCTCTCCTGTGCCTCCGAGGCC
CCCAGCTGGAAGTGCCTTGTTCCTCTGCCCCTTTGAAGTCGGAACAATTCCTAGCACCTGTGGAAGGTCAAGGC
CAAAGGCAAATTCAAGGCCAGACTGTGACAAACCCAGGGCTGAGGCCTGCCCATGAAGAGGCTGAGCCCCCTGA
AACCCCTGCCCTTGTGGTACATTCCAGAGGCGCAGGGGCTGGGGGATATGAAGCTAGGGAAGCCCCCTGCTTC
GATTCCTCCACTGCCCTTGTCTGGATCCAACACCAATAAAAAGAAACAAGTGAAGTAAAAAAAAAAAAAAAAAAAA
AAA

1135/6881
FIGURE 1058

MDIDKDLEAPLYLTPEGWSLFLQRYYQVVHEGAELRHLDTQVQRCEDILQQLQAVVPQIDMEGDRNIWIVKPGAK
SRGRGIMCMDHLEEMLKLVNGNPVVMKDGKWVVQKYIERPLLIIFGTFDLRQWFLVTDWNPLTVWIFYRDSYIRFS
TQPFSLKNLDNSVHLCNNSIQKHLENSCHRRHPLLPDNNMWSSQRFQAHLOEMGAPNAWSTIIVPGMKDAVIHALQ
TSQDTVQCRKASFELYGADFVFGEDFQPWLEINASPTMAPSTAVTARLCAGVQADTLRVVIDRMLDRNCDTGAF
ELIYKQPVTTSFASPTRPSCLLPMYSDTRARSSDDSTASWWALRPCRQARP

1136/6881
FIGURE 1059

GTCCTGGCTCGGGAGATGGACGGCCGCCGTGTTTTGGGCCGGTTCTGGAGTGGCTGGCGGCCGGGCCTGGGTGTC
CGCCCAAGTGCCCGAGGACGCAGGCTTTGGCACCAGCCGAGCCGATCAGAGGCAACCCCGCGGCTCCTGCCAACGG
TCGGGGCCCCCTCGGGGACCAGCCCTTCGCGGGGCTGCTGCCAAAAACCTCAGTCGGGAGGAGCTGGTTGATGCG
CTGCGGGCAGCCGTGGTGGACCGGAAAGGAAAACCAGGAGAGCTGACGTTGTTCTCAGTGCTGCCAGAGCTGAGC
CAGTCCCTAGGGCTCAGGGAGCAGGAGCTTCAGGTTGTCCGAGCATCTGGGAAAGAAAGCTCTGGGCTTGTAATC
CTCTCCAGCTGTCCCCAGACAGCTAGTCGCCTCCAGAAGTACTTCACCCATGCACGGAGAGCCCAAAGGCCACCA
GCCACCTACTGTGCTGTCACTGATGGGATCCCAGCTGCTTCTGAGGGGAAGATCCAGGCTGCCCTGAAACTGGAA
CACATTGATGGGGTCAATCTCACAGTTCCAGTGAAGGCCCATCCCGAAAGGACATCCTGGAAGGTGTCAAGAAG
ACTCTCAGTCACTTTCGTGTGGTAGCCACAGGCTCTGGCTGTGCCCTGGTCCAGCTGCAGCCACTGACAGTGTTT
TCCAGTCAACTACAGGTGCACATGGTACTACAGCTCTGCCCTGTGCTTGGGGACCACATGTACTCTGCCCCGTGTG
GGCACTGTCTTGGGCCAGCGATTTCTGCTGCCAGCTGAGAACAAAGCCCCAAAGACAGGTCTTGGATGAAGCC
CTCCTCAGACGCCTCCACCTGACCCCTCCCAGGCTGCCAGCTGCCCTTGACCTCCACCTACATCGGCTCCTT
CTCCAGGCACCAGGGCCAGGGACACCCCTGTTGAGCTCCTGGCACCCTGCCCCCTTATTTCTCCAGGACCCTA
CAGTGCCTGGGGCTCCGCTTACAATAGTCCTCCCTCTGTTTCTGACCCCTCACACACACTGGAAAGTGAGGGTG
GGGGCTCTGCAGTCAGACAAACCTAAGATCACATCCTGGACAGGCCACTTGCTTGCTGTGTGGCATTGGGCAAGT
AACTTTACCTCTCTGGACTTGTGATAATAAAAGTTCCTACCTC

1137/6881
FIGURE 1060

ATAGGGTCAGTGGGCCGCTTGGCGGTGTCGTTGCGGTACCAGGTCCGCGTGAGGGGTTTCGGGGGTTCTGGGCAGG
CACA**ATGG**CGTCTCGAGCAGGCCCGCGAGCGGCCGGCACCGACGGCAGCGACTTTCAGCACCGGGAGCGCGTCGC
CATGCACTACCAGATGAGTGTGACTCTCAAGTATGAAATCAAGAAGCTGATCTACGTACATCTGGTCATATGGCT
GCTGCTGGTTGCTAAGATGAGCGTGGGACACCTGAGGCTCTTGTCACATGATCAGGTGGCCATGCCCTATCAGTG
GGAATACCCGTATTTGCTGAGCATTTTGGCCTCTCTCTTGGGCCTTCTCTCCTTTCCCGCAACAACATTAGCTA
CCTGGTGCTCTCCATGATCAGCATGGGACTCTTTTCCATCGCTCCACTCATTTATGGCAGCATGGAGATGTTCCC
TGCTGCACAGCAGCTCTACCGCCATGGCAAGGCCTACCGTTTCCTCTTTGGTTTTTCTGCCGTTTCCATCATGTA
CCTGGTGTTGGTGTTGGCAGTGCAAGTGCATGCCTGGCAGTTGTACTACAGCAAGAAGCTCCTAGACTCTTGGTT
CACCAGCACACAGGAGAAGAAGCATAAA**TGA**AGCCTCTTTGGGGTGAAGCCTGGACATCCCATCGAATGAAAGGA
CACTAGTACAGCGGTTCCAAAATCCCTTCTGGTGATTTTAGCAGCTGTGATGTTGGTACCTGGTGCAGACCAGGC
CAAAGTTCTGGAAAGCTCCTTTTGCCATCTGCTGAGGTGGCAAACTATAATTTATTCCTGGTTGGCTAGAACTG
GGTGACCAACAGCTATGAAACAAATTTAGCTGTTTGAAGTTGAACTTTGAGGTTTTTCTTTAAGAATGAGCTTC
GTCCTTGCTCTACTCGGTCACTCTCCCCATTTCCATCCATTACCCCTTAGCCATTGAGACTAAAGGAAATAGGG
AATAAATCAAATTACTTTCATCTCTAGGTCACGGGTCAGGAAACATTTGGGCAGCTGCTCCCTTGGCAGGCTGTGG
TCTCCTCTGCAAAGCATTTTAATTAAAAACCTCAATAAAGA

1138/6881
FIGURE 1061

MASRAGPRAAGTDGSDFQHRERVAMHYQMSVTLKYEIKKLIYVHLVIWLLLVAKMSVGHLRLLSHDQVAMPYQWE
YPYLLSILPSLLGLLSFPRNNISYLVLSMISMGLFSIAPLIYGSMEMFPAAQQLYRHGKAYRFLFGFSAVSIMYL
VLVLAVQVHAWQLYYSKLLDSWFTSTQEKKKH

1139/6881
FIGURE 1062

GGAAGTTGAGCGGCGGCAAGAAATAATGGCGGCAGCTACGGGGGATCCTGGACTCTCTAAACTGCAGTTTGCCCC
TTTTAGTAGTGCTTGGATGTTGGGTTTTGGCATGAGTTGACCCAGAAGAAGCTGAACGAGTATCGGCTGGATGA
AGCTCCCAAGGACATTAAGGGTTATTACTACAATGGTGACTCTGCTGGGCTGCCAGCTCGCTTAACATTGGAGTT
CAGTGCTTTTGACATGAGTGCTCCCAACCCAGCCCGTTGCTGCCCAGCTATTGGAACACTGTATAACACCAACAC
ACTCGAGTCTTTCAAGACTGCAGATAAGAAGCTCCTTTTGGAACAAGCAGCAAATGAGATATGGGAATCCATAAA
ATCAGGCACTGCTCTTGAAAACCCGTGACTCCTCAACAAGTTCCTCCTCTTGACATTTGCAGATCTAAAGAAGTA
CCACTTCTACTATTGGTTTTGCTATCCTGCCCTCTGTCTTCCAGAGAGTTTACCTCTCATTACAGGGGCCAGTGGG
TTTGATCAAAGGTTTTCACTAAAACAGATTGAAGCACTAGAGTGTGCATATGATAATCTTTGTCAAACAGAAGG
AGTCACAGCTCTTCCTTACTTCTTAATCAAGTATGATGAGAACATGGTGCTGGTTTTCTTGCTTAAACACTACAG
TGATTTCTTCCAAGGTCAAAGGACGAAGATAACAATTGGTGTATATGATCCCTGTAACCTAGCCCAGTACCCTGG
ATGGCCTTTGAGGAATTTTTTGGTCTTAGCAGCCACAGATGGAGTAGCAGTTTCCAGTCTGTTGAAGTTGTTTG
CTTCCGTGACCGTACCATGCAGGGGGCGAGAGACGTTGCCACAGCATCATCTTCGAAGTGAAGCTTCCAGAAAT
GGCATTTAGCCCAGATTGTCTTAAAGCAGTTGGATGGGAAAAGAACCAGAAAGGAGGCATGGGACCAAGGATGGT
GAACCTCAGTGAATGTATGGACCTAAAAGGTTAGCTGAGTCATCAGTGGATCTAAATCTCAAACCTGATGTGTTG
GAGATTGGTTCCCTACTTTAGACTTGGACAAGGTTGTGTCTGTCAAATGTCTGCTGCTTGGAGCCGGCACCTTGGG
TTGCAATGTAGCTAGGACGTTGATGGGTTGGGGCGTGAGACACATCATTGTGGACAATGCCAAGATCTCCTA
CTCCAATCCTGTGAGGCAGCCTCTCTATGAGTTTGAAGATTGCCTAGGGGGTGGTAAGCCCAAGGCTCTGGCAGC
AGCGGACCGGCTCCAGAAAATATTCCCCGGTGTGAATGCCAGAGGATTCAACATGAGCATACTATGCCTGGGCA
TCCAGTGAACCTTCTCCAGTGTCACCTCTGGAGCAAGCCCGCAGAGATGTGGAGCAACTGGAGCAGCTCATCGAAAG
CCATGATGTCGTCTTCCTATTGATGGACACCAGGGAGAGCCGGTGGCTTCTTGCCGTCATTGCTGCAAGCAAGAG
AAAGCTGGTCATCAATGCTGCTTTGGGATTTGACACATTTGTTGTCATGAGACATGGTCTGAAGAAACCAAAGCA
GCAAGGAGCTGGGGACTTGTGTCAAACCACCCTGTGGCATCTGCTGACCTCCTGGGCTCATCGCTTTTTTGCAA
CATCCCTGGTTACAAGCTTGGCTGCTACTTCTGCAATGATGTGGTGGCCCCAGGAGATTCAACCAGAGACCGGAC
CTTGACCAGCAGTGCACTGTGAGTCGTCCAGGACTGGCCGTGATTGCAGGAGCCCTGGCCGTGGAATTGATGGT
ATCTGTTTTGCAGCATCCAGAAGGGGGCTATGCCATTGCCAGCAGCAGTGACGATCGGATGAATGAGCCTCCAAC
CTCTCTTGGGCTTGTGCCTCACCAGATCCGGGGATTTCTTTACGGTTTGATAATGTCCTTCCCGTCAGCCTGGC
ATTTGACAAATGTACAGCTTGTCTTCCAAAGTTCTTGATCAATATGAACGAGAAGGATTTAACTTCCTAGCCAA
GGTGTTTAATTCTTCACATTCTTCTTAGAAGACTTGACTGGTCTTACATTGCTGCATCAAGAAACCCAAGCTGC
TGAGATCTGGGACATGAGCGATGATGAGACCATCTGAGATGGCCCCGCTGTGGGGCTGACTTCTCCCTGGCCGCC
TGCTGAGGAGCTCTCCATCGCCAGAGCAGGACTGCTGACCCAGGCCTGGTGAATCTGGGGCCCTCCTCCATACC
CCGAGGTCTGGGATTCCCCCTCTGCTGCCAGGAGTGGCCAGTGTTCCGGCGTTGCTCGGGATTCAAGATACCAC
CAGTTCAGAGCTAAATAATAACCTTGGCCTTGGCCTTGCTATTGACCTGGGAAAAAAAAAAAAAAAAAAAAA

1140/6881
FIGURE 1063

MAAATGDPGLSKLQFAPFSSALDVGFWHELTQKKLNEYRLDEAPKDIKGYYYNGDSAGLPARLTLEFSAFDMSAP
TPARCCPAIGTLYNTNTLESFKTADKKLLEQAANEIWESIKSGTALENPVLLNKFLLLTfADLKKYHFYYWFCY
PALCLPESLPLIQGPVGLDQRFSLKQIEALECAYDNLCQTEGVTALPYFLIKYDENMVLVSLLKHYSDFQGGQRT
KITIGVYDPCNLAQYPGWPLRNFLVLAHRWSSSFQSVVVCFRDRTMQGARDVAHSIIFEVKLPMAFSPDCPK
AVGWEKNQKGGMGRMVNLSECMDBPKRLAESSVDLNLKLMCWRLVPTLDLDKVVSVKCLLLGAGTLGCNVARTLM
GWGVRHITFVDNAKISYSNPVRQPLYEFEDCLGGGKPKALAAADRLQKIFPGVNARGFNMSIPMPGHPVNFSSVT
LEQARRDVEQLEQLIESHDVVFLMDTRESRWLPAVIAASKRKLVINAAALGFDTFVVMRHGLKKPKQQGAGDLCP
NHPVASADLLGSSLFANIPGYKLGCFNDVVAPGDSTRDRTLDDQCTVSRPGLAVIAGALAVELMVSVLQHPEG
GYAIASSSDDRMNEPPTSLGLVPHQIRGFLSRFDNVLPVSLAFDKCTACSSKVLDQYEREGFNFLAKVFNSSHSF
LEDLTGLTLLHQETQAAEIWDMSDDETI

1141/6881
FIGURE 1064

TCTTCCTCGGCGCTGCCTACGGAGGTGGCAGCCATCTCCTTCTCGGCATCATGGCCGCCCTCAGACCCCTTGTGA
AGCCCAAGATCGTCAAAAAGAGAACCAAGAAGTTCATCCGGCACCAGTCAGACCGATATGTCAAAATTAAGCGTA
ACTGGCGGAAACCCAGAGGCATTGACAACAGGGTTCGTAGAAGATTCAAGGGCCAGATCTTGATGCCCCAACATTG
GTTATGGAAGCAACAAAAAACAAGCACATGCTGCCCAGTGGCTTCCGGAAGTTCCTGGTCCACAACGTCAAGG
AGCTGGAAGTGCTGCTGATGTGCAACAAATCTTACTGTGCCGAGATCGCTCACAATGTTTCCTCCAAGAACCGCA
AAGCCATCGTGGAAGAGCTGCCCACTGGCCATCAGAGTCACCAACCCCAATGCCAGGCTGCGCAGTGAAGAAA
ATGAGTAGGCAGCTCATGTGCACGTTTTCTGTTTAAATAAATGTAAAACTGCCATCTGGCATCTTCCTTC

1142/6881
FIGURE 1065

MAALRPLVKPKIVKKRTKKFIRHQSDRYVKIKRNWRKPRGIDNRVRRRFKGQILMPNIGYGSNKKTKHMLPSGFR
KFLVHNVKELEVLLMCNKSYCAEIAHNVSSKNRKAIVERAAQLAIRVTNPARNLRSEENE

1143/6881
FIGURE 1066

TCGGAGGAGCCAGCCGAAATCCTGCCGCCTGCCCGGGACGAGGAGGAGGAGGAGGAAGAGGGGATGGAGCAGGGG
CTGGAGGAGGAAGAAGAGGTGGATCCCCGGATCCAGGGAGAACTGGAGAAGTTAAATCAGTCCACGGATGATATC
AACAGACGGGAGACTGAACTTGAGGATGCTCGTCAGAAAGTTCCGCTCTGTTCTGGTTGAAGCAACGGTGAAACTG
GATGAACTGGTGAAGAAAATTGGCAAAGCTGTGGAAGACTCCAAGCCCTACTGGGAGGCACGGAGGGTGGCGAGG
CAGGCTCAGCTGGAAGCTCAGAAAGCCACGCAGGACTTCCAGAGGGCCACAGAGGTGCTCCGTGCCGCCAAGGAG
ACCATCTCCCTGGCCGAGCAGCGGCTGCTGGAGGATGACAAGCGGCAGTTCGACTCCGCCTGGCAGGAGATGCTG
AATCACGCCACTCAGAGGGTTCATGGAGGCGGAGCAGACCAAGACCAGGAGCGAGCTGGTGCATAAGGAGACGGCA
GCCAGGTACAATGCCGCCATGGGCCGCATGCGACAGCTGGAGAAGAACTCAAGAGAGCCATCAACAAGTCCAAG
CCTTATTTTGAATCAAGGCAAAGTACTATGTGCAGCTCGAGCAACTGAAAAAGACTGTGGATGACCTGCAGGCC
AAACTGACCCTGGCAAAAAGCGAGTACAAGATGGCCCTGAAGAACCTGGAGATGATCTCAGATGAGATCCACGAG
CGGCGGCGCTCCAGTGCCATGGGGCCTCGGGGATGCGGTGTTGGTGCTGAGGGCAGCAGCACATCTGTGGAGGAT
CTGCCAGGGAGCAAACCTGAGCCTGATGCCATTTCTGTGGCCTCGGAGGCCTTTGAAGATGACAGCTGTAGCAAC
TTTGTGTCTGAAGATGACTCGGAAACCCAGTCCGTGTCCAGCTTTAGTTCAGGACCAACAAGCCCGTCTGAGATG
CCTGACCAGTTCCCTGCGGTTGTGAGGCCTGGCAGCCTGGATCTGCCAGCCCTGTGTCCCTGTCTAGAGTTTGGG
ATGATGTTCCAGTGTTGGGCCCTCGAAGTGAATGCAGCGGGGCCCTCCTCCCTGAATGTGAAGTAGAACGAGGA
GACAGGGCAGAAGGGGCAGAGAATAAAACAAGTGACAAAGCCAACAACAACCGGGGCCCTCAGCAGTAGCAGTGCC
AGTGGTGGCAGCAGTAAGAGCCAAAGCAGCACCTCCCCTGAGGGCCAGGCCTTGAGAAACCGGATGAAGCAGCTC
TCCCTACAGTGCTCAAAGGGAAGAGATGGAATTATTGCTGACATAAAAAATGGTGCAGATTGGCTGATTCATCCTG
GGCCCTGGCCGATGTGCATATCAACATTTATACATGGAAGTGGAGAACATTGTGCCAATAATCATTTAATATATG
CCAAATCTTACAGCTCTACTCTAACTGCTCTAATGAAGTTTCAGTGACCTTGAGGGCTAAAGATTGTTCTTCTG
GGTAAGAGCTCTTGGGCTGGTTTTTTCAGAGCAGAGTCTTGTGTGGGTAGACTGTGACTAGGTTTCACAGCCTTT
GTGGAACATTCCGTATAACGGCATTGTGGAAGCAATAACTAGTTCCTATGAAAGAACCAGAGCTGGGAAGATGGC
TGGGAAGCCAGGCCAAAGTGGGGGCAACAGCTTGCTTCTCTTTCTCTTCTCACCCTCAGTTTGTATGGGAAAATG
GAGATGTCCTCTCCACTTTATCCCACGATATCTAAATGAAAAAGAAAAGAAAACCCACACACAAAGCAAAAACTCA
AGTATTAAGAGCACATATTTTTGACCCAGTGGAGGCTTAAAAAAGGCTGATGCTGGGATACCCATTAAACCATTTTCTAGAAGG
CACCTCTGGTGTTCAGAGGGGGCTTTTAAAAAAGCGTGTATGCTGGGATACCCATTAAACCATTTTCTAGAAGG
CTACCATGAGCTGCACTTTTTGGGGTGGGAAAGGTGAATGCCAGTGGGGATGCGGGGGGATGAGGGTAGGAGGGA
CTTATAGAAGGGGATTTGTGGCTGTGGGGGAGAAGGTTCTACAGCATAAGCCTTATCCTGCCAGCCAAGGGGATT
TATTCTAAGAGAAGTGCAATGTGAAGAATGGTTGCCACTGTTATTAGATTGACAAGATGTTAATTTCTCTGTAGGT
TGTAACCTTTAAAAATAAATGAAATTATTTAAGGGTTATGCTGCACTAGTATTCCTTAGAGGAAACAGTTCTTTAA
AGTTAGGAAAGGGAGTAGGCAGGCATGTGTTGGCAAAGGCTGTTAATAGTAGTTAAGTGTTAAGACTGCTTTTCT
TTAACGTTTTTCATGGTAATGCATATTTAGAGCACTGTATTTTTGTCTTGTTAAGAAAATTTAGCATTTTCTAAAAAG
AAAAAAGCAACCCTCTTTCAAAGTGTAAATCTGTACAGCCTGTATATTTAGTCATTGTAAATCTCTTCATA
CAATAGTGACTTCTTTTTTGGACTGATACAGTATCTTAATTACAAGGTTATTTTGTACTTGTCTTAATACACTAAG
TGTAATAAAAACGGCTTGAG

1144/6881
FIGURE 1067

MEQGLEEEEEVDPRIQGELEKLNQSTDDINRRETELEDARQKFRSVLVEATVKLDELVKKIGKAVEDSKPYWEAR
RVARQAQLEAQKATQDFQRATEVLRAAKETISLAEQRILLEDDKRQFDSAWQEMLNHATQRVMEAEQTKTRSELVH
KETAARYNAAMGRMRQLEKKLKRAINKSKPYFELKAKYYVQLEQLKKTVDDLQAKLTLAKGEYKMALKNLEMISD
EIHERRRSSAMGPRGCGVGAEGSSTSVEDLPGSKPEPDAISVASEAFEDDSCSNFVSEDDSETQSVSSFSSGPTS
PSEMPDQFFAVVRPGSLDLPSPVSLSEFGMMFPVLGPRSECSGASSPECEVERGDRAEGAENKTSKANNNRGLS
SSSGSGSSKSKQSSTSPEGQALENRMKQLSLQCSKGRDGIADIKMVQIG

1145/6881
FIGURE 1068

CATGGCAAAAGAACTCCCGGATAATCCGAATTCGTGGTCCTCAGAATTGGTTTAGGGTTGTTTCGCGGTTCTTCC
CGTATTCTGCCTCCGAGGCCAGTGGGGCTGGCTGTGGGGTGAGTGCGCCTGGCCCTAGCCCTGCAGCCCCCTGT
GCTGTTTGAGGCGTGAACTCACCTCAGGAAATGTATCTGATCCATTAGCGTGGATTTCATATTATTGGTGATGG
AGAATCTTCAGCTGTGTTAAGTGTTACCGTCAGTTTCAGAGATGGCTTCTTTGCAAAGGAAAGGGCTGCAGGCAA
GGATTCTCACCTCTGAAGAAGAGGAGAACTGAAAAGAGACCAAACCTTTGGTGTCTGATTTTAAACAGCAGAAAT
TGGAACAAGAGGCTCAGAAAAATTGGGATCTTTTTTACAAAAGAAATAGCACTAATTTCTTCAAAGACAGACACT
GGACCACCAGAGAGTTTGAGGAGCTAAGATCATGTAGAGAGTTTGAAGATCAAAGTTAAACAATGCTTGAAGCTG
GCTGTGGGGTTGGAACTGTTTATTCCCACTTTTAGAAGAAGATCCGAATATCTTTGCCTATGCCTGTGATTTTT
CTCCAAGAGCCATTGAATATGTTAAGCAAAATCCTTTATATGATACAGAAAGATGCAAGGTATTCCAGTGTGATC
TGAATAAGATGATCTTCTGGATCATGTACCGCCAGAGTCTGTGGATGTTGTTATGTTGATATTTGTGCTGTGACG
CTGTTTCATCTGATAAGATGCACCTTGTCTTACAAAACATTTACAAGGTATTTAAACCAGGCAAAAAGTGTCTTGT
TTCGTGACTACGGACTGTATGATCATGCCATGCTTAGGTTTAAAGCCAGCAGCAAACCTTGAGAAAACTTTTATG
TTAGACAAGATGGGACCAGATCATATTTTTTTACTGATGACTTCCTGGCTCAGCTCTTTATGGACACAGGTTATG
AAGAAGTGGTAAACGAGTATGTGTTTCGAGAGACGGTGAATAAAAAAGAAGGCCTGTGTGTGCCAAGAGTTTTCC
TTCAGAGCAAATTTCTAAAGCCTCCTAAGAACCCATCTCCTGTGGTCCTGGGCCTGGATCCTAAGTCCTGACCTT
TCATGAGGTTGGCATTATACCTTCCCTTGAAGAGGAAAATTTAAAATCACTCTTTCGTCTGGGTGCGGTGGCTC
AIGCCTGTAATCCCAGCACTTCGGGAGGCCGAGGTTGGGGGATCATCTGAGGTCAGGAGTTTGAGACCAGCCTGG
CCAACATGGTGAGACCCCATCTCTACTAAAAATACAAAAAAATTAGCTGGGCATAGTGGCGAGTGCCTGTAATCC
CAGCTACTCAGGAGGCTGAGGCAAGAGAATCGCTTGAACCCAAGAGGCGGAGACTGCAGTGAGCCAAGATCATGC
CATTGCACTCCAGCCTGGGCGACAGAGTGAGACCCTGTTTCATAAAATAAAATAAAATCACTCTTTTTACTTTATAT
ATTTTTTGAGACAGGATCTTGTGGTACGCAGGCTGGAGTGCAAGTGGTGTGTGATCACAGCTCATTGTAGCCTCGA
CCTCCCCTGGGCTCAAGCAGTCTTCCTGCCTCAGCCTCCTGAGTAGCTAGGACTACAGGTGTAAGCCACCATGCC
TGGCCCTTAATTTTTTTTAAATGAGCATGTACAGTAGTCCCGCTTTATCCATGGTTTCACCTACCACAATTTCAAT
TACCTGTTTTTCAACTGCAGTCAGTTACTTTTCTTAAGATATTTGAGGGTTATAGGCTCATGCCTATAACCCAG
CACTTTGAGAGGCCAAGGCCAGCAGATCCCTTGAGCCAGGAGTTCAAGACCAGTGTGGGCAACATGGTGAAACT
CTGTCTCTACAGAAAATACAAAAATTAGCCAAATGTGGTGGCATGTGCCTGTAGTCCCAG

1146/6881
FIGURE 1069

MASLQRKGLQARILTSEEEKLKRDQTLVSDFKQQKLEQEAQKNWDLFYKRNSTNFFKDRHWTTREFEELRSCRE
FEDQKLTMLEAGCGVGNCLFPLLEEDPNIFAYACDFSPRAIEYVKQNPLYDTERCKVFQCDLTKDDLLDHVPPES
VDVVMLIFVLSAVHPDKMHLVLQNIYKVLKPGKSVLFRDYGLYDHAMLRFKASSKLGENFYVRQDGTRSYFFTDD
FLAQLFMDTGYEEVVNEYVFRETVNKKEGLCVPRVFLQSKFLKPPKNPSPVVLGLDPKS

1147/6881
FIGURE 1070A

GACAATGAAAAGCGAACCCCATTTGCACGCCGCAGCTTACCTTGGAGATGCAGAAATCATTGAACTTCTTATTTTA
TCTGGAGCTAGAGTTAATGCCAAAGACAGCAAATGGTTGACACCTTTACACAGAGCAGTTGCATCTTGTAGTGAG
GAAGCAGTTCAGGTACTTTTGAAGCATTCTGCAGATGTTAATGCTCGAGACAAAAATTGGCAAACCCCTTTACAT
ATAGCTGCTGCTAATAAAGCTGTAAAGTGTGCTGAAGCTTTGGTACCTCTTCTGAGTAATGTAAACGTATCTGAT
CGAGCAGGGAGGACTGCATTACATCATGCAGCTTTCAGTGGACATGGTGAGATGGTCAAACCTACTCTTGTCTAGA
GGTGCCAATATTAATGCTTTTGACAAGAAAGATAGGCGTGCTATCCATTGGGCAGCATATATGGGTACATTGAA
GTAGTGAAATTGCTTGTGTCGCTGGAGCTGAAGTGACATGCAAGGATAAAAAGTCTTATACACCTCTTCATGCA
GCAGCCTCTAGTGGAATGATCAGCGTAGTCAAGTACCTTCTAGATCTTGGAGTTGATATGAATGAACCAAATGCC
TATGGAAATACACCTCTTCATGTAGCCTGCTATAATGGACAAGATGTTGTAGTGAATGAACCTTATAGACTGTGGT
GCTATTGTGAATCAAAAAGATGAAAAGGATTTACTCCTTTGCACTTTGCTGCTGCATCAACACATGGAGCATTG
TGTTTAGAGCTTCTAGTTGGCAATGGGGCCGATGTCAATATGAAGAGTAAAGATGGGAAAACCCCACTACACATG
ACTGCTCTCCACGGTAGATTCTCCCGATCACAAACCATTATCCAGAGTGGAGCTGTAATCGACTGTGAGGATAAG
AATGGAAATACCCCTTTGCACATAGCAGCACGGTATGGCCATGAGCTGCTGATCAACACTCTTATTACAAGTGGT
GCTGACACTGCAAAGCGTGGCATAACATGGAATGTTCCCCCTCCATTTGGCAGCCTTAAGCGGCTTTTCAGATTGC
TGCAGAAAACCTTCTTTCTTCAGGATTTGATATAGATACCCCAAGATGATTTTGGCAGGACTTGTCTACATGCAGCT
GCAGCTGGAGGGAATTTGGAGTGCCTAAACCTTCTGCTGAATACTGGTGCAGACTTTAATAAAAAGGACAAATTT
GGGAGATCTCCACTGCACTACGCTGCTGCCAACTGCAATTACCAGTGCCTGTTTGTCTTGTGGGATCAGGAGCA
AGTGTGAATGACCTTGATGAAAGAGGCTGCACACCCCTGCACTATGCAGCTACATCAGACACAGATGGCAAGTGC
CTGGAATACTTATTAAGAAACGATGCAATCCAGGGATCCGTGATAAGCAAGGATAACAACGCAGTTCATTATTCA
GCTGCTTATGGTCACCGTCTATGTCTTCAGCTGATTGCAAGTGAACTCCTCTAGATGTTTTAATGGAAACCTCA
GGAACAGACATGCTGAGTGATTAGATAATAGAGCAACAATAAGCCCTTTACACTTGGCTGCCTATCATGGTCAC
CATCAAGCACTGGAAGTGTGGTACAGTCTTTGTTAGATCTTGATGTCAGAAATAGTAGTGAAGAACACCCCTA
GATCTTGCAGCTTTTAAGGGCCATGTTGAATGTGTGGATGTACTCATTAAATCAGGGAGCCTCAATCTTAGTAAAA
GATTACATTTTGAAGAGGACACCTATTTCATGCAGCAGCAACAAATGGTCATTTCAGAATGCTTACGGCTATTAATA
GGAAATGCAGAACACAGAAATGCAGTGGATATTCAAGATGGAAATGGACAGACGCCTCTGATGCTATCTGTTCTC
AACGGGCACACAGACTGTGTTTACTCATTGCTGAACAAAGGAGCAAAATGTAGATGCCAAAGATAAGTGGGGAAAGG
ACAGCGTTGCATAGAGGGGCAGTTACAGGCCATGAAGAATGTGTAGATGCATTACTTCAACATGGTGCTAAGTGC
TTACTTCGGGATAGCAGGGGGCCGACGCCTATACACCTGTCTGCTGCCTGTGGACACATTGGTGTTCTTGGAGCC
CTTTTGCAGTCAGCAGCATCTATGGATGCAAATCCAGCCACAGCAGACAATCATGGATATACGGCACTTCACTGG
GCTTGCTACAATGGTCACGAGACATGTGTAGAAGTCTTTTTAGAACAGGAAGTTTTCCAGAAAACCGGAAGGAAAT
GCTTTTAGTCCATTGCATTGTGCCGTGATAAATGACAACGAAGGTGCTGCTGAGATGTTAATTGATACATTAGGT
GCCAGCATTGTGAACGCCACAGATTCAAAGGAAGAAGTCTCTCCATGCAGCCGCCTTCACAGACCATGTAGAG
TGTTTACAGCTGCTGCTCAGCCATAATGCTCAAGTCAATTCTGTGGACTCTACAGGGAAAACACCTCTTATGATG
GCTGCAGAAAATGGACAAACAAATACAGTTGAGATGCTGGTTAGCAGTGCTAGTGCAGAACTGACTTTACAAGAT
AACAGTAAAAATACTGCCCTCCATTTGGCTTGTAGCAAGGGTCATGAACTAGTGCCTTGTTAATACTGGAAAAG
ATAACAGATAGAAACCTCATCAATGCAACCAACGCAGCCTTGCAAACACCTCTGCATGTTGCTGCCCCGAAATGGG
CTAACAATGGTGTTTTCAGGAACTTTTGGGAAAAGGAGCAAGTGTGCTTGCAAGTAGATGAAAATGGCTATACCCCA
GCTTTGGCCTGTGCTCCCAATAAGGATGTGGCTGATTGCCTGGCTCTCATTTTGGCCACCATGATGCCTGTCTCA
TCAAGTAGTCTTTATCATCCTTAACATTCAATGCCATTAAACGTTATACCAACACCTCAAAAACAGTCAGCTTT
GAAGCTTTGCCCATCATGAGGAATGAACCTAGCTCCTATTGCAGTTTCAATAACATTGGAGGGGAACAGGAGTAC
TTATACACTGACGTGGATGAGCTCAACGACTCCGATTCTGAGACCTACTGAGAGGCTGAGGAGGAGGGAGTTCTC
ACAGTAAAGCTTCAAACCTGTGCTTTTTTCAGGAAAAGGCACTTTGATATTACGTTAGAAATTCACCTAAGAGGA
AAGATCCACAGTGAGCCAATGTTAAGAGATCTGATGGCATTAGGAGGAAGAGTTTTAAAGGCAAGTTTTACAAA
AGGAACTTCTAGAATCTTGAAATAGACCTGACTGAGGAAAACACATTGATGTCAGAAATCTTTGTGGAATTGTTT
AATTTGGTTTTGCAGTGCCAGGAACAATTGGGGACACTGTGCACTCTAACCTGCTTACACAAGCAACACTATTGT
AACAGAAGAAATAAAGACACTAGATTTAAATTTTATCAATAAAATTAACAATAAATTTAAAGGCAATAAAAGTTT
GGTACAGTAGGCATTATGTGCACAGCAAATTGCAAAGGACCAATAAAGTGAAGGTTTTTTTTAATAAAATGCCA
TTTTGTGGAACCTGGAGTAGATTAAATGAAACATTACCTAAACCAAACCTGCAATATTTCTGGAATGAAGCTGAG

1148/6881
FIGURE 1070B

ATTGTTTAAATGTTGAGTTTTTTGGGTTTTGTTTTTTTTTAAGAAAACATCTGAAAGCCTTCCAATGCTG
TATTAAACCATGAGAGAAAGCAGATGTATTTTTACATTTTTTCTTTTACAGAACTATTTCAAATTTCCAATTTT
TATACTATTAGAATTAAAAACCAGCTGACTGGGTGCAATACGGGTGAAAATACTTGTGACATAGACATTGAGATG
GATTGGGGTCAGGCTGTTGCCCTGTTTTGAATGGTTTGGGTTTAAATAGTACTATTTTTGTTTGAAAATGTAA
GAATTCCTAGAAAAAATTCATGAAATCAAAAAGTAGACTATTTACCCTATTGCAGCTAAGTGGTCCTGGGGC
ATGGAGTCTTCAACCTCTCTATGAATGGCACACCTTAGTCACCTATGTTACTTTTGTGTCCCCACCATGGGTTGG
GGGATTTTTTGTATTCTGATCTATGAGTTTTGAAAAAGTGAATAATCAAAGGAAAAATAATTCCTTGTGTTC
ATAAATTAAGCATCACTAAAGTCTCTTGAAAGGCATTTCTGTATTGGGCAAGATTTAAATACTAAAGCCTTAGG
TCCTATTCATATTTAAAGTAGCATGTTTGTAACCTGTTACTATTTGGAGAGAGAAGCAGTTGCCTGCCAAATTGA
AGACTACCTTTCAAATAGCAAAAGAGAGAGAGAAGGCTGATATTTGCGCTTTTAAATAAAGATTTGTGTGGTTCT
GCTTTTACTGTAACTGTCACTTTCCAGTGAAAAATGATTTTCATATACATTGAGGGTCTTACAGGTATGGGTAAAG
TTCTATAAATTGCAACAAAATGATACCCAATTTTCATTTTATCCTTTTTGTATTGTGAACTGGAACTTTATGAC
ATTGTAAATTATCAGCTGGTTTTTCTGAATATAAAGTGTGAAAACACAGAACAGTATTTGATCTATTTGATAAT
TTTGTGGGTTTTTTGAAGAATTAATGAGCATGTACATAGAAATAGTGACTGCTTGAATACTGTATTTACTTGCAC
TCTTTCAGTACATCAAGATTCCCTGTATATTTTAGAGTATAATAAAACACAGATGTGAGTTGTATTTAATGAATA
TGTATTTGTATCTGTGCATATTATCTACAAATCTATAAAGTTTCTAGGGCATTGACTACTAGATTTTAAGCATTT
TTTCTAAAATATTTACAGAAATTATAAATCTAATCCCCCATCTTTTCTTTATAATATAAAGAAGTCATAATGAAC
CCTTCCTAATTATTAGTAGTAGGAAGGTGAATATGCATTTTAATGACAGTGGACTACATTTTCTATTGTACCTTT
TGAAAAAATAAATCAAGCAGATTCTAAAAGTATACATATGTGTGCTTTCTCTTTCCTTTTAGGAATTCTCTT
CTGAATTCCTGAGGGAATTTTCTAGAATCTCAGAATTGAAAGAGACCTGAGGTTTCATCCAGTCTCTAACCTCTT
AACAAATGCAGGAGTCCCTTCTACAAGGGTGATCTTTCCACCTTGAACACTTCCAAGTGACTCTACCTCACCAAG
CAGTCCATTAGTTGTTGAGCAGCTCTAACTGTTAGAAAGGTCTTCCTTAGATGGAGTTGAAGCCTCCCTCCCGG
TAACTTCTGTCTTTGGGCCTGGGTCTGTCTCCAGAGAACCCTGAGAATGTTGGAAGGATGAATCTCGCACATT
CTGCCATGTCTTCTCTTTTACAGGCTGTTTGACTTCTCTGCTGAAGTGATTTCCAGAAGGACTCATTTGACACAC
TATTAGATTTACCACATCTAATGAAATCCAAGGTGTAGCTATAAAGTGACAAGCTGTTTTTAATTTATCACATAC
ACCAGAACTTCTATCCTGCATCACTTATATGTAAATGATGCTGTTACCAAAAACATTAAGGTAGTTCTTGCGAAT
GCCACCCCACTAAGAAAATATTTTATTACTTTTGTAAATCCATCTGTGAGAGTCTGCCCCCAGCTTAACCACTT
CCTTTGGTCTGCACCAATGAAGGGAAACCCCAAAGTACTGTCTCAAATGGTATTTGAACTACG

1149/6881
FIGURE 1071

MVKLLLSRGANINAFDKKDRRAIHWAAYMGHIEVVKLLVSHGA EVTCKDKKSYTPLHAAA SSGMISVVKYLLDLG
VDMNEPNAYGNTPLHVACYNGQDVVVNELIDCGAIVNQKNEKGFTPLHFAA ASTHGALCLELLVGNGADVNMKSK
DGKTPLHMTALHGRFSRSQTI IQSGAVIDCEDKNGNTPLHIAARYGHELLINTLITSGADTAKRGIHGMFPLHLA
ALSGFSDCCRKLLSSGFDIDTPDDFGRTCLHAAAAGGNLECLNLLLNTGADFNKKDKFGRSPLHYAAANCNYQCL
FALVGSGASVNDLDERGCTPLHYAATSDTDGKCLEYLLRNDANPGIRDKQGYNAVHYSAAYGHRCLCLQLIASETP
LDVLMETSGTDMLS DSDNRATISPLHLAAYHGHHQALEVLVQSLLDLVNRSSGRTPDLAAFKGHVECV DVLIN
QGASILVKDYILKRTP IHAAATNGHSECLRL LIGNAEPQNAVDIQDGNGQTPLMLSVLNGHTDCVYSLLNKGANV
DAKDKWGRTALHRGAVTGHEECVDALLQHGA KCLLRDSRGRTP IHLSAACGHIGVLGALLQSAASMDANPATADN
HGYTALHWACYNGHETCVELLLEQEVFQKTEGNAFSPLHCAVINDNEGAAEMLIDTLGASIVNATDSKGRTP LHA
AAFTDHVECLQ LLLSHNAQVNSVDSTGKTPLMMAAENGQTNTVEMLVSSASAELTLQDNSKNTALHLACSKGHET
SALLILEKITDRNLINATNAALQTP LHVAARNGLTMVVQELLGKGASVLAVDENGYPALACAPNKDVADCLALI
LATMMPVSSSSPLSSSLTFNAINRYTNTSKTVSFEALPIMRNEPSSYCSFNNIGGEQEYLYTDVDELNDS DSETY

1150/6881
FIGURE 1072

CTTCCTGACAGCACACAACCTTGATTAGGAGGGGCTGGGAGGGAGGATCGATGAGCCCCTGACCCCTGGGTCTG
AGGCTGCCAGGGTCGCTTGACAGCTCGGCCGCGTGAGAGTGACCGGGCGGAACCTCCGAGGGGGCGCGGGGAGAGCT
GGGCGGGCCCAACCGCTCCAGCGGCTGCTGTAGGGGGCCGCGAGGCTTTCCCTGAAGATGCAGCGTAGCATATTTT
GCACATGAGTTTCAAGGAAGAGGAAGTGTAGCCGGCGGACGCGCGGGCGGGCGGGGGCGCGTTCGGGGCTGG
AGCCGGAGCGCGCCGGGCGCTGGGCGCAGCGAGCGAGAGCGCGGGCGGGCGGGCTCCGGCGAGGGACAGACGCA
CCGATCGCCGGAGGGACAGACACACGACCACGCGGCGCCACCGCCACGCCTCCACCCACCGGCGCCCAAGTCCT
CCCCGCGCCGCTCCTCTGTATGGCACAACTTTCTCCCGGACGGAACACGCTGCCTCAGGGAGCCCGCGACC
GCGCCTTCTCCTCCGCGGTCCCATACGCTGCTGAAATCGGTTGCGGATTGAACAAGTTAGAGAAACGTGATGAA
AAACGGCCTGGGAATATTTATTCAACTTTGAAGAGGCCCTCAGGTGGAAACCAAGATAGATGTGTCTATGAATAC
CGCTTCTGAGTTTACGACTCTGAGTGCTGCGGAGCTCCCTGGGTCTCAGCAGTGAGGCTGGCCTCCCTGCGT
GACCTGCCCCCGCAGCTCCTGGAGCTGTACCAGCAGGGCTTCTCGCTGGCGGCCCTGCACCCCTTCGTGCAGCCC
ACCCATGAGCGGGAGAAGACGCCCCCTGGAGCACATCTTTAGAGCCATCCTGATCAAGAAAACCGACAGATCTCAG
AAAAGTATCTTACAAATGAAGGCTACATCTTGAATTAGATTGCTGTTCTCCTTAGACCACCCGACAGACCAG
AAACTCATCCCAGAGTTCATTAAGAAGATCCAGGAGGCTGCAAGCCAGGGCCTGAAATTCGTTGGTGTTATACCT
CAGTACCATTCTCTGTGAACCTCGGCAGGCAGCAGTGCTCCGGTGTCTACTGCCAACAGCACCGAGGATGCCAGA
GATGCAAAAAACGCACGTGGGGATCACGCGTCACTGGAGAATGAGAAACCGGGGACTGGGGATGTGTGCAGTGCT
CCGGCTGGGAGAAACCAAAGCCAGAGCCCAGCTCAGGCCCCAGAGGGGAGGTGCCCCCTCGCCAAGCAGCCCAGC
TCACCCCTCCGGAGAGGGAGATGGTGGAGAACTTTACCCACAGGGGGTGAGCAAGACACTGGATGGACCGGAGAGC
AACCCCTTGGAGGTGCATGAAGAGCCACTCTCAGGGAAAATGGAGATCTTACCCCTTTTCAACAAACCGAAGAGC
CATCAGAAGTGCCGGCAATACTACCCCTGTACCATTCCTCTCCATGTCTCCAAGAATGGCCAGACAGTGAGCGGT
TTGGACGCCAACTGGTTAGAGCACATGAGCGACCACTTCCGGAAAGGAGGCATGCTGGTGAACGCAGTCTTCTAC
CTTGGAATAGTGAATGATTTCCTTACATGGCTTGACAGATGGAGTATTTCATCTTTGAAGCTGTTTCCACAGAAGAT
AGCAAAACCATAACAGGGCTATGATGCTATTGTGGTTGAACAATGGACAGTCCTGGAAGGTGTGCAAGTGCAGACA
GACTACGTGCCCTGCTGAACCTCGCTGGCGGCCTATGGCTGGCAGCTCACCTGTGTGCTACCAACTCCCGTCGTC
AAGACTACCAGCGAGGGGAGTGTATCCACCAAGCAGATTGTCTTTCTTACAGAGACCTTGTCTACCTCAGAAAATC
AAGAAGAAGGAATCGAAGTTTTCAGTGGCGATTCTCCAGAGAAGAAATGCACAACAGGCAGATGAGGAAATCAAAA
GGTAAACTCAGTGCCAGAGACAAACAACAAGCAGAAGAAAATGAGAAGAACTTAGAAGACCAGTCTTCCAAAGCT
GGAGACATGGGAAACTGTGTTTTCAGGACAGCAGCAGGAGGGTGGAGTCTCCGAGGAGATGAAGGGCCCTGTCCAA
GAGGACAAGGGAGAACAGCTGTCCCTGGTGGCTGCTGTGTGGGGTGGGTGTGGAGGGTGAGGCTGTGCAGAAT
GGTCTGCCAGCCACAGCAGGGCCCTGGTGGGGATTGCACTGGGCACTCCAATCCTGGAGAGGATGCCAGGGAC
GGGGATGCTGAGGAAGTCAGAGAGCTTGGTACGGTTGAAGAAAATGAGTCTTGGGCAATTTGTGCTAAAACCTAG
GTGAGTTGCCAAACCCAAGGCATCTTACCAACAGCTGGTTTGGGGGCTGGTTTCCCTGGTGTGTGTGTACCTA
CCCTTTGGCTTGGCTTGACCTCTCCTTGTGAGCTCACCTGAGCCCTCCAGGGCCAGGTTCTTGACAGTGTGGT
TTTTGCACATCCACTGGAAAGGTGTCAATTAATGACCCAGTGTTAGAATGCAAGAGGTCAGGTTATTCTAGCCCTC
ATGGCTGAAGGCCAGTCTGGCTCCACCACTCCTCCAGCCAGAGGGTCTGGACCATCCAGTGCCTGTCTCGCC
ACAGGGCCTCCAGGGAGCATTGGGTCAAAATCCATGGACACCCTGGGCTACAAACCAAGGCTGCTGTTTCATCCCA
CATCGTGTGGGGCAGTGTCCATCCCTGCAGCTACTTGGTGACTTAACAACCTCCAGGAGCCCTGTCAGCTGCCCT
CCTCCACCTAAACCCCTTCGACTCTTCTGCTTTGACAAAGAAAATGACATTGGGGAGGGGAGGTGCTCCGCCTCC
CAGCTTTTCTCAAAATAGTCCTATAGATACTGGTAATCTGGAATGAAGAAGTAATTCTGTCTCTGCACCTACTT
TTGCAGAATGTTCAAGGAAGTATTCTGTGTTAGTATTAATGCCAAAAGTTGTTTTTAAAGGTTTTGTACTCAGC
ACATCATACAAACCACATTACTTCTGTCACCTCAGGGCATCGGGACTGGCTGGCGCCCTTGTATGTGCTATTTT
AATCAGTGTAACTTGGTCAAGTTGTTACCATGTATGCTGTGTTTATCATGTGTATATCGTCCAGAAAGTATTA
AGGCTTTAGGTAGATGCAACTGGCGAACCTTGGAGAGGGAATGCTGATTGTCTTGACCAAACCCACAGCCTGTCT
CTTCTCTGTTTAGTTACTTACGGCAATAAATCATCTATGAGTT

1151/6881
FIGURE 1073

MGCGLNKLEKRDEKRPGNIYSTLKRPQVETKIDVSYEYRFLEF'TTLSAAELPGSSAVRLASLRDLPAQLLELYQQ
GFSLAALHPFVQPTHEREKTPLEHIFRAILIKKTDRSQKTDLHNEGYLELDCCSSLDHPTDQKLIPEFIKKIQE
AASQGLKFVGVIPQYHSSVNSAGSSAPVSTANSTEDARDAKNARGDHASLENEKPGTGDVCSAPAGRNQSPEPSS
GPRGEVPLAKQPSSPSGEGDGGELSPQGVSKTLDGPESNPLEVHEEPLSGKMEIFTLFNPKPKSHQKCRQYYPVTI
PLHVSKNGQTVSGLDANWLEHMSDHFRKGGMLVNAVFYLGIVNDSLHGLTDGVFIFEAVSTEDSKTIQGYDAIVV
EQWTVLEGVEVQTDYVPLLNSLAAYGWQLTCVLPTPVVKTTSEGSVSTKQIVFLQRPCLPQKIKKKESKFQWRFS
REEMHNRQMRKSKGKLSARDKQQAENEKNLEDQSSKAGDMGNCVSGQQQEGGVSEEMKGPVQEDKGEQLSPGGL
LCGVGVEGEAVQNGPASHSRALVGICTGHSNPGEDARDGDAEEVRELGTVEEN

1152/6881
FIGURE 1074

GCAATAGCACTAGAGTGCATCTATACCTGTGAACGAAATGATCAACTCTGTCTTTGCTATGACCTACTAGAATGT
CTGCCAGAAAAGAGGATATGGTGATAAGACAGAGGCCAACCAAGCTTCATGACATGGTAGACCAACTGGAACAA
ATTCTCAGTGTGTCAGAGCTTTTGGAAAAACATGGACTCGAGAAACCAATTTCAATTTGTTAAAAAACTCAATCT
AGCTCAGAAGAGGCACGCAAGCTGATGGTTAGATTGACGAGGCACACTGGCCGGAAGCAGCCTCCTGTGATGAG
TCTCATTGGAGAACGTTGCTGCAAGACATGTTAACTATGCAGCAGAATGTATACACATGTCTAGATTCTGATGCC
TGCTATGAGATATTTACAGAAAAGCCTTCTGTGCTCTAGTCGCCCTTGAAAACATCCACCTGGCTGGACAGATGATG
CACTGCAGTGCTTGTTGAGAAAATCCTCCAGCTGGTATAGCCCATAAAGGGAAACCCCACTACAGGGTCAGCTAC
GAAAAGAGTATTGACTTGGTTTTGGCTGCCAGCAGAGAGTACTTCAATTTCTTCTACCAACCTCACTGATAGCTGC
ATGGATCTAGCCAGGTGCTGCTTACAACCTGATAACAGACAGACCCCTGCCATTCAAGAGGAGCTAGATCTTATC
CAAGCCGTTGGATGCTTGAAGAATTTGGGGTAAAGATCCTGCCCTTGCAAGTGCGATTGTGCCCTGATCGGATC
AGTCTCATCAAGGAGTGATTTCCCAGTCCCCACATGCTATAAAACATCCACCAAGCTTCTGGGCCTTGCTGAG
CTGCTGAGGGTTGCAGGTGAGAACCAGAAAGCGGGGACAGGTTCTAATCCTTTTAGTGGAGCAGGCACTTC
GCTTCCATGACTACAAAGCAGCCAGTATGCATTGTGAGGAGCTGATGGCCACAGGTTATCCTAAAAGTTGGGATG
TTTGTAGCCAGTTAGGACAATCAGAAGTTACCAGGACTTGGCCACTCGTCAAGAGCTCATGGCTTTTGTCTTTGA
CACATTGCCCTCCTAGCAGCATTGAATTTCTTTTGGCAGCTAGCAGCTCTCTGCAGACAGAAATTTCTTTATCAAA
GAGTGAATTTCCAGATCCATCATGAAGGAGGGGAAAATATCAGTGCTTCACCATTAACTAGTAAAGCAGTACAAG
AGGATGAAGTAGGTGTTCCAGGTAGCAATTCAGCTGACCTATTGCGCTGGACCACTGCTACCACCATGAAAGTCC
TTTCCAACACCACAACCACCACCAAAGCGGTGCTGCAGGCCGTCAGTGATGGGCAGTGGTGAAGAAGTCTTTAA
CTTACCTTCGACCCCTTCAGGGGCAAAAATGTGGTGGTGATATCAAATCGGAACTACAGCCAATGAAGATCTAG
AGAAACAAGGGTGTATCCTTTTTATGAATCTGTCTATCTCAAATCCTTTTGTGCTGAGTCTGAAGGGACCTATG
ACACCTATCAGCATGTTCCAGTGGAAGCTTTGCAGAAGTATTGCTGAGAACTGGAAAATTGGCAGAGGCTAAAA
ATAAAGGAGAAGTATTTCCAACAACCTGAAGTTCTCTTGCAACTAGCAAGTGAAGCCTTGCCAAATGACATGACCT
TGGCTCTTGCTTACCTTCTTGCCCTTACCACAAGTGTAGATGCTAACCAGTGTCTTTGAAAAGCAGTCCCCCTCTG
CATTATCTCTCCAGCTGGCAGCGTATTACTATAGCCTCCAGATCTATGCCCGATTGGCCCCATGTTTCAGGGACA
AGTGCCATCCTCTTTACAGGGCTGATCCCAAAGAACTAATCAAGATGGTCACCAGGCATGTGACTCGACATGAGC
ACGAAGCCTGGCCTGAAGACCTTATTTCACTGACCAAGCAGTTACACTGCTACAATGAACGTCTCCTGGATTTC
CTCAGGCGCAGATCCTTCAGGGCCTTCGGAAGGGTGTGGACGTGCAGCGGTTTACTGCAGATGACCAGTATAAAA
GGGAAACTATCCTTGGTCTGGCAGAACTCTAGAGGAAAGCGTCTACAGCATTGCTATTTCTCTGGCACAACGTT
ACAGTGTCTCCCGCTGGGAAGTTTTTATGACCCATTTGGAGTTCTCTTCACGGACAGTGGTTTTGTCCACACTAG
AAATTGAAAATAGAGCCCCAAGACCTTCATCTCTTTGAGACTTTGAAGACTGATCCAGAAGCCTTTACCAGCACA
TGGTCAAGTATATTTACCCTACTATTGGTGGCTTTGATCACGAAAGGCTGCAGTATTATTTCACTCTTCTGGAAA
ACTGTGGCTGTGCAGATTTGGGGAACCTGTGCCATTAAACCAGAAACCCACATTCGACTGCTGAAGAAGTTTAAGG
TTGTTGCATCAGGTCTTAATTACAAAAAGCTGACAGATGAAAACATGAGTCCTCTTGAAGCATTGGAGCCAGTTC
TTTCAAGTCAAAATATCTTGTCTATTTCCAAACTTGTTCCTCAAAATCCCTGAAAAGGATGGACAGATGCTTTCCC
CAAGCTCTCTGTACACCATCTGGTTACAGAAGTTGTTCTGGACTGGAGACCCCTCATCTCATTAAACAAGTCCAG
GCTCTTACCAGGAGTGGCTTCATGCCTATGATGTCTGCATGAAGTACTTTGATCGTCTCCACCCAGGTGACCTCA
TCACTGTGGTAGATGCAGTTACATTTTCTCCAAAAGCTGTGACCAAGCTGTCTGTGGAAGCCGTAAGAGATGA
CTAGAAAGGCTATTAAGACAGTCAAACATTTTATTGAGAAGCCAAGGAAAAGAACTCAGAAGACGAAGCTCAAG
AAGCTAAGGATTCTAAAGTTACCTATGCAGATACTTTGAATCATCTGGAGAAATCACTTGCCACCTGGAAACCC
TGAGCCACAGCTTCATCCTTTCTCTGAAGAATAGTGAGCAGGAAACACTGCAAAAATACAGTCACCTCTATGATC
TGTCCCGATCAGAAAAAGAGAACTTCATGATGAAGCTGTGGCTATTTGTTTAGATGGTCAGCCTCTAGCAATGA
TTCAGCAGCTGCTAGAGGTGGCAGTTGGCCCTCTTGACATCTCACCCAAGGATATAGTGCAGAGTGAATCATGA
AAATAATTTCTGCATTGAG

1153/6881
FIGURE 1075

GCAGTACATTGAGCTCCATAGAGACAGCGCCGGGGCAAGTGAGAGCCGGACGGGCACTGGGCGACTCTGTGCCTC
GCTGAGGAAAAATAACTAAACATGGGCAAAGGAGATCCTAAGAAGCCGAGAGGCAAAATGTCATCATATGCATTT
TTTGTGCAAACCTGTCTGGGAGGAGCATAAGAAGAAGCACCCAGATGCTTCAGTCAACTTCTCAGAGTTTTCTAAG
AAGCCCGTTATGAAAGAGAAATGAAAACCTATATCCCTCCCAAAGGGGAGACAAAAAGAAGTTCAAGGATCCCA
ATGCACCCAAGAGGCTTCCTTCGGCCTTCTTCCTCTTCTGCTCTGAGTATCGCCCCAAAATCAAAGGAGAACATC
CTGGCCTGTCCATTGGTGATGTTGCGAAGAACTGGGAGAGATGTGGAATAACACTGCTGCAGATGACAAGCAGC
CTTATGAAAAGAAGGCTGCGAAGCTGAAGGAAAAATACGAAAAGGATATTGCTGCATATCGAGCTAAAGGAAAGC
CTGATGCAGCAAAAAAGGGAGTTGTCAAGGCTGAAAAAAGCAAGAAAAAGAAGGAAGAGGAGGAAGATGAGGAAG
ATGAAGAGGATGAGGAGGAGGAGGAAGATGAAGAAGATGAAGAAGAAGATGATGATGATGAATAAGTTGGTTGTA
GCGCAGTTTTTTTTTCTTGTCTATAAAGCATTTAACCCCCCTGTACACAATTCACCTCTTTTTTAAAGAAAAAAATTG
AAATGTAAGGCGGTGTAAGATTTGTTTTTAACTGTACAGTGCTTTTTTTGTATAGTTAACACACTACCGAATG
TGTCTTTAGATAGCCCTGTCCTGGTGGTATTTTCAATAGCCACTAACCTTTGCCTGGTACAGTATGGGGGTTGTAA
ATTGGCATGGAAATTTAAAGCAGGTTCTTGTTGGTGCCAGCACAAATTAGTTATATATGGGGATGGTAGTTTTT
TCATCTTCAGTTGTCTCTGATGCAGCTTATACGAAATAATTGTTGTTCTGTAACTGAATACCACTCTGTAATTG
CAAAAAAAAAAAGTTGCAGCTGTTTTGTTGACATTCTGAATGCTTCTAAGTAAATACAATTTTTTTTATTA

1154/6881
FIGURE 1076

CCTTTCCGTCTGGCGGCAGCCATCAGGTAAGCCAAGATCGGGTGCATACAAGTACATCCAGGAGCTATGGAGAAAAG
AAGCAGTCTGATGTCATGCGCTTTCTTCTGAGGGTCCGCTGCTGGCAGTACCGCCAGCTCTCTGCTCTCCACAGG
GCTCCCCGCCCCACCCGGCCTGATAAAGCGCGCCGACTGGGCTACAAGGCCAAGCAAGGTTACGTTATATATAGG
ATTCTGTGTTCCCGTGGTGGCCGAAAACGCCAGTTCTTAAGGGTGCAACTTACGGCAAGCCTGTCCATCATGGT
GTTAACCAGCTAAAGTTTGCTCGAAGCCTTCAGTCCGTTGCAGAGGAGCGAGCTGGACGCCACTGTGGGGCTCTG
AGAGTCCTGAATTCTTACTGGGTTGGTGAAGATTCCACATACAAAATTTTTTGAGGTTATCCTCATTGATCCATT
CATAAAGCTATCAGAAGAAATCCTGACACCCAGTGGATCACCAACCAGTCCACAAGCACAGGGAGATGCGTGGG
CTGACATCTGCAGGCCGAAAGAGCCGTGGCCTTGGAAGGGGCCACAAGTTCCACCACACTATTGGTGGCTCTCGC
CGGGCAGCTTGGAAGAGCGCAATACTCTCCAGCTCCACCGTTACCGCTAAATATAAGTAAAGTTTGTAATAATTCA
TACTTAATAAACAATTTAGGACAGTCATGTCTGCTTACAGGTGTTATTTGTCTGTTAAACTAGTCTGCAGATGT
TTCTTGAATGCTTTGTCAAATTAAGAAAGTTAAAGTGCAATAATGTTTGAAGACAATAAGTGGTGGTGTATCTTG
TTTCTAATAAGATAAACTTTTTTGTCTTTGCTTTATCTTATTAGGGAGTTGTATGTGTCAGTGTATAAAACATACTG
TGTGGTATAACAGGCTTAATAAATCTTTAAAGGAGAGAACTGAAACTAGCCCTGTAGATTTGTCTGGTGCATG
TGATGAAACCTGCAGCTTTATCGGAGTGATGGCAATGCTCTGCTGGTTTATTTTCAAGTGGCTGCGTTTTTTTTTA
GTTTGGCAGGTGTAGACTTTTTTAAGTTGGGCTTTAGAAAATCTGGGTTAGCCTGAAGAAAATTGCCTCAGCCTCC
ACAGTACCATTTTAAATTCACATAAAAGGTGAAAGCTCCTGGTTTCAAGTGCCATGGCTTCATGGCATTCAAGTGATT
AGTGGTAATGGTAAACACTGGTGTGTTTTGAAGTTGAATGTGCGATAAAATTATTAGCCTTAAGATTGGTAAGCT
AGCAATGAATGCTAGGGTGGGAAGCTGGTGTAGCCAGTGGCCATTAGATAAATACCTTTCAAGTGTGAGCTTAGAC
GTCAACCCTAAAATACTTAACCGTAATGCTAATTGTGATCATTATGAATCCCTTCAGTCACATTAGGGGGAAAGT
AGTTGGCTATAAGTACGTCATTCTTAGTCCAGTCAGTCTTAAAAACATCTTGGGTTACCCACTCTGTCCACTCCC
ATAGGCTACAGAAAAAGTCACAAGCGCATGGTTTCCAACCATATGTGTTTTCTGCAGTTATTTCTCTTGTCTG
CCAAACAACCCTAAAAATCCTTACCATTCCACAAAGTTGGACCATCACTTGTGCACCCACTTTGACTATGAGTAT
ACCACCACATTGCATTTCTGTTTGCACCATGTCTTCCAGGAGACTAGACTACTGTTGTCCAGGGTCAATTTGAGT
GTAAAGAAAATGTAGACAAGGAATTGCCCAATTTTAAATTCTGACTTTGCTGACTTAATTTAAATGCTCGTTCTG
AACCAATTTTCTCCTATCTTCTCTAGGGGTTTCAAAGACTCAGTTAATTGATTTCCAGGAAGTACTCATAGCAA
GTCATAAAAGTTCTTGAGACCTAAATTTCTTCACAAAAAAGAAAAGATCTTAAGTCATACATTTTAATTGTGT
AGAGGTTGTTCAACTGAAGGAATAAATGTCTATTAACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

1155/6881
FIGURE 1077

MGAYKYIQELWRKKQSDVMRFLLRVRCWQYRQLSALHRAPRPTRPDKARRLGKAKQGYVIYRIRVRRGGRKRPV
PKGATYGKPVHHGVNQLKFARSLQSVAEERAGRHCALRVLNSYWVGEDSTYKFFEVLIDPFHKAIRNPDTQW
ITKPVHKKHREMRLTSAGRKSRGLGKGHKFHHTIGGSRAAWRRRNTLQLHRYR

1156/6881
FIGURE 1078

GTGACAGAAGTAGTAGGAAGTGAGCTGTTTCAGAGGCAGGAGGGTCTATTCTTTGCCAAAGGGGGGACCAGAATTC
CCCCATGCGAGCTGTTTGAGGACTGGGATGCCGAGAACGCGAGCGATCCGAGCAGGGTTTGTCTGGGCACCGTCCG
GGGTAGGATCCGGAACGCATTTCGGAAGGCTTTTTTGCAAGCATTACTTGGAAAGGAGAACTTGGGATCTTTCTGGG
AACCCCCCGCCCCGGCTGGATTGGCCGAGCAAGCCTGGAAAATGGTAAATGATCATTGGATCAATTACAGGCTT
TTAGCTGGCTTGTCTGTCATAATTCATGATTTCGGGGCTGGGAAAAAGACCAACAGCCTACGTGCCAAAAAAGGGG
CAGAGTTTGATGGAGTTGGGTGGACTTTTCTATGCCATTTGCCTCCACACCTAGAGGATAAGCACTTTTGCAGAC
ATTCAGTGCAAGGGAGATCATGTTTGACTGTATGGATGTTCTGTCTAGTGAGTCCTGGGCAAAATCCTGGATTTCTA
CACTGCGAGTCCGTCTTCCTGCATGCTCCAGGAGAAAAGCTCTCAAAGCATGCTTCAGTGGATTGACCCAAACCGA
ATGGCAGCATCGGCACACTGCTCAATCAATTGAAACACAGAGCACCAGCTCTGAGGAACCTCGTCCCAAGCCCCC
ATCTCCACTTCTCCCCCTCGAGTGTACAAACCCTGCTTCGTCTGCCAGGACAAATCATCAGGGTACCCTATGG
GGTCAGCGCTGTGAGGGATGTAAGGGCTTTTTCCGCAGAAGTATTGAGAAGAATATGATTTACACTTGTACCCG
AGATAAGAACTGTGTTATTAATAAAGTCACCAGGAATCGATGCCAATACTGTCTGACTCCAGAAGTGCTTTGAAGT
GGGAATGTCCAAAGAATCTGTCTAGGAATGACAGGAACAAGAAAAAGAGGAGACTTCGAAGCAAGAATGCACAGA
GAGCTATGAAATGACAGCTGAGTTGGACGATCTCAGAGAGAAGATCCGAAAAGCTCACCAGGAAACTTTCCCTTC
ACTCTGCCAGCTGGGTAAATACACCACGAATTCAGTGCTGACCATCGAGTCCGACTGGACCTGGGCCTCTGGGA
CAAATTCAGTGAACCTGGCCACCAAGTGCATTATTAAGATCGTGGAGTTTGCTAAACGTCTGCCTGGTTTCACTGG
CTTGACCATCGCAGACCAAATTACCCTGCTGAAGGCCGCTGCCTGGACATCCTGATTCTTAGAATTTGCACCAG
GTATACCCAGAACAAGACACCATGACTTTCTCAGACGGCCTTACCCTAAATCGAACTCAGATGCACAATGCTGG
ATTTGGTCCTCTGACTGACCTTGTGTTACCTTTGCCAACAGCTCCTGCCTTTGGAAATGGATGACACAGAAAC
AGGCCTTCTCAGTGCCATCTGCTTAATCTGTGGAGACCGCCAGGACCTTGAGGAACCGACAAAAGTAGATAAGCT
ACAAGAACCATTGCTGGAAGCACTAAAAATTTATATCAGAAAAAGACGACCCAGCAAGCCTCACATGTTTCCAAA
GATCTTAATGAAAAATCACAGATCTCCGTAGCATCAGTGCTAAAGGTGCAGAGCGTGTAATTACCTTGAAAAATGGA
AATTCCTGGATCAATGCCACCTCTCATTCAAGAAATGCTGGAGAATTCTGAAGGACATGAACCTTGACCCCAAG
TTCAAGTSGGAACACAGCAGAGCACAGTCCTAGCATCTCAGCCAGCTCAGTGGAAAACAGTGGGGTCAGTCAGTC
ACCACTCGTGCAATAAGACATTTTCTAGCTACTTCAAACATTCCCCAGTACCTTCAGTTCCAGGATTTAAAAATGC
AAGAAAAAACATTTTTTACTGCTGCTTAGTTTTTGGACTGAAAAGATATTTAAACTCAAGAAGGACCAAGAAATTT
TCATATGTATCAATATATATACTCCTCACTGTGTAACCTTACCTAGAAATACAACTTTTCCAATTTTAAAAAATC
AGCCATTTTCATGCAACCAGAACTAGTTAAAAGCTTCTATTTTCTCTTTGAACACTCAAGATTGCATGGCAAAG
ACCCAGTCAAAATGATTTACCCCTGGTTAAGTTTCTGAAGACTTTGTACATACAGAAGTATGGCTCTGTTCTTTC
TATACTGTATGTTTGGTGCTTTCTTTTGTCTTGCATACTCAAAAATAACCATGACACCAAGGTTATGAAATAGAC
TACTGTACACGTCTACCTAGGTTCAAAAAGATAACTGTCTTGTCTTTCATGGAATAGTCAAGACATCAAGGTAAGG
AAACAGGACTATTGACAGGACTATTGTACAGTATGACAAGATAAGGCTGAAGATATTCTACTTTAGTTAGTATGG
AAGCTTGTCTTTGCTCTTTCTGATGCTCTCAAACCTGCATCTTTTATTTTCATGTTGCCAGTAAAAGTATACAAAT
TCCCTGCACTAGCAGAAGAGAATTCTGTATCAGTGTAAGTCCAGTTCAGTTAATCAAATGTCATTTGTTCAATT
GTTAATGTCACCTTTAAATTAAAAGTGGTTTATTACTTGTTTAAATGACATAACTACACAGTTAGTTAAAAAAATTT
TTTTTACAGTAATGATAGCTCCAAGGCAGAAACACTTTTCAGTGTTAAGTTTTTGTCTTACTTGTTCACAAGCCA
TTAGGGAAATTTTCATGGGATAATTAGCAGGCTGGTCTACCACCTGGACCATGTAACCTCTAGTGTCTTCTCTGATT
CATGCCTGATATTGGGATTTTTTTTTTCCAGCCTTCTTGATGCCAAGGGGCTAATTAATATTAACTCCCAAAG
AAACAGGCATAGAATCTGCCTCCTTTGACCTTGTTCATCACTATGAAGCAGAGTGAAAGCTGTGGTAGAGTGGT
TAACAGATACAAGTGTCTGTTTCTTAGTTCTCATTTAAGCACTAGTGGAATTTTTTTTTTTTGTATATATTAGCAA
GTCTGTGATGTACTTTCACTGGCTCTGTTTGTACATTGAGATTGTTTGTTTAACAATGCTTTCTATGTTTCATATA
CTGTTTACCTTTTTTTCATGGAGTCTCCTGGCAAAGAATAAAATATATTTATTTT

1157/6881
FIGURE 1079A

ATGGCCAAGTCGGGTGGCTGCGGCGCGGGAGCCGGCGTGGGCGGCGGCAACGGGGGCACTGACCTGGGTGAACAAT
GCTGCAAAAAAGAAGAGTCAGAACTGCCAACAAAAATGATTCTTCAAAGAAGTTGTCTGTTGAGAGAGTGTAT
CAGAAGAAGACACAACCTTGAACACATTCTTCTTCGTCTGATACATATATTGGGTCAGTGGAGCCATTGACGCAG
TTCATGTGGGTGTATGATGAAGATGTAGGAATGAATTGCAGGGAGGTTACCTTTGTGCCAGGTTTATACAAGATC
TTTGATGAAATTTTGGTTAATGCTGCTGACAATAAACAGAGGGATAAGAACATGACTTGTATTAAAGTTTCTATT
GATCCTGAATCTAACATTATAAGCATTGGAATAATGGGAAAGGCATTCCAGTAGTAGAACACAAGGTAGAGAAA
GTTTATGTTCTGCTTTAATTTTTGGACAGCTTTTAACATCCAGTAACTATGATGATGATGAGAAAAAGTTACA
GGTGGTCGTAATGGTTATGGTGCAAACTTTGTAATATTTTCAGTACAAAGTTTACAGTAGAAACAGCTTGCAAA
GAATACAAACACAGTTTTAAGCAGACATGGATGAATAATATGATGAAGACTTCTGAAGCCAAAATTAACATTTT
GATGGTGAAGATTACACATGCATAACATTCCAACCAGATCTGTCCAAATTTAAGATGGAAAACTTGACAAGGAT
ATTGTGGCCCTCATGACTAGAAGGGCATATGATTTGGCTGGTTCGTGTAGAGGGGTCAAGGTCATGTTTAATGGA
AAGAAATTGCCTGTAAATGGATTTGCGAGTTATGTAGATCTTTATGTGAAAGACAAATTGGATGAAACTGGGGTG
GCCCTGAAAGTTATTCATGAGCTTGCAATGAAAGATGGGATGTTTGTCTCACATTGAGTGAAAAAGGATTCCAG
CAAATCAGCTTTGTAAATAGTATTGCAACTACAAAAGGTGGACGGCACGTGGATTATGTGGTAGATCAAGTTGTT
GGTAACTGATTGAAGTAGTTAAGAAAAAGAACAAAGCTGGTGTATCAGTGAAACCATTTCAAGTAAAAAACCAT
ATATGGGTTTTTTATTAATTGCCTTATTGAAAATCCAACCTTTTGATTCTCAGACTAAGGAAAACATGACTCTGCAG
CCCAAAGTTTTGGGTCTAAATGCCAGCTGTGAGAAAATTTTTTAAAGCAGCCTCTAATTGTGGCATTGTAGAA
AGTATCCTGAAGTGGGTGAAATTTAAGGCTCAGACTCAGCTGAATAAGAAGTGTTCATCAGTAAATACAGTAAA
ATCAAAGGTATTTCCCAAACCTGGATGATGCTAATGATGCTGGTGGTAAACATTCCTGGAGTGTACACTGATATTA
ACAGAGGGAGACTCTGCCAAATCACTGGCTGTGTCTGGATTAGGTGTGATTGGACGAGACAGATACGGAGTTTTT
CCACTCAGGGGCAAAATTTCTTAATGTACGGGAAGCTTCTCATAACAGATCATGGAAATGCTGAAATAAATAAT
ATTATTAATAAGTTGGTCTACAATATAAGAAAAGTTACGATGATGCAGAATCTCTGAAAACCTTACGCTATGGA
AAGATTATGATTATGACCGATCAGGATCAAGATGGTTCTCACATAAAAGGCCTGCTTATTAATTTTCATCCATCAC
AATTGGCCATCACTTTTGAAGCATGGTTTTCTTGAAGAGTTCATTACTCCTATTGTAAAGGCAAGCAAAAATAAG
CAGGAACCTTTCCTTCTACAGTATTCTGAATTTGACGAATGGAAAAACATATAGAAAACCAGAAAGCCTGGAAA
ATAAAGTACTATAAAGGATTGGGTACTAGTACAGCTAAAGAAGCAAGGAATATTTTGCTGATATGGAAAGGCAT
CGCATCTTGTTTAGATATGCTGGTCTGAAGATGATGCTGCCATTACCTTGGCATTTAGTAAGAAGAAGATTGAT
GACAGAAAAGAATGGTTAACAAATTTTATGGAAGACCGGAGACAGCGTAGGCTACATGGCTTACCAGAGCAATTT
TTATATGGTACTGCAACAAAGCATTGACTTATAATGATTTTCATCAACAAGGAATTGATTCTCTTCTCAAACCTCA
GACAATGAAAGATCTATACCATCTCTTGTTGATGGCTTTAAACCTGGCCAGCGGAAAGTTTTATTTACCTGTTTT
AAGAGGAATGATAAACGTGAAGTAAAGTTGCCAGTTGGCTGGCTCTGTTGCTGAGATGTCGGCTTATCATCAT
GGAGAACAAGCATTGATGATGACTATTGIGAATTTGGCTCAGAACCTTTGTGGGAAGTAACAACATTAACCTTGCTT
CAGCCTATTGGTCAGTTTGGAACTCGGCCTCATGGTGGCAAAGATGCTGCAAGCCCTCGTTATATTTTCACAATG
TTAAGCACTTTAGCAAGGCTACTTTTTCTGCTGTGGATGACAACCTCCTTAAGTTCCTTTATGATGATAATCAA
CGTGTAGAGCCTGAGTGGTATATTCTTATAATTCCCATGGTTTTAATAAATGGTGCTGAGGGCATTGGTACTGGA
TGGGCTTGTAACCTACCCAACTATGATGCTAGGGAAATTGTGAACAATGTCAGACGAATGCTAGATGGCCTGGAT
CCTCATCCCATGCTTCCAACTACAAAACCTTTAAAGGCACGATTCAAGAACTTGGTCAAACACAGTATGCAGTC
AGTGGTGAAATATTTGTAGTGGACAGAAACACAGTAGAAATTACAGAGCTTCCAGTTAGAAGTTGGACACAGGTA
TATAAAGAACAGGTTTTAGAACCTATGCTAAATGGAACAGATAAAACACCAGCATTAAATTTCTGATTATAAAGAA
TATCATACTGACACAACCTGTGAAATTTGTGGTGAAGTGAAGAGAACTAGCACAAGCAGAAGCTGCTGGA
CTGCATAAAGTTTTTAAACCTCAAACCTACTCTTACTTGTAAATCCATGGTACTTTTTGATCATATGGGATGTCTG
AAGAAATATGAACTGTGCAAGACATTCTGAAAGAATTCTTTGATTTACGATTAAGTTATTACGTTTTACGTAAG
GAGTGGCTTGTGGGAATGTTGGGAGCAGAATCTACAAAGCTTAACAATCAAGCCCCGTTTTATTTAGAGAAGATA
CAAGGGAAAATTACTATAGAGAATAGGTCAAAGAAAGATTTGATTCAAATGTTAGTCCAGAGAGGTTATGAATCT
GACCCAGTGAAAGCCTGGAAAGAGCACAAGAAAAGGCAGCAGAAGAGGATGAAACACAAAACCAGCATGATGAT
AGTTCCCTCCGATTACAGGAACCTTCAGGCCAGATTTTAATTATATTTTAAATATGTCTCTGTGGTCTCTTACT
AAAGAAAAAGTTGAAGAACTGATTAAACAGAGAGATGCAAAAGGGCGAGAGGTCAATGATCTTAAAGAAAAATCT
CCTTCAGATCTTTGGAAAGAGGATTTAGCGGCATTTGTTGAAGAACTGGATAAAGTGAATCTCAAGAACGAGAA

1158/6881
FIGURE 1079B

GATGTTCTGGCTGGAATGTCTGGAAAAGCAATTAAAGGTAAAGTTGGCAAACCTAAGGTGAAGAACTCCAGTTG
GAAGAGACAATGCCCTCACCTTATGGCAGAAGAATAATTCCTGAAATTACAGCTATGAAGGCAGATGCCAGCAAA
AAGTTGCTGAAGAAGAAGAAGGGTGATCTTGATACTGCAGCAGTAAAAGTGGAATTTGATGAAGAATTCAGTGGA
GCACCAGTAGAAGGTGCAGGAGAAGAGGCATTGACTCCATCAGTTCCTATAAATAAAGGTCCCAAACCTAAGAGG
GAGAAGAAGGAGCCTGGTACCAGAGTGAGAAAAACACCTACATCATCTGGTAAACCTAGTGCAAAGAAAGTGAAG
AAACGGAATCCTTGGTCAGATGATGAATCCAAGTCAGAAAGTGATTTGGAAGAAACAGAACCTGTGGTTATTCCA
AGAGATTCTTTGCTTAGGAGAGCAGCAGCCGAAAGACCTAAATACACATTTGATTTCTCAGAAGAAGAGGATGAT
GATGCTGATGATGATGATGATGACAATAATGATTTAGAGGAATTGAAAGTTAAAGCATCTCCCATAAACAAATGAT
GGGGAAGATGAATTTGTTCCCTCAGATGGGTTAGATAAAGATGAATATACATTTTCACCAGGCAAAATCAAAAAGCC
ACTCCAGAAAAATCTTTGCATGACAAAAAAGTCAGGATTTTGGAATCTCTTCTCATTTTCCTTCATATTCTCAG
AAGTCAGAAGATGATTCAGCTAAATTTGACAGTAATGAAGAAGATTCTGCTTCTGTTTTTTCACCATCATTTGGT
CTGAAACAGACAGATAAAAGTTCCAAGTAAACCGGTAGCTGCTAAAAAGGAAAACCGTCTTCAGATACAGTCCCT
AAGCCCAAGAGAGCCCCAAAACAGAAGAAAGTAGTAGAGGCTGTAAACTCTGACTCGGATTGAGAATTTGGCATT
CCAAAGAAGACTACAACACCCAAAAGGTAAAGGCCGAGGGGCAAAGAAAAGGAAAGCATCTGGCTCTGAAAATGAA
GGCGATTATAACCTTGGCAGGAAAACATCCAAAACAACAAGCAAGAAACCGAAGAAGACATCTTTTGATCAGGAT
TCAGATGTGGACATCTTCCCCTCAGACTTCCCTACTGAGCCACCTTCTCTGCCACGAACCGGTCGGGCTAGGAAA
GAAGTAAAATATTTTGCAGAGTCTGATGAAGAAGAAGATGATGTTGATTTTGCAATGTTTAATTAAGTGCCCCAA
GAGCACAAACATTTTCAACAAATATCTTGTGTTGTCCTTTTGTCTTCTGTCTCAGACTTTTGTACATCTGGC
TTATTTTAATGTGATGATGTAATTGACGGTTTTTTATTATTGTGGTAGGCCTTTTAACATTTTGTTCCTTACACAT
ACAGTTTTATGCTCTTTTTTACTCATTGAAATGTCACGTACTGTCTGATTGGCTTGTAGAATTGTTATAGACTGC
CGTGCAATTAGCACAGATTTTAATTGTCATGGTTACAACTACAGACCTGCTTTTTGAAATGAAATTTAAACATTA
AAAATGGAACGTG

1159/6881
FIGURE 1080

MAKSGGCGAGAGVGGGNGALTWVNNAAKKEESETANKNDSSKKLSVERVYQKKTQLEHILLRPDTYIGSVEPLTQ
FMWVYDEDVGMNCREVTFVPGLYKIFDEILVNAADNKQRDKNMTCIKVSIDPESNIISIWNNGKGIPVVEHKVEK
VYVPALIFGQLLTSSNYDDDEKKVTGGRNGYGAKLCNIFSTKFTVETACKEYKHSFKQTWMNNMMKTSEAKIKHF
DGEDYTCITFQPDLSKFKMEKLDKDIVALMTRRAYDLAGSCRGVKVMFNGKKLPVNGFRSYVDLYVKDKLDETGV
ALKVIHELANERWDVCLTLSEKGFQQISFVNSIATTKGGRHVDYVVDQVVGKLIIEVVKKKNKAGVSVKPFQVKNH
IWFVINCLIENPTFDSQTKENMTLQPKSFGSKQLSEKFFKAASNCGIVESILNWVKFKAQTQLNKKCSSVKYSK
IKGIPKLDDANDAGGKHSLECTLILTEGDSAKSLAVSGLGVIGRDRYGVFPLRGKILNVREASHKQIMENAEINN
IIKIVGLQYKKSYYDDAESLKTLYGKIMIMTDQDQDGSNIKGLLINFIIHNWPSLLKHGFLEEFITPIVKASKNK
QELSFYSIPEFDEWKKHIENQKAWKIKYYKGLGTSTAKEAKEYFADMERHRILFRYAGPEDDAAITLAFSKKKID
DRKEWLTNFMEDRRQRRHLHGLPEQFLYGTATKHLTYNDFINKELILFSNSDNNERSIPSLVDGFKPGQRKVLFTCF
KRNDKREVKVAQLAGSVAEMSAYHHGEQALMMTIVNLAQNFVGSNNINLLQPIGQFGTRLHGGKDAASPRYIFTM
LSTLARLLFPAVDDNLLKFLYDDNQRVEPEWYIPIIPMVLINGAEGIGTGWACKLPNYDAREIVNNVRRMLDGLD
PHMPLPNYKNFKGTIQELGQNQYAVSGEIVVDRNTVEITELPVRTWTQVYKEQVLEPMLNGTDKTPALISDYKE
YHTDTTVKFVVKMTEEKLAQAEAAAGLHKVFKLQTTLTCSNMVLFDHMGCLKKYETVQDILKEFFDLRLSYGLRK
EWLVGMLGAESTKLNNQARFILEKIQGKITIENRSKKDLIQMLVQRGYESDPVKAWKEAQEKAAEEDETQNHDD
SSSDSGTPSGPDFNYILNMSLWSLTKEKVEELIKQRDAKGREVNDLKRKSPSDLWKEDLAAFVEELDKVESQERE
DVLAGMSGKAIKKGKVGKPKVKKLQLEETMPSPYGRRIIPEITAMKADASKKLLKKKKGDLDTAAVKVEFDEEFSG
APVEGAGEEALTPSVPINKGPKPKREKKEPGTRVRKTPPTSSGKPSAKKVKKRNPWSDDESKSESLEETEPVVIP
RDSLLRRAAAERPKYTFDFSEEEDDDADDDDDNNDLEELKVKASPIITNDGEDEFVPSDGLDKDEYTFSPGSKA
TPEKSLHDKKSQDFGNLFSFSPSYSQKSEDDSAKFDSDNEEDSASVFSFSGLKQTDKVPSTVAACKGKPSDTP
KPKRAPKQKKVVEAVNSDSDSEFGIPKKTTPKGGKRGAKKRKASGSENEGDPYNGRKTSTTSKKPKKTSFDQD
SDVDIFPSDFPTEPPSLPRTGRARKEVKYFAESDEEEDDVDFAMFN

1160/6881
FIGURE 1081

GAGAAGGCCCCAGGAAGTGACGGCCGCCTCCCGGCTACCGGGGACTTCTGGAGTCCGAGAAGTCAACGGCGCGGTT
GCTGCGGCCCGCCGCGCTCCCCGGCCCGAGGCG**ATG**GAGAACGGAGCGGTGTACAGCCCCACTACGGAGGAGGACC
CGGGCCCCCGCAGAGGCCCGGAGCGGCCTCGCTGCCTACTTTTTTCATGGGCCGGCTCCCATTGCTCCGGCGCG
TTCTCAAGGGCTTGACAGCTGTTGCTGTCTCTGCTGGCCTTCATCTGTGAAGAAGTTGTATCACAATGTACTTTAT
GTGGAGGACTTTATTTTTTTGAGTTTGTAAGCTGCAGTGCCTTTCTTCTGAGTCTCCTTATACTGATTGTGTATT
GCACTCCATTTTATGAGAGAGTTGATACCACAAAAGTAAATCATCGGATTTTATATTACTTTGGGAACAGGAT
GTGTGTTTTTGTGGCATCCAATCATTTTTGTTTCCACACATGACAGGACTTCAGCTGAGATTGCTGCAATTGTGT
TTGGATTTATAGCAAGTTTTATGTTCTACTTTGACTTTATCACTATGCTGTATGAAAAACGACAGGAGTCCCAGC
TGAGAAAACCTGAAAATACCACTAGGGCTGAAGCCCTCACTGAGCCACTTAATGCC**TAA**AGACTCTGGGGAGCAG
ATGTTACCTAAGGTAGTGACCCTGCATTGTGGTGCCTGAGCCCTGGCAGAAGCTCTTGTAATAATTTGTTAATTGT
TTAAACCACTTCTTTTGGAGAGCAAGGGGAAGGTCAAGAAGGCAGTTTTATCAATATTGTGTGAGTCACCACAAA
GTAGGCCAGATAAGTTAAAAAAATTTTTTTTTAAATAATAATTGAACTTATCTCAAATGGAGATTTTGGTGGG
AGGAGGAGAAAACAATTGTTTTTAAATCACACAGCTCAACGGTTGATAAATGATTCTGTCAATTCTGTTACAGGTC
ATTCTTTTACTAGGCTTAGCTTCCAAATTATGCTTTATAGCTGTATAAACATCGTGATTATATTCACTACTTAG
AAATTGTTTTATTTTTAAATTAATTTGCTTAGCTGTTGTTTTGATGCTTAGATTATGTTCTGTTAATGGGAATT
TAACATATTTAAGAAACCAATATTTAAATGTTGGTCTAGGTTTTTTTCCCTTAACATATATTACCAGGCTTTACT
GTATTTCACTCAGCCTTAAATGTTATAATATTTTTGGATAACGGTTATTAATTCTTTGAGACCTTCGTATAGCCT
ATAAAATGTATGGGAGATGTTGGTATTTTATGTGTATAAAAGCAACAATATCAGCAACTTCGTGTTTATACTGCA
CCTTGGTTGTTGATGTCAAGTAAAAAAAGATTGTTTTGTAACACATAAAAAAATGGAAGAACTGATACCACAC
CTAAGGACCAAAGATAAGAAAGACTTTTTGCCCAAGACAGTGAAAGTAATTATAAAAACAAGCTTTGACCACTTA
CCAAGTATCTGAAGAGATGAGTTCATACTATGATTTAGAAAGTGGTTCGATTCCCCTGTTGGCATATGATTATTT
TTACTAAAATTAATACAGCTCTGTGGGTCTTCCTTAGTGTTTTCTTTGAAGCCAATCTGTTTTTTTTTAGGACACC
AGCCTTTGGTTTTTCATCTGTTTCGAGATGCCTCTTCTCTGTCTCCTTATCAGATAGAAATGGAGTCATGTGCTGC
TGCTTCATCTAGCAGAGGTTGGCCTCTGGCTCTGACACTTTTGTGAGTTGTCTTTAGGTGGTCCTGAATCTTGG
GCCCTTTTGATTGTGAATACTGTGTAGCAGGATCTTGAGAGTCCTTGTTCTTACATAGGCATTGCTCTAGTTGT
CTTTGGCAAAAAAAAAAAAAAAAAAAAAA

1161/6881
FIGURE 1082

MENGAVYSPTTEEDPGPARGPRSGLAAYFFMGRLEPLLRRVLKGLQLLLSLLAFICEEVVSQCTLCGGLYFFEFVS
CSAFLLSLLILIVYCTPFYERVDTTKVKSDFYITLGTGCVFLLASIIFVSTHDRTSAEIAAIVFGFIASFMFLL
DFITMLYEKRQESQLRKPENTTRAERALTEPLNA

1162/6881
FIGURE 1083

ATGGATGCTGTGTGCTATGGTGAAGCTGTTTCTTCCCAGCAGCAGGGAGAGAAAAAGGAGAAGAGGAAACACAAG
AAGAAATGCGTGGTGCAGAGCCTCAATTCCTACTTCATGGATGTGAAATGCCCAGGATGCTATAAAATCACTACA
GCAGTTTCTAATTCCTGCAATTTTCCCCTTAATGGCTCTCCGGATGTTGCCACTGATTATGGTGCCGTTTCATGGC
TCTTCAGCAGGTGCTGGGCATAGGCACCAGGAAGCCCTGTTTAATAGTGTGTCTGCCTTTTCCTTTACATGCTCCC
TCGGGTGAAGCAAGGCAGATGGAGAAGGCTTTAGCAGACAGCGTGGGCATGTTTCCAAGCCCTCAGGCTGCTGAG
CAACAATGCCGATGCCAGCACCAACAGGCTGAGGTGGCTTCTTCATTT**TAG**

1163/6881
FIGURE 1084

MDAVCYGEAVSSQQQGEKKEKRKHKKKCVVQSLNSYFMDVKCPGCKYKITTAVSNSCNFPLNGSPDVATDYGAVHG
SSAGAGHRHQEALFNSVSAFPLHAPSGEARQMEKALADSVGMFPSPQAAEQQCRCQHQQAEVASSF

1164/6881
FIGURE 1085

GCTAAAGGTGATGTGGCCGCCCTCAACCGACGCATCCAGCTCGTTGAGGAGAAGTTGGACAGGGCTCAGGAAAGA
CTGGCCACGGCCCCGAGAAGCTGGAGGAGGCAGAAAAAGCTGCAGATGAGAGTGAGAGAGGAATGAAGGTGATA
GAAAACCGGGCCATGAAGGATGAGGAGAAGATGGAAATTCAGGAGCTGCAGCTCAAAGAGGCCAAGCACATTGCG
GAAGAGGCTGACCGCAAATACTGGGAGGTAGCTCGTAAGCTGGTCTTCCTGGAGGGTGAGCTGGAGAGGGCAGAG
GAGCGTGTGGAGGTGTCTGAACTAAAATGTGGTGACCTTGAAGAAGAACTCAAGAATGTTACTAACAATCTGAAA
TCTCTGGAGGCTGCGTCTGAAAAGTATTCTGAAAAGGAGGACAAATGTGAAGAAGAAATTAACTTCTGTGTGAC
AAACTGAAAGAGGCTGAGACCCGTGCTGAATTTGCAGAGAGAACGGTTGCAAACTGGAAAAGACAATTGATGAC
CTGGAAGAGAACTTGCCCAGGCCAAAGAAGAGAACGTGGGCTTACATCAGACACTGGATCAGACACTAAACGAG
CTTAACTGTATATAAGCAAAACAGAAGAGTCTTGTTCCAACAGAACTCCGGAGCTCCGTGGGTCTTTCTCTTCT
CTTGTAAGAAGTTCCTTTTGTTATTGCCATCTTCGCTTTGCTGGAAATGTCAAGCAAATTATGAATACATGACCA
AATATTTTGTATTGGAGAAGCTTTGAGCACGAGTTAAATCTCATGCCTTCCCTTTTTTTGTCAAATGGCACCAAC
TTTTTCAGCTCTCTTATTTTTTTCCTTAAGTTGCATTTATTCTTAAGGTAGGCAGGGTATTTCTAGTAAGCATAG
TTTCTTAAGACAGAGGCCATTTGGTTCCTGGGAGAATAGGCAGCCCCACACTTTGAAGAACACAGACCCCCAGTAT
CTAGTCGTGGATATGATTAAAACGCTGAAGACCACAACCTTTTTGGGTCAACTGTTGGTCAAACATATAGGAGAGAC
CAGGGACCACCCCACTCCTATTTATTCAGCACCACACTACCCAGGAAATACACTAGCAAATTGTGCAATGGAATA
AAATCCACACTTTACTTTAGATTCTTGCAACTGTATCATATGTAATAGTATCACTTTTTTCTACATTTTGGTCAAA
TAAATTTTTTACATAAACTAC

1165/6881
FIGURE 1086

AGCTCATCCACACTTCCAATCACTTTCCGGAGTGCTTCCCTCCCTCCGGCCCGTGCTGGTCCCGACGGCGGGCC
TGGGTCTCGCGCGCGTATTGCTGGGTAACGGGCCTTCTCCCGCGTCGGCCCGGCCCTCCTGCCTCGGCTCGTCC
CTCCTTCCAGAACGTCCCGGGCTCCTGCCGAGTCAGAAGAAATGGGACTCCCTCCGCGACGTGCCCGGAGCAGCT
CCCTTCGCTGTGGAAGCGGCGGTGTCTTCAAGAAACCGGAAGCCCGTGGTGACCCCTGGCGACCCGGTTTGT
TCGGTCCGTTTCCAAACACTAAGGAATCGAACTCGGCGGCCTTGGGGGCGGCCCTACGTAGCCTGGCTTCTGGT
TGTC**ATG**GATGCACTGGTAGAAGATGATATCTGTATTCTGAATCATGAAAAAGCCATAAGAGAGATACAGTGAC
CCCAGTTTCAATATATTCAAGGAGATGAATCTGTTGCTTCCCATTTTGCTCTTGTCACATATGAAGACATCAA
AAAACGACTTAAGGATTCAAGAGAAAGAGAACTCTTTGTTAAAGAAGAGAATAAGATTTTGAAGAAAAGCTAAT
AGCTCGATTTGAAGAAGAAAACAAGTTCGTTGGGACGAGAAACAAGTAAATAAGGCCTATCATGCATATCGAGAGGT
TTGCATTGATAGAGATAATTTGAAGAGCAAACCTGGACAAAATGAATAAAAGACAACCTCTGAATCTTTGAAAGTATT
GAATGAGCAGCTACAATCTAAAAGAGTAGAACTCCTCCAGCTGAGGACAGAGGTGGAAGCTCAGCAGGTGATGAG
GAATTTAAATCCACCTTCATCAAACTGGGAGGTGGAAGGTTGAGCTGTGACCTGAAGATCCATGGTTTGAAGACA
AGAGCTGGAAGCTGATGAGGAAAAGATGTAGCGATCTCAAAATAGAACTACAGAAAGCCAAACAAACGGATCCATA
TCAGGAAGACAATCTGAAGAGCAGAGATCTCCAAAACTAAGCATTTCAGTGATAATATGCAGCATGCATACTG
GGAAGCTGAAGAGAGAAATGTCTAATTTACATCTGGTGACTCAAGTACAAGCTGAAGTACTAAGAAAAGCTGAAAAC
CTCAACTGCAATCAAGAAAGCCTGTGCCCTGTAGGATGCAGTGAAGACCTTGAAGAGACAGCACAAAAGCTGCA
CTTGATGAATTTTACTGCAACATACACAAGACATCCCCCTCTCTTACCAAATGGCAAAGCTCTTTGTCATACCAC
ATCTTCCCCTTTACCAGGAGATGTAAAGGTTTTATCAGAGAAAGCAATCCTCCAATCATGGACAGACAATGAGAG
ATCCATTCCCTAATGATGGTACATGCTTTTCAAGAACACAGTTCTTATGGCAGAAATTCTCTGGAAGACAATTCCTG
GGTATTTCCAAGTCCCTCTAAATCAAGTGAGACAGCATTGTTGGGAAACTAAAAGCTTTGCTTTTACCCAA
CCTTCCACCACTGCATTACTTGGATCAACATAATCAGAACTGCCTTTATAAGAAT**TAA**TTTGAAGAGATTACAG
ATTTACCATGAGGACACTTATCTCTTTTCAAGTGGTCTCCCAAGAAATTATTTAACAACTGAAAGGAGATTTTG
ATTAAAATTTTGCAGAGGTCTTCAAGTATCTATATTTGAACACACTGTACAATAGTACAAAACCAACATAGTTGG
TTTTCTAGTATGAAAGAGCACCTCTAGCTCCATATTCTAAGAATCTGAAATATGCTACTATACTAATTAATAAG
TAACTTAAGGTGTTTTAAAAAACTCTGCCTTCTATATTAATTGTAATTTTGCCTCTCAGAAGAATGGAATTGG
AGATTGTAGACGTGGTTTTACAAAATGTGAAATGTCTAAATATCTGTTTCAATAAAATAAAAGGAAAACATGTTTC
TTCAAATTGCATAATGGAACAAATGGCAATGTGAGTAGGTTACATTTCTGTTGTTATAATGCGTAAAGATATTGA
AAATATAATGAAATAAAAGCATCTTAGGTTATACCATCTTTATATGCTATTGCGTTTCAATATTTAAGATTTAAA
GTGATTTTTTGGTCACAGTGTGTTTGTGATAAAATTTTTTTAGAATTGAAGTTTGAATTCTAAGACTTGAAACAA
CCTGATCATTGAAGCCAACCTTTGTCCCAGCACATTCCTTAAGTCCTAATTGGGAAAAAAAAAAAAAAAAAAAAA

1166/6881
FIGURE 1087

MDALVEDDICILNHEKAHKRDTVTPVSIYSGDESVASHFALVTAYEDIKKRLKDSEKENSLLKKRIRFLEEKLIA
RFEEETSSVGREQVNKAYHAYREVCIDRDNLKSKLDKMNKDENSESLKVLNEQLQSKEVELLQLRTEVETQQVMRN
LNPPSSNWEVEKLSCDLKIHGLEQELELMRKECSDLKIELQKAKQTDPTYQEDNLKSRDLQKLSISSDNMQHAYWE
LKREMSNLHLVTQVQAELLRKLTSTAIAKACAPVGCSEDLGRDSTKLHLMNFTATYTRHPPLLNGKALCHTTS
SPLPGDVKVLSEKAILQSWTDNERSIPNDGTCFQEHSSYGRNSLEDNSWVFPSPPKSSETAFGETKTKTLPLPLNL
PPLHYLDQHNQNCCLYKN

1167/6881
FIGURE 1088

GCGATGGAGCCGGGGCGCCGGGGGGCCGCGGCGCTGCTAGCGCTGCTGTGCGTGGCCTGCGCGCTGCGCGCCGGG
CGCGCCCAATACGAACGCTACAGCTTCCGAGCTTCCCACGGGACGAGCTGATGCCGCTCGAGTCGGCCTACCGG
CACGCGCTGGACAAGTACAGCGGCGAGCACTGGGCGGAGAGCGTGGGCTACCTGGAGATCAGCCTGCGGCTGCAC
CGCTTGCTGCGCGACAGCGAGGCCCTTCTGCCACCGCAACTGCAGCGCCGCGCGCACTGCCTCAAGCGCTGCAAGCAG
CTCGCCAGCTATCCCGAGCTGCGCCTCTTCGGGGGCGCTGCTGCGCCGCGCGCACTGCCTCAAGCGCTGCAAGCAG
GGCCTGCCAGCCTTCCGCCAGTCCCAGCCCAGCCGCGAGGTGCTGGCGGACTTCCAGCGCCGCGAGCCCTACAAG
TTCCTGCAGTTTCGCTTACTTCAAGGCAAATAATCTCCCCAAAGCCATCGCCGCTGCTCACACCTTTCTACTGAAG
CATCCTGATGACGAAATGATGAAGAGGAACATGGCATATTATAAGAGCCTGCCTGGTGCCGAGGACTACATTAA
GACCTGGAAACCAAGTCATATGAAAGCCTGTTTCATCCGAGCAGTGCGGGCATAACAACGGTGAGAACTGGAGAA
TCCATCACAGACATGGAGCTGGCCCTTCCCGACTTCTTCAAAGCCTTTTACGAGTGTCTCGCAGCCTGCGAGGGT
TCCAGGGAGATCAAGGACTTCAAGGATTTCTACCTTTCCATAGCAGATCATTATGTAGAAGTTCTGGAATGCAAA
ATACAGTGTGAAGAGAACCTCACCCAGTTATAGGAGGCTATCCGTTGAGAAATTTGTGGCTACCATGTATCAT
TACTTGAGTTTGCCTATTATAAGTTGAACGACCTGAAGAATGCAGCCCCCTGTGCAGTCAGCTATCTGCTCTTT
GATCAGAATGACAAGGTCATGCAGCAGAACCTGGTGTATTACCAGTACCACAGGGACACTTGGGGCCTCTCGGAT
GAGCACTTCCAGCCCAGACCTGAAGCAGTTCAGTTCTTTAATGTGACCACACTCCAGAAGGAGCTGTATGACTTT
GCTAAGGAAAATATAATGGATGATGATGAGGGAGAAGTTGTGGAATATGTGGATGACCTCTTGGAAGTGGAGGAG
ACCAGCTAGCCACAGCAACCAAAGAGACTTCCTCTTGGCGTTGAGGAAACACAGATTCTTTGTCTTTTCCCAA
CAGCCCAGGCTGTTGATACCTCAGAGCCTTCTCTTTACTCTCCAAAGTGAAAGGGAAGCCCCCGTCTCTCTAACT
GCATGTCATCAGGGGTGAGCCTGCCTTTCTATCTTCACACCTGCCACCTCATGTTACACCTATCTTTCTCACC
TTTTTTTTTGAGATGGAGTCTCGCTCTCTTGGCCAGGCTGGAGTGCAATGGCACGTTCTCAGCTCACTGCAACCTC
CGCCTCTTGGGTTCAAGCAATCTGCTGCATCAGCCTCCCGAGTACCTGGGATTACAGGCATGTGCCACCACGCC
CGGCTAATTTTGTATTTTGTAGTAGAGACGGGGTTTTGCCATGTTGGCCAGGCTGGTCTCGAACTCTTGACTTCAG
ATGATCCATCTGCCTTGGCCTCCACAGTGTGGGATTACAGGCGTGAGCCACCATGCCCGGCTCTTTCTCACC
TTTACACCTGTCTTCTTATCCTCACATCTGTTTTTACACCTTCATCCCTGTCTTCCTCATGTTACACCTTGTCTT
CCCCATGTTTCATAGCTGCCTTTCTTACCATTTTGGTTTGAAGGGCAGTCTTCTCTGGCTTGTTTTTTTGTTC
CCAGAAAATCAGTATTATTTTTTAAATAAGAAAAACATTCCTAGAAGATGATAATTGTGAAAACCTCCTTTGGCT
TATTTGCTTTTCCAGATTTTGTCTCTCTTCTCCCCATCCGGGAAAGATGGTGGAAGACATAGGCTAAATTTCTC
CAGCCTCACAATGGTCTTCACTTGGTCTGACTTGTACCAATTCTAGCACCCTGAAAAACAAGTTGAGTAGAGA
GTGTAGAGTGACAGAAATGTGGCTTTTGCCCCACTTTGCATCTCCAAAATTACAACGGTTGGCCGATCCCATTTGA
GGACAATGCTTAGTTATAAGTCTCCGAGTTGGAAAAGGAAGAAAGCCAGAGCTGTCTAGTTTTCATTTCATTCTTC
AGTAAATATTTATTGAGT

1168/6881
FIGURE 1089

GAATTCGGGCGCGAAGCGGCCGGCCTGGGCGCCGACTGCAGAGCCGGGAGGCTGGTGGTCA**ATG**CCGGGGTTTCCTG
GTTTCGCATCCTCCTTCTGCTGCTGGTTCTGCTGCTTCTGGGCCCTACGCGCGGCTTGCGCAATGCCACCCAGAGG
ATGTTTGAAATTGACTATAGCCGGGACTCCTTCCTCAAGGATGGCCAGCCATTTCGCTACATCTCAGGAAGCATT
CACTACTCCCGTGTGCCCCGCTTCTACTGGAAGGACCGGCTGCTGAAGATGAAGATGGCTGGGCTGAACGCCATC
CAGACGTATGTGCCCTGGAACTTTCATGAGCCCTGGCCAGGACAGTACCAGTTTTCTGAGGACCATGATGTGGAA
TATTTTCTTCGGCTGGCTCATGAGCTGGGACTGCTGGTTATCCTGAGGCCCGGGCCCTACATCTGTGCAGAGTGG
GAAATGGGAGGATTACCTGCTTGGCTGCTAGAGAAAGAGTCTATTCTTCTCCGCTCCTCCGACCCAGATTACCTG
GCAGCTGTGGACAAGTGGTTGGGAGTCCTTCTGCCAAGATGAAGCCTCTCCTCTATCAGAATGGAGGGGCCAGTT
ATAACAGTGCAGGTTGAAAATGAATATGGCAGCTACTTTGCCTGTGATTTTGACTACCTGCGCTTCCTGCAGAAG
CGCTTTCGCCACCATCTGGGGGATGATGTGGTTCTGTTTACCAGTATGGAGCACATAAAACATTTCCTGAAATGT
GGGGCCCTGCAGGGCCTCTACACCACGGTGGACTTTGGAACAGGCAGCAACATCACAGATGCTTTTCCTAAGCCAG
AGGAAGTGTGAGCCCAAAGGACCCCTTGATCAATTCTGAATTCTATACTGGCTGGCTAGATCACTGGGGCCAACT
CACTCCACAATCAAGACCGAAGCAGTGGCTTCCTCCCTCTATGATATACTTGCCCGTGGGGCGAGTGTGAACCTG
TACATGTTTATAGGTGGGACCAATTTTGCCTATTGGAATGGGGCCAACTCACCTATGCAGCACAGCCACCAGC
TACGACTATGATGCCCCACTGAGTGAGGCTGGGGACCTCACTGAGAAGTATTTTGCTCTGCGAAACATCATCCAG
AAGTTTGAAAAAGTACCAGAAGGTCCTATCCCTCCATCTACACCAAAGTTTGATATGGAAAGGTCACCTTGGAA
AAGTTAAAGACAGTGGGAGCAGCTCTGGACATTCTGTGTCCCTCTGGGGCCATCAAAGCCTTTATCCCTTGACA
TTTATCCAGGTGAAACAGCATTATGGGTTTGTGCTGTACCGGACAACACTTCCTCAAGATTGCAGCAACCCAGCA
CCTCTCTCTTACCCCTCAATGGAGTCCACGATCGAGCATATGTTGCTGTGGATGGGATCCCCAGGGAGTCCTT
GAGCGAAACAATGTGATCACTCTGAACATAACAGGGAAAGCTGGAGCCACTCTGGACCTTCTGGTAGAGAACATG
GGACGTGTGAACTATGGTGCATATATCAACGATTTTAAGGGTTTGGTTTCTAACCTGACTCTCAGTTCCAATATC
CTCACGGACTGGACGATCTTTCCACTGGACACTGAGGATGCAGTGCGCAGCCACCTGGGGGGCTGGGGACACCGI
GACAGTGGCCACCATGATGAAGCCTGGGCCCACTCATCCAACACAGCTCCCGGCCCTTTTATATGGGGAACT
TTCTCCATTCCCAGTGGGATCCCAGACTTGCCCCAGGACACCTTTATCCAGTTTCCTGGATGGACCAAGGGCCAG
GTCTGGATTAATGGCTTTAACCTTGCCGCTATTGGCCAGCCCGGGGCCCTCAGTTGACCTTGTTTGTGCCCCAG
CACATCCTGATGACCTCGGCCCCAAACACCATCACCGTGCTGGAAGTGGAGTGGGCACCCTGCAGCAGTGATGAT
CCAGAACTATGTGCTGTGACGTTCTGTGGACAGGCCAGTTATTGGCTCATCTGTGACCTACGATCATCCCTCCAAA
CCTGTTGAAAAAAGACTCATGCCCCACCCCGCAAAAAAACAAGATTTCATGGCTGGACCATGTAT**TGAT**GATGA
AAGCCTGTGTCTTTGAGGGATTCTACCCTGAACATACCTCACAGATCCTCCCTGTATGCCACATTTCACTGATT
GGAATGTGGAATGGAAAAGGAATTTAGGATGTGCATTTTACCTGAGGTTTCCCTGCATCCCTGCAGTGCCAAA
GCCCCACCTTCAGGGACCACCTGGAATGTGTGAGGGGCTGACAGCACAGTAACGTGCATACATATCTGCAGGGCT
GGAATGGAAGCTTTAAAGGIGGTAGTGATTTTTATTTTGAAGAATCATGTTACCTTTTTGTAAATAAAATTTG
CCCGAATTC

1169/6881
FIGURE 1090

MPGFLVRILLLLLVLVLLLGPTRGLRNATQRMFEIDYSRDSFLKDGQPFRIYISGSIHYSRVPRFYWKDRLLKMKMA
GLNAIQTYVPWNFHEPWPQYQFSEDHDVEYFLRLAHELGLLVILRPGPYICAEWEMGGLPAWLLEKESILLRSS
DPDYLAAVDKWLGVLPLPKMKPLLYQNGGPVITVQVENEYGSYFACDFDYLRFQKRFRHHLGDDVVLF TTDGAHK
TFLKCGALQGLYTTVDFTGSNITDAFLSQRKCEPKGPLINSEFYTGWLDHWGQPHSTIKTEAVASSLYDILARG
ASVNLYMFI GGTNFAYWNGANSPYAAQPTS YDYDAPLSEAGDLTEKYFALRNIIQKFEKVPEGPIPPSTPKFAYG
KVTLEKLKTVGAALDILCPGPIKSLYPLTFIQVKQHYGFVLYRTTLPQDCSNPAPLSSPLNGVHDRAYVAVDGI
PQGVLERNNVITL NITGKAGATDLLVENMGRVNYGAYINDFKGLVSNLTLSSNILDWTIFPLDTEDAVRSHLG
GWGHRDSGHHDEAWAHNSSNYTLPAFYMGNFSIPSGIPDL PQDTFIQFPGWTKGQVWINGFNLGRYWPARGPQLT
LFVPQHILMTSAPNTITVLELEWAPCSSDDPELCAVTFVDRPVIGSSVTYDHPSKPVEKRLMPPPPQKNKDSWLD
HV

1170/6881
FIGURE 1091

CGCAGGCGGAGCGCAAGTCTGTCAGCCAGTCAGTCCGCCAGTCCGCCAGCCCAGTACCTCTCTCTCCTCGGCCCT
CGTAAGCTGTCCGCGGTCTGTTTGGCCCGAACGGCGGCGGAGGCGCTGATCATGGCGACATTTCATCTCGGTGCAG
CTGAAAAAGACCTCAGAGGTGGACCTGGCCAAGCCGCTGGTGAAGTTCATCCAGCAGACTTACCCAAGCGGCGGG
GAAGAGCAGGCCCAGTACTGCCGCGCGGCGGAGGAGCTCAGCAAGCTGCGCCGCGCCGAGTCGGTTCGTCCGCTG
GACAAGCACGAGGGCGCGCTCGAGACGCTCCTGAGATATTATGATCAGATTTGTTCTATTGAACCCAAATTCCCA
TTTTCTGAAAATCAGATCTGCTTGACATTTACCTGGAAGGATGCTTTTCGATAAAGGTTCACTTTTTGGAGGCTCT
GTAAACTGGCTCTTGCAAGCTTAGGATATGAAAAGAGCTGTGTGTTGTTCAATTGTGCAGCCTTAGCTAGCCAA
ATTGCAGCAGAACAGAACCTGGATAATGATGAAGGATTGAAAATCGCTGCTAAACATTACCAGTTTGCTAGTGGT
GCCTTTTTACATATTAAAAGAGACGGTTTTATCTGCCTTAAGTCGAGAGCCGACCCTGGACATATCTCCAGATACT
GTTGGGACCCTCAGTCTTATTATGCTGGCACAGGCTCAAGAAAGTATTTTTTTTAAAAGCCACAAGAGATAAAAATG
AAAGATGCCATCATAGCTAAATTGGCTAATCAGGCTGCAGATTATTTTGGTGATGCTTTCAAACAGTGTCAATAC
AAAGATACTCTCCCCAAGGAGGTGTTCCCTGTCTTGGCTGCAAAGCACTGTATCATGCAGGCCAATGCTGAGTAC
CATCAGTCTATCCTGGCAAAACAGCAGAGAAGAAATTTGGAGAAGAAATTGCAAGGTTACAGCATGCAGCAGAACTG
ATTAAAACAGTGGCATCTCGCTATGATGAATATGTTAATGTGAAGGATTTTTCTGACAAAATCAATCGTGCCCTT
GCTGCAGCAAAGAAGGATAATGACTTCATTTATCATGATCGAGTTCAGACCTTAAAGATCTAGATCCTATTGGC
AAAGCCACACTTGTGAAATCTACCCCGGTCAATGTACCCATCAGTCAGAAATTTACTGATCTGTTTGAGAAGATG
GTTCCCGTGTGAGTACAGCAGTCTTTGGCTGCCTATAATCAGAGGAAAGCCGATTTGGTTAACAGATCAATTGCT
CAGATGAGAGAAGCCACCCTTTGGCAAATGGGGTGCTAGCTTCCCTTAATCTTCCAGCAGCAATTGAAGATGTG
TCTGGAGACACTGTACCTCAGTCTATATTGACTAAATCCAGATCTGTGATTGAACAGGGAGGCATCCAGACTGTT
GATCAGTTGATTAAAGAACTGCCTGAATTACTGCAACGAAATAGAGAAATCCTAGATGAGTCATTAAGGTTGTTG
GATGAAGAAGAAGCAACCGATAATGATTTAAGAGCAAAATTTAAGGAACGTTGGCAAAGGACACCATCCAATGAA
CTGTATAAGCCTTTAAGAGCAGAGGGAACCAACTTCAGAACAGTTTTAGATAAAGCTGTGCAGGCAGATGGACAA
GTGAAAGAATGTTACCAGTCTCATCGTGACACCATCGTGCTTTTGTGTAAGCCAGAGCCTGAGCTGAATGCTGCC
ATCCCTTCTGCTAATCCAGCAAAGACCATGCAGGGCAGTGAGGTTGTAAATGTCTTAAATCCTTATTGTCAAAT
CTTGATGAAGTAAAGAAGGAAAGAGAGGGTCTGGAGAATGACTTGAAATCTGTGAATTTTGACATGACAAGCAAG
TTTTTGACAGCCCTGGCTCAAGATGGTGTGATAAATGAAGAAGCTCTTCTGTTACTGAACTAGATCGAGTCTAT
GGAGGTCTTACAATAAGTCCAAGAATCTCTAAAGAAACAGGAGGGACTTCTTAAAAATATTAGGTCTCACAT
CAGGAATTTTCAAAAATGAAACAATCTAATAATGAAGCTAACTTAAGAGAAGAAGTTTTGAAGAATTTAGCTACT
GCATATGACAACCTTTGTTGAACTTGTAGCTAATTTGAAGGAAGGCACAAAGTTTTACAATGAGTTGACTGAAATC
CTGGTCAGGTTCCAGAAACAAATGCAGTGATATAGTTTTTGCACGGAAGACAGAAAGAGATGAACTCTTAAAGGAC
TTGCAACAAAGCATTGCCAGAGAACCTAGTGCTCCTTCAATTCCCTACACCTGCGTATCAGTCTCACCAGCAGGA
GGACATGCACCAACTCCTCCAACCTCCAGCGCCAAGAACCATGCCGCTACTAAGCCCCAGCCCCAGCCAGGCCCT
CCACCACCTGTGCTTCCAGCAAATCGAGCTCCTTCTGCTACTGCTCCATCTCCAGTGGGGGCTGGGACTGCTGCG
CCAGCTCCATCACAAACGCTGGCTCAGCTCCTCCTCCACAGGCGCAGGGACCACCCTATCCACCTATCCAGGA
TATCCTGGGTATTGCCAAATGCCCATGCCCATGGGCTATAATCCTTATGCGTATGGCCAGTATAATATGCCATAT
CCACCAGTGTATCACCAGAGTCTTGACAGGCTCCATACCCGGGACCCCAGCAGCCTTCATACCCCTTCCCTCAG
CCCCACAGCAGTCTTACTATCCACAGCAGTAATATGTCTGCTCAGCAGCTCAGCTGATTGAGATCAGAGGGAAA
GAAATACCAACCCTGCAATAAGTGTAATAACTCTACGCTCTGGTTAATGTAATGTACTCTCCTGGACTGAATGC
AGTGATAATTTCTGTCTACAGCTAGAAGCTGTGCCCCAGTTCACATTTGATTACACATGTGAGATTTGCTGCT
GTTGCAGTATAAACACTAGGTATAATAGGATTTGAAATTGCATTACAGTTCATAAAAATTGAAAATGAGAAATTA
AACCTGCAAGTGAACATTTGAAACGATTATACTTTCTACATAAGACATGGTTGGGACATCAGATACTTACAAAG
ATGGTTTAAAGTATGGATACTAGAGAAAATTAAGTTTTCTTCTCTTTGGTTTATTGATTGGTTTAAATTTCCATT
ATGCTATTTTGCATAATCAAGGCAGTGTAAATCTTATAATTTTAAATAAATTACTTAAGAAC

1171/6881
FIGURE 1092

MATFISVQLKKTSEVDLAKPLVKFIQQTYPSSGEEQAQYCRAAEELSKLRRAAVGRPLDKHEGALETLLRYDQI
CSIEPKFPFSENQICLTFTWKDAFDKGSLSFGGSVKLALASLGYEKSCLFNCAALASQIAAEQNLDNDEGLKIAA
KHYQFASGAFLHIKETVLSALSREPTVDISPDTVGTLSLIMLAQAQEVFFLKATRDKMKDAIIAKLANQAADYFG
DAFKQCQYKDTLPKEVFPVLAAKHCIMQANA EYHQSILAKQQKKFGEEIARLQHAAELIKTVASRYDEYVNVKDF
SDKINRALAAAKKDNDFIYHDRVDPDLKDLDP I GKATLVKSTPVNVPISQKFTDLFEKMVPVSVQQSLAAYNQKKA
DLVNRSIAQMREATTLANGVLASLNLPA AIEDVSGDTV PQSILTKSRSVIEQGGIQTVDQLIKELPELLQRNREI
LDESLRLLDEEEATDNDLRKFKERWQRTPSNELYKPLRAEGTNFRTVLDKAVQADGQVKECYQSHRDTIVLLCK
PEPELNAAIP SANPAKTMQGSEVVNLKSLLSNLDEVKKEREGLENDLKS VNFDMTSKFLTALAQDGVINEEALS
VTELD R VYGGLT TKVQESLKKQEGLLKNIQVSHQEF SKMKQSNNEANLREEVLKNLATAYDNFVELVANLKEGTK
FYNELTEILVRFQNKCS DIVFARKTERDELLKDLQQSIAREPSAPS IPTPAYQSSPAGGHAPTPTPTAPRTMPPT
KPQPPARPPFPVLPANRAP SATAPSPVGAGTAAPAPSQTTPGSAPPPQAQGPPYPTYPGYPGYCMMPMGMGNPYA
YGQYNMPYPPVYHQSPGQAPYPGPQQPSYFPFPQPPQQSYYPQQ

1172/6881
FIGURE 1093A

TTGGCCCGTGCCTGGGGCTGGGGTGGAGGGCGGGACAGAGGGGCTGGGCCAGGCAAAGCTTCTGTGCTGCTGC
TGCGGAGGCCGAGGACAGGACGTGGGCTGGGCCGGGCAGTGCCGGACTCGGAGGAGCAGGAGGCGAGGTCCGCCG
GAGCTCTGAACCCCCGCTGCTCTGCCGCGCGGTGACCCGCGCCCCGCGCCGTCCGACCCGTGGCTGTTCCGAG
ACGATTGGTGGGGGCGCGGCGGCGGCGGCGGCGGCTGTTGGGGGTGGGGAGACGCGCGGCGAGGAGACGAGCGAG
GTCAGCGAGTTTGAGGGAGGACCGCGAGCCGCTGCCGCCGTCATGTCGGAAGACTCGAGCGCCCTGCCCTGGTCC
ATCAACAGGGACGATTACGAGCTGCAGGAGGTGATCGGGAGTGAGCAACTGCTGTAGTCCAAGCAGCTTATTGT
GCCCCATAAAAGGAGAAAAGTGGCAATCAAACGGATAAACCTTGAGAAAATGTCAAAC TAGCATGGATGAACTCCTG
AAAGAAATTCAGCCATGAGTCAATGCCATCATCCTAATATTGTATCTTACTACACATCTTTTGTGGTAAAAGAT
GAGCTGTGGCTTGTTCATGAAGCTGCTAAGTGGAGGTTCTGTTCTGGATATTATTAAGCACATTGTGGCAAAAGG
GAACACAAAAGTGGAGTCCCTAGATGAATCTACCATTGCTACGATACTCCGAGAAGTACTGGAAGGGCTGGAATAT
CTGCATAAAAATGGACAGATCCACAGAGATGTGAAAGCTGGAAACATTCTTCTTGGAGAAGATGGCTCAGTACAG
ATTGCAGACTTTGGGGTTAGTGTCTTTTTAGCAACTGGTGGTGATATTACCCGAAATAAAGTGAGAAAGACCTTT
GTTGGCACCCCTTGTGGATGGCACCTGAAGTTATGGAACAGGTCCGTGGTTATGATTTCAAAGCTGATATTTGG
AGTTTTGGAATTACAGCAATTGAATTGGCTACAGGGGCGGCTCCTTATCATAAATATCCACCAATGAAGGTTTTA
ATGCTGACACTGCAGAACGATCCTCCTTCTTTGGAACTGGTGTTCAAGATAAAGAAATGCTGAAAAAATATGGA
AAATCATTTAGAAAAATGATTTCAATTGTGCCTTCAAAAAGATCCAGAAAAAGACCAACAGCAGCAGAACTATTA
AGGCACAAAATTTTCCAGAAAGCAAAGAATAAAGAATTTCTTCAAGAAAAACATTGCAGAGAGCACCAACCATT
TCTGAAAGAGCAAAAAAGGTTCCGAGAGTACCAGGTTCCAGTGGGCGTCTTCATAAGACAGAGGATGGAGGCTGG
GAGTGGAGTGATGATGAATTTGATGAAGAAAGTGAGGAAGGGAAAGCAGCAATTTCACTCAGGTCTCCCCGA
GTGAAAGAATCAATATCAAATTCGTAGCTCTTTCCAACAACCTGATCCTGTGGGTACTTTGCTCCAAGTTCCAGAA
CAGATCTCTGCTCATCTACCTCAGCCAGCTGGGCAGATTGCTACACAGCCAACCTCAAGTCTCTCTCCACCCACC
GCAGAGCCAGCAAAAACAGCTCAGGCTTTGTCTTCAGGATCAGGTTTCAAGAAACCAAGATCCCCAATCAGTCTA
GTACTAAGATTAAAGGAATTCAAAAAAGAACTAAATGATATTGATTTGAATTTACTCCTGGGAGAGATACAGCA
GAGGGTGTCTCTCAGGAACCTCATTTCTGCTGGCCTGGTTCGACGGAAGGGATTTAGTAATAGTGGCAGCTAATTTG
CAGAAAATTTGTGAAGAACCTCAGTCAAATCGATCTGTCACTTTCAAACCTGGCATCTGGTGTGCAAGGCTCAGAT
ATTCTGTATGATGGTAAACTGATAGGATTTGCCAGCTCAGCATCAGCTAAACCACAACCTGGAAGAGGCGGCC
TAAGGAGATTCCACACATGCGTATCTCTGTTGCTTCTATTGGCCTAAACCCACTACTGCCAAAGAACCCAGCAAC
AAACCTCCCGGCTAGGAGCTTTAGAAGTCTTTATGTTCTTCTGCCATCATTCTCTCTTTTCCACAGGGAAAGA
AAAGTTGGATCACTAGTGGCCAGCATCCCCAGAGTTCCGTTAGTAAACTTACTTCATATGTCCCTGTCTTCTC
CATCTGAGAAGTGGCCCATGTGCTTCAAGGCCAGGAGGGAGATCTGTCACTCATTCTTGCTTACTCCAATGA
TGGCCAGGTGGAAGTAGCAGCTGTATCGGGCTTCTCATCCTGCCTGTTCCCCCACACCTGCCAGGATATGG
ACATCTTGGGATATCTCTTTACCACTGAAGTAGAATTGATTGTTTCACTGGAGCCAGAGAATTTAATTTAATGT
TTTTTCTTTGTACCTGATGTGAATTCTAGCAACCTTTGTTAGGAAAAAGCACAGCCTCAGATGGAGGCAGCCTAA
ACTGTGTTCTTGTGTTTGTTCATGGTGTGTTCTAAGCGTTTGTGCTGAAGCTGCTCTCAGGCACCCCTTCTTCATTG
CTCTCTCCAGAAAGGGTTGCTAGCCTTAACCTCAGCTGGTGCAAAACATCTGACTGTAGCCGAACTTCAGCCATC
AGATCCTTCAAAGTGAACCTTTGGATTGTTTTTACAGACAACATCGAGTAATGGCTTGTAATGTGAATTTTGCC
AGAGGTGGTTTTTTGAACAGGAAAATCATAATTCATATCATTGGAGAAGTATTTATTTTCAAATATCAAATTGAAG
AAAAACTCAATCCTCCCATGAAAATCAGTTGCGCTGGCCTCCAAGTCGTGAGGAAATGGGTATGCAAGGCTGAGA
TTTCTACAGCAATAAAGGAGACACACACTGGGCCAGAGAGGCTGCCTTCTGCCTGCTCTCCTGCACTGACCCTT
TGGAGGGGGTCTCTGTGTGCTGAAGCTAACTCAAGATGGAAGTGAACCACATGTGCCGTGACCTTTAGGTTTT
ATGAGTAGACAGTGTTCAATTTGATTTTTCTACAGAAATAATATAAATTATTCTTTAGGTTTTAAAAAGAGCACTCA
TAATGCAATATGTGAATAATCAGTGAGGTTGATTTTTCTTTTTTCTACCGTTTCATAGTCTTTGTCTAAGTGT
AGTAACCCCTACCGAGTTTTATATATGAGTGGGATACTCAATCTGGCCTTAAAAAGATACACAAAGATGGGCTGTG
GGTCCCTGGAAGGGGGAGAGTTGCCCTTTACAGAATCACTCGAGCCCTTTCCAGCACTGTTGGTCTGATGAACA
AGGTTGTTTTACCTTATTTTCTCTTGAACATATCTGAAAACCTTCCCACAAATAAAGTTGTCACACCTTTTGT
TCATTCTGAGTCTTTAGTTTTAGTCATGGGCTTTCTTCACCTGCTCTAGGTGCAAAGGCATGTTGGGAAAGAGAT
GGATGTTGGGGAGGAAGAGAGGAGATGGATTTCAAGTTGGGAGTTAGGAGGAGAGTAGGTGAGATGATCAGACACC
GGAGTTCAACGTCCCAGCAGTCTTGGTAAAAGGAGGGAGCCTGCTGAGCCAGGAGGGAGAAAAGAAGATTGACCA

1173/6881
FIGURE 1093B

GCTTGCTAGAAAAATACTTAGCTTTTCTTTTCTTTTGTGGAGGGGGACGGAGAGGAACAAGGATGGGGAG
GTAGGAATGAGGTATAGAAAAGAGATAGCATCTTCTTTGGCACAAGAATAGTGGCTTACCGCTTACCTTAGAGTT
TTGTTTTTTTTTTTCAAACCCATCAAATCTACTTATTTATGAATCCAAGGGGTGGCAGCATCACTCTGTTCTA
GCATTCTTTGTGGAGATGGTCTGGTGCCTAGCTGGGAGTGAGCAGCAGCCCATCCCCTGTTCACTTTCTCTAGCC
CATCATTACCTGTGAAGTGCAGTGGGGCAGTCATGGCAAATAGAATTGGGCTGGGGTTTCTCCTTCTTTTCAGTT
CATTGTTTGCCCTGCTAGGAATTAGAAGACAGACACCATGTCCCAGGACAGTGTTACTTCTTCTGCATGATGTGT
GGTAGACTCCCTTTGCTGGCTTGTGCAGTGATACTGAGAAAATACATGAACAGAAACTGCCAGGTGGAACAGCA
CGTAACCTAGTGAGTGACTGTACTCCTTTCTAGGAATGCTGATTCAGAGTGCACCTCTTTGACTAGGTCCCAGGA
TCCCCTTGTCCTGGAGTAGGGACTAACTATAGCACAAAGTAATATGTGCCAATGCTATTTGTGAAATGTTTGGT
CTTTCTAAACGACTAAAGGATTTGTTGGGTTTTTGCTTAAGTTTGAACCAAATCCTAGAGCCAGCTGATAATAT
TTAATAATCTGGAGGAGAGAATAATGATGTACCAATAAGTGGAGATTCTCCTTATGATGTATGCTAGGTTATGG
AAGATGTAAATATTCAACTTTTCTCCTTTTTTTGGACTTTGTATTTTACTGCATGTTTTCTTCATTTTTAAT
CAATAAAGAGTAAATTGTC

1174/6881
FIGURE 1094

MSEDSSALPWSINRDDYELQEVI GSGATAVVQAAYCAPKKEKVAIKRINLEKCQTSMD ELLKEIQAMSQCHHPNI
VSYYTSFVVKDELWLV MKLLSGGSVLDIIKHIVAKGEHKSGVLDESTIATILREVLEGL EYLHKNGQIHRDVKAG
NILLGEDGSVQIADFGVSAFLATGGDITRNKVRKTFVGTFCWMAPEVMEQVRGYDFKADIWSFGITAI ELATGAA
PYHKYPPMKVLM LTLQNDPPSLETGVQDK EMLKKYGKSFRKMISLCLQKDPEKRPTAAELLRHKFFQKAKNKEFL
QEKT LQRAPTISERAKKVRRVPGSSGRLHKTEDGGWEWSDD EFD ESEEGKAAISQLRSPRVKESISNSELFPTT
DPVGTLLQVPEQISAHLPQPAGQIATQPTQVSLPPTAEPAKTAQALSSGSGSQETKIPISLVLRLRNSKKELNDI
RFEFTPGRDTAEGVSQELISAGLVDGRDLVIVAANLQKIVEEPQSNRSVTFKLASGVEGSDIPDDGKLIGFAQLS
IS

1175/6881
FIGURE 1095

ATGCGACCCGACCGCGCTGAGGCTCCAGGACCGCCCGCC**ATG**GCTGCAGGAGGTCCCGGCGCGGGGTCTGCGGCC
CCGGTCTCCTCCACATCCTCCCTTCCCCTGGCTGCTCTCAACATGCGAGTGCGGCGCCGCCTGTCTCTGTTCTTG
AACGTGCGGACACAGGTGGCGGCCGACTGGACCGCGCTGGCGGAGGAGATGGACTTTGAGTACTTGAGATCCGG
CAACTGGAGACACAAGCGGACCCCACTGGCAGGCTGCTGGACGCCTGGCAGGGACGCCCTGGCGCCTCTGTAGGC
CGACTGCTCGAGCTGCTTACCAAGCTGGGCCGCGACGACGTGCTGCTGGAGCTGGGACCCAGCATTGAGGAGGAT
TGCCAAAAGTATATCTTGAAGCAGCAGCAGGAGGAGGCTGAGAAGCCTTTACAGGTGGCCGCTGTAGACAGCAGT
GTCCACGGACAGCAGAGCTGGCGGGCATCACCACACTTGATGACCCCTGGGGCATATGCCTGAGCGTTTCGAT
GCCTTCATCTGCTATTGCCCCAGCGACATCCAGTTTGTGCAGGAGATGATCCGGCAACTGGAACAGACAACTAT
CGACTGAAGTTGTGTGTCTGACCGCGATGTCCTGCCTGGCACCTGTGTCTGGTCTATTGCTAGTGAGCTCATC
GAAAAGAGGTGCCGCCGATGGTGGTGGTTGTCTCTGATGATTACCTGCAGAGCAAGGAATGTGACTTCCAGACC
AAATTTGCACTCAGCCTCTCTCCAGGTGCCCATCAGAAAGCGACTGATCCCATCAAGTACAAGGCAATGAAGAAA
GAGTTCCCCAGCATCCTGAGGTTTCACTGTCTGCGACTACACCAACCCCTGCACCAAATCTTGGTTCTGGACT
CGCCTTGCCAAGGCCTTGTCCCTGCCCT**TGA**AGACTGTTCTGAGGCCCTGGGTGTGTGTGTATCTGTCTGCCTGTC
CATGTACTTCTGCCCTGCCTCCTCCTTTTCGTTGTAGGAGGAATCTGTGCTCTACTTACCTCTCAATTCCTGGAGA
TGCCAACTTCACAGACACGTCTGCAGCAGCTGGACATCACATTTTATGTCTGCATGGAACCAAGTGGCTGTGAGT
GGCATGTCCACTTGCTGGATTATCAGCCAGGACACTATAGAACAGGACCAGCTGAGACTAAGAAGGACCAGCAGA
GCCAGCTCAGCTCTGAGCCATTACACATCTTCACCTCAGTTTCTCACTTGAGGAGTGGGATGGGGAGAACAG
AGAGTAGCTGTGTTTGAATCCCTGTAGGAAATGGTGAAGCATAGCTCTGGGTCTCCTGGGGGAGACCAGGCTTGG
CTGCGGGAGAGCTGGCTGTTGCTGGACTACATGCTGGCCACTGCTGTGACCACGACACTGCTGGGGCAGCTTCTT
CCACAGTGATGCCTACTGATGCTTCACTGCTCTGCACACCGCCCATTCCTTCTCCTTCCCCACAGGGCAGG
TGGGGAAGCAGTTTGGCCCAGCCCAAGGAGACCCCATCTTGAGCCTTATTTCTTAATGGGTCCACCTCTCATCTG
CATCTTTCACACCTCCCAGCTTCTGCCCAACCTTCAGCAGTGACAAGTCCCCAAGAGACTCGCCTGAGCAGCTTG
GGCTGCTTTTTCATTTCCACCTGTCAGGATGCCTGTGGTCATGCTCTCAGCTCCACCTGGCATGAGAAGGGATCCT
GGCCTCTGGCATATTTCATCAAGTATGAGTTCTGGGGATGAGTCACTGTAATGATGTGAGCAGGGAGCCTTCTCTCC
CTGGGCCACCTGCAGAGAGCTTTCCCAACCTTTGTACCTTGATTGCCTTACAAAGTTATTTGTTTACAAACAG
CGACCATATAAAAGCCTCCTGCCCCAAAGCTTGTGGGCACATGGGCACATACAGACTCACATACAGACACACACA
TATATGTACAGACATGTACTCTCACACACACAGGCACCAGCATAACACACGTTTTTCTAGGTACAGCTCCCAGGAA
CAGCTAGGTGGGAAAGTCCCATCACTGAGGGAGCCTAACCATGTCCCTGAACAAAAATTGGGCACTCATCTATTC
CTTTTCTCTTGTGTCCCTACTCATTGAAACCAAACCTCTGGAAAGGACCCAATGTACCAGTATTTATACCTCTAAT
GAAGCACAGAGAGAGGAAGAGAGCTGCTTAAACTCACACAACAATGAACTGCAGACACAGCTGTTCTCTCCCTCT
CTCCTTCCCAGAGCAATTTATACTTTACCCTCAGGCTGTCTCTGGGGAGAAGGTGCCATGGTCTTAGGTGTCTG
TGCCCCAGGACAGACCCTAGGACCCTAAATCCAATAGAAAATGCATATCTTTGCTCCACTTTCAGCCAGGCTGGA
GCAAGGTACCTTTTCTTAGGATCTTGGGAGGGAATGGATGCCCCCTCTCTGCATGATCTTGTGAGGCATTTAGCT
GCCATGCACCTGTCCCCCTTTAATACTGGGCATTTTAAAGCCATCTCAAGAGGCATCTTCTACATGTTTTGTACG
CATTAATAATAATTTCAAAGATATCTGAGAAAAGCCGATATTTGCCATTCTTCTATATCCTGGAATATATCTTGC
ATCCTGAGTTTATAATAATAATAATATTCTACCTTGAAAAAAAAAAAAAAAAA

1176/6881
FIGURE 1096

MAAGGPGAGSAAPVSSTSSLPLAALNMRVRRRLSLFLNVRTQVAADWTALAEEMDFEYLEIRQLETQADPTGRLL
DAWQGRPGASVGRLLELLTKLGRDDVLLELGPSIEEDCQKYILKQQQEEAEKPLQVAAVDSSVPRTAELAGITT
DDPLGHMPERFDAFICYCPSDIQFVQEMIRQLEQTNYRLKLCVSDRDVLPGTCVWSIASELIEKRCRMVVVSD
DYLQSKCEDFQTKFALSLSPGAHQKRLIPIKYKAMKKEFPSILRFITVCDYTNPCTKSWFWTRLAKALSLP

1177/6881
FIGURE 1097

ATGTGGTTCTGCGCGTGTGCGGACGGCTGTCTGTAACTCCGCGGTCA GTTCCCGGACTGGTGGCTGGTCTGCAG
GGTTGACCTGCGCAATGCAGAGGCTGCAGGTAGTGCTGGGCCACCTGAGGGGTCCGGCCGATTCCGGCTGGATGC
CGCAGGCCGCGCCTTGCCCTGAGCGGTGCCCCGCAGGCCTCGGCCGCGGACGTGGTGGTGGTGCACGGGCGGCGCA
CGGCCATCTGCCGGGCGGGCCGCGGCGGCTTCAAGGACACCACCCCGACGAGCTTCTCTCGGCAGTCATGACCG
CGTTTCTCAAGGACGTGAATCTGAGGCCGGAACAGCTGGGGGACATCTGTGTGCGAAATGTGCTGCAGCCTGGGG
CCGGGGCAATCATGGCCCGAATCGCCAGTTTCTGAGTGACATCCCGGAGACTGTGCCTTTGTCCACTGTCAATA
GAÇAGTGTTTCGTGCGGGCTACAGGCAGTGGCCAGCATAGCAGGTGGCATCAGAAATGGGTCTTATGACATTGGCA
TGGCCTGTGGGGTGGAGTCCATGTCCCTGGCTGACAGAGGGAACCTTGAAATATTACTTCGCGCTTGATGGAGA
AGGAGAAGGCCAGAGATTGCCTGATTCTATGGGGATAACCTCTGAGAATGTGGCTGAGCGGTTTGGCATTTCAC
GGGAGAAGCAGGATACCTTTGCCCTGGCTTCCCAGCAGAAGGCAGCAAGAGCCCAGAGCAAGGGCTGTTTCCAAG
CTGAGATTGTGCCTGTGACCACCACGGTCCATGATGACAAGGGCACCAAGAGGAGCATCACTGTGACCCAGGATG
AGGGTATCCGCCCCAGCACCAACCATGGAGGGCCTGGCCAAACTGAAGCCTGCCTTCAAGAAAGATGGTTCTACCA
CAGCTGGAAACTCTAGCCAGGTGAGTGATGGGGCAGCTGCCATCCTGCTGGCCCGGAGGTCCAAGGCAGAAGAGT
TGGGCCTTCCCATCCTTTGGGGTCTTGGGTCTTATGCAGTGGTTGGGGTCCCACCTGACATCATGGGCATTGGAC
CTGCCTATGCCATCCCAGTAGCTTTGCAAAAAGCAGGGCTGACAGTGAGTGACGTGGACATCTTCGAGATCAATG
AGGCCTTTGCAAGCCAGGCTGCCTACTGTGTGGAGAAGCTACGACTCCCCCCTGAGAAGGTGAACCCCTGGGGG
GTGCAGTGGCCTTAGGGCACCCACTGGGCTGCACTGGGGCACGACAGGTCAACACGCTGCTCAATGAGCTGAAGC
GCCGTGGGAAGAGGGCATAACGAGTGGTGTCCATGTGCATCGGGACTGGAATGGGAGCCGCTGCCGTCTTTGAAT
ACCCTGGGAACTGAGTGAGGTCCCAGGCTGGAGGCGCTACGCAGACAGTCCTGCTGCTCTAGCAGCAAGGCAGTA
ACACCACAAAAGCAAAACCACATGGGAAAACCTCAGCACTGGTGGTGGTGGCAGTGGACAGATCAAGGCACTTCAA
CTCATTTGGAAAATGTGAACACTGATGACATGGTATAGGAGTGGGTGGGGTGTGAGCCACCCATCAGACCCTCT
TTAGCTGTGCAAGATAAAAGCAGCCTGGGTACCCAGGCCACAAGGCCATGGTTAATTCTTAAGGCAAGGCAAAAT
CCATGGATGAGAAGTGCAATGGGCATAGTAAAAGTGCATGAATTT

1178/6881
FIGURE 1098

MQRLQVVVLGHLRGPADSGWMPQAAPCLSGAPQASAADV VVHGRRTAICRAGRGGFKDTPDELLSAVMTAVLKD
VNL RPEQLGDI CVGNVLQPGAGAIMARIAQFLSDIPETVPLSTVNRQCSSLQAVASIAGGIRNGSYDIGMACGV
ESMSLADRGNP GNITSRLMEKEKARDCLIPMGITSENV AERFGISREKQDTFALASQQAARAQSKGCFQAEIVP
VTTTVHDDKGTKRSITVTQDEGIRPSTTMEGLAKLKPAFKKDGSTTAGNSSQVSDGAAAILLARRSKAEELGLPI
LGVLRSYAVVGVPDIMGIGPAYAIPVALQKAGLTVSDVDIFEINEAFASQAAYCVEKLRLPPEKVNPLGGAVAL
GHPLGCTGARQVITLLNELKRRGKRAYGVVSMCIGTGMGAAAVFEYPGN

[illegible]

1180/6881
FIGURE 1100

MIPPSSPREDGVDGLPKEAVGAEQPPSPASTSSQESKLQKLKRSLSFKTKSLRSKSADNFFORTNSEDMKLQAHM
VAEISPSSSPLPAPGSLTSTPARAGLHPGGKAHAFQEYIFKKPTFCDVCNHMIVGTNAKHGLRCKACKMSIHHKC
TDGLAPQRCMGKLPKGFRRYYSSPLLIHEQFGCIKEVMP IACGNKVDPVYETLRFGTSLAQRTKKGSSGSGSDSP
HRTSTSDLVEVP EEEANGPGGGYDLRKRSNSVFTYPENGTD DFRDPAKNINHQGSLSKDPLQMNTYVALYKFVPQE
NEDLEMRPGDIITLLEDSNEDWWKGKIQDRIGFFPANFVQRLQONEKIFRCVRTFIGCKEQGQITLKENQICVSS
EEEQDGFIRVLSGKKKGLIPLDVLENI

1181/6881
FIGURE 1101

GCCGCGGGCTTCGTTTGTGAGGAAGGGGGCCTAGGCCCGGGCCTGCGGTGGTGGGGGTGCTGCGCGCCGGGGGT
CGCTCCTGCTGTGTCTTCCGCTCCAGCTTCGCCCCTTCCCCTTGCCAGCGGGGTGGGCGCGGAGAAGACCTGCC
GGAGCCATGGAGGACGAAGTGGTCCGCTTTGCCAAGAAGATGGACAAGATGGTGCAGAAGAAGAACGCGGCTGGA
GCATTGGATTTGCTAAAGGAGCTTAAGAATATTCTATGACCCTGGAATTACTGCAGTCCACAAGAATCGGAATG
TCAGTTAATGCTATTTCGCAAGCAGAGTACAGATGAGGAAGTTACATCTTTGGCAAAGTCTCTCATCAAATCCTGG
AAAAAATTATTAGATGGGCCATCAACTGAGAAAGACCTTGACGAAAAGAAGAAAGAACCTGCAATTACATCGCAG
AACAGCCCTGAGGCAAGAGAAGAAAGTACTTCCAGCGGCAATGTAAGCAACAGAAAGGATGAGACAAATGCTCGA
GATACTTATGTTTCATCCTTTCTCGGGCACCAAGCACTTCTGATTCTGTGCAGTTGAAGTGTAGGGGAGATGCTT
GCTGCAGCTCTTCGAACAGGGGATGACTACATTGCAATTGGAGCTGATGAGGAAGAATTAGGATCTCAAATTGAA
GAAGCTATATATCAAGAAATAAGGAATACAGACATGAAATACAAAAATAGAGTACGAAGTAGGATATCAAATCTT
AAAGATGCAAAAAATCCAAATTTAAGGAAAAATGTCCTCTGTGGGAATATTCTCCTGACTTATTTTGCTAGAATG
ACAGCAGAGGAAATGGCTAGTGATGAGCTGAAAGAGATGTGGAAAACTTGACCAAAGAAGCCATCAGAGAGCAT
CAGATGECOAAGACTGGTGGGACCCAGACTGACTTGTTTACATGTGGCAAATGTAAAAAGAAGAATTGCACCTTAC
ACACAGGTACAAACCCGTAGTGCTGATGAACCAGTGACAACATTTGTTGTCTGTAATGAATGTGGAAATCGATGG
AAGTTCTGTTGAGTTGGAAGAATTGGCAAAATATCTGGACCATTAAGAAAACGGATTTTGTAAGTAGCTTTAAAC
TAGGCCAAGCAACTAGTTTTCTGCAAATCAAATTTTTAAAGCAACTTGAGTTAGACTTTGTTTTTGACCTAACA
TCCCTTCCTTAAATGCCTTCTGTAGTTTCAGATCAGTAGGGAGACCATATAATAATTGTATGGTACCTGTTTCAA
AACATATTTTTTCTGTTTTTATAAGTAAGTTGATATTAATTAACCTCTTGGCAATATTTCTTCTTTCTTAAAGGA
AAATACACCTTAACCTTTTTTCTTTTACACTGTGAAACATACACAGTAGAAATTCTGTTACTCTCTGTATTAAAT
ACATAAATGAAAATACTTTTTTTTCCATATTGGCATGTAGCTACAAATATTAAAGGAGGAGAAAAGGTAATATAA
TTTTAGGTTTACCAAATATGGTGTGTATTCAAATAATACTTGACCAGCTTATCTAAATGTACATAATTTTGAGG
TAGCTTATGAATTTGATTTTAATTATTATGTTTACAAGCTTGGAATATTAGATATTATTTTGCATCTGTAACATA
CCGTGATCATCATCTCTTGTAATTTCTGTACATGTATATTACTTGTCTTAATAGATTTTGGAAACAAGACTT
TATTGAGATCAGTTTGGTTTTCTGTAAATTTACCTGTTTGACTTTATAATGTGTTTTAGTTTTGCAGAAGAACA
CTGTTGTAGTTTAGAAGGCTTTTCATAAATCCCTCATAGGCCAAAGATGAGAACTTCCCCTATTTTTTTCCCCT
CTTAGGAAGACATACTGGAAAGAAAATGTTTAGCATCTTAGTGTAAGTATAGCTATTGTAAACAGTTTATGACTAG
ATTTTGATTTCGAAATCTATACTGACCAAGGATTAATCTTAAGGACTGTATAATTCATTAAAGCGGTGGTCTTTC
CATGTGGAGACTGATAGAAAATAATTTGTCCCAAGTCTTATTGCTGACTTTTTCTGTCAATGAGTGAGATTGT
TGAACAACTGAATATATGGGCTATAGCAAGTAGCTTTACAGTACAGATCTTACAATTAAGTTTTGCTTTTGTTA
AAGTGTGTACCATTTTTTCTGTTTGGAGTAAGACAAAAATTGTTTTGACATAGGTTCCCTAGGGTACACTTGCTC
TAGCATACTTTAAAGGCCACTGTTGCAAAGTCTACATTTTATGCTGAATCTGCATTCTGTGAGGCACCCGTAGAA
AGACCTCAGTACATGCTTTGCACTCTCCTTTGCTCCCTTTTTCCAATTTCTTATTGCATATCATTGTTGTTAAT
ACAGAAAGCAGCATTTTTTAAATGTCCATGTTAAGAATTGGCCCACTGGTACCGACTCACCTCTATTTTGTGAGTT
CATAGTTGAAGATTTTGTGTTTTATTTCAAAAACAAAGTACATTTTTGAAATAATGTTTCAGAATAAAATAATCTCA
CTTTTAAATTAAGTGATCCATTTTAAATTTGTAATTCATAAAGTTTTTTTTGTTGTTAAACAT

1182/6881
FIGURE 1102

MEDEVVRFAKKMDKMOVQKKNAAGALDLLKELKNIPMTLELLQSTRIGMSVNAIRKQSTDEEVTSLAKSLIKSWKK
LLDGPSTEKDLDEKKKEPAITSQNSPEAREESTSSGNVSNRKDETNARDTYVSSFPRAPSTSDSVQLKCREMLAA
ALRTGDDYIAIGADEEELGSQIEEAIYQEIRNTDMKYKNRVRSRISNLKDAKNPNLRKNVLCGNIPDLPFARMTA
EEMASDELKEMWKNLTKEAIREHQMAKTGGTQTDLFTCGKCKKKNCTYTQVQTRSADEPVITFVVCNECGNRWKF
C

1183/6881
FIGURE 1103

AGGTCCCACCGCTCCTACCAGCAGCCTGACCCAGGATCGCTCTACTCCCCAGCCTTCAATCCCCTGGACCTGGGTT
TGGAATTAGGAGACTTCCGTCGAGGGTCAATTGTGCGGGATCCTGGCCATTCCATACAAAATCTCACGACTGGCA
AAAGAGAGGGGGACCCCTCGAGCAGAGGTCAGATATCACAAAGGGACCCGGGTTTTTCCACCCCGCCCTCATTCCC
AGCGTGGGGTCTCAGATGAGTGGGAAAACCTCAAATATGGATCAGAAATCATGCAAGTTCGGACTCTGGCCTTAG
GAGAAAACCTCTTAACGGAGATGGAATGTCACGAGGGATCCAGCCACCCCATCCACTCATTGACTGGATGAAGTT
TTGCGATGGGAAAATCCAGGTCAGGAGTTACGGACGACCTGCACCGCCCGGAGCTCCTTCTGGGTCCGGAGTTTG
GGAAAAGTGC GG GTTAGGGGTAAAGGTCACGGAAGAACTTCCCCACTCCCCCGCCTCTTTCGTCCGCGGGCCG
GTTCAAGAGGTATTCGGAACCAGGGGAGGAGAGCGGCGGCCATCGTACCTGAGCAGGAGCCAGCGCCTGCTGGAG
CTGCTGCTGCTCCTCGCTGATCTTTTGCTTCAGTTTCTTGAACATGGCGCAGCGTACGTACGGTCTCTGAGTGTCA
ACGAAACCTGAAGGGCGAGAGCCCCGGGGAGTCCCGGCCGCGACGGCTACGGCGACTTCTTTACACCAGGGACAGC
GGGGGCCGGGCCTCGCCGTCTCCTCCTTGAGGCTGTGGGCAAGTCCGGACACTCGTCTTGAGGGTGTGCGCGTCCG
CCGCCGCCGCTCTCTTTCTTCCGGGTGCCACTGGCTGGCCTCGGCCCCCATCCAGCCCCGGGAGCCGCGGGCGG
CGACGACAACGGCAGCAGGTGAACGTGTGCGCCAAGGGCGCTTGC GCGGCCCTACGTGGAGCTCACAGAGGCTAACT
ACGGAGCACCGGATGGGACAAGCACAAATGTCGGGTCCCGCACATGCGCGCTCGGCCGGTTCGCTTCCGAACCTCGCT
GCACTGGAGGACGCAAGGTTTCGGTCTGCTGATTTCTTGTGCTGCGGAGACCGCCGTTCGCGGCTCAGAACC GGA
GCGTGGGCTAGTCTGAACACTACCCTGACTCTCACCTGGGCTTTGGCCCTGCGAAATCAGACGGGGAGAGTGCTG
CTTCTATCGATGGCAGCAGGGCCGACGGGCCCCACCGCAAAGAACACAGGGATGAGCGTCAAGGATGGGAGAAGGG
GAGATCCAGAGAACCTGACGCGGGCCCTAATTGATAGTGTTCTTTCTTTAGTAGCTGTAGCTAGGATTCTGTGT
CTTCGGTGCCAGAGGGGGCCGCTTCCCTTCCCTGAACTCTTCCAGCGTCGGGAAGTCCCTGATACCAGGCGCCAG
GGGTCCAAATGTTTTATGCCAATACTGTAAAACCTCAAGTGTTTGGACACCTGCTTTATTCTTTCTTCCACCGAA
ATCGTGTATTTACGAATTCATTCAAAAACCTTTATCAGGCCTTGGAGATGTTAAAAGAATTTACAGCCTAGTGG
AAGACACAGATTCTAATTAGTCCAAATTTACTCCTAACACCTGCAATCATCCTACAAGATCTTAATGTTTATGT
GCCTCATTTATCTAAAACCTGAACTTTGGCTGCCTGTGAATCCTCAGGTCCATTTTCAGCAACCCACTTTTGCAT
GCTGTACCTTTGATATCATCTGAAACTGCTTACATTGTCTCCGGTATCAGAATCTAACAGTATATGCTGATCTCC
ACGTTCTAGCAAATTTTGTTTACCAGCAATAATAGGAGCAACCTGCTCTCGAGAGTCCATATTCTGATCCCTAAA
TGATTAGAGCCACAGTGGGGCCTGGAACACTGCCTTAACACCTGGGCTAAGTCCCTCTTATATCTCGTAGTGAAC
ACCTTATGTATGTAAGGTGTCCCCAGCCCCCGGGCCACAAACGGGTACCAGCCCCATGGCCTGTTAGGAACCGGGC
TACACAGCAAGAAGTGAATCTCTGGCAAGCCAGGGAAGCTTAATCTGTATTTACAGCTGCTCCCCATGGTTTACA
TTATCGTCTGAGCTCCACCTCCTGTGATCAGCTGTGGCATGAGATTCTCATAGGAGCTGGAACACTGTGAAC
TAGGCATGAGAGGGATCTAGGTTATGCTCCTTAAGAGAATCTAATGCCTGATGATCTGTCACTGTCTCCCATCAC
CCCCAGATGGGACCATCTAGTTGCAGGAAAATAAGCTCAGGGCTCCACCGATTCTACATTATGGTGAGTTGTGT
AATTGTTTCATTATATATTACAATGCAATAATAATAGAAATAAAGGGCACATAAATAT

1184/6881
FIGURE 1104

MALLPSLQSLDLGLELGDFRRGSIVRDPGHSIQNLTTGKREGDPSSRGQISQGTRVFPPRPHSQRGVSDIEWENLK
YGSEIMQVRTLALGENS

1185/6881
FIGURE 1105

CTCTTCCGGTTCTAGGTGCTTCGGGAGCCGCGGCTTAAGGTGTAGACATGGCGAAGTCCAAGAACCACACCACAC
ACAACCAGTCCCGAAAATGGCACAGAAATGGTATCAAGAAACCCCGATCACAAAGATACGAATCTCTTAAGGGGG
TGGACCCCAAGTTCCTGAGGAACATGCACCTTTGCCAAGAAGCACAACAAGAAGGGCCTAAAGAAGATGCAGGCCA
ACAATGCCAAGGCCATGAGTGCACGTGCCGAGGCTATCAAGGCCCTCGTAAAGCCCAAGGAGGTAAAGCCCAAGA
TCCCAAAGGGTGTGAGCCGCAAGCTCGATCGACTTGCCTACATTGCCCATCCCAAGCTTGGGAAGCGTGCTCGTG
CCCGTATTGCCAAGGGGCTCAGGCTGTGCCGGCCAAAGGCCAAGGCCAAGGATCAAACCAAGGCCCAGGCTGCAG
CTCCACCTTCAGTTCCAGCTCAGGCTCCCAAAGGTGCCCAGGCCCTACAAAGGCTTCAGAGTAGATATCTCTGC
CAACATGAGGACAGAAGGACTGGTGTGACCCCTACCCCGCCCTGGGCTACCATCTGCATGGGGCTGGTCCTC
CTGTGCTATTTGTACAAATAAACCTGAGGCAGG

1186/6881
FIGURE 1106

ATTGCCACATGGTCCACATTGCATGCAAGATTGCTGAGCTGAAGGAAAAGATTGATTGCCGTTCTGGTAAAAAGC
CAGAAGATTGCCCTAAATTCTTGAAGTCTGATGATGCTGCCATCATTGACATGGTTCCTGGCAAGCCCATGTGTG
TTGAGAGCTTCTCAGAACTGTTTGTTCATTGGCCATTTAAGTTTAGTAGTAAAAGACTGGTTAATGATAACAA
TGCATCATAAAACCTTCAGATGGAAAGGAGAATGTTTGTGGACCACTTTGGTTTTCTTTTTTGCATCTGGCAGT
TTTAAGTTATTAGTTTTTAAAATCAGTACTTTTTAATGGAA

1187/6881
FIGURE 1107

MVHIACKIAELKEKIDCRSGKKPEDCPKFLKSDDAAIIDMVP GKPMC VESFSELFVSIGHL SLVVKDWL MITMHH
KTRWKGECFVDHFGFLFCIWQF

1188/6881
FIGURE 1108

TGCCTGTCCTTTTCCGTGCTACCTGCAGAGGGGTCCATACGGCGTTGTTCTGGATTCCCGTCGTAACCTTAAAGGGA
AACTTTCACAATGTCCGGAGCCCTTGATGTCCTGCAAATGAAGGAGGAGGATGTCCTTAAGTTCCTTGCAGCAGG
AACCCACTTAGGTGGCACCAATCTTGACTTCCAGATGGAACAGTACATCTATAAAAGGAAAAGTGATGGCATCTA
TATCATAAATCTCAAGAGGACCTGGGAGAAGCTTCTGCTGGCAGCTCGTGCAATTGTTGCCATTGAAAACCCCTGC
TGATGTCAGTGTTATATCCTCCAGGAATACTGGCCAGAGGGCTGTGCTGAAGTTTGCTGCTGCCACTGGAGCCAC
TCCAATTGCTGGCCGCTTCACTCCTGGAACCTTCACTAACCAGATCCAGGCAGCCTTCCGGGAGCCACGGCTTCT
TGTGGTTACTGACCCAGGGCTGACCACCAGCCTCTCACGGAGGCATCTTATGTTAACCTACCTACCATTTGCGCT
GTGTAACACAGATTCTCCTCTGCGCTATGTGGACATTGCCATCCCATGCAACAACAAGGGAGCTCACTCAGTGGG
TTTAATGTGGTGGATGCTGGCTCGGGAAGTTCTGCGCATGCGTGGCACCATTTCCTGTAACACCCATGGGAGGT
CATGCCTGATCTGTACTTCTACAGAGATCCTGAAGAGATTGAAAAAGAAGAGCAGGCTGCTGCTGAGAAGGCAGT
GACCAAGGAGGAATTTAGGGTGAATGGACTGCTCCCGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAGA
CTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCTATTACAGCAATTCCTACTGAAGACTGGAGCGCTCAGCCTGC
CACGGAAGACTGGTCTGCAGCTCCCACTGCTCAGGCCACTGAATGGGTAGGAGCAACCACTGACTGGTCTTTAAGC
TGTTCTTG CATAGGCTCTTAAGCAGCATGGAAAAATGGTTGATGGAAAATAAACATCAGTTTCT

1189/6881
FIGURE 1109

MSGALDVLQMKEEDVLKFLAAGTHLGGTNLDFQMEQYIYKRKSDGIYIINLKRTWEKLLLAARAIVAIENPADVS
VISSRNTGQRAVLKFAAATGATPIAGRFTPGFTNQIQAAFREPRLLVVTDPRADHQPLTEASYVNLPTIALCNT
DSPLRYVDIAIPCNNKGAHSVGLMWWMLAREVLRMRGTISREHPWEVMPDLYFYRDP EEIEKEEQAAAEKAVTKE
EFQGEWTAPAPEFTATQPEVADWSEGVQVPSVPIQQFPTEDWSAQPATEDWSAAPT AQATEWVGATTDWS

FIGURE 1110

[illegible]

1191/6881
FIGURE 1111

MVFRRFVEVGRVAYVSFGPHAGKLVAIVDVIDQNRALVDGPCTQVRRQAMPFKCMLTDFILKFPHTSAHQKYVRQ
AWQKADINTKWAATRWAKKIEARERKAKMTDFDRFKVMKAKKMRNRIKNEVKKLQKAALLKASPKKAPGKGT
AAAAAAAAAAKVPAKKITAASKKAPAQKVPAQKATGQKAAPAPKAQKGQKAPAQKAPAPKASGKKA

1192/6881
FIGURE 1112

GACTCCTAGGGGCTTGCAGACTAGTGGGAGAGAAAAGAACATCGCAGCAGCCAGGCAGAACCAGGACAGGTGAGGT
GCAGGCTGGCTTTCCTCTCGCAGCGCGGTGTGGAGTCCTGTCTGCCTCAGGGCTTTTCGGAGCCTGGATCCTCA
AGGAACAAGTAGACCTGGCCGCGGGGAGTGGGGAGGGAAGGGGTGTCTATTGGGCAACAGGGCGGGGCAAAGCCC
TGAATAAAGGGGCGCAGGGCAGGCGCAAGTGGCAGAGCCTTCGTTTGCCAAGTCGCCTCCAGACCGCAGACATGA
AACTTGTCTTCCTCGTCCTGCTGTTCTCGGGGCCCTCGGACTGTGTCTGGCTGGCCGTAGGAGGAGTGTTCAGT
GGTGCGCCGTATCCCAACCCGAGGCCACAAAATGCTTCCAATGGCAAAGGAATATGAGAAAAGTGCCTGGCCCTC
CTGTCTAGCTGCATAAAGAGAGACTCCCCATCCAGTGTATCCAGGCCATTGCGGAAAACAGGGCCGATGCTGTGA
CCCTTGATGGTGGTTTCATATACGAGGCAGGCCTGGCCCCCTACAACTGCGACCTGTAGCGGGCGGAAGTCTACG
GGACCGAAAGACAGCCACGAACCTCACTATTATGCCGTGGCTGTGGTGAAGAAGGGCGGCAGCTTTCAGCTGAACG
AACTGCAAGGTCTGAAGTCTGCCACACAGGCCTTCGCAGGACCGCTGGATGGAATGTCCCTATAGGGACACTTC
GTCCATTCTTGAATTGGACGGGTCCACCTGAGCCCATTGAGGCAGCTGTGGCCAGGTTCTTCTCAGCCAGCTGTG
TTCCCGGTGCAGATAAAGGACAGTTCCCCAACCTGTGTGCCTGTGTGCGGGACAGGGGAAAACAAAATGTGCCT
TCTCCTCCCAGGAACCGTACTTCAGCTACTCTGGTGCCTTCAAGTGTCTGAGAGACGGGGCTGGAGACGTGGCTT
TTATCAGAGAGAGCACAGTGTGTTGAGGACCTGTCTAGACGAGGCTGAAAGGGACGAGTATGAGTTACTCTGCCAG
ACAACACTCGGAAGCCAGTGGACAAGTTCAAAGACTGCCATCTGGCCCGGGTCCCTTCTCATGCCGTTGTGGCAC
GAAGTGTGAATGGCAAGGAGGATGCCATCTGGAATCTTCTCCGCCAGGCACAGGAAAAGTTTGGAAGGACAAGT
CACCGAAATTCAGCTCTTTGGCTCCCCTAGTGGGCAGAAAGATCTGCTGTTCAAGGACTCTGCCATTGGGTTTT
CGAGGGTGGCCCCGAGGATAGATTCTGGGCTGTACCTTGGCTCCGGCTACTTCACTGCCATCCAGAAGTTGAGGA
AAAGTGAGGAGGAAGTGGCTGCCCGGCGTGC CGGGTCTGTGTGGTGTGCGGTGGGCGAGCAGGAGCTGCGCAAGT
GTAACCACTGGAGTGGCTTGAGCGAAGGCAGCGTGACCTGCTCCTCGGCCTCCACCACAGAGGACTGCATCGCCC
TGGTGTCTGAAAGGAGAAGCTGATGCCATGAGTTTGGATGGAGGATATGTGTACACTGCAGGCAAATGTGGTTTGG
TGCCTGTCTTGGCAGAGAACTACAAATCCCAACAAAGCAGTGACCCTGATCCTAACTGTGTGGATAGACCTGTGG
AAGGATATCTTGCTGTGGCGGTGGTTAGGAGATCAGACACTAGCCTTACCTGGAAGTCTGTGAAAGGCAAGAAGT
CCTGCCACACCGCCGTGGACAGGACTGCAGGCTGGAATATCCCCATGGGCCTGCTCTTCAACCAGACGGGCTCCT
GCAAATTTGATGAATATTTTCAGTCAAAGCTGTGCCCTGGGTCTGACCCGAGATCTAATCTCTGTGCTCTGTGTA
TTGGCGACGAGCAGGGTGAGAATAAGTGCCTGCCAACAGCAACGAGAGATACTACGGCTACACTGGGGCTTTCC
GGTGCCTGGCTGAGAATGCTGGAGACGTTGCATTTGTGAAAGATGTCACTGTCTTGAGAACACTGATGGAAATA
ACAATGACGCATGGGCTAAGGATTTGAAGCTGGCAGACTTTGCGCTGCTGTGCCTCGATGGCAAACGGAAGCCTG
TGAAGGCTAGAAAGCTGCCATCTTGCCATGGCCCCGAATCATGCCGTGGTGTCTCGGATGGATAAGGTGGAAC
GCCTGAAACAGGTGTTGCTCCACCAACAGGCTAAATTTGGGAGAAAATGGATCTGACTGCCCCGACAAGTTTTGCT
TATTCAGTCTGAAACCAAAAACCTTCTGTTCAATGACAACACTGAGTGTCTGGCCAGACTCCATGGCAAAAACAA
CATATGAAAAATATTTGGGACCACAGTATGTGCGAGGCATTACTAATCTGAAAAAGTGCTCAACCTCCCCCTCC
TGGAAGCCTGTGAATTCCTCAGGAAGTAAAACCGAAGAAGATGGCCCAGCTCCCCAAGAAAGCCTCAGCCATTCA
CTGCCCCCAGCTCTTCTCCCCAGGTGTGTTGGGGCCTTGGCCTCCCCCTGCTGAAGGTGGGGATTGCCCATCCATC
TGCTTACAATTCCCTGCTGTCTGCTTAGCAAGAAGTAAAATGAGAAATTTTGTGATATTC

FIGURE 1113

GCTTCTAAACAACCTACCCCTCTCCCAATTTTCTGTGGTGCCAACTACCTTCGGCGATCCCAGGCTTGGCGGGGG
ACCGCTTGGCCTCTCCCGTTCCTTTAGGCTGCCGCCGCTGCCTGCCGCCATCGCAGAGTTGGGCCTAAATGAGAC
CCATCAAAATGAAGTTATTAATTATATGCGTTTTGCTCGTTCAAAGAGAGGCTTGAGACTCAAACTGTAGATTCT
CTGCTTCCAAGACCTCAAGGAGAGCAGGCTGGTGGAGGACACCTTACCATAGATGAAGTCTCTGAAGTCTCTCAA
TGGATTACAAGCTGTGGTTCATAGTGAGGTGGAATCTGAGCTCATCAACACTGCCTATACCAATGTGTTACTTCT
GCGACAGCTGTTTGCACAAGCTGAGAAGTGGTATCTTAAGCTACAGACAGACATCTCTGAAGTTGAAAACCGAGA
ATTATTAGAACAAGTTGCAGAATTTGAAAAAGCAGAGATTACATCTTCAAACAAAAGCCCATCTTAGATGTCAC
AAAGCCAAAACCTTGCTCCACTTAATGAAGGTGGAACAGCAGAAGCTCCTAAACAAGGAAATTTTAAGACTTCAAGA
AGAGAATGAGAAATTGAAGTCAAGGTTGAAGACCATTGAAATACAGGCTACAAATGCACTGGATGAAAAGTCAAA
ACTAGAAAAAGCACTGCAAGATTTACAGCTTGATCAAGGAAATCAAAGGATTTTATAAAGGCCCAAGACTTAAG
TAAGTTAGAAAAACACTGTCGCTGCCTTAAAGAGTGAGTTTCAGAAGACACTTAATGACAAGACAGAAAACCAGAA
GTCAGTGGAGGAGAAATCTGGCGACAGCCAAGCACGATCTACTCAGGGTTTCAGGAGCAGCTGCACATGGCTGAAAA
GGAATTAGAAAAAGAAATTTACAGCAAACAGCAGCTTATCGAAACATGAAAGAGATTCTTACCAAGAAGAATGACCA
AATCAAAGATCTGAGGAAAAGACTGGCACAATATGAACCTGAAGATTAAAGTGAAGATTTTCTCTGGAAGCTAC
CACATGCAAAACATACAAGCAGTCTCACCTCAGGCATGTATTTTGAAGAGCATTGTTGTCATATCCCCTCTCCTTAT
TTTTCTAATATTTAGACTTTGAATATTTAGAAGTAGAGTTCCTATTTTTCAGCTAGTTGAAAACAGAGAAAACCTA
GTGATTCTGTCTGGTTCATCCACACACCTCTCTACTGAGTGCTCCAGAGTCTTAGCTCACATGCACTGAGAATTC
TTTACAGCAAAGAAGAGATTTTATAGAGTGGGAAGAAGAGGCTTATCCTTCTGCATTAGTATAAAGAGTCTGTATT
TTTAATAAATGTTAAATAAGCTAACAAATGTTTGTACTTATGCATTCCCATGGGTAAAAATAAATAATAGCATTG
TTAAAGATAGTTATTACCAAAAAAAGAGAGTTATTACAAATAAATATGTCTCTTTATTTTTAAAAATGAAATCTT
AATTCATTTACTCTATTTGATGATAAACTATAAATTCATTGAAAATGTGAATTCATTATGGGTAGCCTTTTTTAC
CAATTATAAGGAAAAATTTACAGCAGTGAACATGAACATTCAGTTAGCTTCTCAGTCTCTCCATCTTAAAGATCA
TTTATCAGAGGAGGTTTCAGCATTTTTTGCAGCATAACTTTTCATGAGTCTGTATTACTAATGGATAAGTCAAATC
CATCCTGCAGTTCTACAGTTTGAAGATCTGGACTCAGAATAAATGTAATATTTATACTTGTGTTCCAGAATGT
TATTTTACATTTTATGTTCAATAAGAACACTTTTTTAAAGACGTATATTCAACATAAAATCAGCTATCAGACTTC
AGATTAGACTTTTATTTATGTGGGTCTATAATAATTGTATTTTCAAGAGGTTTTTACTATATTTGTATTGGCCTGG
TTTTCTCAGACGATTTTGGACAAATCATTAGAACTGGGCATCATATCCACAGTTATGTAAGGCAGTGATATACT
ATAAGGATAAAACAAAGTCAAGTCCATAAAGCAATAATCCCTCAGAAGGAAAGTCCCTTACTTTTACATATTAATA
TTTAGTAATTTTTCTGCTTCTAAAAAGTGAGAGTATCACACCCTAAATGAACACTGTCTACTAAGAGACATCATT
CCATTTCCACAAATGAAGATTTTTATTCCAAAGAAACGAGTTTACTGATTGGAGCATAGGGCTTGTGTTATTTTTA
TTCAAGCTTTTAGTAATAGCCTTGAATTTATTATTTTTCTTATAGGCTTTTTGTTAAAAATAGTGAAGGAACAAAT
GTTAAAGGGTAAGATAATTTCCCTGCAAAAGGACACAGAAGGCAGTCTTAAGAAGATGAATGGATGAGAGAAGGG
AGAGAATAAAATGCAATAACGAGCCAGCATTACTATGTATTTTCTCCTCACCTGCTCTCCATATTTAGGTCAC
TTACCAGTTTCTGTGCCCTTTTGGAGCTTTTGTGAGGGCTTCATTCTCACCTGTATTTCTTTAGCCCTAAAT
GACACTCTCTCCAAAAATCCATTCCATTGTCTGTGGACCAAGATGTTCTATGTAATTCAGAAGCAGAAGCTCTTGG
CTAAAGGGCTAGTGTGGCCTTCAGAAAACATTCAATTATTTTCTCCCTACACCTTTGTGAGTTTGAAACAGTGA
GAAAAAAGGTATGTTGATAAGAAAACCTATATTGCTAGGTAGAATTTGTACTTGTGTTTCTTGGTAGCAGTTTTGA
AATATTCTGTACAGTACGTTTCTATTGTTTAAATAATAAATTCAAAAATATTTCTAAAACCTTAAACCAACTATG
CCAAGCATTAAAGATAAAACAAATATGATGTTCTTTGACGTAAATCAACGTGATGATTCTTTACATGTAAACACAT
TTTAGTGTTTCTGGTTTTGTCAATTTTTGTTGTTGTTGTTGTTGTTGTTGTTTATTACTCTATACCCTTTAGCAAAATAC
AGTTTTAAATTTTTTATTGTTTTTAGTAGTTTTCCCAACTTTAAGACTTATCTAATTTAACTGAGAAAGAAAGCCTT
TTTCATATATATATATATTGGATTTCTAAGGATGGTGGTTTGAGCCTTGATTAGACTTTTGATGTGCTAAGCCAG
ACAGGCAGTCTGTACATTGATGGCCATCACAATGCAGCTTTGGTTTAATTTAATTCAGGCCTGCTGCTGAGTTAT
GCACAGACTTTTTGTTGACCAAAATAAAATATAAAGGGTTTTCTCTGTTTGACATTTGTGTTCAATTTTTTCTCT
TTATGTATTACATTTTAACCTATATTAAATAAATGTTTAAATGATAATTTGCTTATGTCTTATAAACTCAGCAT
AAGAAAAAT

1194/6881
FIGURE 1114

MAELGLNEHHQNEVINYMRFARSKRGLRLKTVDSQDLKESRLVEDTFTIDEVSEVLNGLQAVVHSEVESELIN
TAYTNVLLLRQLFAQAEKWYLKLQTDISELENRELLEQVAEFEKAEITSSNKKPILDVTKPKLAPLNEGGAELL
NKEILRLQEENEKLKSRLKTIEIQATNALDEKSKLEKALQDLQDQGNQKDFIKAQDLSNLENTVAALKSEFQKT
LNDKTENQKSLEENLATAKHDLRLVQEQQLHMAEKELEKKFQQTAAAYRNMKEILTKKNDQIKDLRKRLAQYEPED

1195/6881
FIGURE 1115

AGATGACGTGCGGCTCGTGGGGCAGCTCGGCAGCATGGCGTCCGTGACGCTGAGCGAGGCGGAGAAGGTGTACAT
CGTG CATGGCGTCCAGGAAGACCTCCGTGTGGATGGCCGTGGCTGTGAGGACTACCGATGTGTGCGAAGTGGAAAC
TGATGTGGTGTCCAACACTAGTGGGTCCGCCAGGGTCAAGCTGGGTACACAGACATCTTGGTGGGAGTGAAAGC
AGAAATGGGGACGCCGAAGCTGGAGAAACCAAATGAAGGCTACTTGGAGTTCTTTGTTGACTGTTTCAGCCAGTGC
TACCCCTGAATTTGAAGGTAGAGGAGGTGATGACCTTGGCACCGAGATCGCTAACACCCTCTATCGGATATTTAA
CAATAAAAGCAGTGTGCGACTTAAAGACCCTCTGCATTAGTCCTCGGGAGCACTGCTGGGTTCTCTATGTGGATGT
GCTGCTTCTGGAATGTGGTGGAAATTTGTTTGATGCCATTTCCATTGCTGTAAAGGCTGCTCTCTTCAATACAAG
GATACCAAGGGTTCGAGTTTTGGAGGATGAAGAGGGGTGCAAGGACATTGAATTGTCAGATGACCCTTATGACTG
CATACGACTAAGTGTGGAGAATGTCCCCTGCATTGTCACTCTGTGCAAGATTGGCTATCGGCATGTGGTGGATGC
TACTCTTCAGGAGGAGGCCTGCTCGCTGGCCAGCTTGCTGGTGTGCGTGACCAGCAAGGGAGTTGTGACGTGCAT
GAGGAAAGTGGGGAAGGGCAGCCTGGACCCAGAGAGCATCTTCGAGATGATGGAGACTGGCAAGCGTGTGGGCAA
GGTACTGCATGCCTCCTTGAGAGTGTTGTGCACAAGGAAGAAAGCCTGGGGCCCAAGAGACAGAAAGTTGGATT
CCTGGGATGATTTGCACATCAACTGCTCAACTGTGGATTGTTTTTTACTTTTCCTTTTAAACCGGTTTCGTATATA
TTTTTCTTCGCTGTTACGAATTTACAGCAGCATTTGTACATGTAAAATTAAAGGCTATTTTCTGGTCTGGTT

1196/6881
FIGURE 1116

MASVTLSEAEKVYIVHGVQEDLRVDGRGCEDYRCVEVETDVVSNTSGSARVKLGHTDILVGVKAEMGTPKLEKPN
EGYLEFFVDCSASATPEFEGRGDDLGTETIANTLYRIFNNKSSVDLKTLCISPREHCWVLYVDVLLLECGGNLFD
AISI AVKAALFNTRIPRVRVLEDEEGSKDIELSDDPYDCIRLSVENVPCIVTLCKIGYRHVV DATLQEEACSLAS
LLVSVTSKGVVTCMRKVGKGS LDPESIFEMMETGKRVGKVLHASLQSVVHKEESLGPKRQKVGF LG

1197/6881
FIGURE 1117

CACCGTGCCCAAGAGAAAGGCTGAAGGGGATGCTAAAGGAGATAAAGCCAAGGTGAAGGATGAACCACAGAGAAG
ATCCATGAGGTTTTCTGCTAAACCTGCTCCTCCAAAGCCAGAGCCCAAGCCTAAAAAGGCCCTGCAAAGAAGGG
AGAGAAGATACCCAAAGGGAAAAAGGGAAAAGCTGATGCTGGCGAGGAGGGGAATAACCCTGCAGAAAACGGAGA
TGCCAAAACAGACCAGGCACAGAAAGCTGAAGGTGCTGGAGGTGCCAAGTGAAGCATGTGCATTTTTTATAACTG
TGTACTTTTGATGACTGTACAGCTTGAAATACTATTTTTATCAAGTTTTATAAAAATGCAGAATTTTGTCTTACT
TTTTTTTTTAAAGCTATGCTATTAGCACACAGAACTTCAGTGTGTGTGTAGGGAGAAGGGGCATATGTCACTA
ATAGAATGTCCCAAAGCTGGATTGATGTGGGGAAAACACCTTTCCCTTCTAGCTTTGAGAGACTTCCTCTTGGC
TCCAGGAGGAGGGATTCCCTGACTTTGACACAGATGGTCACCTTGGCACAAAAGCCTTGTAGGATGGAAAAACA
AATTTGTTTTTATGTCCTCTTCTCCCTTTCCATCCTTCAGCATAGACTTAACTCCCTTAAGCCCAGACATCTGTT
GGGACCTGACCCCCAGTCATTGGTTACCAGTGTGTCAGGCAATCTGGACTTTCCAGTGATGCCACTGAGATGGCA
CCTGTCAAAAACAGCGGTGGTTCCATTTCTAGACTGTGGATCTTCAGATAAATTCTGCCATTTTCATTTCACTTCC
TGAAACTCAGGGTCGGCTTGTGAAAAGCTGTTAAACAACATGCTAAATGTGAAATGTCAACCCCTCACTCTAAACT
TTCCCTGTTTCAGAGCATCAGACGAAAACCTTCATTGGGTTTTATAGTGGCTTTCAGATTTTTGGTAGTCAATTGAA
GAAGGGAGTTTTAAATTTGTTGTATACTGTTTCATGATTGTCTGCCCATGTCCTGCCTGAAATACCATGATTGTTT
ATGGAAAGTATCTTTAATAAAGCTGGATACAGTTTGGC

1198/6881
FIGURE 1118

VPKRKAEGDAKGDKAKVKDEFQRRSMRFSAKPAPPKPEPKPKKAPAKKGEKIPKGKKGKADAGEEGNNPAENGDA
KTDQAQKAEGAGGAK

FIGURE 1119

[illegible]

1200/6881
FIGURE 1120

GGGACTGCGAGCCAGGGACTCGGGCCGCGGGGCGGGAAGAAGTGGGGCAGCGCTTGGCCAGGCCGAAAGGACTTT
GGGGGTGGGGGCTGGGAGTCCGTGTCTCGAATGAGGGAGGAGAGGTGGAGTTGCCGGGGCTCAGGCCCGGCCTCG
AGCATGGGCGGATGAGAGGAGTCGGGAGCCGAGGCCTAGGGTCCTTCGGGTGAGGGGAGACGGAGCCAGCGAGGA
GATGGAGCAGAAGCTTGTGGAGGAGATTCTTCAAGCAATCACTATGTCAACAGACACAGGTGTTTCCCTTCCTTC
ATATGAGGAAGATCAGGGATCAAACTCATTGAAAAGCTAAAGAGGCACCATTTCGTACCCGTTGGAATAGCGGG
TTTTGCAGCAATTGTTGCATATGGATTATATAAACTGAAGAGCAGGGGAAATACTAAAATGTCCATTCATCTGAT
CCACATGCGTGTGGCAGCCCAAGGCTTTGTTGTAGGAGCAATGACTGTTGGTATGGGCTATTCCATGTATCGGGA
ATTCTGGGCCTTTAGTTAGATGTCTTATTATTAAAGTTACCTATTATTGTTGGAAATAAACTAATTTGTATGGGT
TTAGATGGTAACATGGCATTTTGAATATTGGCTTCCTTTCTTGACGGCTTGATTTGCTTGGTGACCGAATTACTA
GTGACTAGTTTACTAACTAGGTCATTCAAGGAAGTCAAGTTAACTTAAACATGTCACCTAAATGCACTTGATGGT
GTTGAAATGTCCACCTTCTTAAATTTTAAAGATGAACTTAGTTCTAAAGAAGATAACAGGCCAATCCTGAAGGTA
CTCCCTGTTTGCTGCAGAATGTCAGAT

1201/6881
FIGURE 1121

TGGTGCTGACCAGCCACTTACCCACAGGAGCCACATCCAACCTCGGCTCTCAGCTGAGGAAGCAGCCCATCGCCTT
GCACGCCTGGACACTAACTCACCTAGCATCTTCCAGCACCTGGACGAACTCAAGGCATTCTTCGCAGAGGTTGTC
AGTGATGGTGTACCCCTGGTGCTAGCCCTGGTCCCCACCGGCAGCCCCACTCCTTCATCACCCAGGGTTCCCCA
GACCTGTTGGTGACTGTGAGTGCCAGTGGGCTGCTGGGCACCCACAGCTGGTTGCCCTATGACCGCAACATAAGC
AACTACTTCAGCTTCAGCAAAGACCCACCATGGGCAGCCACAAGACGCAGCGACTGCTGAGTGGCCCCGTGGGTG
CCAGGCAGTGGTGTGAGTGGACAAGCACTGGCAGTGGCCCCGGATGGAAAGCTGCTATTACAGCGGTGGCCACTGG
GATGGCAGCCTGCGGGTGACTGCACTACCCCGTGGCAAGCTGTTGAGCCAGCTCAGCTGCCACCTTGATGTAGTA
ACCTGCCTTGCACTGGACACCTGTGGCATCTACCTCATCTCAGGCTCCCGGGACACCACGTGCATGGTGTGGCGG
CTCCTGCATCAGGTGTGCCTCGTGGGCAGCTCTGTGGGGCCCCCGTAGCCAGACCTGCAGCCCATCCGTCCCTC
AGTGGCCTTCCAGTCCTGTCCTCCTCTAGTC

1202/6881
FIGURE 1122A

AGTTGCAGCGGCCGGGGAAGATGGTGGAGGACGGCGCGGAGGAGCTGGAGGATCTGGTGCACCTTCTCCGTGTCTG
AGTTGCCTAGTCGCGGCTACGGCGTCATGGAGGAGATCCGGCGGCAGGGCAAGCTGTGCGACGTGACCCTCAAGA
TTGGGGACCACAAATTCAGTGCCACCGGATTGTCTTAGCAGCCTCGATCCCGTATTTCCATGCTATGTTTACAA
ATGACATGATGGAGTGCAAGCAGGATGAGATTGTAATGCAAGGAATGGACCCAAGTGCCCTGGAGGCTCTGATCA
ACTTTGCCTACAACGGCAACCTTGCCATTGACCAGCAAAATGTCCAGTCATTGCTGATGGGGGCGAGCTTCCTGC
AGCTGCAGAGCATCAAAGACGCCCTGCTGCACATTCCCTTCGAGAACGGCTTCACCCAAAAAACTGCCTGGGTGTGC
GCCAGTTTGCTGAGACAATGATGTGTGCTGTGCTGTACGACGCTGCCAACAGCTTCATCCACCAGCACTTTGTGG
AGGTGTCCATGTGAGAAAGATTCCCTGGCCCTGCCCTTGGAAGACGTGCTTGAGCTGGTGTCTCGGGATGAGCTGA
ATGTCAAATCTGAGGAGCAGGTCTTTGAAGCTGCATTGGCCTGGGTGAGATACGACCGGGAGCAGAGGGGTCCCT
ACCTGCCTGAGCTGCTGTCCAATATCCGCCTGCCCTCTGTGCGCCCCAGTTCCTTTTCCAGACAGAGTACAGCAGG
ATGACCTGGTGCCTTGCTGCCACAAATGCAGGGACCTGGTAGACGAAGCAAAGGACTACCACCTCATGCCAGAGC
GCCGGCCCCACCTGCCAGCTTTTCAAGACCCGGCCACGCTGCTGCACATCCATCGCTGGACTTATCTACGCTGTAG
GGGGCCTCAACTCAGCAGGTGATTCCCTGAATGTGGTGGAAAGTGTTCGACCCCATTGCCAATTGCTGGGAGAGAT
GCCGTCCCATGACAACAGCCCGCAGCCGCGTTGGCGTGGCTGTGGTGAACGGGCTTCTCTATGCCATCGGAGGAT
ATGACGGCCAGCTACGGCTGAGCACTGTGGAGGCCTACAACCCGAGACAGACACATGGACCAGAGTGGGGAGCA
TGAATAGCAAGAGAAGTGCCATGGGGACAGTCGTGCTGGATGGGCAGATCTACGTCTGTGGGGGCTACGATGGCA
ACTCTTCCCTCAGCTCCGTGGAGACCTACTCACCTGAGACGGACAAATGGACAGTGGTGACCTCGATGAGCTCGA
ATCGCAGTGCTGCTGGGGTTACAGTCTTTGAGGGCAGGATATATGTGTGTCAGGCGGCCATGATGGTTTGCAGATCT
TCAGCAGTGTGGAACACTACAACCACCACACAGCCACCTGGCACCTGCAGCTGGCATGCTCAACAAGCGCTGCC
GGCACGGAGCCGCCCTCCCTGGGGAGCAAGATGTTTGTCTGCGGGGGCTACGATGGCTCTGGCTTCCTCAGCATTG
CCGAGATGTACAGCTCTGTGGCAGACCAAGTGGTGCCTGATTGTCCCCATGCACACGCGCAGGAGCCGGGTCTCCC
TGGTGGCCAGCTGTGGGCGCCTCTACGCTGTTGGGGGCTACGACGGACAGTCAAACCTAAGCTCAGTGGAGATGT
ATGACCCAGAGACAGACTGCTGGACATTATGCCCCCATGGCGTGCCATGAGGGAGGGGTGCGTGTGGGCTGCA
TCCCTCTCCTCACCATCTAAGGCAGAGGATGGGATGTGGTGGGGCAGGGATCTGGTACAGACATAGGCGCTTCCT
TCCAGGAACAGTCCCTCAGGAGAGGCAGTGGACCAGAAGAGATGGCGAAACGTGAGCTCGCCGGAGGTACAGTTT
TTCCAGGTGCTTAAGCCCTCCCCACTGTGCCACCCTTGTGACCTTCAGGCTTGGGTTCATCAAGATGCACAGCAT
GGAACACAAGCTCCTCTGGATCCTGCAGCTGGTGACATGGAAGTGTTCCTGCTGTCACATGAACACAGGCTCCAT
CCAGGCCAGCTCCTACCCACCGCCTCTCTGTGGGCCAGCTGTTACAGAAAGGCCTTCATCTGATGCTCCCCAT
CGCCTGCTTGCTCTCCAGCCGAGTCTGGCCAATTTGCCATGGGGAGGCTGCAGTGTCCAAGCCTGCTGGAAACTG
GGATGTAGCTGGGGACGAAAGGACAGACCCAAGCGTTCTCCCTGCCTGAGATGGTGTGGCCACAGCAGTGGAAAGG
CTGCACACAGGCACATTCCCTTCTTCCACAGTGGGGCACCAAGGATTCTGTCTCATTGCTGGGTAAAGCAGGGAGA
AGAGAAGTTTTTCCCCATGTCTAATTTTGGGATTTTTCAGTGAGGCCTTTTGTCTGTCCAGGAGAACAGAAAGGGAAA
AAAAGATACTTGAAAGAACTGAAGGAAATTTAAACAAAAGAAACACTTGAAAGAACTGGAAAGAAAAATAATTT
TTTTATGTGAACAAATTTTGCAAGAAGAAAAAGCATAAAAAGACACTAACGGCAAATCTATGTTTAAATGGAAAA
TCGTCTAACTGGAGAAGGGCGGTATCCACCCACATTCCGGATCCCAGGGTCCTGAGGCCTCGCATTGAGCTGGGG
GTTCCCTCTGAGCCCCAGTGTGTGTGGAATCAGTGCACTCTTGACTGGGCCTGTAGTAAGGTGCTCATGGGGTTT
GTCTTCTCACCCACCATCAGAGGACTTTTAAATCATAGGCGTAGAGAGTTAGGCTATCTGCTGAATTACTGCCA
CTCTTCTTGGTGGGGGCTCCTAGCTGTGGCTGGGGGCTCCAGGCGCCCTGTGATTACCTCCTACTGCCACCATG
GCGCTCATTAGATTCCCACTCTACTAACATTGCTTCCTTTTTTGACCAGCAGGAAACAGCAGGTCTGGCCAG
ATTCTCACTTGCCCATCAATCTCGTTCTTGGATGATTTCCCTCATTGTGATGCTTCTGGGGCACGTTGACCATAT
GCACCTCTAGAACCTAACCAGGGCTTCCTTCTACCAGCTGTGGGCGGGCTTGGTCTGGTAACCTTGTCTGCTCTG
CCATTCCACTGCTCCTCCATCCACTCGCCAATCCCAAGAGTCTGGCCTCCCTCCAGCCCTGGGCAGACTGACCAG
CAAGGTGGACCTTTACATTCAAGCACAGCTGGCTTTTATGACATAAAGAACTAAAGGCCGAAAGAATCTCTTGCT
GCTGCAAAGAACAGATTTTATATTTCTTCTCTAATCTTGGCAAAATGACCTTTACCTTTTGGAAAGATTTTCATAT
TGCTTCCTCCTCCCTGGATAGGACCTAATGTAGCACAGCGGGACTCAAAGAGGAGGACATTTTCTCTTGCCAGTG
CACTGGGCAGTGGGGCTGTCTTCAACTGCTGCTGCCAAAATGGTTTTCTAAAATTCTTCCAGTAGAGACTAAA
AGAAGATTCAATTCCTGTAACCCAAGACTGAGTCTTAGGGCTCCAGTCTCCACCTGCTTGGTTTTCTATCCTTTG
CTGCCTGCCTGGGGTGGCCTGGAAGCCTGTTTCAGAAAGGCACAATGTGGAGCCTGGGGTGTCTCCCCCACCACAG

1203/6881
FIGURE 1122B

GACCGTCAGGTTTACCAGTGTGTGCAATCGCCATGTATTCAGAGGGAAGTACCTTTGTTACCTACAACCTTAGGAG
CTAGGCCTCTGCTACAAGCACTTGAAAATGATATTTTATTTTAAACGTCTCAACAATCTGATATCGGATGTCGT
TTAACCTGGGCTCGTGGTAGGGCTCCAGCATTTCTCCCTCCTTCCTGGTTTGCCTGTAGGGGTAGACTCGGAAGG
TGGGTGGGGTGTGCATTTCTGTAGGAGTGTATCAGTGCTTGTCTTATTATAAGCCCCTTTCTTTTGTGAATTT
GAAGTAGCACCAACAAGCCTGGATTGTGAAGGTATTAAGAATCGGTCTGTGGGCTACTGAGTGGGTCCTTAGGAT
ACTGGCCCAGATTTTGCCACTGGGTATGGCAGATCATTTTCTACCATGGCCTGCTGCTCTTGTAGTGGACTTCCT
GAGTCCAATCCCACCTCCTGGTGTAGAATTTACTGCTGCACCTGAGGTCGATGTTTCAAAGTAAGATCAAGCC
AGTGTTTTGATCTGGGCTCTGAGCACAAGTCAGGAAACACCAACATATTCACACTCTCCCAGTAGGTTCCCTCAGT
CCGATGGTGAAATGGCTATTTCGTAAATGGCTGGTCTGGCTCTTTGGTGTTGGAGCCTTTCCAATAGCCCCATGAAA
AGAAGCATCACCCAAGGATATTGTAAAAAGGATGTAACAAGGAGATAGGGTAGACATTGTACTCAGTGGGCCTTG
GGCCTAGCCCAGCTCTGAGCAGAGGACTGTGGCATTCACTGTCCTTGAGTGTTTACCTTCTTGATAACACAC
GGGCCTTCTCTTCTGGATTTTCATCAGAGATTACAGCCAGATGGGGGCTGAAGACCATCCTCTTGACCACAGAGGT
GTGACTGTGGGAATTCCTCCCAATTTATGGTTTTCCAGAAAATCTTAGTTCCTTTTATTTATAGAATGCATGTCT
TTTGTGTTAAGAAACCAAAGAGAAATAAAGAGAACTCCTAAT

1204/6881
FIGURE 1123A

AGAGAGGGAGGGCGCCACGCACCGGACTGCGGGCCGAGAGCGCGCACGCCGCGCTCCGCCCTGCTGCCGCCCCC
GTCGCGCGCCGCCGCCGCCGCGCAGCTTGGGAGGTGCTGCCACCACAGGTACCTGCACATGTTGTTCTTTGTTCAG
TGCTGTCAAGTGTGTGCCAGGGTGATCCATGGTCACTTTCCGGGATGGCAGCAAGGTGACTTCGGCTGAGGATGA
CCCTGACTGAAAGGCTGCGTGAGAAGATATCTCGGGCCTTCTACAACCATGGGCTCCTCTGTGCATCCTATCCCA
TCCCCATCATCCTCTTCACAGGGTTCTGCATCTTAGCCTGCTGCTACCCACTGCTGAAACTCCCCTTGCCAGGAA
CAGGACCTGTGGAATTCACCACCCCTGTGAAGGATTACTCGCCCCACCTGTGGACTCTGACCGCAAACAAGGAG
AGCCTACTGAGCAGCCTGAGTGGTATGTGGGTGCCCGGTGGCTTATGTCCAGCAGATATTTGTGAAGTCCTCAG
TGTTTCCCTGGCACAAGAACCTCCTGGCAGTAGATGTATTTCTGTTACCTTTGTCCCGGGCATTCCAACCTGGTGG
AGGAGATCCGGAACCACGTGCTGAGAGACAGCTCTGGGATCAGGAGCTTGGAGGAGTTGTGTCTGCAAGTGACCG
ACCTGCTGCCAGGCCTTAGGAAGCTCAGGAACCTACTCCCTGAGCATGGATGCCTGCTGCTGTCCCCTGGGAACT
TCTGGCAGAATGACTGGGAACGCTTCCATGCTGATCCTGACATCATTGGGACCATCCACCAGCACGAGCCTAAAA
CCCTGCAGACTTCAGCCACACTCAAAGACTTGTTATTTGGTGTTCCTGGGAAGTACAGCGGGGTGAGCCTCTACA
CCAGGAAGAGGATGGTCTCCTACACCATCACCCCTGGTCTTCCAGCACTACCATGCCAAGTTTCTGGGCAGCCTGC
GTGCCCCCCTGATGCTTCTGCACCCAGCCCCAACTGCAGCCTTCGGGCGGAGAGCCTGGTCCACGTGCACTTCA
AGGAGGAGATTGGTGTGCTGAGCTCATCCCCCTTGTGACCACCTACATCATCTTGTTTGCCTACATCTACTTCT
CCACGCGGAAGATCGACATGGTCAAGTCCAAGTGGGGGCTGGCCCTGGCTGCCGTGGTTCACAGTGCTCAGCTCGC
TGCTCATGTCTGTGGGACTCTGCACACTCTTCGGCCTGACGCCCCACCTCAATGGCGGCGAGATTTTCCCCTACC
TTGTGGTGGTTATTGGGTAGAGAATGTGTTGGTGCTACCAAGTCTGTGGTCTCAACCCCGGTAGACCTGGAGG
TGAAGCTGCGGATCGCCCAAGGCCTAAGCAGCGAGAGCTGGTCCATCATGAAGAACATGGCCACGGAGCTGGGCA
TCATCCTCATCGGCTACTTCACCCTAGTGCCCGCCATCCAGGAGTTCTGTCTCTTTGCTGTGCTGGGGCTGGTGT
CTGACTTCTTCTTCAGATGCTGTTTTTTACCACCTGTCTGTCCATTGACATTGCGCCGGATGGAGCTAGCAGACC
TGAACAAGCGACTGCCCCCTGAGGCCTGCCTGCCCTCAGCCAAGCCAGTGGGACAGCCAACGCGCTACGAGCGGC
AGCTGGCTGTGAGGCCGTCCACACCCACACCATCACGTTGCAGCCGTCTTCTTCCGAAACCTGCGGCTCCCCA
AGAGGCTGCGTGTTGTCTACTTCTTGCCCCGACCCGCTGGCACAGCGCCTCATCATGGCTGGCACCGTTGTCT
GGATTGGCATCCTGGTATACACAGACCCAGCAGGGCTGCGCAACTACCTCGCTGCCCAGGTGACGGAACAGAGCC
CATTGGGTGAGGGAGCCCTGGCTCCCATGCCCGTGCTAGTGGCATGCTGCCCCCAGCCACCCGGACCTGCCT
TCTCCATCTTCCACCTGATGCCCTAAGCTACCTGAGAACCAGACGTCGCCAGGCGAGTCACCTGAGCGTGGAG
GTCCAGCAGAGGTTGTCCATGACAGCCAGTCCAGAGGTAACCTGGGGGCTGAGGATGAGGAACCTTTGGAGGA
AATTGTCTTCCGCCACTGGCCGACGCTCTTCAGCTATTACAACATCACACTGGCCAAGAGGTACATCAGCCTGC
TGCCCGTCATCCAGTCAAGCTCCGCTGAACCCGAGGGAGGCTCTGGAGGGCCGGCACCCCTCAGGACGGCCGCA
GTGCTGGCCCCCACCAGGGGCCATACCTGCTGGGCACTGGGAAGCAGGACCCAAGGGCCAGGTGGGGTGCAGG
CCCATGGAGACGTACGCTGTACAAGGTGGCGGCGCTGGGCCTGGCCACCGGCATCGTCTTGGTGTGCTGCTGC
TCTGCCCTTACC GCGTGCTATGCCGCGCAACTACGGGCAGCTGGGTGGTGGGCCGGGCGGAGGCGCGGGG
AGCTGCCCTGCGACGACTACGGCTATGCGCCACCCGAGACGGAGATCGTGCCGCTTGTGCTGCGCGGCCACCTCA
TGGACATCGAGTGCTTGGCCAGCGACGGCATGCTGCTGGTGAGCTGCTGCCCTGGCAGGCCACGTCTGCGTGTGGG
ACGCGCAGACCGGGGATTGCCTAACGCGCATTCCGCGCCAGGGCAGCGCCGGGACAGTGGCGTGGGCAGCGGGC
TTGAGGGCTCAGGAGAGCTGGGAACGACTTTCAGATGGTGGGAAGGCTGGTCCAGAGGAGCCTGGGGACAGCCCTC
CCCTGAGACACCGCCCCCGGGGCCCTCCGCCGCTTCCCTCTTCGGGGACAGCCTGACCTACCTGCTTAATTG
ACACCAACTTTTCAGCGCAGCCTCGGTCTCACAGCCCACTCAGCCCGAGCCCCGGCACCGGGCGGTCTGTGGCC
GCTCTCGGGACTCCCCAGGCTATGACTTCAGCTGCCTGGTGCAGCGGGTGTACCAGGAGGAGGGGCTGGCGGCCG
TCTGCACACCAGCCCTGCGCCACCCCTCGCTGGGCCCGGTGCTGTCCAGGCCCTGAGGACGAGGGTGGCTCCC
CCGAGAAAGGCTCCCCTTCCCTCGCTGGGCCCCAGTGCCGAGGGTTCCATCTGGAGCTTGGAGCTGCAGGGCA
ACCTCATCGTGGTGGGGCGGAGCAGCGGCCGCTGGAGGTGTGGGACGCCATTGAAGGGGTGCTGTGCTGCAGCA
GCGAGGAGGTCTCCTCAGGCATTACCGCTCTGGTGTCTTGGACAAAAGGATTGTGGCTGCACGGCTCAACGGTT
CCCTTGATTTCTTCTCCTTGGAGACCCACACTGCCCTCAGCCCCCTGCAGTTTAGAGGGACCCAGGGCGGGGCA
GTTCCCCTGCTCTCCAGTGTACAGCAGCAGCGACACAGTGGCCTGTACCTGACCCACACAGTGCCTGTGCAC
ACCAAAAACCCATCACAGCCCTGAAAGCGCTGCTGGGCGCTTGGTGACTGGGAGCCAAGACCACACACTGAGAG
TGTTCCGTCTGGAGGACTCGTGCTGCCTCTTACCCTTCAGGGCCACTCAGGGGCCATCACGACCGTGTACATTG

1205/6881
FIGURE 1123B

ACCAGACCATGGTGCTGGCCAGTGGAGGACAAGATGGGGCCATCTGCCTGTGGGATGTACTGACTGGCAGCCGGG
TCAGCCATGTGTTTGCTCACCGTGGGGATGTCACCTCCCTTACCTGTACCACCTCCTGTGTCATCAGCAGTGGCC
TGGATGACCTCATCAGCATCTGGGACCGCAGCACAGGCATCAAGTTCTACTCCATTACAGCAGGACCTGGGCTGTG
GTGCAAGCTTGGGTGTCATCTCAGACAACCTGCTGGTGACTGGCGGCCAGGGCTGTGTCTCCTTTTGGGACCTAA
ACTACGGGGACCTGTTACAGACAGTCTACCTGGGGAAGAACAGTGAGGCCAGCCTGCCCAGCAGATCCTGGTGC
TGGACAACGCTGCCATTGTCTGCAACTTTGGCAGTGAGCTCAGCCTGGTGTATGTGCCCTCTGTGCTGGAGAAGC
TGGACTGAGCGCAGGGCCTCCTTGCCCAGGCAGGAGGCTGGGGTGCTGTGTGGGGGCCAATGCACTGAACCTGGA
CTTGGGGGAAAGAGCCGAGTATCTTCCAGCCGCTGCCTCCTGACTGTAATAATATTAAACTTTTTTAAAAAACCA
TATCATCATCTGTCAGGCACTTTGGGA

1206/6881
FIGURE 1124

MTLTERLRREKISRIFYNHGLLCASYPIPIILFTGFCILACCYPLLKLELPGTGPVEFTTPVKDYSPPPVDSDRKQ
GEPTTEQPEWYVGAPVAYVQQIFVKSSVFPWHKNLLAVDVFRSPLSRAFLVEEIRNHVLRDSSGIRSLLEELCLQV
TDLLPGLRKLRLNLLPEHGCLLLSPGNFWQNDWERFHADPDIIGTIHQHEPKTLQTSATLKDLLFGVPGKYSVSL
YTRKRMVSYTITLVFQHYHAKFLGSLRRLMLLHPSPNCSLRAESLVHVHFKEEIGVAELIPLVTITYIILFAYIY
FSTRKIDMVKSKWGLALAAVTVLSSLLMSVGLCTLFGLTPTLNGGEIFPYLVVVIGLENVLVLTKSUVSTPVDL
EVKLRIAQGLSSESWSIMKNMATELGIIILIGYFTLVPAIQEFCLFAVVGLVSDFFLQMLFFTTVLSDIRRMELA
DLNKRLPPEACLP SAKPVGQPTRYERQLAVRPSTPHTITLQPSFRNLRLPKRLRVVYFLARTRLAQRLIMAGTV
VWIGILVYTDPAGLRNYLAAQVTEQSPLGEGALAMPVPVSGMLPPSHPDPAFSIFPPDAPKL PENQTS PGESPER
GGPAEVVHDSVPVEVTWGPEDDEELWRKLSFRHWPTLFSYYNITLAKRYISLLPVIPVTLRLNP REALEGRHPQDG
RSAWPPPGPI PAGHW EAGPKGPGGVQA HGDVTLYKVAALGLATGIVLVLLLLCLYRVLCP RNYGQLGGGPGRRRR
GELPCDDYGYAPPETEIVPLVLRGHLMDIECLASDGMLLVSCCLAGHVCVWDAQTGDCLTRIPRPGQRRDSGVGS
GLEAQESWERLSDGGKAGPEEPGDSPLRHRPRGPPPSLFGDQPDLTCLIDTNFSAQPRSSQPTQPEPRHRAVC
GRSRDSPGYDF SCLVQRVYQEEGLAAVCTPALRPPSPGPVLSQAPEDEGGSP EKGSPSLAWAPSAEGSIWSLELQ
GNLIVVGRSSGRLEVWDAIEGVLCCSSEEVSSGITALVFLDKRIVAARLNGSLDFFSLEHTALSPLQFRGTPGR
GSSPASPVYSSSDTVACHLTHTVPCA HQKPITALKAAAGRLVTGSQDHTLRVFRLEDSCCLFTLQGHSGAITTVY
IDQTMVLASGGQDGAICLWDVLTGSRVSHVFAHRGDVTSLTCTTSCV ISSGLDDLISIWDRSTGIKFYSIQQDLG
CGASLGVISDNLLVTGGQGCVSFWDLNYGDL LQTVYLGNKNS EAQPARQILVLDNAAIVCNFGSEL SLVYVPSVLE
KLD

1207/6881
FIGURE 1125

GTTCTCTTCGCCCCGGTCCCTGCCGCGCACAGGCCTCGGGGTGCGCGGGAGCACGATGGCGGCCGCTAGGAGACTC
ATGGCGCTGGCCGCGCGGCATCTCTCCGCGCCTGCAGCCGCTGGGTCCCCGCGCTGCTGGGCGACAGGGTCGCTCG
CGCGGCTTCTCTTCAAGCTGCGCCCACCCCGACCACACCAAGGAAGCCGCCGAGGCCGAGTCAGGGATGGCCCCC
GGCGGGCCTGGGGAAGGCGACGGAAGCTTGGTGAACGCTTCTAGGGACCTATTAAAAGAGTTCCACAGCCCCAAA
AATCTTCTCAACAGTGTGATTGGAAGAGCCCTCGGCATCTCACATGCAAAAGACAACTAGTCTACGTGCACACA
AATGGACCGAAGAAAAAGAAAGTCACACTGCACATAAAATGGCCCCAAGAGCGTGGAGGTAGAAGGCTATGGCAGC
AAGAAGATCGATGCTGAGCGGCAGGCTGCAGCTGCAGCCTGCCAGCTGTTCAAGGGTTGGGGTCTGCTAGGTCCC
CGGAATGAGTTGTTTGACGCAGCCAAATACCGAGTGCTAGCTGATCGCTTTGGCTCCCCTGCCGACAGCTGGTGG
CGTCCGGAACCCACCATGCCCCCTACTTCCTGGCGGCAGCTGAATCCAGAGAGTATTTCGACCAGGGGGACCTGGG
GGCCTATCCCGCTCTTTAGGCCGGAAGAAGAGGAGGACGAGGAGGAAGAGCTAGAAGAAGGGACCATAGATGTT
ACCGACTTCTTGTCCATGACCCAGCAGGATTCCACGCTCCACTCAGGGACTCAAGGGGGAGTTCCCTTTGAGATG
ACAGATGACGACAGTGCCATTAGGGCTCTGACCCAGTTTCCACTTCCCAAGAACCTTCTGGCCAAGGTGATTCAG
ATTGCAACGTCACTCTCCACAGCTAAGAACCTCATGCAGTTCCATACTGTGGGCACCAAGACCAAGCTGTCTACA
CTCACCCCTGCTCTGGCCCTGCCCATGACCTTTGTTGCCAAAGGGCGCCGCAAAGCAGAGGCTGAGAATAAGGCG
GCAGCCTTGGCCTGCAAGAACTGAAGAGCCTGGGCCTGGTGGACAGGAACAACGAACCGCTTACACACGGTTAC
GGAGCCGATGGCTTGACGTATTTTCATGGCAGTCAAGTCCAATGGCAGCGTCTTCGTCCGGGACTCCTCTCAGGTGC
ACCCGCTAGCTGTGCTGCTGCTGACCGACGGGGACGTGCACATCCGTGATGACGGGCGCCGGGCCACCATCTCAC
TGAGCGACAGTGACCTGCTGCGGCTGGAGGGTGACTCGCGTACCGTGCGGCTGCTGAAGGAGCTGCGGCGGGCCC
TGGGCCGCATGGTGGAGCGGAGCCTGCGCAGCGAGCTGGCTGCACTTCCCCCAGCGTACAGGAGGAGCACGGGC
AGCTGCTTGCGCTACTGGCAGAGCTGCTGCGAGGACCCTGTGGCAGCTTTGATGTGCGCAAGACAGCTGACGACT
GAGCCCTGCTTCTGCTGGGGCTGTGTACAGAGTGCAAATGTTTATTTAAAATAAAGTTCTATTTATCCCTTGTG

1208/6881
FIGURE 1126

MAAARRLMALAAGISPRQLGPRAGRQGRSRGFSSSCAHPDHTKEAAEAESGMAPGGPGEGDGSILVNASRDLL
KEFPQPKNLLNSVIGRALGISHAKDKLVYVHTNGPKKKKVTLHIKWPKSVEVEGYGSKKIDAERQAAAAACQLFK
GWLLGPRNELFDAKYRVLADRFGPSADSWWRPEFTMPPTSWRQLNPESIRPGPGGLSRSLGREEEEEDEEEEL
EEGTIDVTDFLSMTQQDSHAPLRDSRGSSFEMTDDDSAIRALTQFPLPKNLLAKVIQIATSSSTAKNLMQFHTVG
TKTKLSTLTLLWPCPMTFVAKGRRKAEAEENKAAALACKKLKSLGLVDRNNEPLTHGYGADG

1209/6881
FIGURE 1127

CGAAAGGCCGGCCTGGCTGCGACAGCCTGGGTAAGAGGTGTAGGTCGGCTTGGTTTTCTGCTACCCGGAGCTGGG
CAAGCGGGTGGGAGAACAGCGAAGACAGCGTGAGCCTGGGCCGTTGCCTCGAGGCTCTCGCCCGGCTTCTCTTGC
CGACCCGCCACGTTTGTGTTGGATTAACTTTCAGGTTGCCGGCGCCCGCCCGCTGGCCTCGCGGTGTGAGA
GGGAAGCACCCGTGCCTGTGGCTGGTGGCTGGCGCCTGGAGGGTCCGCACACCCGCCCGCGCGCGCTTGCCC
GCGGCAGCCGCGTCCCTGAACCGCGGAGTCGTGTTTGTGTTTGACCCGCGGGCGCCGGTGGCGCGCGGCCGAGGC
CGGTGTGCGCGGGGCGGGGCGGTTCGCGGCGGAGGCAGAGGAAGAGGGAGCGGGAGCTCTGCGAGGCCGGGCGCCG
CCATGGAACTGGGCCCCGAGCCCCCGCACCGCCGCGCCTGCTCTTCGCCTGCAGCCCCCTCCCGCGTCGCAGC
CCGTCGTGAAGGCGCTATTTGGCGCTTCAGCCGCGGGGGACTGTGCGCTGTCACCAACCTGACCGTCACTATGG
ACCAGCTGCAGGGTCTGGGCAGTGATTATGAGCAACCACTGGAGGTGAAGAACAACAGTAATCTGCAGAGAATGG
GCTCCTCCGAGTCAACAGATTTCAGGTTTCTGTCTAGATTCTCCTGGGCCATTGGACAGTAAAGAAAACCTTGAAA
ATCCTATGAGAAGAATACATTCCCTACCTCAGAAGCTGTTGGGATGTAGTCCAGCTCTGAAGAGGAGCCATTCTG
ATTCTCTTGACCATGACATCTTTCAGCTCATCGACCCAGATGAGAACAAGGAAAATGAAGCCTTTGAGTTTAAGA
AGCCAGTAAGACCTGTATCTCGTGGCTGCCTGCACTCTCATGGACTCCAGGAGGGTAAAGATCTCTTCACACAGA
GGCAGAACTCTGCCCCAGCTCGGATGCTTTCCTCAAATGAAAGAGATAGCAGTGAACCAGGGAATTTTATTCTC
TTTTTACACCCCAGTCACCTGTGACAGCCACTTTGTCTGATGAGGATGATGGCTTCGTGGACCTTCTCGATGGAG
AGAATCTGAAGAATGAGGAGGAGACCCCTCGTGCATGGCAAGCCTCTGGACAGCTCCTCTCGTCATGAGAACTA
CAAACCTTGACAACCGATGCAAGCTGTTTGACTCCCTTCCCTGTGTAGCTCCAGCACTCGGTCACTGTTGAAGA
GACCAGAACGATCTCAAGAGGAGTCTCCACCTGGAAGTACAAAGAGGAGGAAGAGCATGTCTGGGGCCAGCCCCA
AAGAGTCAACTAATCCAGAGAAGGCCCATGAGACTCTTCATCAGTCTTTATCCCTGGCATCTTCCCCCAAAGGAA
CCATTGAGAACATTTTGGACAATGACCCAAGGGACCTTATAGGAGACTTCTCCAAGGGTTATCTCTTTCATACAG
TTGCTGGGAAACATCAGGATTTAAAATACATCTCTCCAGAAATTATGGCATCTGTTTTGAATGGCAAGTTTGCCA
ACCTCATTAAGAGTTTGTATCATCGACTGTGATACCCATATGAATACGAGGGAGGCCACATCAAGGGTGCAG
TGAACCTGCACATGGAAGAAGAGGTTGAAGACTTCTTATTGAAGAAGCCCATGTACCTACTGATGGCAAGCGTG
TCATTGTTGTGTTTCACTGCGAGTTTTCTTCTGAGAGAGGTCCCCGCATGTGCCGGTATGTGAGAGAGAGAGATC
GCCTGGGTAATGAATACCCCAAACCTCACTACCCTGAGCTGTATGTCTGAAGGGGGGATACAAGGAGTTCTTTA
TGAAATGCCAGTCTTACTGTGAGCCCCCTAGCTACCGGCCCATGCACCACGAGGACTTTAAAGAAGACCTGAAGA
AGTTCCGCACCAAGAGCCGGACCTGGGCAGGGGAGAAGAGCAAGAGGGAGATGTACAGTCGTCTGAAGAAGCTCT
GAGGGCGGCAGGACCAGCCAGCAGCAGCCCAAGCTTCCCTCCATCCCCCTTTACCCTCTTTGCTGCAGAGAACT
TAAGCAAAGGGGACAGCTGTGTGACATTTGGAGAGGGGGCCTGGGACTTCCATGCCTTAAACCTACCTCCACAC
TCCAAGGTTGGAGCCAGGGCATCTTGCTGGCTACGCCTCTTCTGTCCCTGTTAGACGTCCTCCGTCCATATCA
GAACTGTGCCACAATGCAGTTCTGAGCACCGTGTCAAGCTGCTCTGAGCCACAGTGGGATGAACCAGCCGGGGCC
TTATCGGGCTCCAGCCATCTCATGAGGGGAGAGGAGACGGAGGGGAGTAGAGAAGTTACACAGAAATGCTGCTGG
CCAAATAGCAAAGA

1210/6881
FIGURE 1128

GAATTCCGGCCATGAAAGACCCAAAGGAATGGCCACTCCCTGGGGCGGTGGTCACTGGTGCTCCTGCTGCTGGGCC
TGGTGATGCCTCTGGCCATCATTGCCCAGGTCTCAGCTACAAGGAAGCTGTCCTTCGTGCTATAGATGGCATCA
ACCAGCGGTCTCTGGATGCTAACCTCTACCGCCTCCTGGACCTGGACCCCAGGCCCACGATGGATGGGGACCCAG
ACACGCCAAAGCCTGTGAGCTTCACAGTGAAGGAGACAGTGTGCCCCAGGACGACACAGCAGTCACCAGAGGATT
GTGACTTCAAGAAGGACGGGCTGGTGAAGCGGTGTATGGGGACAGTGACCCTCAACCAGGCCAGGGGCTCCTTTG
ACATCAGTTGTGATAAGGATAACAAGAGATTTGCCCTGCTGGGTGATTTCTTCCGAAATCTAAAGAGAAGATTG
GCAAAGAGTTTAAAAGAATTGTCCAGAGAATCAAGGATTTTTTGC GGAATCTTGTACCCAGGACAGAGTCCTAGT
GTGTGCCCTACCCTGGCTCAGGCTTCTGGGCTCTGAGAAATAAACTATGAGAGCAATTTCAAAAAAAAAAAAAAA
AAAAAACCGGAATTC

1211/6881
FIGURE 1129

MKTQRNGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTMDGDPDTPK
PVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKRFBALLGDFFRKSKEKIGKEF
KRIVQRIKDFLRNLVPTES

1212/6881
FIGURE 1130

CGTGCGTGCGCGCGCAGATGTGGGCCCCGCGGGAGCAGCTACTGGGCTGGACTGCGGAAGCTCTGCCTGCCAAGG
ATTCTGCCTGGCCCTGGGAAGAGAAGCCTAGATATCTGGTTCCAGTGGCAGATGGGGCACTGGCCAGAGGGGTTA
GGAGGATTTGGACTCTCCTTGGGAGTCGCTGTGATACGGCCTTCAATTATAGTTGTCTTTCTTCTTGGAATTTCC
ACCACTTCCCTGAAACCACGAGCTGGAAGCTGAGACCAGCTGGTCACTGCTGGGCCTGCTAGGAGCCCCACACGGA
AGCTGCCCCACAGCCAGACACCAGAGCCTCAAAGGCCGCCATCTTGAAAAACCAACCCTGACCTCCACAATGATTG
ATTTTCAAATGTTGAACCAGCTTTGCAGAACTATAATAAACCCAAAGTGTGATACCCTGTCTCAAGTATTGTGGTG
ATCAAATAGGACCAGTGACTTTTCGAGGATGTGGCTGTGCTTTTCACTGAGGCAGAGTGGAAGAGACTGAGCCTTG
AGCAGAGGAACCTATACAAAGAAGTGATGCTGGAAAATCTCAGGAATCTGGTCTCATTGGAATCAAAGCCAGAAG
TCCATACCTGCCCTTCTTGCCCTCTGGCCTTTGGCAGTCAGCAGTTCCCTCAGCCAAGATGAGCTACACAATCATC
CTATTCCAGGTTTCCATGCAGGAAATCAACTCCACCCAGGAAATCCCTGCCCAGAGGATCAGCCACAGTCACAAC
ATCCTTCTGATAAAAATCACAGGGGGGCTGAAGCAGAAGATCAACGAGTGGAAGGAGGCGTCAGACCCCTTGTTTT
GGAGTACAAATGAAAGGGGGGCTTTAGTGGGTTTCTCTAGCCTGTTCCAGAGACCACCAATAAGCTCTTGGGGAG
GCAACAGAATATTAGAGATACAGCTCAGTCCAGCCCAGAATGCAAGCTCTGAGGAAGTAGACAGAAATTTCCAAGA
GGGCAGAAAACCCAGGGTTTGGAGCAGTCACGTTTGGGGAGTGTGCACTAGCTTTTAACCAGAAGTCAAACCTGT
TCAGACAGAAAGGCAGTCACAGCAGAAAAATCTTCAGACAAAAGGCAGTCACAGGTGTGCAGGGAGTGTGGGCGAG
GCTTTAGCAGGAAGTCACAGCTCATCATACACCAGAGGACACACACAGGAGAAAAGCCTTATGTCTGCGGAGAGT
GTGGGCGAGGCTTTATAGTTGAGTCAGTCCTCCGCAACCACCTGAGTACACACTCCGGGGAGAAACCTTATGTGT
GCAGCCATTGTGGGCGAGGCTTTAGCTGCAAGCCATACCTCATCAGACATCAGAGGACACACACAAGGGAGAAAT
CGTTTATGTGCACAGTGTGTGGGCGAGGCTTTTCGTGAAAAGTCAGAGCTCATTAAAGCACCAGAGGTGTCAAGTGA
CGGTCCCTTGGAGGAATGGTCTTTGCATCTGACTACTTCCCTCTGCAACTGTGTTCTTCCATTAGCTTCCATGA
CACTCTCCTGCTTTATTTTTTTTCTACATCTCTAGCCTTTGCTGTTTCCCTCTCCTACCCACCTTTAGATTTTACT
CAGAGTTCACTCTCCAGCCCTACAATCTGAGGGACACCTTTACCAGGTCCCTTCCCTAACCTCCAGTCCCAAAT
CCAAGATTCTTTAACACACTCTAAAAGTTCTTCAGACTCAGGACTTAAACATAGCCACGCCACCTTGGCCTTCA
ATGACAGGGATCTAGCAATGCTGCATCATCAGCCTTCCAATACCAGGTTTAAGGGTATTTTAAACACAGCTCCTC
TTAAATCCTCCAATCTCAGTACCCAGTGTTTTAGCCATGCTCGGGTGGCTAAATTACATCCAGGAATGGTGCCAG
GGCCTTTAGCCATTTGTCTCTCTCCTCACACTCCAGGGCCCATATGGCCCAGGTTCTGACAGTTTGCTTACTCCCT
TGGGCTGGGGCTAGCCCTACCTGATACCCTGTGTCAATGAGTGTACCTTGGAGAGCTATCCACTCAGGCCCCAGT
GCCTCTATTTGCTAAGGGACTCTGCCACAGAAAAGAAGGGGAGAGATGTTTCATGTAACCTCAAATACTTAGGCT
TGGTTTTGATGCTAGAGAGGAAAAAGGACTTGGAGAGAGAGAAGGAATGGCTGGTCCAGAGGCTTTTGTCCACTC
CCTCTCACTGGAAGTGGTTGATCTCCAGGGAATCCCCAAGGTTAGCCTGCTTAGGGGAAGGGCTAGGGGTACCTG
GAATGTAGGATCTCCCCATGCCTGGCCTACCACCCTAATGTGTCTGGAATTGGTGGGTTCTTGGTCTTGCTGAC
TTCAAGAATGAAGCCGTGGACCTCACGGTGAGTGTACAATTCTTAAA

1213/6881
FIGURE 1131

CAGCGTGCCTGCCAGTGTAGAGCCGGTGGAGCAGCTGGGCTCGGCGCTGAGGTTTCGCCCTGGCTACAACGACCC
CATGTCAGGGTTCGGAGCGACCTTGGCCGTTGGCCTGACCATCTTGTGCTGTCTGTCGTCACTATCATCATCTG
CTTACCTGCTCCTGCTGCTGCCTTTACAAGACGTGCCGCCGACCACGTCCCTCCAAGTGTGCCGCCCAGCTACC
CTGGACCAAGCTACCAGGGCTACCACACCATGCCGCCTCAGCCAGGGATGCCAGCAGCACCCCTACCCAATGCAGT
ACCCACCACCTTACCCAGCCCAGCCCATGGGCCCACCGGCCTACCACGAGACCCTGGCTGGAGGAGCAGCCGCGC
CCTACCCCGCCAGCCAGCCTCCTTACAACCCGGCCTACATGGATGCCCCGAAGGCGGCCCTCTGAGCATTCCCTG
GCCTCTCTGGCTGCCACTTGGTTATGTTGTGTGTGTGCGTGAGTGGTGTGCAGGCGCGGTTTCCTTACGCCCCATG
TGTGCTGTGTGTGTCCAGGCACGGTTCCTTACGCCCCATGTGTGCTGTGTGTGTCTGCCTGTATATGTGGCTTC
CTCTGATGCTGACAAGGTGGGGAACAATCCTTGCCAGAGTGGGCTGGGACCAGACTTTGTTCTCTTCCTCACCTG
AAATTATGCTTCCTAAAAATCTCAAGCCAAACTCAAAGAATGGGGTGGTGGGGGGCACCCCTGTGAGGTGGCCCCCTG
AGAGGTGGGGGCCTCTCCAGGGCACATCTGGAGTTCTTCTCCAGCTTACCCTAGGGTGACCAAGTAGGGCCTGTC
ACACCAGGGTGGGCGCAGCTTTCTGTGTGATGCAGATGTGTCCCTGGTTTCGGCAGCGTAGCCAGCTGCTGCTTGAG
GCCATGGCTCGTCCCCGGAGTTGGGGGTACCCGTTGCAGAGCCAGGGACATGATGCAGGCGAAGCTTGGGATCTG
GCCAAGTTGGACTTTGATCCTTTGGGCAGATGTCCATTGCTCCCTGGAGCCTGTATGCCTGTTGGGGATCAGG
CAGCCTCCTGATGCCAGAACACCTCAGGCAGAGCCCTACTCAGCTGTACCTGTCTGCCTGGAETGTCCCTGTCC
CCGCATCTCCCTGGGACCAGCTGGAGGGCCACATGCACACACAGCCTAGCTGCCCCAGGGAGCTCTGCTGCCC
TTGCTGGCCCTGCCCTTCCCACAGGTGAGCAGGGCTCCTGTCCACCAGCACACTCAGTTCTCTTCCCTGCAGTGT
TTTCATTTTATTTTAGCCAAACATTTTGCCTGTTTTCTGTTTCAAACATGATAGTTGATATGAGACTGAAACCCC
TGGGTTGTGGAGGGAAATTGGCTCAGAGATGGACAACCTGGCAACTGTGAGTCCCTGCTTCCCGACACCAGCCTC
ATGGAATATGCAACAACTCCTGTACCCAGTCCACGGTGTCTGGCAGCAGGGACACCTGGGCCAATGGGCCATC
TGGACCAAAGGTGGGGTGTGGGGCCCTGGATGGCAGCTCTGGCCCAGACATGAATACCTCGTGTTCCTCCTCCCT
CTATTACTGTTTACCAGAGCTGTCTTAGCTCAAATCTGTTGTGTTTCTGAGTCTAGGGTCTGTACACTTGTTTA
TAATAAATGCAATCGTTTGG

1214/6881
FIGURE 1132A

AGCGAACCATCGGGGCGGCCGGGAGCCATGTTGGAGCGGCGGGAGGCGGCAGCAGCGTCGGGGATGCTGTGGTGG
GGGCGGAAAAAGCCAGGGGCCACGCCGAGGGGCTCCGGCCGCGGAGTAGATGGTGCCAGAGGGCGGCGGGGG
TGCGGAGAGACAGGCGGAGGGGCGGGGGCCCGGGGCGGCGGCAGGGGCCGGGAGGGGGCCCCGAGCGGCGGGGCC
AGCCCAAGGCCCGACCGGGGCGGGGGCGGTGGAGGCCGTGCAGGGAGGCGGGAGATGATGCGGAGGCGGCCGC
CGTGGCGGGGCTCGGGGAACGGTCGACCCCCATACTCTGCTCCTTCTCCTCTCTTTGTTCCCCCTCAGCCAGG
AGGAGCTGGGGGGCGGTGGGCACCAGGGCTGGGACCCAGGCTTAGCTGCCACTACGGGGCCAAGGGCGCATATCG
GTGGCGGAGCCTTAGCTCTTTGTCCGAGTCTTCCGGGGTCCGGGAGGATGGGGGGCCTGGCCTGGGGGTCAGGG
AGCCTATCTTCGTGGGGCTCCGAGGGAGAAGGCAAAGCGCCCGGAATAGTCGAGGGCCCCCTGAGCAGCCGAATG
AGGAGCTGGGGATTGAACACGGCGTCCAGCCATTGGGCGAGCCGCGAACGAGAGACAGGACAGGGACCAGGGTCTG
TGTTATACTGGCGCCCAGAGGTCTCCTCTTTCGGGGCGGACAGGACCTTTGCAAAGAGGTAGTCTGTACCCAGGGG
CTCTGTCTCAGGGGTCCCGGGCTCGGGGAACAGCTCGCCCCCTCCCTTCAGACTTTTTTGATTCCGGCACCACGGTC
CCAAGCCGGTGTCTCTCCAGCGGAACGCTGGGACAGGCTCCCGCAAAGAGTGGGCACCGCGCGCTGCTGTGGGG
AATTATGGGCAACAGGGAGCAAGGGTCAGGGCGAGAGAGCCACGACATCCGGAGCAGAAAGGACAGCCCCCGGC
GGAACGTGTCTTCCAGGGGCTCGGGATCTGGCCCCGAGCTGGATTTCAGACCACGCACGGCGAGGACAGCTCCTG
CATCAGGTTTCAGCACCCCGCGAGTCTCGGACAGCTCCCGAGCCGCGCCCAAGCGCATGCGCTCCCGGGGTCTCT
TCCGCTGCCGCTTCTCTCCCGCAGCGCCCCGGGCCGCGTCCCCCGGACTCCCGGGCCGCTCTGAAGCCAGGAAAG
TAACCTCGGCGAACCGGGCAGCTTTTCGTGCGCGCGCAAACCGCCACCCGAGTTTCCGCGAGTACAACCTACCAGA
CGCTGGTGCCGAGAATGAGGCAGCAGGCACCGCGGTGCTACGCGTGGTTGCTCAGGACCCGGACGCCGGCGAGG
CCGGGCGCCTAGTCTACTCGCTGGCGGCACCTCATGAACAGCCGCTCGCTGGAGCTGTTTCAGCATCGACCCGCGA
GCGGCCTTATCCGTACGGCGGCAGCTCTGGACCGCGAGAGCATGGAGCGTCACTACCTGCGTGTGACCGCGCAGG
ACCACGGGTGCGCGCGCTCTCGGCCACCACGATGGTGGCCGTGACAGTAGCCGACCGCAACGACCACTCGCCGG
TTTTTGAGCAAGCGCAGTACCGGGAGACCCTTCGCGAGAATGTGGAGGAGGGCTACCCTATCCTGCAGCTGCGTG
CCACTGACGGCGACGCGCCCCCAACGCCAACCTGCGCTACCGCTTCGTGGGGCCGCCAGCTGCGCGCGCTGCAG
CTGCCGCGCCTTCGAGATTGATCCACGCTCCGGCCTCATCAGCACCCAGCGGCCGAGTGGACCGCGAGCACATGG
AAAGCTATGAGCTGGTGGTGGAAAGCCAGCGACCAGGGCCAGGAACCCGGGCCGCGCTCGGCCACTGTGCGCGTAC
ACATAACTGTGCTAGACGAGAACGACAATGCTCCTCAGTTTCAGCGAGAAGCGCTACGTGGCGCAGGTGCGCGAGG
ATGTGCGCCCCACACAGTCTGTGCTGCGCGTCACGGCCACTGACCGGGACAAGGACGCCAACGGATTGGTGCCT
ACAACATCATCAGTGGCAATAGCCGTGGACACTTTGCCATCGACAGCCTCACTGGCGAGATCCAGGTGGTGGCAC
CTCTGGACTTCGAGGCAGAGAGAGATGCTTGCATCAGGGCGCAGGATGCTGGCCGGCCACCGCTGTCCA
ACAACACGGGCCTGGCCAGCATCCAGGTGGTGGACATCAATGACCACATTCTATTTTTGTCAGCACGCCCTTCC
AAGTTTCTGTCTTGGAAAATGCTCCCTTGGGTCACTCAGTCATCCACATTTCAGGCAGTCGATGCAGACCATGGGG
AGAATGCCAGATTGGAGTACTCCCTAACTGGTGTGGCACCTGATACTCCTTTTGTGATAAACAGCGCCACTGGCT
GGGTCTCTGTGAGTGGTCCCCTGGACCGTGAGTCTGTGGAGCATTACTTCTTTGGTGTGGAGGCTCGAGACCATG
GCTACCCCCACTCTCTGCCTCAGCCAGTGTACCGTGACTGTGCTGGACGTTAATGACAATCGGCCTGAGTTCA
CAATGAAGGAGTACCACCTACGACTGAATGAGGATGCAGCTGTGGGCACCGAGTGTGGTCAGCGTGACCGCAGTAG
ACCGTGATGCCAACAGTGCCATCAGCTACCAGATCACAGGCGGCAACACCCGGAATCGCTTTGCCATCAGCACCC
AGGGGGGTGTGGGTCTGGTGACTCTGGCTCTGCCACTGGACTACAAGCAGGAACGCTACTTCAAGCTGGTACTAA
CTGCATCTGACCGTGCCCTTCATGATCACTGCTATGTGCACATCAACATCACAGATGCCAACACTCATCGGCCGG
TCTTTCAAAGTGCCCACTACTCAGTGAGTGTGAATGAAGATCGGCCAATGGGTAGCACCATAGTGGTCATCAGTG
CCTCTGATGATGACGTGGGTGAGAATGCTCGTATCACCTATCTCTGGAGGACAACCTGCCCCAGTTCCGCATTG
ATGCAGACTCAGGAGCCATTACATTACAGGCCCCATTAGACTATGAGGACCAGGTGACCTACACCCTGGCTATCA
CAGCTCGGGACAATGGCATCCACAGAAGGCAGACACTACTTATGTGGAGGTGATGGTCAATGACGTGAATGACA
ATGCTCCACAATTTGTGGCCTCCCACTATACAGGGCTGGTCTCTGAGGATGCCCCACCTTTACCAGTGTCTGTC
AGATCTCAGCCACTGACCGGGATGCTCATGCCAATGGCCGGGTCCAGTACACTTTCCAGAATGGTGAAGATGGGG
ATGGAGATTTTACCATTGAGCCACCTCTGGAATTGTCCGTACAGTAAGGCGGCTAGACCGGGAGGCAGTATCAG
TGTATGAGTTGACTGCCTACGCAGTGGACAGAGGTGTGCCCCCACTCCGGACTCCAGTCAGTATCCAGGTGATGG
TGCAGGATGTGAACGACAATGCACCTGTCTTCCAGCTGAGGAGTTTGGAGGTGCGGGTGAAAGAGAATAGCATTG
TGGGCTCAGTGGTGGCCAGATCACTGCAGTGGACCCTGACGAAGGCCCAATGCCCATATAATGTACCAGATCG

1215/6881
FIGURE 1132B

TGGAGGGGAACATCCCTGAGCTGTTCCAAATGGACATCTTCTCTGGAGAAGTACGGCACTCATTGACCTAGACT
ATGAGGCTCGCCAAGAATATGTGATTGTGGTGCAGGCCACATCTGCTCCTTTGGTCAGCCGGGCCACTGTGCACG
TCCGCTGTTGACCAGAATGACAACAGCCCTGTGCTCAACAACCTTCCAGATCCTCTTCAACAACCTATGTATCCA
ACCGTTCAGACACCTTCCCGTCGGGCATTATTGGGCGCATCCCAGCTTATGACCCCGATGTCTCCGACCACCTCT
TCTACTCCTTTGAGCGTGGCAATGAGCTGCAGCTGCTGGTAGTCAACCAGACCAGTGGGGAGCTGCGACTCAGCC
GAAAGCTAGACAATAACCGCCCACTGGTGGCCTCCATGTTGGTGAAGTGTACAGATGGCCTGCACAGCGTGACGG
CGCAGTGTGTGCTGCGCGTGGTCATCATCACGGAGGAGTTGCTGGCCAACAGCCTGACCGTGCAGCCTTGAGAACA
TGTGGCAGGAGCGCTTCCCTGTACCGCTGCTGGGCCGCTTCCCTGAGGGCGTGGCTGCGGTGCTCGCTACGCCCG
CTGAGGACGTCTTCATCTTCAACATCCAGAACGACACAGACGTAGGGGGCACCGTGTCAATGTGAGTTTCTCGG
CGCTAGCTCCACGTGGGGCCGGGGCGGGCGCTGCAGGGCCCTGGTTCAGCTCCGAGGAGCTGCAGGAGCAGTTGT
ACGTGCGCCGGGCGGCGCTGGCGGCTCGCTCCCTGCTCGACGTACTGCCCTTCGACGACAACGTGTGCCTGCGAG
AGCCCTGTGAGAACTACATGAAATGCGTGTCCGTGCTCCGCTTTGACTCGTCCGCGCCCTTCCCTGGCCTCGGCCT
CCACGCTGTTCCGACCCATCCAGCCCATCGCTGGCCTGCGCTGCCGCTGCCCGCCCGGATTACGGGAGACTTTT
GCGAGACCGAGCTCGACCTCTGCTACTCCAACCCATGTGCAACGGCGGAGCCTGCGCGCGGCGCGAGGGAGGCT
ACACGTGCGTCTGCCGCCCGCGCTTACCGGAGAGGACTGCGAGCTGGACACCGAGGCGGGCGGCTGCGTGCCGG
GCGTCTGCCGCAACGGGGGCACCTGCACCGACGCGCCCAACGGCGGCTTTGCTGCCAGTGCCCGGCAGGCGGCG
CCTTCGAGGGGCCGCGCTGCGAGGTGGCTGCGCGCTCCTTCCCGCCAGTTTGGTTCGTATGTTTTCGCGGCTGC
GGCAGCGATTCCACCTTACGCTGTCCCTCTCGTTGCGACAGTGCAGCAGAGCGGGCTGCTCTTCTACAACGGGC
GCCTGAACGAGAAGCAGACTTCCCTGGCCCTGGAACCTCGTGGCTGGCCAAGTGGGCTCACATATTCCACGGGTG
AATCCAACACCGTGGTTCAGCCCCACAGTTCCAGGGGGCTTGAGTGACGGGCAATGGCATAAGTGCATCTGAGAT
ACTACAACAAGCCCCGGACAGATGCCCTAGGGGGTGCACAGGGCCCTCCAAGGACAAGGTGGCTGTGCTAAGCG
TGGATGATTGTGATGTGGCCGTGGCTCTGCAGTTTGGTGTGAGATTGGCAACTACTCATGCGCGGCTGCTGGTG
TGCAACAAGCTCCAAGAAGTCCCTGGACCTGACGGGCCCTCTTCTTCTGGGAGGTGTCCCAACCTCCCCGAGA
ACTTCCCCGATCCCATAGGACTTCATCGGCTGTATGCGGGACCTGCACATTGATGGCCGCCGAGTGGACATGG
CGGCTTTTGTGCAATAATGGCACCATGGCAGGCTGCCAAGCCAAGCTACACTTTTGTGACTCAGGCCCTGCA
AGAACAGTGGCTTCTGCTCGGAGCGTGGGGCAGCTTCAGCTGCGACTGCCCTGTGGGCTTCGGCGGCAAGACT
GTCAGCTTACTATGGCCCATCCCCACCATTTCCGTGGCAACGGCACACTGAGCTGGAACCTTTGGAAGTGACATGG
CTGTGTCTGTGCCATGGTACCTGGGGCTGGCATTTCGGACACGGGCAACGCAGGGGGTCTGATGCAAGTGCAGG
CTGGGCCACACAGCAGCTCCTTTGCCAGCTAGATCGGGGGTACTGTCTGTGACAGTGACCAGGGGCTCGGGCC
GTGCTTCCCATCTCCTTCTGGACCAGGTGACTGTGAGTGATGGCCGGTGGCACGATCTGCGGCTGGAGTTGCAGG
AGGAACCAGGTGGCCGGCGGGGCCACCATGTCTTATGGTCTCACTGGACTTTAGCCTCTTCCAGGACACCATGG
CGGTGGGGAGTGAGCTGCAGGGCCTGAAGGTAAAGCAGCTCCACGTGGGAGGCCTGCCCCCGGCAGTGCAGAGG
AGGCTCCTCAGGGTCTGGTTGGCTGCATCCAGGGGGTGTGGCTCGGCTCCACACCCTCTGGCTCCCCGGCCCTGC
TACCCCCCAGCCACCGAGTGAATGCGGAGCCTGGCTGTGTTGTGACCAACGCCTGTGCCTCTGGGCCCTGCCAC
CTCACGCAGACTGCCGGGACCTCTGGCAGACCTTTTCTTGACCTGCCAGCCAGGTTACTACGGCCAGGCTGTG
TGGATGCCTGCCTCCTGAACCCCTGTGAGAACCAGGGATCATGCCGGCACCTGCCAGGAGCCCCCATGGCTATA
CCTGTGACTGTGTGGGTGGCTATTTCGGGCACCACTGTGAGCACAGGATGGACCAGCAGTGCCACGGGGCTGGT
GGGGGAGCCCAACCTGTGGCCCCCTGCAACTGTGATGTTACAAAGGTTTGTATCCCAACTGCAACAAGACAAATG
GGCAGTGTCACTGCAAGGAGTTCCACTACCGACCGCGGGGAGTGAAGTCTTGCCTCCCATGTGACTGCTACCTG
TGGGCTCCACCTCGCGCTCATGTGCACCCACAGCGGGCAGTGGCCCTGTGCGCCAGGAGCCCTTGGCCGCCAGT
GCAACAGCTGTGACAGTCCCTTCGAGAGGTGACAGCCAGCGGCTGCCGGGTGCTCTATGATGCCTGCCCTAAGT
CCCTGAGATCTGGTGTGTGGTGGCCCCAGACAAAGTTTGGCGTCTTGGCCACAGTGGCCTGTCCCCGGGGGGCC
TGGGTGCTGCTGTGCGGCTGTGTGATGAGGCCAGGGTTGGCTGGAGCCCGACCTCTTCAACTGTACCTCCCCTG
CCTTCGAGAGCTCAGTCTGCTGCTGGATGGCCTAGAGCTGAACAAGACGGCACTGGATACCATGGAGGCCAAGA
AGCTGGCTCAGCGGCTACGGGAGGTGACTGGCCACACTGACCACTATTTTAGCCAAGATGTTTCGAGTCACTGCCC
GCCTGCTGGCCACCTGCTGGCCTTCGAGAGCCATCAGCAGGGCTTCGGGCTGACAGCCACACAGGATGCCCACT
TCAATGAGAATCTGCTGTGGGCCGGCTCTGCACTGCTTGGCCAGAGACAGGGGACTTGTGGGCGGCGCTGGGGC
AGCGGGCCCCCTGGGGGCTCCCCAGGCAGCGCGGGACTGGTGAGGCACCTGGAGGAGTATGCAGCCACACTCGCAA

1216/6881
FIGURE 1132C

GGAATATGGAAC TCACATACCTGAATCCCATGGGGCTGGTGACGCCTAATATCATGCTCAGCATTGACCGCATGG
AGCACCCCAGTTCTCCCCGGGGGGCCCGTCGCTACCCTCGCTACCATAGCAACCTCTTTTCGAGGCCAGGATGCCT
GGGATCCTCACAACCATGTGCTGCTGCCTTCCCAGTCCCCACGGCCATCCCCATCTGAAGTTCTGCCCACAAGCA
GCAGCATAGAAAAC TCACCACCTCAAGTGTGGTCCCCCACCAGCCCCGCCAGAGCCAGAGCCTGGGATCTCCA
TTATCATTCTCCTCGTTTACCGCACCTTAGGGGGACTGCTCCCTGCCAGTTCCAGGCAGAACGCCGAGGTGCCA
GGCTTCCTCAGAACCCCGTCATGAACTCCCCGGTGGTCAGCGTGGCTGTGTTCCACGGACGCAACTTCCTAAGGG
GAATCCTGGAGTCCCCCATCAGCCTAGAGTTTCGCCTGCTACAGACAGCGAATCGGAGCAAGGCGATCTGTGTGC
AGTGGGACCCACCTGGCCTGGCGGAGCAGCATGGTGTGTGGACAGCACGGGACTGCGAGCTGGTGCACAGGAATG
GGTCCCACGCACGGTGTGCTGCAGCCGGACAGGGACCTTTGGGGTCTCTATGGATGCCTCTCCCCGTGAGAGGC
TGGAGGGCGACCTGGAGCTGCTGGCTGTGTTACCCACGTGGTTCGTGGCTGTGCTGTGGCTGCGCTGGTGTGTA
CTGCAGCCATCCTGCTGAGCCTGCGCAGCCTCAAGTCCAATGTGCGTGGGATCCATGCCAATGTGGCAGCCGCCC
TGGGGGTGGCAGAGCTCCTCTTCCTGCTGGGGATTACAGGACCCACAATCAGCTGGTGTGCACTGCAGTCGCCA
TCCTCCTGCAC TACTTCTTCCTCAGCACCTTCGCGTGGCTCTTCGTGCAGGGGCTGCACCTCTACCGCATGCAGG
TTGAGCCACGCAACGTGGACCGCGGGCGCCATGCGCTTCTACCATGCCCTGGGCTGGGGCGTCCCTGCTGTGCTGC
TGGGCCCTTGCTGTGGGCTGGACCTGAGGGCTATGGGAACCTGACTTCTGCTGGATCTCAGTCCACGAGCCCC
TCATCTGGAGCTTTGCTGGCCCTGTTGTCTGGTCATAGTGATGAACGGGACCATGTTTCTCCTCGCTGCCCCGA
CATCCTGCTCCACAGGGCAGAGGGAGGCCAAGAAGACCTCTGCACTGACCCTTCGCAGCTCCTTCCTGCTGCTTC
TGCTGGTCAGTGCTCCTGGCTCTTTGGGCTCCTGGCAGTCAACCACAGCATCCTAGCCTTCCACTACCTCCATG
CTGGACTCTGCGGCCTCCAGGGCCTGGCGGTGCTGCTGCTCTTCTGTGCTCTAAATGCAGATGCTCGGGCTGCCT
GGATGCCAGCCTGTCTGGGCAGGAAGGCAGCGCCTGAGGAGGCAAGGCCAGCACCTGGGCTGGGACCTGGGGCCT
ACAACAACACGGCTCTCTTTGAGGAGAGTGGCCTCATCCGCATCACTCTGGGCGCCTCCACCGTCTCCTCTGTGA
GCAGTGCCCGCTCCGGCCGACCCAGGACCAGGACAGCCAGCGGGGCCGAGCTACCTCAGGGACAATGTCTTGG
TTCGACATGGCTCAGCCGCTGACCACACTGACCACAGCCTCCAGGCTCATGCTGGCCCCACTGACCTGGACGTGG
CCATGTTCCATCGAGATGCTGGCGCAGACTCCGACTCTGACAGTGACCTGTCTTGGAGGAGGAGAGGAGTCTCT
CCATTCCATCTTCAGAAAGCGAGGACAATGGCCGGACGCGGGGGCGCTTCCAACGGCCACTCTGCCGAGCAGCCC
AGAGTGAGAGGCTCCTCACCCACCCCAAAGATGTGGATGGCAATGACCTCCTGTCTACTGGCCAGCCCTGGGGG
AGTGCAGAGCAGCCCCCTGTGCTCTGCAGACTTGGGGCTCTGAAAGCGCCTGGGGCTGGACACCAGCAAGGATG
CAGCTAACAACAACCAGCCAGACCCGGCCCTGACCAGTGGGGATGAGACTTCTCTGGGCCGGGCCAGCGCCAGA
GGAAAGGCATCCTGAAGAACC GGTTGCAATACCCACTGGTGCCACAGACCCGAGGTGCCCTGAGCTGTCTTGGT
GCCGTGCAGCCACCTTGGGCCACCGTGCAGTGCCAGCTGCCTCTTACGGTTCGCATCTATGCTGGCGGGGGCACGG
GCAGCCTTTACAGCCAGCCAGCCGCTACTCTTCTAGAGAACAGCTGGACCTGCTCCTCCGGCGGCAACTGAGCC
GTGAGCGACTAGAGGAAGCCCCTGCCCCGTGTTCTACGTCCCCCTGAGCCGGCCAGGGTCCCAGGAATGCATGGATG
CTGCACCAGGCGGACTGGAGCCCAAAGATCGGGGCAGCACCTGCCACGGAGGCAGCCACCTCGGGACTACCCCTG
GCGCCATGGCTGGCCGCTTCGGGTACGCGGATGCGCTCGACTTAGGGGCACCTCGAGAGTGGTTGAGCACGCTGC
CTCCGCCCCGCGCACCCGGGACCTTGACCCACAGCCCCACCTCTGCCCCGTGTCTCCCCAGCGGCAACTCTCAA
GGGACCCCCCTCTTGCCATCCCGGCCGCTGGACTCTCTGTCTAGGAGCTCGAATCTCGGGAGCAGCTGGACCAGG
TGCTTAGCCGGCACCCCTCACGAGAAGCCCTTGGGCCACTCCCGCAGCTGCTCAGAGCTAGGGAGGACTCGGTCA
GTGGCCCCAGCCATGGCCCCCTCCACAGAACAGTTGGACATTCTTCTCCATCCTTGCCCTTTTCAACTCCTCGG
CCCTCTCCTCTGTGCAATCTTCAAGCACACCCTTGGGCCCTCACACCACTGCCACACCTTCTGCCACAGCCTCTG
TGCTTGGGGCCTCCACGCCACGTTCTGCCACGTCTCACAGCATCTCGGAGCTGTCGCCAGACTCAGAAGTTCCCA
GAAGTGAGGGTCACTCCTGAAGGGGATGACGGCGTGGACGAGGAACAGCTGAGGGCGACAGAGGATCTAGGCTAAC
AGGAGAGACTCCAGGAGTGGGGGCAGATCCCAAGGCAGCCTCCTGCTCCCCAGTGGTGGGTGCCCCAGCTCTACC
TGGTGTGGCAGGGCTGAGGCTCCATGTGCATCTGTGAGCATGCGTGTGACAGGTGCAGAGACGGGGACTGGAGG
GAGACTTTTATACGTTTGTACCTTTGTAACCAGAGAGATGCTTATGTTATTTTTAGCTTTTCTGTCTCCTGGG
GGGTTTGAGGCTGGGCTGGGAGGGGGAGGGAGATAGAGGGAGAGATGCAGTTTGACCCATTTGGGTCTGAGCA
AACCCTATGCTCATCTCTCTCTCTCTCTCTGGGGTGGACTCAGATGGGTGGGACACATGCCTTCTCCCCCTATT
CACCCCAAGTTGATCTGAGTATCGTCAGGGGCCCAAAGTACAGAATTGTTCTTTGCTTTTATTGAATGCTCCA
AAGGCCAAACTTCTGGGGCTGGGGGTGGTCTTGGAACAGGGGTCTCTGACTTCTCATGGGGGCTTGCTCAT

1217/6881
FIGURE 1132D

ACCGCCCCCTCCTGGTGGATGTGTGTGTTTATTATGTGGAGTCCCTGCCACTTACTGCCTTATGACCTAGGACTGA
TGCTGTGGGGTGCTGGTGGAGCAGCTGATGTCGTGTTTACAGAGCAAGGCTTCCCTGTCTCCACGGGGAGGGGC
TCGGGCCTCTAGTCAGACATTCCCTGCAGAGGGTCGGTGGAGGGGTCATTACCTGCCCCTGCAGCAAGCAAAAGT
TGTCTGTGGTGCCATTGATTCCCTGACACTGCCCCCTGCTTGAATTGATTCCGAAGGGTAGGGTGGGAAGGTGA
GCAAAGGGAGCAGAAACAAGGGAATTCAAGACCCAGAATGTAGGTGCCACTGCCTCCTATGTTTACAGGATCCTC
CGTGGCCCTAGGCACCTGGGCTGCAGGAAGTGACTCCGTTCCACTCCTCCTTTATTCCCTTAAAAAGGGAAAAAT
GACTGTTACGACCCTGTTACAAAACCTCTTACTTTTGCTATTTTGTCTGCTGTCCAGAACTGAAGACTTTAAAT
TTTGTTACTGTTTACAAGTCCAGATTCAAAAAATGTTTTTACTTTGTTTACAACCTCAAACTTTGAGTTTACAC
TTTGTTTACAGTAGATAATTTTTTTTTCCTTTGTTTCCAAGTGAAAGGTAGGGAAAGTGGGAGAGGGACTTGGAGG
ACCCACCTGTGAGGACCCCTGACCTGGCCATCTTGAGGGGTTTTCTAACCCCCAGGTCTCCCAGGCCGAAGGTCAG
CCTTGAGTCCCGTTTAACAGCAGATCCAGAAGACCTTGAGAGTAGGCGTCTCTAACCACGGGGGAGAGTGGCTG
TGCAGGGCTGGGGGGTGGTCTGTGCAGACACCTCCTCACCCACCACCCCATGCATACTCTTGGGAAGCAGCTTCC
TGGGAGATTAGAAATTCTACTTCCCTGACTGGAGCTAAATCCCACCAGCCAGGACCCAACTCTCCTTACCGAGA
AGGACCCCAGCTCTTGAAGGGCTGAGTGGCCTGCTGGGGGTGGGAGGGTGTCTTTACTATGTCTAGGTTTCGTA
GATGCCCCCTCTCTGGGGTTCCTCCTCCAGCCCAGCGGCCCTCTTTCCTGTCTGTGTAAATTGTTCCCGTGAAGC
CGCGCTCTGTTTGGGAATAAACTTCTATAGAAAACAAAA

1218/6881
FIGURE 1133

MMARRPPWRGLGERSTPILLLLLLLSLFPLSQEELGGGGHQGWDPGLAATTGPRAHIGGGALALCPESSGVREDGG
PGLGVREPIFVGLRGRRQSARNRSGPPEQPNEELGIEHGVQPLGSRERETGQGPGSVLYWRPEVSSCGRTGFLQR
GSLSPGALSSGVPFSGNSSPLPSDFLIRHHGPKPVSSQRNAGTGSRKRVGTARCCGELWATGSKGQGERATTSGA
ERTAPRRNCLPGASGSGPELDSAPRTARTAPASGSAPRESRTAPEPAPKMRSGLFRCRFLPQRPGPRPPGLPA
RPEARKVTSANRARFRRAANRHPQFPQYNYQTLVPENEAAGTAVLRVVAQDPDAGEAGRLVYSLAALMNSRSLEL
FSIDPQSGLIRTAALDRESMERHYLRVTAQDHGSPRLSATTMVAVTVADRNDHSPVFEQAQYRETLRENVEEGY
PILQLRATDGDAPPNANLRYRFVGPAAARAAAAAFEIDPRSGLISTSGRVDREHMESYELVVEASDQGOEPGPR
SATVRVHITVLDENDNAPQFSEKRYVAQVREDVRPHTVVLVLTATDRDKDANGLVHYNIIISGNSRGHFAIDS LTG
EIQVVAPLDFEAEREYALRIRAQDAGRPPLSNNTGLASIQVVDINDHIPIFVSTPFPQVSVLENAPLGHSVIHIQA
VDADHGENARLEYSLTGVAPDTPFVINSATGWVS VSGPLDRESVEHYFFGVEARDHGSPPLSASASVTVTVLVDVN
DNRPEFTMKEYHLRLNEDAAVGTSSVSVTAVDRDANS AISYQITGGNTRNRFAISTQGGVGLVTALPLDYKQER
YFKLVLTASDRALHDHCYVHINITDANTHRPVFQSAHYSVSVNEDRPMGSTIVVISASDDDVGENARITYLLEDN
LPQFRIDADSGAITLQAPLDYEDQVITYTLAITARDNGIPQKADTTYVEVMVNDVNDNAPQFVASHYTGLVSEDAP
PFTSVLQISATDRDAHANGRVQYTFQNGEDGDGDF TIEPTSGIVRTVRRLDREAVSVYELTAYAVDRGVPLRTP
VSIQVMVDVNDNAPVFPAEEFEVRVKENSIVGSVVAQITAVDPDEGPNAHIMYQIVEGNIPELFQMDIFSGELT
ALIDLDYEARQEYVIVVQATSAPLVSRATVHVR LVDQNDNSPVLNNFQILFN NYVSNRSDTFPSGIIGRIPAYDP
DVSDHLFYSFERNELQLLVVNQTS GELRLSRKLDNNRPLVASMLVTVDGLH SVTAQCVLRVVITTEELLANSL
TVRLENMWQERFLSPLLGRFLEGVA AVLATPAEDVFIFNIQNDTDVGGTVLNVFSALAPRGAGAGAAGPWFSS E
ELQEQLYVRAALAARSLLDVLFPDDNVCLREPCENYMKCVSVLRFDSAPFLASASTLFRPIQPIAGLRCRCPP
GFTGDFCETELDLCYSNPCRNCGACARREGGYTCVCRPRFTGEDCELDTEAGRCVPGVCNRNGGTCTDAPNGGFRC
QCPAGGAFEGPRCEVAARSFPPSSFVMFRGLRQRFHLTLSLSFATVQQSGLLFYNGRLNEKHDFLAL ELVAGQVR
LTYSTGESNTVVSPTVPGGLSDGQWHTVHLRYYNKPRTDALGGAQGPSKDKVAVLSVDDCDVAVALQFGAEIGNY
SCAAAGVQTSSKKS LDTGPLLGGVNPENFPVSHKDFIGCMRDLHIDGRRVDMAAFVANNGTMAGCQAKLHF
CDSGPCKNSGFCSERWGSFSCDCPVGFGGKDCQLTMAHPHHFRGNGTLSWNFGSDMAVSVPWYLG LAFRTRATQG
VLMQVQAGPHSTLLCQLDRGLLSVTVTRGSGRASHLLLDQVTVSDGRWHDRLRLELQEEPGGRRGHHVLMVSLDFS
LFQDTMAVGSELQGLKVKQLHVGG LPPGSAEEAPQGLVGCIQGVWLGSTPSGSPALLPPSHRVNAEPGCVVTNAC
ASGPCPPHADCRDLWQTF SCTCQPGYYGPGCVDA CLLNPCQNQGSCRHLPGAPHGYTCD CVGGYFGHHCEHRMDQ
QCPRGWWGSPTCGPCNCDVHKGFDPNCNKTNGQCHCKEFHYRPRGSDSCLPCDCYPVGSTSRSCAPHSGQCPCR P
GALGRQCNSCDSPPFAEVTASGCRVLYDACPKSLRSGVWWPQTKFGVLATVPCPRGALGA AVRLCDEAQGWLEPDL
FNCTSPAFRELSLLLDGLELNKTALDTMEAKKLAQRLREVTGHTDHYFSQDVRVTARLLAHL LAFESHQQGFGLT
ATQDAHFNENLLWAGSALLAPETGDLWAALGQ RAPGGSPGSAGLVRHLEEYAATLARNMELTYLNP MGLVTPNIM
LSIDRMEHPSSPRGARRYPRYHSNLF RQDAWDPHTHVLLPSQSPRPSPEVLEPTSSSIENSTTSSVPPPPAPPE
PEPGISIIILLVYRTLGGLLPAQFQAERRGARLPQNPVMNSPVVSVAVFHGRNFLRGILESPISLEFRLLQTANR
SKAICVQWDPPGLAEQHGVTARDCELVHRNGSHARCRCRSTGTFGVLM DASPRERLEGDLELLAVFTHVVAVS
VAALVLTAAILLSLRSLKSNVRGIHANVAAALGVAELLFLLGIHRTHNQLVCTAVAILLHYFFLSTFAWL FVQGL
HLYRMQVEPRNVDRGAMRFYHALGWGVP AVLLGLAVGLDPEGYGNPDFCWISVHEPLIWSFAGPVVLVIVMNGTM
FLLAARTSCSTGQREAKKTSALT LRSSFLLLLLV SASWLFGLLAVNHSILAFHYLHAGLCGLQGLAVLLLFCVLN
ADARAAWMPACLGRKAAP EEARPAPGLGPGAYNNTALFEESGLIRITLGASTVSSVSSARSGR TQDQDSQRGRSY
LRDNVLVRHGSAADHTDHS LQAHA GPTDL DVAMFHRDAGADSDSDSL SLEEERSLSIP SSESEDNGRTRGRFQR
PLCRAAQSERLLTHPKDVDGNDLLSYW PALGECEAAPCALQTWGSERRLGLDTSKDAANNQPDAL TSGDETS L
GRAQRQRKGILKNRLQYPLVPQTRGAPELSWCRAATLGHRAVPAASYGRIYAGGGTGSLSQPASRYSSREQLDLL
LRRQLSRERLEEAPAPVLRPLSRP GSGQECMDAAPGRLEPKDRGSTLPRRQPPRDYPGAMAGRFGSRDALDLGAPR
EWLSTLPPPRTRDLD PQQPPLPLSPQRQLSRDPLPSRPLDSLRSNSNREQLDQVPSRHP SREALGPLPQLLR
AREDSVSGPSHG PSTEQLDILSSILASFNS SALS SVQSSSTPLGPHTTATPSATASVLGPSTPRSATSHSISELS
PDSEVPRSEGH S

1219/6881
FIGURE 1134

TACTGACTTTTCAGCACCAACTTGTGGTCCCAGGTAAGTTTCCACGCTGGTACTTTAGCCCTGGGCTCGAACCTGC
GGACACGCTGTGGCTGCAACTCCCCGCCCAGACCTCAGTACGCAGCGCGGCTGGTGAGAAACATAATGCACT
CTGACTTCCACGCGTGGAATGGGGAGATGGACTGCACGGCGGGCGGACCTGCTCGGGCTGATGGACGGCAGGTGG
ACTGATGTGCGCAGGGACTGGCGGCAGCGCGGTGAGAGCCAGTCAGCCAAAGCCAGGCCAGCACAAATAGACTGTC
CCGGTTCCCGCCAGGAGGCGGCCGAGCACCAACTGTACGGTACTGCGCCTGCGCCGCGACCGCCAACGCGCCCAG
TCTACGCTTGCGCGGCGCAACAGGGCCGACTGCAGCTGGAAGATGCGCGGCGTCCGTGGTCTGTCTGGGCCGCTACC
GCCGGGGCACAAGTGCTATTGCGCGCCGCGCTGCGCGGCCCTGCTGCGGACGCCAGCCTTGCGGAGTACGGCA
ACCTTCGCTCAGGCGCTCCAGTTCGTGCCGAGACGCAGGTTAGCCTGCTGGACAACGGCCTGCGTGTGGCCTCC
GAGCAGTCCTCTCAGCCCACTTGACGGTGGGAGTGTGGATTGATGTTGGCAGCCGTTTTTGAGACTGAGAAGAAT
AATGGGGCAGGCTACTTTTTGGAGCATCTGGCTTTCAAGGGAAACAAGAATCGGCCTGGCAGTGCCCTGGAGAAG
GAGGTGGAGAGCATGGGGGCCATCTTAATGCCTACAGCACCCGGGAGCACACAGCTTACTACATCAAGGCGCTG
TCCAAGGATCTGCCGAAAGCTGTGGAGCTCCTGGGTGACATTGTGCAGAACTGTAGTCTGGAAGACTCACAGATT
GAGAAGGAACGTGATGTGATCCTGCGGGAGATGCAGGAGAATGATGCATCTATGCGAGATGTGGTCTTTAACTAC
CTGCATGCCACAGCATTCCAGGGCACACCTCTAGCCCAGGCTGTGGAGGGGCCAGTGAGAATGTCAGGAAGCTG
TCTCGTGCAGACTTGACCGAGTACCTCAGCACACATTACAAGGCCCTCGAATGGTGTGGCAGCAGCTGGAGGA
GTGGAGCACCAGCAACTGTTAGACCTCGCCCAGAAGCACCTCGGTGGCATCCCATGGACATATGCAGAGGACGCT
GTGCCACTCTTACTCCATGCCGCTTCACTGGCAGTGAGATCCGCCACCGTGATGATGCTCTACCTTTTGCCAC
GTGGCCATTGCAGTAGAGGGTCTGGCTGGGCCAGCCCGGACAGTGTGGCCTTGCAAGTGGCCAATGCCATCATC
GGCCACTATGACTGCACTTATGGTGGTGGCGTGACCTGTCCAGCCCACTGGCTTCAGGTGCTGTGGCCAACAAG
CTATGCCAGAGTTTCCAGACCTTCAGCATCTGCTATGCAGAGACGGGCTTGCTGGGTGCACACTTTGTCTGTGAC
CGAATGAAAATCGATGACATGATGTTTCGTCTGCAAGGGCAGTGATGCGCCTGTGTACCAGTGCCACGGAGAGT
GAGGTGGCCCCGGGGCAAAAACATCCTCAGAAATGCCCTGGTATCTCATCTAGATGGCACTACTCCTGTGTGTGAG
GACATCGGACGCAGCCTCCTGACCTATGGCCGCCGCATCCCCCTGGCTGAATGGGAAAGCCGGATTGCGGAGGTG
GATGCCAGTGTGGTACGTGAGATCTGCTCCAAGTACATCTATGACCAGTGCCAGCAGTGCGTGGATATGGCCCC
ATTGAGCAGCTCCCAGACTACAACCGGATCCGTAGCGGCATGTTCTGGCTGCGCTTCTAGCGGGAAGCCTATGT
AAGCAAGAGGGCAGGGCCGGGTTTGTGGTCCCCCCCCACCACAAACACAGCACTTCGGCTCCTCTAACCTGTG
CCACAGGTGACCACCAATAAAATCCTCTGCTGAGA

1220/6881
FIGURE 1135

MAASVVCRAATAGAQVLLRARRSPALLRTPALRSTATFAQALQFVPETQVSLDNGLRVASEQSSQPTCTVGVI
DVGSRFETEKNNAGYFLEHLAFKGTKNRPGSALEKEVESMGAHLNAYSTREHTAYYIKALSKDLPKAVELLGDI
VQNCSEDSQIEKERDVILREMQENDASMRDVVFNYLHATAFQGTPLAQAVEGPSENVKLSRADLTEYLSHYK
APRMVLAAAGGVEHQQLDLAQKHLGGIPWTYAEDAVPTLTPCRFTGSEIRHRDDALPFAHVAIAVEGPGWASPD
SVALQVANAIIGHYDCTYGGGVHLSSPLASGAVANKLCQSFQTFSCICYAETGLLGAHFVCDRMKIDMMFVLQGO
WMRLCTSATESEVARGKNILRNALVSHLDGTTVCEDIGRSLTYGRRIPLAEWESRIAEVDASVVREICSKYIY
DQCPAVAGYGP IEQLPDYNRIRSGMFWLRF

1221/6881
FIGURE 1136

TCCGACTCATCCCGGCCCCGGGATGGCGTCCCCACGGGAATTGACACAGAACCCCCCTGAAGAAGATCTGGATGCC
ATACAGCAATGGGCGGCCCCGCTCTGCACGCTTGCCAGCGCGGTGTGTGCATGACCAACTGCCCAACTCTCATTGT
CATGGTGGGCCTGCCCGCCAGGGGCAAGACCTACATCTCCAAGAAGCTGACTCGATACCTGAACCTGGATTGGTGT
GCCCCTCGGGAGTTCAATGTTGGCCAGTATCGCCGGGACGTGGTCAAGACCTACAAATCTTTGAATTTTTTCT
CCCCGACAATGAAGAGGGCCTGAAAATCAGGAAGCAGTGTGCCCTGGCAGCCCTCCGTGACGTCCGGCGGTTCCCT
TAGTGAGGAGGGGGGACATGTGGCGGTTTTTGTATGCCACAAACACCACCCGAGAACGGAGAGCGACCATCTTTAA
TTTTGGAGAACAGAATGGCTACAAGACCTTTTTTGTGAGTCCATCTGTGTGGATCCTGAGGTCATAGCTGCCAA
CATCGTGCAAGTGAAACTGGGCAGCCCTGACTATGTCAACCGCGACAGTGATGAGGCTACGGAGGACTTCATGAG
GCGCATTGAGTGCTATGAGAACTCCTACGAGTCGCTAGATGAGGACCTGGATAGGGACCTGTCCTATATCAAGAT
CATGGATGTGGGCCAGAGCTACGTGGTGAACCGTGTGGCTGACCACATCCAGAGCCGCATCGTATATTACCTCAT
GAACATCCACGTGACCCCCCGCTCCATCTACCTCTGCCGGCACGGGGAGAGCGAGCTCAACCTCAAGGGCCGGAT
TGGCGGGGACCCAGGACTGTCCCCCTCGGGGACGGGAGTTTGCCAAGAGTCTAGCCCAAGTTCATCAGTGACCAAAA
TATCAAGGATCTGAAGGTCTGGACAAGCCAGATGAAGAGGACAATCCAGACGGCTGAGGCACTGGGTGTGCCCTA
TGAACAGTGGAAGGTCCTCAACGAGATCGATGCGGGCGTCTGTGAGGAAATGACCTACGAGGAAATTCAGGATAA
TTATCCACTGGAGTTGCGCCCTGCGGGACCAGGACAAGTACCGGTACCGGTACCCCTAAAGGGGAGTCTACGAGGA
CCTGGTCCAGAGACTGGAGCCTGTCAATCATGGAGCTGGAGAGGCAAGAGAATGTGCTGGTCACTGTGCCACCAGGC
TGTGATGCGCTGCTGTGGCCTACTTCCTCGACAAGGCAGCAGAACAGCTGCCCTACCTCAAGTGTCCGCTGCA
CACAGTCTGAAGCTGACTCCTGTGGCATATGGTTGTAAAGTGGAGTCCATATTCCTGAACGTGGCTGTGTGAA
CACGCACCGGGACAGGCCTCAGAACGTGGACATCTCAAGACCTCCAGAGGAAGCCCTTGTACGGTGCCTGTCTCA
CCAGTGACCATGTTTCACTCACTGTGACCACTAGGCAGGCACTGCTCTCTGCAGAGGGGGTCAATCCAGGCCCTCC
AGTGTGTGTGATAGTCACCATGCCATGCAGGGATATTCTTGAAGCCACACATGGCTGGCGGAACCCAGAGCCCCC
ACCCAGCCCACCTGGCTCTTTGTTGACAGTCGGCGACAAGGTTGTGCGTGGCTCCTGACCTGCTGCTAAGAGTC
ACTTGACCAGACTGCATCTGCATGGGCTGCGCGGAGGTTGCCAGCCCCAGTTTCTTCCGGCGCAGCTCTTAGGT
GTTCACTCTCGCCAGCTCAGTTGGCTTTGTGAAGTGTGAAACCCTACAATGTGAAAGGAAAGTGCTTGCTGTGAT
GTTCCCTACTGTGGCCCAGCTGCCAGCAIGGACCTGGTGACTCTCCACAGGGCCTCTACCATCCTCTCTGTGGCC
ACTTCTGAGCCAGAGGCCAGGTCTTCAIGGGGCCCTGAGCTTCTGCTGCCTCTGGTGAGAGGGAGAGCCCTTCC
CATCCTTACCCACCAGGAACTAGAGCCCCAACCCACAGCAGATGCTTCCTGGGCAGCCACTGGCCAGGCCGTTGTA
TCCATGTCACCCCTTAGTTGTGGGCATTATGAAAGCAATGCGCTTGCTTCAGCACATTGGGATGCACAGAAACGT
GAGGGCAGGGGGGAGTTGTGGTCGCCCCCTCCCCAGTTGTGCATGTACCCGGCTACTTAGGTATGCTTAGGGGAG
CTGGTGGCCAGGGGTGCCCTTCAGGCCGTCTCTACAGTGAAACCACTTCAAGACAGGGCAGGAAGTTACCTTC
CTGGTGCACACACCGAAGTGCTCGAGGGAGAGGCTGCCGCCCCCTCTCCCCCTTCCCTGGCTGTGGACACTGGCAG
CCAATGGGGAGGCGGCTCTCCCCCTGTTGCTGCCCGTGTCCACACAGGAATGTACACTGGTGGCAGAAACATGCA
TTTGCCATAAATAATTCAGAAAC

1222/6881
FIGURE 1137

AGCAATGGCTGCCATCCGGAAGAACTGGTGATTGTTGGTGATGGAGCCTGTGGAAAGACATGCTTGCTCATAGT
CTTCAGCAAGGACCAGTTCCCAGAGGTGTATGTGCCCACAGTGTTTGAGAACTATGTGGCAGATATCGAGGTGGA
TGGAAAGCAGGTAGAGTTGGCTTTGTGGGACACAGCTGGGCAGGAAGATTATGATCGCCTGAGGCCCCCTCTCCTA
CCCAGATACCGATGTTATACTGATGTGTTTTTCCATCGACAGCCCTGATAGTTTAGAAAACATCCCAGAAAAGTG
GACCCCAGAAGTCAAGCATTCTGTCCCAACGTGCCCATCATCCTGGTTGGGAATAAGAAGGATCTTCGGAATGA
TGAGCACACAAGGCGGGAGCTAGCCAAGATGAAGCAGGAGCCGGTGAAACCTGAAGAAGGCAGAGATATGGCAAA
CAGGATTGGCGCTTTTGGGTACATGGAGTGTTTCAGCAAAGACCAAAGATGGAGTGAGAGAGGTTTTTGAAATGGC
TACGAGAGCTGCTCTGCAAGCTAGACGTGGGAAGAAAAAATCTGGGTGCCTTGTCTTGTGTAAACCTTGCTGCAAG
CACAGCCCTTATGCGGTTAATTTGAAGTGCTGTTTATTAATCTTAGTGTATGATTACTGGCCTTTTTTCATTTAT
CTATAATTTACCTAAGATTACAAATCAGAAGTCATCTTGCTACCAGTATTTAGAAGCCAACTATGATTATTAACG
ATGTCCAACCCGCTCTGCCCCACCAGGGTCCTTTTGACACTGCTCTAACAGCCCTCCTCTGCACTCCACCTGACA
CACCAGGCGCTAATTCAGGAATTTCTTAACTTCTTGCTTCTTTCTAGAAAGAGAAACAGTTGGTAACTTTTGTG
AATTAGGCTGTAACTACTTTATACTAACATGTCCTGCCTATTATCTGTCAGCTGCAAGGTACTCTGGTGAGTCA
CCACTTCAGGGCTTTACTCCGTAACAGATTTTGTTGGCATAGCTCTGGGGTGGGCAGTTTTTTGAAAATGGGCTC
AACCAGAAAAGCCCCAAGTTCATGCAGCTGTGGCAGAGTTACAGTTCTGTGGTTTCATGTTAGTTACCTTATAGTT
ACTGTGTAATTAGTGCCACTTAATGTATGTTACCAAAAATAAATATATCTACCCAGACTAGATGTAGTATTTTT
TGTATAATTGGATTTCTAATACTGTCATCCTCAAAGAAAGTGATTGGTTTTTTAAAAAAGAAAGTGATTG
AAATAAAGTCAGATGGAAAATTCATTTTTTAAATTCCTCGTTTTGTCACTTTTTCTGATAAAAGATGGCCATATTA
CCCCTTTTCGGCCCCATGTATCTCAGTACCCCATGGAGCTGGGCTAAGTAAATAGGAATTGGTTTCACGCCTGAG
GCAATTAGACACTTTGGAAGATGGCATAACCTGTCTCACCTGGACTTAAGCATCTGGCTCTAATTCACAGTGCTC
TTTTCTCCTCACTGTATCCAGGTTCCCTCCCAGAGGAGCCACCAGTTCTCATGGGTGGCACTCAGTCTCTCTCT
CTCCAGCTGACTAAACTTTTTTTCTGTACCAGTTAATTTTTTCCAACCTACTAATAGAATAAAGGCAGTTTTCT

1223/6881
FIGURE 1138

MAAIRKKLVIVGDGACGKTCLLIVFSKDQFPEVYVPTVTFENYVADIEVDGKQVELALWDTAGQEDYDRLRPLSYP
DTDVILMCFSIDSPDSLENIPEKWTPEVKHFCPNVPIILVGNKKDLRNDENRRELAKMKQEPVKPEEGRDMANR
IGAFGYMECSAKTKDGVREVFEMATRAALQARRGKKKSGCLVL

1224/6881
FIGURE 1139

TGAGCCCCAGCTAAGCGCTGCCCTTGAGTATGTGCGGAGTCACCCCTTGGACCCCATCGACACTGTGGACTTCGA
GCGGGAATGTGGCGTGGGTGTCATTGTGACCCAGAGCAGATTGAGGAGGCTGTGGAGGCTGCTATTAACAGGCA
CCGGCCCCAGCTCCTGGTGAACGTTACCATTTCAACATGGGGCTGCTGATGGGAGAGGCTCGGGCTGTGCTGAA
GTGGGCAGATGGCAAAATGATCAAGAATGAAGTGGACATGCAGGTCCTCCACCTTCTGGGCCCCAAGTTGGAGGC
TGATCTGGAGAAGAAGTTCAAGGTGGCAAAAGCTCGGCTAGAAGAAACAGACCGGAGGACGGCAAAGGATGTGGT
GGAGAATGGCGAGACTGCTGACCAGACCCTGTCTCTGATGGAGCAGCTCCGGGGGGAGGCCCTTAAGTTCCACAA
GCCTGGTGAGAACTACAAGACCCAGGCTATGTGGTCACTCCACACACCATGAATCTACTAAAGCAGCACCTGGA
GATTACTGGTGGGCAGGTACGTACCCGGTTCCCGCCAGAACCCAATGGAATCCTGCATATTGGACATGCCAAAGC
CATCAATTTCAACTTTGGCTATGCCAAGGCCAACAATGGCATCTGTTTTCTGCGTTTTTGATGACACCAACCCTGA
GAAGGAGGAAGCAAAGTTCTTCACGGCCATCTGTGACATGGTAGCCTGGCTAGGCTACACACCTTACAAAGTCAC
ATATGCGTCTGACTATTTTGACCAGCTATATGCGTGGGCTGTGGAGCTCATCCGCAGGGGCTGCTGGCTTATGTGTG
CCACCAGCGAGGAGAGGAGCTCAAAGGCCATAATACTCTGCCTTCACCCCTGGAGAGACCGTCCCATGGAGGAGTC
ACTGCTGCTCTTTGAGGCAATGCGCAAGGGCAAGTTTTTCAGAGGGCGAGGCCACACTACGGATGAAGCTGGTGAT
GGAGGATGGCAAGATGGACCCTGTAGCCTATCGAGTCAAGTATACACCACACCACCGCACAGGGGACAAATGGTG
CATCTATCCCACCTACGACTACACACACTGCCTCTGTGACTCCATCGAGCACATCACTCACTCACTCTGCACCAA
GGAATTCCAGGCCCG

1225/6881
FIGURE 1140A

GAAGGCAGTTTCCGGAGGGAAGGGGTAGGGTTGGGGTGGGGGCGCTCTCCGCCCGGTGTTGCGCTCCTTCCCAGA
ATCCGCTCCGGCCTTTCCTTCCTGCCGCGATTCCCAACTTTGCTCAAAGTCGCTGGACTCTAAGCTGTTCGGAGGG
ACCGCTGGACAGACCTGGGAACTGACAGAGGGCCTGGAGGGAAACAGGCCAAAGACCCACAGGCAGAGTTGACAC
GGAACCCCAAAGCAAGGAGGAGGGCTCGGGCCCCGAGACCGTTCACCTCCCCTTATCCCTGTTCCCTCTTCAGGA
TGGAGCTGACCTCAAGGGAAAGAGGGAGGGGACAGCCTCTGCCCTGGGAACTTCGACTGGGCCTACTGCTAAGCG
GTGAGAGGGCCTGGTGGGGGCTGGGGGTTGTGGAATGTGATGGTAGTCCCTGGGAGTTGCCCTTGGGGCACATGA
GGTGGAGCCACTGGATAGGAACTCCACGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT
GGCCCCCTGCCCCCGATGXX
XXCACCACAGCGCGGGCAGCCTGGTGGCAGTCAG
AGAATGGTATCCCTGCGGTACCATCCAGCTGGACCTGGAGGCTGAGTTTCATTTACACACCTCATTATGACCT
TCAAGACATTTGCCCTGCTGCCATGCTGGTGGAAACGCTCAGCAGACTTTGGCCGCACCTGGCATGTGTACCGAT
ATTTCTCCTATGACTGTGGGGCTGACTTCCCAGGAGTCCCAGTACGACCCCCACGGCACTGGGATGATGTAGTCT
GTGAGTCCCGCTACTCAGAGATTGAGCCATCCACTGAAGGCGAGGTCATCTATCGTGTGCTGGACCCCTGCCATCC
CTATCCCAGACCCCTACAGCTCACGGATTGAGAAGCTGTTGAAGATCACCAACCTACGGGTGAACCTGACTCGTC
TACACACGTTGGGAGACAACCTACTCGACCCACGGAGGGAGATCCGAGAGAAGTACTACTATGCCCTCTATGAGC
TGGTTGTACGTGGCAACTGCTTCTGCTACGGACACGCCTCAGAGTGTGCACCCGCCCCAGGGGCACAGCCCATG
CTGAGGGCATGGTGCACGGAGCTTGCATCTGCAAACACAACACACGTGGCCTCAACTGCGAGCAGTGTGAGGATT
TCTATCGTGACCTGCCCTGGCGTCCGGCTGAGGACGGCCATAGTCATGCCTGTAGGAAGTGTGAGTGCCATGGGC
ACACCCACAGCTGCCACTTCGACATGGCCGTATACCTGGCATCTGGCAATGTGAGTGGAGGTGTGTGTGATGGAT
GTCAGCATAACACAGCTGGGCGCCACTGTGAGCTCTGTGCGCCCTTCTTCTACCGTGACCCAACCAAGGACCTGC
GGGATCCGGCTGTGTGCCGCTCCTGTGATTGTGACCCCATGGGTCTCAAGACGGTGGTGCCTGTGATTCCCATG
ATGACCCTGCACTGGGACTGGTCTCCGGCCAGTGTGCTGCAAAGAACATGTGGTGGGCACTCGCTGCCAGCAAT
GCCGTGATGGCTTCTTTGGGCTCAGCATCAGTGACCGTCTGGGCTGCCGGCGTATGTCAATGTAATGCACGGGGC
ACAGTGCCTGGGAGCACTCCTTGTGACCCCAACAGTGGATCCTGTTACTGCAAACGTCTAGTGACTGGACGTGGA
TGTGACCGCTGCCTGCCTGGCCACTGGGGCCTGAGCCACGACCTGCTCGGCTGCCGCCCTGTGACTGCGACGTG
GGTGGTGTCTTTGGATCCCCAGTGTGATGAGGGCACAGGTCAATGCCACTGCCGCCAGCACATGGTTGGGCGACGC
TGTGAGCAGGTGCAACCTGGCTACTTCCGGCCCTTCTGAGACCACTAATTTGGGAGGCTGAGGACACCCGAGGG
CAGGTGCTCGATGTGGTGGAGCGCTGGTGAACCCCGGGGAACTCCATCCTGGACTGGCTCAGGCTTCGTGCGG
CTACAGGAAGGTGAGACCTGGAGTTCCTGGTGGCCTCTGTGCCGAAGGCTATGGACTATGACCTGCTGCTGCGC
TTAGAGCCCCAGGTCCCTGAGCAATGGGCAGAGTTGGAAGTGAATGTGTCAGCGTCCAGGGCCTGTGCTGCCAC
AGCCTGTGTGGGCATTTGGTGCCCAAGGATGATCGCATCCAAGGGACTCTGCAACCACATGCCAGGTACTTGATA
TTTCCTAATCCTGTCTGCCTTGAGCCTGGTATCTCCTACAAGCTGCATCTGAAGCTGGTACGGACAGGGGGAAAGT
GCCCAGCCTGAGACTCCCTACTCTGGACCTGGCCTGCTCATTGACTCGCTGGTGTGCTGCCCCGTGTCTGCTG
CTAGAGATGTTTAGTGGGGGTGATGCTGCTGCCCTGGAGCGCCAGGCCACCTTTGAACGCTACCAATGCCATGAG
GAGGGTCTGGTGCCAGCAAGACTTCTCCCTCTGAGGCCTGCGCACCCCTCCTCATCAGCCTGTCCACCCCTCATC
TACAATGGTGCCCTGCCATGTCAGTGCAACCCTCAAGGTTCACTGAGTTCTGAGTGCAACCCTCATGGTGGTCAG
TGCTGTGCAAGCCTGGAGTGGTTGGGGCGCCGCTGTGACCTCTGTGCCCTGGCTACTATGGCTTTGGCCCCACA
GGCTGTCAAGCCTGCCAGTGCAGCCACGAGGGGGCACTCAGCAGTCTCTGTGAAAAGACCAGTGGGCAATGTCTC
TGTGCAACTGGTGCCTTTGGGCTTCGCTGTGACCGCTGCCAGCGTGGCCAGTGGGGATTCCCTAGCTGCCGGCCA
TGTGTCTGCAATGGGCATGCAGATGAGTGCAACACCCACACAGGCGCTTGCTGGGCTGCCGTGATCACACAGGG
GGTGAGCACTGTGAAAGGTGCATTGCTGGTTTCCACGGGGACCCACGGCTGCCATATGGGGGCCAGTGCCGGCCC
TGTCCCTGTCTGAAGGCCCTGGGAGCCAACGGCACTTTGCTACTTCTTGCCACCAGGATGAATATTCCCAGCAG
ATTGTGTGCCACTGCCGGGCAGGCTATACGGGGCTGCGATGTGAAGCTTGTGCCCTGGGCACTTTGGGGACCCA
TCAAGGCCAGGTGGCCGGTGCCAACTGTGTGAGTGCAGTGGGAACATTGACCCAATGGATCCTGATGCCTGTGAC
CCCCACACGGGGCAATGCCTGCGCTGTTTACACCACACAGAGGGTCCACACTGTGCCACTGCAAGCCTGGCTTC
CATGGGCAGGCTGCCCCGACAGAGCTGTACCGCTGCACATGCAACCTGCTGGGCACAAATCCGCAGCAGTGCCCCA
TCTCCTGACCAGTGCCACTGTGATCCAAGCAGTGGGCAGTGCCCATGCCCTCCCAATGTCCAGGGCCCTAGCTGT
GACCGCTGTGCCCCCAACTTCTGGAACCTCACCAGTGGCCATGGTTGCCAGCCTGTGCTGCCACCCAAGCCGG

1226/6881
FIGURE 1140B

GCCAGAGGCCCCACCTGCAACGAGTTACAGGGCAGTGCCACTGCCGTGCCGGCTTTGGAGGGCGGACTTGTTCT
GAGTGCCAAGAGCTCCACTGGGGAGACCCTGGGTGTCAGTGCCATGCCGTGTGATTGTGACTCTCGTGGAATAGAT
ACACCTCAGTGTCACCGCTTACAGGTCAGTGAGCTGCCGCCAGGGGTGTCTGGTGTGCGCTGTGACCAGTGT
GCCCCGTGGCTTCTCAGGAATCTTTCCTGCCTGCCATCCCTGCCATGCATGCTTCGGGGATTGGGACCGAGTGGTG
CAGGACTTGGCAGCCCGTACACAGCGCCTAGAGCAGCGGGCGCAGGAGTTGCAACAGACGGGTGTGCTGGGTGCC
TTTGAGAGCAGCTTCTGGCACATGCAGGAGAAGCTGGGCATTGTGCAGGGCATCGTAGGTGCCCCGCAACACCTCA
GCCGCTCCACTGCACAGCTTGTGGAGGCCACAGAGGAGCTGCGGCGTGAAATTGGGGAGGCCACTGAGCACCTG
ACTCAGCTCGAGGCAGACCTGACAGATGTGCAAGATGAGAACTTCAATGCCAACCATGCACTAAGTGGTCTGGAG
CGAGATAGGCTTGCACTTAATCTCACACTGCGGCAGCTCGACCAGCATCTTGACTTGCTCAAACATTCAAACCTC
CTGGGTGCCTATGACAGCATCCGGCATGCCCATAGCCAGTCTGCAGAGGCAGAACGTGCTGCCAATACCTCAGCC
CTGGCAGTACCTAGCCCTGTGAGCAACTCGGCAAGTGCTCGGCATCGGACAGAGGCACTGATGGATGCTCAGAAAG
GAGGACTTCAACAGCAAACACATGGCCAACCAGCGGGCACTTGCCAAGCTCTCTGCCCATACCCACACCCCTGAGC
CTGACAGACATAAATGAGCTGGTGTGTGGGGCACCAGGGGATGCACCCTGTGCTACAAGCCCTTGTGGGGGTGCC
GGCTGTGAGATGAGGATGGGCAGCCGCGCTGTGGGGGCCTCAGCTGCAATGGGGCAGCGGTACAGCAGACCTA
GCACTGGGCCCGGGCCCCGGCACACACAGGCAGAGCTGCAGCGGGCACTGGCAGAAGGTGGTAGCATCCTCAGCAGA
GTGGCTGAGACTCGTCGGCAGGCAAGCGAGGCACAGCAGCGGGCCAGGCAGCCCTGGACAAGGCTAATGCTTCC
AGGGGACAGGTGGAACAGGCCAACCAGGAACCTTCAAGAACTTATCCAGAGTGTGAAGGACTTCTCAACCAGGAG
GGGGCTGATCCTGATAGCATTGAAATGGTGGCCACACGGGTGCTAGAGCTCTCCATCCCAGCTTCAGCTGAGCAG
ATCCAGCACCTGGCGGGTGCGATTGCAGAGCGAGTCCGGAGCCTGGCAGATGTGGATGCGATCCTGGCACGTACT
GTAGGAGATGTGCGTTCGTGCCGAGCAGCTACTGCAGGATGCACGGCGGGCAAGGAGCTGGGCTGAGGATGAGAAA
CAGAAGGCAGAGACAGTACAGGCAGCACTGGAGGAGGCCAGCGGGCACAGGGTATTGCCCAGGGTGCCATCCGG
GGGGCAGTGGCTGACACACGGGACACAGAGCAGACCCTGTACCAGGTACAGGAGAGGATGGCAGGTGCAGAGCGG
GCACTGAGCTCTGCAGGTGAAAGGGCTCGGCAGTTGGATGCTCTCCTGGAGGCTCTGAAATTGAAACGGGCAGGA
AATAGTCTGGCAGCCTCTACAGCAGAAGAAACGGCAGGCAGTGCCAGGGTCGTGCCAGGAGGCTGAGCAGCTG
CTACGCGGTCTCTGGGTGATCAGTACCAGACGGTGAAGGCCCTAGCTGAGCGCAAGGCCCAAGGTGTGCTGGCT
GCACAGGCAAGGGCAGAACAACTGCGGGATGAGGCTCGGGACCTGTTGCAAGCCGCTCAGGACAAGCTGCAGCGG
CTACAGGAATTGGAAGGCACCTATGAGGAAAATGAGCGGGCACTGGAGAGTAAGGCAGCCCAGTTGGACGGGTTG
GAGGCCAGGATGCGCAGCGTGCTTCAAGCCATCAACTTGAGGTGCAGATCTACAACACCTGCCAGTGACCCCTG
CCCAAGGCCTACCCAGTTCTTAGCACTGCCCCACATGCATGTCTGCCTATGCACTGAAGAGCTCTTGCCCCGGC
AGGGCCCCCAATAAACAGTGTGAACCCCC

1227/6881
FIGURE 1141

AGGGCCGGGAGCCCCGCCAGAGCCCGACTTCAGCCCCAGCCAGATCCCGCGTCAACGGAGGCGGAACGGCGGACC
CCGTACCCCTGCAGCATCGGAGCACCGGCGGGTGAAGGCAAGGTCCCTGGACTGGTCATATACCTCTTGTGGCCC
TGGCAGAATCAAGATGAGGCCCTGTCATGCCTCCCCAGTGAGGCCTACAGTCTGAGCAGACAGCATGGCCTGCCA
CTGGCAGTGAACACCATGTCTGCAGGAGGTGGCCGGGCCTTTGCTTGGCAAGTGTTCCCCCCCATGCCCCTTGC
CGGGTCTATGGCACAGTGGCACACCAAGATGGGCACCTGCTGGTGTGGGGGGTGTGGCCGGGCTGGACTGCCC
CTGGACACTGCTGAGACACTGGACATGGCCTCGCACACATGGCTGGCACTGGCACCCCTGCCACTGCCCCGGGCT
GGTGCAGCTGCGGTAGTTCTGGGCAAGCAGGTGCTAGTGGTGGGTGGTGTGGATGAGGTCCAGAGCCCCGGTAGCT
GCTGTAGAGGCCTTCTGATGGATGAGGGCCGCTGGGAGCGTCGGGCCACCCTCCCTCAAGCAGCCATGGGGGTT
GCAACTGTGGAGAGAGATGGTATGGTGTATGCTCTGGGGGGAATGGGGCCCTGACACGGCCCCCAGGCCCAGGTA
CGTGTGTATGACCCCGTCGGGACTGCTGGCTTTTCGCTACCCCTCCATGCCACACCCCTGCTATGGGGCCCTCCACC
TTCTGACCGGGAACAAGATCTATGTCTGGGGGGCCGCCAGGGCAAGCTCCCGGTGACTGCTTTTGAAGCCTTT
GATCTGGAGGCCCCGTACATGGACCCGGCATCCAAGCCTACCCAGCCGTGCGGCCTTTGCTGGCTGCGCCATGGCT
GAAGGCAGCGTCTTTAGCCTGGGTGGCCTGCAGCAGCCTGGGCCCCACAATTCTACTCTCGCCACACTTTGTC
AACACTGTGGAGATGTTTGACCTGGAGCATGGGTCTGGACCAATTGCCCCGCAGCCTGCGCATGAGGGATAAG
AGGGCAGACTTTGTGGTTGGGTCCCTTGGGGGCCACATTGTGGCCATTGGGGGCCTTGAAACCAGCCATGTCCT
TTGGGCTCTGTGGAGAGCTTTAGCCTTGCACGGCGGCGCTGGGAGGCATTGCCTGCCATGCCACTGCCCCGCTGC
TCCTGCTCTAGTCTGCAGGCTGGGCCCCGGCTGTTTGTATTGGGGGTGTGGCCAGGGCCCCAGTCAAGCCGTG
GAGGCACTGTGTCTGCGTGATGGGTCTGAAGGCTTGGTGGGAGCTGTCCACTGGAGCAGCTCATTGCCAGAGGC
AGCTATTTCTATGGCTCCTTTTGCTGCTGAGGACACTCACTGTGGCTCTGTGGGATGAGAGAGGCATGGGGGTGA
GCACTTGAAACACTGCCTTGGGGCCTTGGGTTAGGGGAGCCTTTGTCTTTAGTGCAGGACACACATATGCTTACA
CCTACCTTTATCACCATTCGTTTCATGAATCATGCCTAGCTCCATCCTTGCCCTGGGACCTACTAGGCCTTCCATC
CAACTGGGAAATGGGGAGAAGCAAAGCTGGCCTCATGCTCTTCAGGGTCAGTTCCTATCTGGAGTTGACCAGGCC
TACCCAGTTGCCATTCTTGAAAAATCTCAGCTGCCAGGCTGCCTTTAGGGTCCCTGCAGACCCAGGAGAGTTGA
GAGGGTGGGGGACACAGAGAGAATAGAGAGGATGTGGAACTGCCAGAGGGCCGGAGCGCAGGAGTTCAAGTGGA
GGAATGCTGGCTTTGAGCCCTCTACACTGCTGGTTGTATGACCTTGGACAAGTCACTTCACCTCTCTGTGCCTCA
GCATCCTCATCTATAAATGGGGATCTCTGAAACCTTCTACCTACCTACCTACAGGGCTGTTGTGAGGACCCA
GGGAGTTTGGATGTGGAAGTAAAAGTGCTGCTAAAACCTA

1228/6881
FIGURE 1142

MSAGGGRAFAWQVFPPMPTCRVYGTVAHQDGHLLVLGGCGRAGLPLDTAETLDMASHTWLALAPLPTARAGAAV
VLGKQVLVVGGVDEVQSPVAAVEAFMLDEGRWERRATLPQAAMGVATVERDGMVYALGGMGPD TAPQAQVRVYDP
RRDCWLSLP SMP TPCYGASTFLHGNKIYVLGGRQGKLPVTAFEAFDLEARTWTRHPSLPSRRAFAGCAMAEGSVF
SLGGLQQPGPHNFYSRPHFVNTVEMFDLEHGSWTKLPRSLRMRDKRADFVVGSLGGHIVAIGGLGNQPCPLGSVE
SFSLARRRWEALPAMPTARCSCSSLQAGPRLFVIGGVAQGSPSQAVEALCLRDGV

1229/6881
FIGURE 1143

GGCGGCAGAGAGGAGACTATGGAAACGTCAGGTGCTGCTGAGCGAGCCCGAGGAGGCGGCGGCTCTGTATCGGGGC
CTTAGCCGCCAGCCCGCGCTGAGCGCCGCTGCCTGGGCCCCGAGGTCACCACGCAGTACGGCGGCCAATACCGG
ACGGTGACACTGAGTGGACCCAGAGGGACCTGGAACGCATGGAGAACATTGATTCTGCCGCCAATACCTGGTG
TTCCATGACGGGGACTCAGTGGTGTTTGCAGGACCTGCAGGCAACAGTGTGGAGACCCGGGGGGAAGTGTGAGC
AGAGAGTCTCCTTCAGGCACCATGAAAGCTGTGCTGCGCAAGGCTGGAGGCACGGGCCCTGGGGAAGAGAAGCAG
TTCCTGGAGGTCTGGGAGAAGAACCGGAAGCTCAAGAGCTTCAACCTGTCAGCGCTGGAGAAACATGGGCCTGTT
TATGAGGATGACTGCTTTGGCTGCCTGTCTGGTGCCTCGGAGACACACTTGTGTATGTGGCAGAGAAGAAG
CGCCCCAAGGCCGAGTCCTTCTTTAGACCAAAGCCTTGGACGTCAGTGCCAGCGATGATGAGATAGCCAGGCTG
AAGAAGCCAGACCAAGCCATCAAGGGGATCAGTTTGTGTTTTATGAAGACTGGGGAGAAAACATGGTTTCCAAA
AGCATCCCTGTGCTCTGCGTGCTGGATGTGAGAGTGGCAACATCTCTGTGCTTGAGGGGGTCCCTGAGAAATGTG
TCCCTGGACAGGCATTTTGGGCCCCCTGGAGATGCTGGTGTGGTGTGTTGTGGGCTGGTGGCATGAGCCCTTCCGG
TTGGGCATCCGCTTTTGCACCAATCGCAGGTGAGCCCTGTATTATGTGGACCTCATCGGGGGGAAGTGTGAGCTC
CTCTCGGATGACTCCCTGGCTGTCTCTTCTCCCCGGCTGAGCCCAGACCAATGTGCGATTGTCTACCTGCAGTAC
CCATCTCTGATCCCCCATCACCAATGCAGCCAGCTGTGCTGTATGACTGGTATACCAAGGTTACCTCAGTGGTG
GTAGATGTTGTGCTCGGCAGCTGGGAGAGAACTTCTCTGGGATCTACTGCAGCCTTCTGCCTTTGGGATGCTGG
TCAGCTGACAGCCAGAGAGTGGTCTTTGACTCGGCTCAGCGCAGCCGGCAGGACCTGTTTGTGCTGTGGACACCCAA
GTGGGCACTGTGACCTCCCTCAGAGCTGGAGGGTCAGGTGGGAGCTGGAAGTTGCTCACAATTGACCAGGACCTC
ATGGTGGCACAGTTTTTCCACACCCAGCCTACCTCCAACCTGAAAGTTGGGTTCCCTGCCTTCTGCAGGGAAGGAG
CAGTCAGTGTGTTGTGGGTGTCCCTGGAGGAGGCCGAGCCATTCCCGACATCCACTGGGGCATCCGGGTGCTACAG
CCACCCCCAGAGCAAGAGAATGTGCAGTATGCTGGCCTTGACTTTGAAGCAATCCTGCTGCAGCCTGGCAGCCCT
CCAGATAAGACCCAAGTGCCCATGGTGGTTCATGCCCCACGGGGGGCCCCATTATCCTTTGTCACTGCCTGGATG
CTGTTCCAGCCATGCTTTGCAAGATGGGCTTTGCGGTACTACTAGTGAAGTATCGTGGCTCCACGGGCTTTGGC
CAGGACAGCATCCTCTCCCTCCAGGCAATGTGGGCCACCAGGATGTGAAGGATGTCCAGTTTGCAGTGGAAACAG
GTGCTCCAGGAGGAACACTTTGATGCAAGCCATGTGGCCCTTATGGGTGGTTCCCATGGTGGCTTCATTTCTGC
CACTTGATTGGTCAGTACCCAGAGACCTACAGGGCCTGCGTGGCCCGGAACCCCGTGATCAACATCGCCTCCATG
TTGGGCTCCACTGACATCCCTGACTGGTGCCTGGTGGAGGCTGGCTTTTCTTTTTCAGCAGTACTGCCTGCCAGAC
CTCAGCGTGTGGGCTGAGATGCTGGACAAATCGCCCATCAGATACATCCCTCAGGTGAAGACACCACTGTTACTG
ATGTTGGGCCAGGAGGACCGCGTGTGCCCTTCAAGCAGGGCATGGAGTATTACCGTGCCCTCAAGACCCGGAAT
GTGCTGTTCGGCTCCTGCTCTATCCAAAAGCACCCACGCATTATCAGAGGTGGAGGTGGAGTCAGACAGCTTC
ATGAATGCTGTGCTCTGGCTACGCACACACTTGGGCAGCTGAAGCCCTGCCATTCTGCATGAGCTGATCAGCCTG
TGCCACACTTCGCTCTTGGAGAGCTCAACGGTCTGGCAGGGCAGCAGGAGGCTTTCTGGGCTCTGGACTCCACGG
ATGCGTGGGCAGAGGAATGTGGGCTATGTAGTCATAATAAATTAGGAC

1230/6881
FIGURE 1144

MERQVLLSEPEEAAALYRGLSRQPALSAACLGPEVTTQYGGQYRTVHTEWTQRDLERMENIRFCRQYLVFHDGDS
VVFAGPAGNSVETRGEILLSRESPSGTMKAVLRKAGGTGPGEEKQFLEVWEKNRKLKSFNLSALEKHGFPVYEDDCF
GCLSWSHSETHLLYVAEKKRPKAESFFQTKALDVSASDDEIARLKKPDQAIKGDQFVFYEDWGENMVS KSIPVLC
VLDVESGNISVLEGV PENVSPGQAFWAPGDAGVVFVGWWHEPFRLGIRFCTNRRSALYYVDLIGGKCELLSDDSL
AVSSPRLSPDQCRIVYLQYPSLIPHHQCSQLCLYDWYTKVTSVVVDVVPRLGENFSGIYCSLLPLGCWSADSQR
VVFDSAQRSRQDLFAVDTQVGTVTSLTAGGSGGSWKLLTIDQDLMVAQFSTPSLPPTLKVGF LPSAGKEQS VLWV
SLEEAEPIPDIIHWGIRVLQPPPEQENVQYAGLD FEAILLQPGSPDKTQVPMVMPHGGPHSSFVTAWMLFPAML
CKMGFAVLLVN YRGSTGFGQDSILSLPGNVGHQDV KDVQFAVEQVLQEEHFDASHVALMGGSHGGFISCHLIGQY
PETYRACVARNPVINIASMLGSTDIPDWCVVEAGFPFSSDCLPDL SVWAEMLDKSPIRYIPQVKTPLLLMLGQED
RRVPFKQGM EYYRALKTRNVPVRLLLYPKSTHALSEVEVESDSFMNAVLWLRTHLGS

1231/6881
FIGURE 1145

TACTCCCGGAGTCACTCATCCCTTAAGCAAGCAGGGTGGGGTTAGGTGCGCGTGCGCGGTTTTAATACTCCTCCC
CGAACTGCCAACTCTTCACGCACGCGAAGTAGGCCCCACCCTGGCTGGGTTTACGCGTGCGCACTAACGGGCCTG
GTCCCGGAAGACCACACGCGTGCGTGGTGGGGACTACGGTGACAGTACCCCGGGTGGGGCGAGGGCCAGTCA**ATGG**
CGGAGTCCTGGTCTGGGCAGGCCTTGCAAGGCTCTGCCGGCCACGGTGCTGGGCGCGCTGGGCAGCGAGTTCTTGC
GGGAGTGGGAGGCGCAGGACATGCGCGTGACCCTCTTCAAGCTGCTGCTGCTGTGGTTGGTGTAAAGTCTCCTGG
GCATCCAGCTGGCGTGGGGGTTCTACGGGAATACAGTGACCGGGTTGTATCACCGTCCAGGTCTGGGTGGTCAGA
ATGGATCCACGCCTGATGGCTCCACGCATTTCCCTTCGTGGGAAAATGGCAGCAAACGAACCTCTCAAAAACCCACA
GAGAA**TAA**GGGAAGGCAGCAGAGGGTCTCCAAGGGCATCACTGGGTCTGCTGGCTTCTACACTGGGTTCTGCTAC
TCCCCAGACCTCAGGGACAACCTGCCGGGGGTTTCAAGGGTTGGTAGCAGGGAGTACCCAGTGCCTACAGGGCTGGGC
CTCTTCTGCTCTTAAGCCTGCTCCCTCACCCAGGCACTGGGCAAGTGAAGAGTTTGCCTGTACTCTTATCTGGG
TGCCTTAAGGAGAGAGATTGTGTTCTTCTCTCTCAGGGGTGATAACTCAGGAAGCCTCTGGGTTGGGAAGACCA
TCAGTTCTTTTGTCTTAGGTTTCTTTTCTGTCCCTCTTCCATCCCCAAGATGTGACCCCATAAAAATTTTCTCT
GAGTTGGCCAGGCATGGTGGCTCACGCCTGTAATCCCAACACTTTGGGAGGCTGAGGCAGGCAGATCACGAGGTC
AGGAGTTCGAGACCAGCCTGACCAACATGGTGAAAACCCCATCTCTACTAAAAATACAAAAATTAGCCGGGTGTG
GTGGCACACACCAGTAATCCCAGCTACTCGGGAGGCTGAAGCAGGAGATTTGCTTGAACCTGGGAGGCAGAGGTT
GCAGTGAGCCAAGATTGCGCCGTTGTACTCCAGCCTGGGCAACAGAGCAAGACCCATCTCAAAAAAAAAAATTTT
TTCCTGAGAGGAAGCCTGAGGTTGACCAGCTCTGGGGTTTGTAAGGCAGGTCTGTTTTCTCTAGGCCCTGAGTT
TTCTGAATCTCTGGTTTTGCTTTGTTGGCAAGGAGCCAGGGAATCCTGACCTGAGCCAGACCTTAAGCTCTATGG
TTATTTAGCTGGCCATTCAGGTATAAGGCAGGGTGGTGTACCTGCTGGCACTATCCAGATGGAGGCACCAAACAC
CCACATACCTGGCCCAACCAGACTTCTCCCGTGAGCCAGGCAAAGGAAATTGTCATCTGCCAACTGTCCTACTCA
TATTCCTCTCAGTCCTTCTTGGGGGTAAGCTGATTACCTGAAGGACAGCTGAACCCCTGGGGTAGCCTCCTATCC
ACCACTGCTTAAGTGCCTATGGGAATGTGGGTCTGCACCTTGTCCCTCATAGGATGGTACCAAGCATTTAGTGC
ACAGTGGCCCCATCATAGCCTGCAGCCTCATCATTTCCCATCTGGACCTGGTACAAATGCACGTACAGGCTCAG
CTCCTCCCCACTAGCATCTTCTCTACCTTCAAGAACCAGGCAGCCCTGCCATGTCACAATAGGCCAGGGGAGTTT
CCAAAGATGTGGGTGGCAAATGCCCTATAGAAACACCAGTACCTGAAAGCACTGTAGCCCTGGACCTGCCTCCT
TCCCTCGGGGCCATACTTCTGTTTCCATCTGCTGGGCCACCAGCCACTTTAGTGACCCCTGCCTACTTCTTCTCT
GTTGGATATCATACTTCCATCTGGCTGCCTTTGCTTAAGCCATCTTTGTGGTAGAGGGGCCCTGGAATTGCAGCT
GTACTGAGGATGATGTTATTACAGCCCTGGGCCACCCACTAATACTACTGCACAGAGTCAGGATCTCACATTT
CACCCCAGGCTCAACTGAGGATGTGGCTTATTAAACACGGAAGTGC

1232/6881
FIGURE 1146

MAESWSGQALQALPATVLGALGSEFLREWEAQDMRVTLFKLLLLWLVLSSLGIQLAWGFYGNVTGGLYHRPGLGG
QNGSTPDGSTHFPSWEMAANEPLKTHRE

1233/6881
FIGURE 1147

CCCGAGTGCTTCCCGCAGAGGGCTGGTGGTGGGAGCGGAGTGGGTGCGGGCGGGCCGAGCCGGGCCGTGGGCCGT
GTGGGGGCCGGGCGGCGGGCCGGGCGGCGGACGGCGGGATCGGCTGCACCGTGAGCGCCGAGGACAAGGCGGCGG
CCGAGCGCTCTAAGATGATCGACAAGAACCTGCGGGAGGACGGAGAGAAGGCGGCGGGGAGGTGAAGTTGCTGC
TGTTGGGTGCTGGGGAGTCAGGGAAGAGCACCATCGTCAAGCAGATGAAGATCATCCACGAGGATGGCTACTCCG
AGGAGGAATGCCGGCAGTACCGGGCGGTTGTCTACAGCAACACCATCCAGTCCATCATGGCCATTGTCAAAGCCA
TGGGCAACCTGCAGATCGACTTTGCCGACCCCTCCAGAGCGGACGACGCCAGGCAGCTATTTGCACTGTCCTGCA
CCGCCGAGGAGCAAGGCGTGCTCCCTGATGACCTGTCCGGCGTCATCCGGAGGCTCTGGGCTGACCATGGTGTGC
AGGCCTGCTTTGGCCGCTCAAGGGAATACCAGCTCAACGACTCAGCTGCCTACTACCTGAACGACCTGGAGCGTA
TTGCACAGAGTGACTACATCCCCACACAGCAAGATGTGCTACGGACCCGCGTAAAGACCACGGGGATCGTGGAGA
CACACTTCACCTTCAAGGACCTACACTTCAAGATGTTTGATGTGGGTGGTCAGCGGTCTGAGCGGAAGAAGTGGA
TCCACTGCTTTGAGGGCGTCACAGCCATCATCTTCTGCGTAGCCTTGAGCGCCTATGACTTGGTGCTAGCTGAGG
ACGAGGAGATGAACCGCATGCATGAGAGCATGAAGCTATTGATAGCATCTGCAACAACAAGTGGTTCACAGACA
CGTCCATCATCTCTTCTCAACAAGAAGGACCTGTTTGAGGAGAAGATCACACACAGTCCCCTGACCATCTGCT
TCCCTGAGTACACAGGGGCCAACAAATATGATGAGGCAGCCAGCTACATCCAGAGTAAGTTTGAGGACCTGAATA
AGCGCAAAGACACCAAGGAGATCTACACGCACTTCACGTGCGCCACCGACACCAAGAACGTGCAGTTCGTGTTTG
ACGCCGTCACCGATGTCATCATCAAGAACAACCTGAAGGACTGCGGCCTCTTCTGAGGGGCGAGCGGGGCTGGCG
GGATGGGCCACCGCGACTTTGTACCCCCCAACCCCTGAGGAAGATGGGGGCAAGAAGATCACGCTCCCCGCCTG
TTCCCCGCGCTTTTCTCCTCTTCTCTCTTTGTTCTCAGCTCCCCCTGTCCCCCTCAGCTCCAGACGTAGGGG
AGGGGTTGCCACAGGCCTCCCTGTTTGAAGCCTGCCCTTGTCTGAGATGCTGGTAATGGCCATGGTACCCCTTC
TGGGCATCTGTTCTGGTTTTTAACCATTGTCTTGTCTGTGATGAGGGGAGGGGGGCACATGCTGAGTCTCCCAA
GGCTGCGTCTGGAGGGGCCCTGCTTCTCCAGCCTGGACCCCAGCTTTGCCCAACACCAGCCCCTGCCCCAGCC
CAAGTCCAAATGTTTACAGGGAGCCTCCTGCCAGTCCCCCAACCCCAGCCGCTCGGAGGCCCCAAAGGAAAAAG
CACAAGAAGCGTGAGACGCCACCATTCCTGGAAACCACAGTCC

1234/6881
FIGURE 1148

MGCTVSAEDKAAAERSKMIDKNLREDGEKAAREVKLLLLGAGESGKSTIVKQMKIIHEDGYSEEECRQYRAVVYS
NTIQSIMAIVKAMGNLQIDFADPSRADDARQLFALSCTAEEQGVLPDDLSGVIRRLWADHGVQACFGRSREYQLN
DSAAYYLNDLERIAQSDYIPTQQDVLRTVRVKTGTGIVETHFTFKDLHFKMFDVGGQRSEKRWIHCFFEGVTAIIFC
VALSAYDLVLAEDEEMNRMHESMKLFDSICNNKWFTDTSIILFLNKKDLFEKITHSPLTICFPPEYTGANKYDEA
ASYIQSKFEDLNKRKDTKEIYTHFTCATDTKNVQFVFDVTDVVIKNNLKDCGLF

1235/6881
FIGURE 1149

TCTGTGATTGTGGCCAGGCGGGGCACCCTCGGAGGGGAGGGTTTCGGAAGTGGAATGCGACCCCCAGCCTCTTTC
CCCTAGGGGCTGTAATCTGATCCCTGGGGACTCCCCCCTAGCCTCCCGCCCTCGCCCTCACTGCTGACTCCTCT
TCCAGATCCTGGGGCAGAGTCCAGGGCAGCTCAAGGCTCCTCCACACACACACCCGCTGAACCCTGAGCACCCCTG
AGCTGCTGAGATGCGGGCGGGCCGGGGCTGCCGCCGTGATCCCGGGCCTGGCCCTGCTCTGGGCAGTGGGGCTGGG
GAGTGCCGCCCCCAGCCCCCAGCCTTTCGGCTCTCCTTCCAAGAGCTCCAGGCCTGGCATGGTCTCCAGACTTT
CAGCCTGGAGCGAACCTGCTGCTACCAGGCCTTGTGTTGGATGAGGAGCGTGGACGCCTGTTTGTGGGTGCCGA
GAACCATGTGGCCTCCCTCAACCTGGACAACATCAGCAAGCGGGCCAAGAAGCTGGCCTGGCCGGCCCCCTGTGGA
ATGGCGAGAGGAGTGCAACTGGGCAGGGAAGGACATTGGTACTGAGTGCATGAACTTCGTGAAGTTGCTGCATGC
CTACAACCGCACCCATTTGCTGGCCTGTGGCACGGGAGCCTTCCACCCAACCTGTGCCTTTGTGGAAGTGGGCCA
CCGGGCAGAGGAGCCCGTCTCCGGCTGGACCCAGGAAGGATAGAGGATGGCAAGGGGAAGAGTCCTTATGACC
CAGGCATCGGGCTGCCTCCGTGCTGGTGGGGGAGGAGCTATACTCAGGGGTGGCAGCAGACCTCATGGGACGAGA
CTTTACCATCTTTTCGCAGCCTAGGGCAACGTCCAAGTCTCCGAACAGAGCCACACGACTCCCGCTGGCTCAATGA
GCCAAGTTTGTCAAGGTATTTTGGATCCCGGAGAGCGAGAACCAGACGACGACAAAATCTACTTCTTCTTCG
TGAGACGGCGGTAGAGGCGGCGCCGGCACTGGGACGCCTGTCCGTGTCCCGCGTTGGCCAGATCTGCCGGAACGA
CGTGGGCGGGCCAGCGCAGCCTGGTCAACAAGTGGACGACGTTCCCTGAAGGCGCGGCTGGTGTGCTCGGTGCCCGG
CGTCGAGGGCGACACCCACTTCGATCAGCTCCAGGATGTGTTTCTGTTGTCTCGCGGGACCACCGGACCCCGCT
GCTCTATGCCGTCTTCTCCACGTCCAGCAGCATCTTCCAGGGCTCTGCGGTGTGCGTGTACAGCATGAACGACGT
GCGCCGGGCCTTCTTGGGACCCTTTCACACAAGGAGGGGCCCATGCACCAAGTGGGTGTCATACCAGGGTCGCGT
CCCCTACCCGCGGCCAGGCATGTGCCCCAGCAAGACCTTTGGCACCTTCAGTTCACCAAGGACTTCCAGACGA
TGTATCCAGTTTGC GCGGAACCACCCCTCATGTACAACCTCTGTCTGCCACTGGGGGGCGCCCTCTTTTCTCT
ACAAGTTGGAGCCAATTACACCTTCACTCAAATTGCCGCGGACCGGGTGCAGCCGCTGACGGACACTATGACGT
CCTCTTCATTGGCACAGACGTTGGCACGGTGTGTAAGGTGATCTCGGTCCCCAAGGGCAGTAGGCCAGCGCAGA
GGGGCTGCTCCTGGAGGAGCTGCACGTGTTTGGAGACTCGGCCGCTGTACACAGCATGCAAATTTCTTCCAAGAG
GCACAGCTGTACGTAGCTCGCGGAGCGCGGTGGCCAGATCGCGTTGCACCGCTGCGCTGCCACGGCCGCGT
CTGCACCGAATGCTGTCTGGCGCGTGACCCCTACTGCGCCTGGGACGGGGTTCGCGTGCACGCGCTTCCAGCCAG
TGCCAAGAGGCGGTTCCGGCGGCAAGACGTAAGGAATGGCGACCCAGCACGTTGTGCTCCGGAGACTCGTCTCG
TCCCGCGCTGCTGGAACACAAGGTGTTCCGGCTGGAGGGCAGCAGCGCCTTTCTGGAGTGTGAGCCCCGCTCGCT
GCAGGCGCGCGTGGAGTGGACTTTCCAGCGCGCAGGGGTGACAGCCCACACCCAGGTGCTGGCAGAGGAGCGCAC
CGAGCGCACCGCCCGGGGACTACTGCTGCGCAGGCTGCGGCGCCGGGACTCGGGCGTGTACTTGTGCGCCGCCGT
CGAGCAGGGCTTTACGCAACCGCTGCGTGCCTGTGCTGCACGTGTTGAGTGCTACGCAGGCCGAACGACTGGC
GCGGGCCGAGGAGGCTGCGCCCCGCCGCGCGGGGCCCAAACCTCTGGTACCGGGACTTTCTGCAGCTGGTGGGA
GCCGGGCGGAGGTGGCAGCGCGAACTCCCTGCGCATGTGCCGCCCGCAGCCTGCGCTGCAGTCACTGCCCTTGGGA
GTGCGCGAGAAAGGGCCGTAACCGGAGGACCCACGCCCCCTGAGCCTCGCGCTGAGCGGGGGCCGCGCAGCGCAAC
GCACTGGTGAACAGACTGTCCCCACGCCGGAACCAAGCAGGAGACGACAGGCGAGAGAGGAGCCAGACAGACCC
TGAAAAGAAGGACGGGTGGGGCCGGGCACATTGGGGGTACCGGCCGATGGAGACACCAACCGACAGGCCCTGG
CTGAGGGCAGCTGCGCGGGCTTATTTATTAACAGGATAACCTTGAATGTAGCAGCCCCGGGAGGGCGGCACAGG
TCGGGCGCAGGATTAGCCGGAGGGAAGGGACGGGGAAGCCGAGCTCCAGAGCAACGACCAGGGCCGAGGAGGTG
CCTGGAGTGCCACCCCTGGGAGACAGACCCACCTCCTTGGGTAGTGAGCAGTGAGCAGAAAGCTGTGAACAGGC
TGGGCTGCTGGAGGTGGGGCGAGGCAGGCCGACTGTACTAAAGTAACGCAATAAACGCATTATCAGCCA

1236/6881
FIGURE 1150

MGRAGAAAVIPGLALLWAVGLGSAAPSPPRRLRLSFQELQAWHGLQTFSLERTCCYQALLVDEERGRLFVGAENHV
ASLNLDNISKRAKKLAWPAPVEWREECNWAGKDIGTECMNFVKLLHAYNRTHLLACGTGAFHPTCAFVEVGHRAE
EPVLRLLDPGRIEDGKGKSPYDPRHRAASVLVGEELYSGVAADLMGRDFTIFRSLGQRPSLRTEPHDSRWLNPKF
VKVFWIPESENPDDDKIYFFFRETAVEAAPALGRLSVSRVGQICRNDVGGQRSLVNKWTTFLLKARLVCSVPGVEG
DTHFDQLQDVFLLSRDHRTPLLYAVFSTSSSIFQGSAVCVYSMNDVRR AFLGPF AHKEGPMHQWVS YQGRVPYP
RPGMCPSKTFTGTFSSTKDFPDDVIQFARNHPLMYNSVLPTGGRPLFLQVGANYTFTQIAADRVAADGHYDVLFI
GTDVGTVLKVISVPKGSRPSAEGLLLEELHVFEDSAAVTSMQISSKRHQLYVASRSAVAQIALHRCAAHGRVCTE
CCLARDPYCAWDGVACTRFQPSAKRRFRQQDVRNGDPSTLCSGDSSRPALLEHKVFGVEGSSAFLECEPRSLQAR
VEWTFQRAGVTAHTQVLAEERTERTARGLLLRLRRRDSGVYLCAAVEQGFTQPLRRLSLHVLSATQAERLARAE
EAAPAAPP GPKLWYRDFLQLVEPGGGGSANSLRMCRPQPALQSLPLESRRKGRNRRTHAPEPRAERGPR SATHW

1237/6881
FIGURE 1151

ATGGGCCCCAAAAATCTTGCGAAGTCACCTTTTTTCCACTGCCTGAGGTTTGGCTGTTGCTCCTGTTATCCCAA
GCTCTAAGCCCTTCCCATGGTCCCCAGACCCAGGCAGGGGTAGGTCTCGTCTGGAGTGTCCCGCTGCCAAGTGCC
CTGAGAAGCCAGTCCCTGCCTTGGTGCTCCACTGAGGGACGCTTCGGAGTTAACACCGTGCACTTGTTCCTCGACG
CGGGGCTGGGGCGCGCGCAGGGCATTGTGGGTGCATAGTTTCAGCCAGCGCGTCGTCTGGCTGCTAGCCGCCGTCGC
CTGCGCGCTCAGGCCTCTGGGATTAGTAGTTTTAGCCTCGTGATGGCGGGGCGCCTCGCGAAGATGGTGGCGCG
CGTGGCGTGTGGCTCCCGTCGTCTGGCCAAGTCTCAGCGCAGCGCACCGGCCGGCGTCTCGTTGGCCTGGAGCCC
ACACCCACCGGGTCCCTGACCCCGCGCCCCCGCGCCCGGTTCCCGGCATGCCTCGCGCCCGTAAGGGCAACACG
CTCCGGAAGGGTGGTCAGCGCCGTGGAGGAGGTGCCCCGAGCAGTGCCCCAAGCTGACTCGGGTTCCAGTGACGAT
GAGGCAGCCAGTGAGGCCCCGACGACCGCCAGTGAATGCCCCAGCCTTCTCAGCACCAGTGCAGAGGACAGCCCTT
GGGGGGGATGTGCTGGATGAGCAGGGCCAGCAGGAAGACCTTGAGGAAAAGCTGAAGGAGTATGTGGACTGTCTC
ACAGACAAGAGTGCCAAGACCCGGCAGGGTGCTCTTGAGAGCCTGCGCCTGGCCCTAGCGTCCCGCCTACTCCCC
GACTTCTTGCTGGAGCGCCGCTCACGCTAGCCGATGCCCTGGAAAAGTGCTCAAGAAAGGGAAGGGCGAGGAA
CAAGCCCTGGCTGCTGCTGTGCTAGGCCTGCTCTGCGTGACAGTGGGCCCTGGACCTAAGGGTGAGGAGCTGTTT
CACAGCCTGCAGCCTCTGCTGGTCTCTGTGCTCAGTGACAGCACAGCTAGCCCTGCTGCCCCGCTCCACTGTGCT
TCTGCCCTTGGCCTGGGCTGCTACGTGGCTGCCGCTGACATCCAGGACCTGGTCTCTTGCTTGCCTTGCTTAGAA
AGTGTTTTTAGCCGGTTCTATGGCTTGGGGGGCAGCTCCACAAGTCTGTGGTTCTTGCCAGCCTGCACGGCCTG
CTCTCTGCTGCCCTGCAGGCCTGGGCATTGCTGCTACCATCTGCCCTAGCACCCAAATCAGCCACATCCTTGAC
AGGCAGCTGCCCCGGCTGCCCCAGCTCTTGCTCCAGTGAAAGTGTGAACCTGCGGATCGCTGCCGGTGAAACCAT
GCACTGCTCTTTGAGCTTGCCCGGGACCTTGAGGAGGAGTTTGTTTACGAGGACATGGAGGCCCTCTGCAGTGTC
CTGCGCACTCTGGCCACTGACAGTAACAAGTACCGTGCCAAGGCTGATCGTCGGCGCCAGCGCTCTACTTTCCGC
GCCGTGCTGCACTCCGTGGAGGGCGGTGAATGCGAAGAAGAGATAGTGCGCTTCGGCTTTGAGGTGCTCTACATG
GACAGCTGGGCTCGGCACCGGATCTACGCTGCCTTCAAGGAAGTGCTGGGTTGCGGCATGCACCACCACCTCCAG
AACAAATGAGCTACTCCGTGACATCTTTGGCCTGGGCCCTGTGCTGTTGCTGGATGCCACTGCCCTGAAGGCCTGC
AAGGTTCCACGCTTTGAGAAGCACCTGTACAATGCTGCTGCCTTCAAAGCCCGGACCAAGGCTCGAAGCCGTGTG
CGGGACAAGCGGGCAGACATCCTGTGAAAGCAGGACCTGCTGAAGAGGAGACTTTCTATGCCCTTGGTCCGTATTT
TTAACAGAAGACAGTGCAACAAGTGGTCTCCACCAGTATTTGTCACTTTATTTTTTTTAAATGACAAAACCAAAAA
CAGACATGGGGTGGGTAGCTGGGGGCCCGGACACTTGGGACCCTGACCCCTTTGTCCCTGCACTCAGCCCTGTGG
CCCCTTCTGTCTGTCTCAGGCCAGGCTAAATATGTGCCTTCTCAGGGCTGTGGGGCAGGCACTAGGGGGCCT
TTCCCTTCTTTCTTTCTCAGGCCTTGCTCCCCCAGGATGACCCACTCTTAGGGGGGTGGTGGCATCTGGACAA
ATGCCACCACAGCAGGTGGGGTGGCAAAAGCTACCTGGAATGGATTTGTGTGCTGATTTTTTAAGGATTATTACAGA
TAATTAAACAGAACGGTCAGCCTTCAAAAAAAAAAAAAAAAAAAAAATTCCTGCGGCCGCAAGGC

1238/6881
FIGURE 1152

MGPKKSWRSHFFPLPEVWLLLLLSQALSPSHGPQTQAGVGLVWSVPLPSALRSQSCLGAPLRDASELTTVHLFPT
RGWGARRALWVHSSASASSAASRRRLRAQASGISSFSLVDGGAPREDGGARGVWLPSSGQVSAQRTGRRLVGLEP
TPTGSLTPRPPRPVPGMPRARKGNTLRKGGQRRGGGARSSAQADSGSSDDEAASEARSTASECPSLLSTTAEDSL
GGDVVDEQGQQEDLEEKLKEYVDCLTDKSAKTRQGALESRLALASRLLPDFLLERRLTLADALEKCLKKGKGEE
QALAAAVLGLLCVQLGPGPKGEELFHSLOPLLVSVLSDSTASPAARLHCASALGLGCVAAADIQDLVSCIACLE
SVFSRFYGLGGSSTSPVVPASLHGLLSAALQAWALLLTICPSTQISHILDRQLPRLPQLLSSES VNLRIAAGETI
ALLFELARDLEEEFVYEDMEALCSVLRTLATDSNKYRAKADRRRQRSTFRAVLHSVEGGECEEEIIVRFGFEVLYM
DSWARHRIYAAFKEVLGSGMHHLQNNELLRDIFGLGPVLLLDATAALKACKVPRFEKHLYNAAAFKARTKARSRV
RDKRADIL

1239/6881
FIGURE 1153

TGCGGCCGCGTTTCCGTGGAGACAGCCGAGCCTGCGGAAGGCGGCGGCGGCACCTGCGATCAGCGGCTGGGG
CAGGTTATGGTAGTGCGGACTGCGGTGTGAGCAGAGCGGCCACGGGGCCGCCATGCGCCGGCGGCCCTGACATG

GGCGCCAGCGGGTCCAAAGCTCGGGGCGCTGTGGCCCTTCGCCTCGGCGGCGGAGGCGGCGGCTCAGAGGCAGCA
GGAGCTGAGCAAGCTTTGGTGCGGCCTCGGGGCCGAGCTGTGCCCCCTTCGTATTACGCGCCGCGGCTCTATG
TTCTATGATGAGGATGGGGATCTGGCTCACGAGTTCTATGAGGAGACAATCGTCACCAAGAACGGGCAGAAGCGG
GCCAAGCTGAGGCGAGTGCATAAGAATCTGATTCCCTCAGGGCATCGTGAAGCTGGATCACCCCGCATCCACGTG
GATTTCCCTGTGATCCTCTATGAGGTGTGACCCTGGGAGGTGGCAGACAGAAGCACCCCTGCCCGGCAAGAAA
CTCCCAGGCTCAATCAAGGTGTGGCTTCCATTGAGGAGCCCAGGCTGGGGCCACAACCCTGAATAAACTCTGTTG
GCCCCATAACCTTCAGCTGTGAGCGGGTCCGTCCCACAGTATTGGTTGGGTGTTGGTTTGTGTGTGGACAAGAGGT
GGTTGGTGGGTGGTGAAGGCTAATGGCAGAGTTAGCACCCCACTCTCCCAAGCCACCCCTGCAAGCAGCATAGCA
GGGCATATACCAGTCAGGAATGCCCGTTACCTGGTTCCTTGCTTGGTCTGCTTTCTTCCAAGTTTGCCTGGGGCC
TAGCCCTGCTAGAGGCTACAGCACTTTACAAGCAAGGTATGCTTTCTTCCAGCCCTAGGCTGTGGGCACTGTAT
ACAAGTAGGAACCTTCCTTTCTTCACTTCCCTTTTAACCCCTAGTCAGAGCATTTTCAGCCGTTTGCTACCTCGAT
TCCTCCTGTGTTGGACAGAGGCTGGGGGCGAGTGCCAGCCTGATTCTTCCGACCTACCTGCCATTTGTTCCCGCCT
TCAGATGGATGGACAGTTTGTCTGGCTATTGATAGGAGTGGGGACTGGGTGGGGGCTTCTCCCTCTACCCAGGGCT
GGGCTGATCCCCCTACTGCAACTAACTGTTGCCCCCAACCCCGAACCCCAAGTTGAGGAGTTGAGAGAGTGCAG
GCTGGGGTCAGGACAGGCTGCGGATGCTTGTGCCTATGGGGAGTTACTCCAACCCACCTATTCTGTCTAATCTCC
ATGGCTTTGCACCAAATCCTCCACCCCTCCAATTGGGAGGGGACTGTTACACACCTTGTGGTAAGGGACAACACC
CTAAGGCTGGTGCCAGTAGTTATGAGTAGCCTACCACCCCTCCCTTACAGTAACCCCAACCCCTTCAGGATCAG
TCAAGGGAAAGCACTAGAACCCCTGGGTAGGGAAAGAAAGGAGGGAAAAACCATAAAAGGAATACTTATAATGTG
AAGGTTTGTAATAGTCCATGATGATGTCGTGGCAGAGTCTGATTTCTATATAGAGGTGACTTTTTTTTTTAAGTA
CTGTGCAAGCTCTGTGCTTCTATAATGTGGGAAATGGCTTGGGGAGGATGGCCCTAGCTTAGGAAGACTGTTGT
GTTATTTGTTCAATTTCAATAAAATGATTTGTAGATCCTGC

1240/6881
FIGURE 1154

MGASGSKARGLWPFASAAGGGGSEAAGAEQALVRPRGRAVPPFVFTRRGSMFYDEDGDLAHEFYEETIVTKNGQK
RAKLRRVHKNLIPQGIVKLDHPRIHVDFPVILYEV

1241/6881
FIGURE 1155

GGCACGAGGCTGCGGCCGCCAGCTCCCGCGACCGCCTCTCCTGCCCTCGCCGGTACCTCAGCAAGGTGCCACTA
GAAGCGCCAGGCTGGGGCCGCCTCTGAGCGCCCCGCGGGGCCATGGATGGTGAAACAGCAGAGGAGCAGGGGGG
CCCTGTGCCCCCGCCAGTTGCACCCGGCGGACCCGGCTTGGGCGGTGCTCCGGGGGGGCGGCGGGAGCCCAAGAA
GTACGCAGTGACCGACGACTACCAGTTGTCCAAGCAGGTGCTGGGCCTGGGTGTGAACGGCAAAGTGCTGGAGTG
CTTCCATCGGCGCACTGGACAGAAGTGTGCCCTGAAGCTCCTGTATGACAGCCCCAAGGCCCGCAGGAGGTAGA
CCATCACTGGCAGGCTTCTGGCGGGCCCCCATATTGTCTGCATCCTGGATGTGTATGAGAACATGCACCATGGCAA
GCGCTGTCTCCTCATCATCATGGAATGCATGGAAGTGGTGAGTTGTTTACGACAGGATTCAGGAGCGTGGCGACCA
GGCTTTCACTGAGAGAGAAGCTGCAGAGATAATGCGGGATATTGGCACTGCCATCCAGTTTCTGCACAGCCATAA
CATTGCCACCGAGATGTCAAGCCTGAAAACCTACTCTACACATCTAAGGAGAAAGACGCAGTGCTTAAGCTCAC
CGATTTTGGCTTTGCTAAGGAGACCACCCAAAATGCCCTGCAGACACCCTGCTATACTCCCTATTATGTGGCCCC
TGAGGTCTTGGGTCCAGAGAAGTATGACAAAGTCATGTGACATGTGGTCCCTGGGTGTCATCATGTACATCCTCCT
TTGTGGCTTCCCACCCTTCTACTCCAACACGGGCCAGGCCATCTCCCCGGGGATGAAGAGGAGGATTGCGCTGGG
CCAGTACGGCTTCCCCAATCCTGAGTGGTGTCAGAAAGTCTCTGAGGATGCCAAGCAGCTGATCCGCCTCCTGTTGAA
GACAGACCCACAGAGAGGCTGACCATCACTCAGTTCATGAACCACCCCTGGATCAACCAATCGATGGTAGTGCC
ACAGACCCCACTCCACACGGCCCCGAGTGCTGCAGGAGGACAAAGACCACTGGGACGAAGTCAAGGAGGAGATGAC
CAGTGCCTTGGCCACTATGCGGGTAGACTACGACCAGGTGAAGATCAAGGACCTGAAGACCTCTAACAACCGGCT
CCTCAACAAGAGGAGAAAAAAGCAGGCAGGCAGCTCCTCTGCCTCACAGGGCTGCAACAACCACTAGCTCATGGG
GCCTTGGAGGAGCCTGGCCTCTCAGCCTGCATAACAGACTGAAATGTGCTCAGGCCCTGGCCAGGAGGGCCCAGG
GTCATTCTTTTAAACAAAAGGATTATTTTGTGTGTTTTAATTTGTCACTCGGAACCTCAGGATGGAGGACCCTGA
CCCTAAGCCTCCTTCAGATCTCTGGCCCAGGCTCAAGCCCTAGAGATGGGCAGGGCCTAGGGGCTGGGAGCTGCC
TGCTGCCATAGCAGCACCTTTAGCTAGGTTGGCCCCGAGTGAGGCCTCTGTGCTGTCCTGCCCTGGTGCATGGCCT
TAGCTTTCTAGGCCACTGGGAGTTGTGGCTGGGCTTCCCATCTTCCACAGAGACATCTCCCTGTGGGATGGGCAG
ATGGGCCTGGCCTTGAGAAAGGCATTGGCCATTGGTTGCCATGGTGACCAGGGACCACGTTGCTGCCTGTGAATG
CTGAGTGAGCGAGTAAGGGAGGAGGGGCGATTGAGGGTTCACCTCTGCCTTGGGGAGGCTGATTTCTCACACACT
GGCTGGCCCTCTCATTCTCACTCCTCCTTGGGCCCTGAGGCTGCTGGATCCGGTCTGCCTGCCTCCCTGTGCAGT
CCAGCCCTGCCTTGCTGCAGCCCCAGCCCAGATGGCACTCAGCGCTCTCCCCTGAGGGAGTCCCTGGGCCTAGCC
ATCCCCTCACTATTCCCGACCCAAAGGGTGACTTTTCATCTGAACTTAAGGTGGGAGATATTTTAACTTTTTTC
CACTTTGGAAAATGTCACTGTGACAAAAGCCAGCATACTTTCCCTGCACCCATCTGCTCACCAGATCTCAGGCAG
GAAAGCCCCCTCTCTGTTGAAGTCAGGGGCTATCTTTTGGTATACTTGTGTGAAAGTGGCTGGTTGGGAGCAGAGC
TAAGTGGCTTCCCATTAACCTGAGGTCTCTTTCTTTACTCTGGGTGAGACCTGAGGTTGGGGAAGGCGACTGAGC
CATGCTCAGAATGTCTGGTCTGGCTTGGGCCTGAGTAGGGCAGAGAGGGCCTTTTCATGGCTGATCAGAGCTTAC
CAGCCCCACCCACCATGGTAGCCTTAGGGTGCTGAGTGCCTGATACTGCCTGACAAGTGCCTGACACGCAGCCT
AGTTCCTTCTGGCCCTCTCTCACTGGCTGGGAAACCTAGACCATGTCAGATAGGACAACACTGCTGGGTTTT
ACATCCAGATAGTAATAAACACCATTTTCATCATT

1242/6881
FIGURE 1156

MDGETAEEQGGPVPPPVPAPGGPGLGGAPGGRREPKKYAVTDDYQLSKQVLGLGVNGKVLECFHRRTGQKCALKLL
YDSPKARQEVDDHHWQASGGPHIVCILDVYENMHHGKRCLLIIMECMEGGELFSRIQERGDQAFTEREAAEIMRDI
GTAIQFLHSHNIAHRDVKPENLLYTSKEKDAVLKLTDFGFAKETTQNALQTPCYTPYYVAPEVLGPEKYDKSCDM
WSLGVIMYILLCGFPPFYNTGQAISPGMKRRIRLGQYGFPNPEWSEVSEDAKQLIRLLLKTDFTERLTITQFMN
HPWINQSMVVPQTPLHTARVLQEDKDHWEVKEEMTSALATMRVDYDQVKIKDLKTSNNRLLNKRRKKQAGSSSA
SQGCNNQ

1243/6881
FIGURE 1157

GGCGGCATTTCTGGTGTCTGAGCCTGGCGCGGAGGCTATGGGCAGCCAGGAGGTGCTGGGCCACGCGGCCCGGC
TGGCCTCCTCCGGTCTCCTCCTGCAGGTGTTGTTTCGGTTGATCACCTTTGTCTTGAATGCATTTATTCTTCGCT
TCCTGTCAAAGGAAATCGTTGGCGTAGTAAATGTAAGACTAACGCTGCTTTACTCAACCACCTCTTCCTGGCCA
GAGAGGCCTTCCGCAGAGCATGTCTCAGTGGGGGCACCCAGCGAGACTGGAGCCAGACCCTCAACCTGCTGTGGC
TAACAGTCCCCCTGGGTGTGTTTTGGTCCTTATTCTGGGCTGGATCTGGTTGCAGCTGCTTGAAGTGCCTGATC
CTAATGTTGTCCCTCACTATGCAACTGGAGTGGTGCTGTTTGGTCTCTCGGCAGTGGTGGAGCTTCTAGGAGAGC
CCTTTTGGGTCTTGGCACAAGCACATATGTTTGTGAAGCTCAAGGTGATTGCAGAGAGCCTGTCGGTAATTCTTA
AGAGCGTTCCTGACAGCTTTTCTCGTGCTGTGGTTGCCCTCACTGGGGATTGTACATTTTCTCTTTGGCCCAGCTTT
TCTATACCACAGTTCTGGTGCTCTGCTATGTTATTTATTTACAAAGTTACTGGGTTCCCCAGAATCAACCAAGC
TTCAAACCTCTTCCTGTCTCCAGAATAACAGATCTGTTACCCAATATTACAAGAAATGGAGCGTTTATAAACTGGA
AAGAGGCTAAACTGACTTGGAGTTTTTTCAAACAGTCTTTCTTGAAACAGATTTTGACAGAAGGCGAGCGATATG
TGATGACATTTTTGAATGTATTGAACTTTGGTGATCAGGCTGTGTATGATATAGTGAATAATCTTGGCTCCCTTG
TGGCCAGATTAATTTTCCAGCCAATAGAGGAAAGTTTTTATATATTTTTTGCTAAGGTGCTGGAGAGGGGAAAGG
ATGCCACACTTCAGAAGCAGGAGGACGTTGCTGTGGCTGCTGCAGTCTTGGAGTCCCTGCTCAAGCTGGCCCTGC
TGGCCGGCCTGACCATCACTGTTTTTGGCTTTGCCTATTCTCAGCTGGCTCTGGATATCTACGGAGGGACCATGC
TTAGCTCAGGATCCGGTCCTGTTTTGCTGCGTTCCCTACTGTCTCTATGTTCTCCTGCTTGCCATCAATGGAGTGA
CAGAGTGTTCACATTTGCTGCCATGAGCAAAGAGGAGGTGACAGGTACAATTTTGTGATGCTGGCCCTGTCCT
CCTCATTCTGGTGTTATCCTATCTCTTGACCCGTTGGTGTGGCAGCGTGGGCTTCATCTTGGCCAACCTGCTTTA
ACATGGGCATTTCGGATCACGCAGAGCCTTTGCTTCATCCACCGCTACTACCGAAGGAGCCCCACAGGCCCTGG
CTGGCCTGCACCTATCGCCAGTCCTGCTCGGGACATTTGCCCTCAGTGGTGGGGTTACTGCTGTTTCGGAGGTAT
TCCTCTGCTGTGAGCAGGGCTGGCCAGCCAGACTGGCACACATTGCTGTGGGGGCCTTCTGTCTGGGAGCAACTC
TCGGGACAGCATTCTCACAGAGACCAAGCTGATCCATTTCTCAGGACTCAGTTAGGTGTGCCCAGACGCACTG
ACAAAATGACATGACTTCAGGGAAGCCTGGACACCCGAGGCACCTGGACCAGCTATGGGTAGTTCTGTGGGTGGA
ACACATTCTGTGTAAGAGCCCCACTGAGGGCTCTGCAGCGGAGTGACAGCAACCCCAAAGATGAGGCACCAGAGA
GTGCCACTGCATGAGACACCTGTGACCATTGCAAGTCTGAAATGCGGGGGGGAGTTTTCATTTTTAAGTGAAGAC
CAAAAGCCCTTTAAAAATAATAGTTTTTTATCATTTTATAGTAAAAAAAAAAAAAAAAAGGGCGGACCATCAATCAG
CACGCAGCAAGAAAAGCACATTCATACTAGACTATACAAAAAAAAAAAAAAAA

1244/6881
FIGURE 1158

MGSQEVLGHAARLASSGLLLQVLFRLITFVLNAFILRFLSKEIVGVVNVRLTLLYSTTLFLAREAFRRACLSGGT
QRDWSQTLNLLWLTVPPLGVFWSLFLGWIWLQLEVPDPNVVPHYATGVVLFGLSAVVELLGEPFWVLAQAHMFVK
LKVIAESLSVILKSVLTAFLVLWLPHWGLYIFSLAQLFYTTVLVLCYVIYFTKLLGSPESTKLQTLPVSRITDLL
PNITRNGAFINWKEAKLTWSFFKQSFLKQILTEGERYVMTFLNVLNFGDQGVYDIVNNLGSLSVARLIFQPIEESF
YIFFAKVLERGKDATLQKQEDVAVAAVLESLLKLALLAGLTITVFGFAYSQALDIYGGTMLSSGSGPVLLRSY
CLYVLLLAINGVTECFTFAAMSKEEVDRYNFVMLALSSSFLVLSYLLTRWCGSVGFILANCFNMGIRITQSLCFI
HRYYYRRSPHRPLAGLHLSPVLLGTFALSGGVTAVSEVFLCCEQGWPARLAHIAVGAFCLGATLGTAFLETETKLIH
FLRTQLGVPRRTDKMT

[illegible]

1246/6881
FIGURE 1160

MESYHKPDQQLQALKDTANRLRISSIQATTAAGSGHPTSCCSAAEIMAVLFFHTMRYKSQDPRNPHNDRFVLSK
GHAAPILYAVWAEAGFLAEAE LLNLRKISSDL DGHVPKQAF TDVATGSLGQGLGAACGMAYTGKYFDKASYRVY
CLLGDGELSEGSVWEAMAFASIYKLDNLVAILDINRLGQSDPAPLQHQM DIYQKRCEAFGWHAIIVDGHSVEELC
KAFGQAKHQPTAIIAKTFKGRGITGVEDKESWHGKPLPKNMAEQIIQEIYSQIQSKKKILATPPQEDAPSVDIAN
IRMPSLPSYKVGDKIATR KAYGQALAKLGHASDRIIALDGD TKNSTFSEIFKKEHPDRFIECYIAEQNMVSI AVG
CATRNRTVPFCSTFAAFFTRA FDQIRMAAISESNINLCGSHCGV SIGEDGPSQMALEDLAMERSVPTSTVFYPSD
GVATEKAVELAANTKGICFIRTSRPENAI IYNNNEDFQVGQAKVVLKSKDDQVTVIGAGVTLHEALAAAE LLKKE
KINIRVLDPFTTIKPLDRKLILDSARATKGRILTVEDHYE GEGIGEAVSSAVVGEPGITVTHLAVNRVPRSGKPAE
LLKMEFGIDRDAIAQAVRGLITKA

1247/6881
FIGURE 1161

AGAAGCCTCCTGGCAGACACTGGAGCCACGATGAAGCCCCAAGGCCTGTCCGTACCTGCAGCAAAGTTCTCGTC
CTGCTTTCACTGCTGGCCATCCACCAGACTACTACTGCCGAAAAGAATGGCATCGACATCTACAGCCTCACCCTG
GACTCCAGGGTCTCATCCCGATTTGCCACACGGTCGTACACCAGCCGAGTGGTCAATAGGGCCAATACTGTGCAG
GAGGCCACCTTCAGATGGAGCTGCCCAAGAAAGCCTTCATCACCAACTTCTCCATGATCATCGATGGCATGACC
TACCCAGGGATCATCAAGGAGAAGGCTGAAGCCCAGGCACAGTACAGCGCAGCAGTGGCCAAGGGAAAAGAGCGCT
GGCCTCGTCAAGGCCACCGGGAGAAACATGGAGCAGTTCCAGGTGTCCGTGTCAGTGTGGCTCCCAATGCCAAGATC
ACCTTTGAGCTGGTCTATGAGGAGCTGCTCAAGCGGCGTTTGGGGGTGTACGAGCTGCTGCTGAAAAGTGC GGCCC
CAGCAGCTGGTCAAGCACCTGCAGATGGACATTACATCTTCGAGCCCCAGGGCATCAGCTTTCTGGAGACAGAG
AGCACCTTCATGACCAACCAGCTGGTAGACGCCCTCACCACTGGCAGAATAAGACCAAGGCTCACATCCGGTTC
AAGCCAACACTTTCCCAGCAGCAAAAGTCCCCAGAGCAGCAAGAAACAGTCCTGGACGGCAACCTCATTATCCGC
TATGATGTGGACCGGGCCATCTCCGGGGGCTCCATTGAGATCGAGAACGGCTACTTTGTACACTACTTTGCCCCC
GAGGGCCTAACCAATGCCCAAGAATGTGGTCTTTGTGTCATTGACAAGAGCGGCTCCATGAGTGGCAGGAAAATC
CAGCAGACCCGGGAAGCCCTAATCAAGATCCTGGATGACCTCAGCCCCAGAGACCAGTTCAACCTCATCGTCTTC
AGTACAGAAGCAACTCAGTGGAGGCCATCACTGGTGCCAGCCTCAGCCGAGAACGTGAACAAGGCCAGGAGCTTT
GCTGCGGGCATCCAGGCCCTGGGAGGGACCAACATCAATGATGCAATGCTGATGGCTGTGCAGTTGCTGGACAGC
AGCAACCAGGAGGAGCGGCTGCCCGAAGGGAGTGTCTCACTCATCATCTGCTCACCAGTGGCGACCCCACTGTG
GGGGAGACTAACCCAGGAGCATCCAGAATAACGTGCGGGAAGCTGTAAGTGGCCGGTACAGCCTCTTCTGCCTG
GGCTTCGGTTTCGACGTCAGCTATGCCTTCCTGGAGAAGCTGGCACTGGACAATGGCGGCTGGCCCGGCGCATC
CATGAGGACTCAGACTCTGCCCTGCAGCTCCAGGACTTCTACCAGGAAGTGGCCAACCCACTGCTGACAGCAGTG
ACCTTCGAGTACCCAAGCAATGCCGTGGAGGAGGTCACTCAGAACAACCTCCGGCTCCTCTTCAAGGGCTCAGAG
ATGGTGGTGGCTGGGAAGCTCCAGGACCGGGGCTGATGTGCTCACAGCCACAGTCAGTGGGAAGCTGCCTACA
CAGAACATCACTTTCAAACGGAGTCCAGTGTGGCAGAGCAGGAGGCGGAGTTCAGAGCCCCAAGTATATCTTC
CACAACCTTCATGGAGAGGCTCTGGGCATACCTGACTATCCAGCAGCTGCTGGAGCAAACCTGTCTCCGCATCCGAT
GCTGATCAGCAGGCCCTCCGGAACCAAGCGCTGAATTTATCACTTGCCCTACAGCTTTGTACGCCTCTCACATCT
ATGGTAGTCACCAAACCCGAIGACCAAGAGCAGTCTCAAGTTGCTGAGAAGCCCATGGAAGGCGAAAGTAGAAAC
AGGAATGTCCACTCAGGTTCACCTTTCTTCAAATATTATCTCCAGGGAGCAAAAATACCAAACCCAGAGGCTTCC
TTTTCTCCAAGAAGAGGATGGAATAGACAAGCTGGAGCTGCTGGCTCCCGGATGAATTTAGACCTGGGGTTCTC
AGCTCCAGGCAACTTGGACTCCCAGGACCTCCTGATGTTCTGACCATGCTGCTTACCACCCCTTCCGCCGTCTG
GCCATCTTGCTGCTTCAGCACCACCAGCCACCTCAAATCCTGATCCAGCTGTGTCTCGTGTATGAATATGAAA
ATCGAAGAAACAACCATGACAACCCAAACCCAGCCCCCATAACAGGCTCCCTCTGCCATCCTGCCACTGCCTGGG
CAGAGTGTGGAGCGGCTCTGTGTGGACCCAGACACCGCCAGGGGCCAGTGAACCTGCTCTCAGACCCTGAGCAA
GGGGTTGAGGTGACTGGCCAGTATGAGAGGGAGAAGGCTGGGTTCTCATGGATCGAAGTGACCTTCAAGAACCCC
CTGGTATGGGTTACGCATCCCTTGAACACGTGGTGGTGAAGTCCGGAACCGAAGAAGCTCTGCGTACAAGTGAAG
GAGACGCTATTCTCAGTATGCCCCGGCCTGAAGATGACCATGGACAAGACGGGTCTCCTGCTGCTCAGTGACCCA
GACAAAGTGACCATCGGCCTGTTGTTCTGGGATGGCCGTGGGGAGGGGCTCCGGCTCCTTCTGCGTGACACTGAC
CGCTTCTCCAGCCACGTTGGAGGGACCCCTGGCCAGTTTTACCAGGAGGTGCTCTGGGGATCTCCAGCAGCATCA
GATGACGGCAGACGCACGCTGAGGGTTTCAGGGCAATGACCACTCTGCCACCAGAGAGCGCAGGCTGGATTACCAG
GAGGGGCCCCCGGAGTGGAGATTTCTGCTGGTCTGTGGAGCTGTAGTTCTGATGGAAGGAGCTGTGCCACCC
TGTACACTTGGCTTCCCCCTGCAACTGCAGGGCCGCTTCTGGGGCCTGGACCACCATGGGGAGGAAGAGTCCAC
TCATTACAAATAAAGAAAGGTGGTGTGAGCCTGGG

1248/6881
FIGURE 1162

GCGGCCGCCAAGCGATCCCTGCTCCGCGCGACACTGCGTGCCCGCGCACGCAGAGAGGCGGTGACGCACTTTACG
GCGGCAGCGTAAGTGCGTGACGCTCGTCAGTGGCTTCAGTTCACACGTGGCGCCAGCGGAGGCAGGTTGATGTGT
TTGTGCTTCCTTCTACAGCCAATATGAAAAGGCCTAAGTTAAAGAAAGCAAGTAAACGCATGACCTGCCATAAGC
GGTATAAAATCCAAAAAAGGTTTCGAGAACATCATCGAAAATTAAGAAAGGAGGCTAAAAAGCGGGGTACAAGA
AGCCTAGGAAAGACCCAGGAGTTCCAAACAGTGCTCCCTTTAAGGAGGCTCTTCTTAGGGAAGCTGAGCTAAGGA
AACAGAGGCTTGAAGAACTAAAACAGCAGCAGAACTTGACAGGCAGAAAGGAAGTAGAAAAGAAAAGAAAACTTG
AACTAATCCTGATATTAAGCCATCAAATGTGGAACCTATGGAAAAAGGAGTTTGGGCTTTTGCAAACTGAGAACA
AAGCCAAGTCGGGCAAAACAGAAATTCAAAGAAGCTGTACTGCCAAGAACTTAAAAAGGTGATTGAAGCCTCCGATG
TTGTCCTAGAGGTGTTGGATGCCAGAGATCCTCTTGGTTGCAGATGTCTCAGGTAGAAGAGGCCATTGTCCAGA
GTGGACAGAAAAAGCTGGTACTTATATTAAATAAATCAGATCTGGTACCAAAGGAGAATTTGGAGAGCTGGCTAA
ATTATTTGAAGAAAGAATTGCCAACAGTGGTGTTTCAGAGCCTCAACAAAACCAAAGGATAAAGGGAAGATAACCA
AGCGTGTGAAGGCAAGAAGAATGCTGCTCCATTGAGAAGTGAAGTCTGCTTTGGGAAAGAGGGCCTTTGGAAC
TTCTTGGAGGTTTTTCAGGAACTTGCAAGCAAGCCATTGCGGTTGGAGTAATTGGTTTCCCAATGTGGGGAAAA
GCAGCATTATCAATAGCTTAAAACAAGAACAGATGTGTAATGTTGGTGTATCCATGGGGCTTACAAGGAGCATGC
AAGTTGTCCCCTTGGACAAACAGATCACAATCATAGATAGTCCGAGCTTCATCGTATCTCCACTTAATTCCTCCT
CTGCGCTTGCTCTGCGAAGTCCAGCAAGTATTGAAGTAGTAAAACCGATGGAGGCTGCCAGTGCCATCCTTTCCC
AGGCTGATGCTCGACAGGTAGTACTGAAATATACTGTCCCAGGCTACAGGAATTCTCTGGAATTTTTTACTGTGC
TTGCTCAGAGAAGAGGTATGCACCAAAAAGGTGGAATCCCAATGTTGAAGGTGCTGCCAACTGCTGTGGTCTG
AGTGGACAGGTGCCTCATTAGCTTACTATTGCCATCCCCCTACATCTTGGACTCCTCCTCCATATTTTAATGAGA
GTATTGTGGTAGACATGAAAAGCGGCTTCAATCTGGAAGAACTGGAAAAGAACAATGCACAGAGCATAAGAGCCA
TCAAGGGCCCTCATTGTTGGCCAATAGCATCCTTTCCAGTCTTCCGGTCTGACAAATGGAATAATAGAAGAAAAGG
ACATACATGAAGAATTGCCAAAACGGAAAGAAAGGAAGCAGGAGGAGAGGGAGGATGACAAAGACAGTGACCAGG
AACTGTTGATGAAGAAGTTGATGAAAACAGCTCAGGCATGTTTGCTGCAGAAGAGACAGGGGAGGCACTGTCTG
AGGAGACTACAGCAGGTGAACAGTCTACAAGGTCTTTTATCTTGGATAAAATCATTGAAGAGGATGATGCTTATG
ACTTCAGTACAGATTATGTGTAACAGAACAATGGCTTTTTTATGATTTTTTTTTTAACATTTTAAGCAGACTGCTA
AACTGTTCTCTGTATAAGTTATGGTATGCATGAGCTGTGTAAATTTTGTGAATATGTATTATATTAACCAGGC
AACTTGAATCCCTAAATTCTGTAAAAAGACAATTCATCTCATTGTGAGTGGAAGTAGTTATCTGGAATAAAAAA
AGAAGATACCTATTG

1249/6881
FIGURE 1163A

ACTCTGTCCTGGACAGCGTGCCCAACCAGCCATGCGGGGGCCCCGGGGCCTCCTCCCACTCTGCCTCCTGGCCTTC
TGCTTGGCAGGCTTCAGCTTCGTCAGGGGGCAGGTGCTGTTCAAAGGCTGTGATGTGAAAACCACGTTTGTCACT
CATGTACCCTGCACCTCGTGCGCGGCCATCAAGAAGCAGACGTGTCCCTCAGGCTGGCTGCGGGAGCTCCCGGAT
CAGATAACCCAGGACTGCCGCTACGAAGTACAGCTGGGGGGCTCTATGGTGTCCATGAGCGGCTGCAGACGGAAG
TGCCGGAAGCAAGTGGTGCAGAAGGCCTGCTGCCCTGGCTACTGGGGTTCCCGGTGCCATGAATGCCCTGGGGGC
GCTGAGACCCCATGCAATGGCCACGGGACCTGCTTGGATGGCATGGACAGGAATGGGACCTGTGTGTGCCAGGAA
AACTTCCGCGGCTCAGCCTGCCAGGAGTGCCAAGACCCCAACCGGTTCCGGGCTGACTGCCAATCGGTGTGCAGC
TGTGTGCACGGAGTGTGCAACCATGGGCCACGTGGGGATGGAAGCTGCCTGTGCTTTGCTGGATACACTGGCCCC
CACTGTGATCAAGAGCTGCCCCGTCTGCCAGGAGCTGCGCTGTCCCCAGAACACCCAGTGCTCCGCAGAGGCTCCC
AGCTGCAGGTGCCTGCCCCGGCTACACACAGCAGGGCAGTGAATGCCGAGCCCCCAACCCCTGCTGGCCATCACCC
TGCTCACTGCTGGCCCAAGTGCTCGGTGAGCCCCAAGGGGCAGGCTCAGTGTCACTGCCCTGAGAACTACCATGGC
GATGGGATGGTGTGTCTGCCCAAGGACCCATGCACTGACAACCTTGGTGGCTGCCCCAGCAACTCTACTTTGTGT
GTGTACCAGAAGCCGGGCCAGGCCCTTCTGCACCTGCCGGCCAGGCCTGGTCAGCATCAACAGCAACGCTTCTGCG
GGCTGCTTCGCCTTCTGCTCCCCCTTCTCCTGCGACCGGTCTGCCACTTGCCAGGTGACCGCTGATGGGAAGACC
AGCTGTGTGTGCAGGGAAGCGAGGTGGGGGATGGGCGTGCCTGCTACGGACACCTGCTCCACGAGGTGCAGAAG
GCCACGCAGACAGGCCGGGTGTTCCTGCAGCTGAGGGTGCCTGTCGCTGATGGACCAGGGCTGCCGGGAAATC
CTTACCACAGCGGGCCCTTTACCCGTGCTGGTGCCATCCGTCTCCTCCTTCTCCTCCAGGACCATGAATGCATCC
CTTGCCAGCAGCTCTGTAGACAGCACATCATCGCAGGGCAGCACATCCTGGAGGACACAAGGACCCCAACAAACA
CGAAGGTGGTGGACGCTGGCCGGGCAGGAGATCACCGTCACCTTTAACCAATTACGAAATACTCCTACAAGTAC
AAAGACCAGCCCCAGCAGACGTCAACATCTACAAGGCCAACACATAGCAGCTAATGGCGTCTTCCACGTGGTC
ACTGGCCTGCGGTGGCAGGCCCTCTGGGACCCCTGGGGATCCCAAGAGAATATCGGACAGATCCTCGCCTCT
ACCGAGGCCTTCAGCCGCTTTGAAACCATCCTGGAGAATGTGGGCTGCCCTCCATCCTGGACGGACCTGGGGCC
TTCACAGTCTTTGCCCCAAGCAATGAGGCTGTGGACAGCTTGCGTGACGGCCGCCTGATCTACCTCTTCACAGCG
GGTCTCTCTAAACTGCAGGAGTTGGTGCGGTACCACATCTACAACCACGGCCAGCTGACCGTTGAGAAGCTCATC
TCCAAGGGTCGGATCCTCACCATGGCGAACCAGGTCTGGCTGTGAACATTTCTGAGGAGGGGCGCATCCTGCTG
GGACCCGAGGGGGTCCCGCTGCAGAGGGTAGACGTGATGGCCGCCAATGGTGTGATCCACATGCTGGACGGCATC
CTGCTGCCCCCGACCATCCTGCCCATCCTGCCCAAGCACTGCAGCGAGGAGCAGCACAAAGATTGTGGCGGGCTCC
TGTGTGGAAGTGCCTGAACACCAGCACGTGTCCCCCAACAGTGTGAAGCTGGACATCTTCCCCAAGGAG
TGTGTCTACATCCATGACCCAACGGGGCTCAATGTGCTAAAGAAGGGCTGTGCCAGCTACTGCAACCAACCATC
ATGGAACAAGGCTGCTGCAAAGGTTTTTTTCGGGCTGACTGCACGCAGTGTCTGGGGGCTTCTCCAACCCCTGC
TATGGCAAAGGCAATTGCAGTGATGGGATCCAGGGCAATGGGGCTGCCTCTGCTTCCAGACTACAAGGGCATC
GCCTGCCACATCTGCTCGAACCCTAACAGCATGGAGAGCAATGCCAGGAAGACTGCGGCTGTGTCCATGGTCTC
TGCGACAACCGCCAGGCTGAGGGGGGTGTGCCAGCAGGGCAGTGTGCCCTGGCTTCACTGGCCGGTTCTGC
AACGAGTCCATGGGGGACTGTGGGCCACAGGGCTGGCCAGCACTGCCACCTGCATGCCCGCTGTGTAGCCAG
GAGGGTGTGGCAGATGTGCTGTCTTGATGGCTTTGAGGGTGATGGCTTCTCCTGCACACCTAGCAACCCCTGC
TCCCACCCGGACCGTGAGGCTGCTCAGAGAATGCTGAGTGTGTCCCTGGGTCCCTGGGCACCCACCACTGCACA
TGCCACAAAGGCTGGAGTGGGGATGGCCGCTGTGTGGCTATTGACGAGTGTGAGCTGGACATGAGAGGTGGC
TGCCACACCGATGCCCTCTGCAGCTATGTGGGCCCCGGGCAGAGCCGATGCACCTGCAAGCTGGGCTTTGCCGGG
GATGGCTACCACTGCAGCCCCATCGACCCCTGCCGGGCAGGCAATGGCGGCTGCCACGGCCTGGCCACCTGCCGG
GCAGTGGGGGGAGGTGAGCGGGTCTGCACGTGCCCCCTGGCTTTGGGGGTGATGGCTTCACTGTTATGGAGAC
ATCTTCCGGGAGCTGGAGGCAATGCCCACTTCTCCATCTTCTACCAATGGCTTAAGAGTGCCCGCATCACGCTT
CCTGCCGACCGCGAGTCACAGCCCTGGTGCCCTCCGAGGCTGCAGTCCGTCAGCTGAGCCCCGAGGACCGAGCT
TTCTGGCTGCAGCCAAGGACGCTGCCGAACCTGGTCAGGGCCCCATTTCTCCAGGGTGCCTCTTCGAGGAGGAG
CTGGCCCGGCTGGGTGGGCAGGAAGTGCCACCCCTGAACCCACACACGCTGGGAGATTGCAACATTAGTGGG
AGGGTCTGGGTGCAGAATGCCAGCGTGATGTGGCTGACCTCCTTGCCACCAACGGTGTCTACACATCCTCAGC
CAGGTCTTACTGCCCCCCCCGAGGGGATGTGCCCGGTGGGCAGGGGTGCTGCAGCAGCTGGACTGGTGCCTGCC
TTCAGCCCTCTTCCGGGAATTGCTGCAGCACCATGGGTGGTGGCCAGATTGAGGCTGCCACTGCCTACACCATC
TTTGTGCCCAACCGCTCCCTGGAGGCCAGGGCAACAGCAGTCACCTGGACGCAGACACAGTGCGGCACCAT

1250/6881
FIGURE 1163B

GTGGTCCTGGGGGAGGCCCTCTCCATGGAAACCCTGCGGAAGGGTGGACACCGCAACTCCCTCCTGGGCCCTGCC
CACTGGATCGTCTTCTACAACCACAGTGGCCAGCCTGAGGTGAACCATGTGCCACTGGAAGGCCCATGCTGGAG
GCCCCTGGCCGCTCGCTGATTGGTCTGTGCGGGGTCTGACGGTGGGCTCAAGTCGCTGCCTGCATAGCCACGCT
GAGGCCCTGCGGGAGAAATGTGTAAACTGCACCAGGAGATTCCGCTGCACTCAGGGCTTCCAGCTGCAGGACACA
CCCAGGAAGAGCTGTGTCTACCGATCTGGCTTCTCCTTCTCCCGGGGCTGCTCTTACACATGTGCCAAGAAGATC
CAGGTGCCGGACTGCTGCCCTGGTTTCTTTGGCACGCTGTGTGAGCCATGCCCAGGGGTCTAGGGGGGGTGTGC
TCAGGCCATGGGCAGTGCCAGGACAGGTTCTTGGGCAGCGGGGAGTGCCACTGCCACGAGGGCTTCCATGGAACG
GCCTGTGAGGTGTGTGAGCTGGGCCGCTACGGGCCCCAACTGCACCGGAGTGTGTGACTGTGCCCATGGGCTGTGC
CAGGAGGGGCTGCAAGGGGACGGAAGCTGTGTCTGTAACGTGGGCTGGCAGGGCCTCCGCTGTGACCAGAAAATC
ACCAGCCCTCAGTGCCCTAGGAAGTGCAGCCCCAATGCCAACTGCGTGCAGGACTCGGCCGGAGCCTCCACCTGC
GCCTGTGCTGCGGGATACTCCGGCAATGGCATCTTCTGTTTACAGAGGTGGACCCCTGCGCCCCACGGCCATGGGGGC
TGCTCCCCCTCATGCCAACTGTACCAAGGTGGCACCTGGGCAGCGGACATGCACCTGCCAGGATGGCTACATGGGC
GACGGGGAGCTGTGCCAGGAAATTAACAGCTGTCTCATCCACCACGGGGGCTGCCACATTCACGCCGAGTGCATC
CCCACTGGCCCCCAGCAGGTCTCCTGCAGCTGCCGTGAGGGTTACAGCGGGGATGGCATCCGGACCTGCGAGCTC
CTGGACCCCTGCTCTAAGAACAATGGAGGATGCAGCCCATATGCCACCTGCAAAAGCACAGGGGATGGCCAGAGG
ACATGTACCTGCGACACAGCCCACACCGTGGGGGACGGCCTCACCTGCCGTGCCCGAGTGGCCTGGAGCTCCTG
AGGGATAAGCATGCCTCATTCTTCAGCCTCCGCCTCCTGGAATATAAGGAGCTCAAGGGCGATGGGCCTTTCACC
ATCTTCGTGCCGCACGCAGATCTAATGAGCAACCTGTGCGAGGATGAGCTGGCCCCGATTCTGTGCGCATCGCCAG
CTGGTGTTCGCTACCACGTGGTTGGCTGTGCGCGGCTGCGGAGCGAGGACCTGCTGGAGCAGGGGTACGCCACG
GCCCTCTCAGGGCACCCACTGCGCTTCAGCGAGAGGGAGGGCAGCATATACCTCAATGACTTCGCGCGCGTGGTG
AGCAGCGACCATGAGGCCGTGAACGGCATCCTGCACCTTATTGACCGTGTCTGCTGCCCCCGAGGCGCTGCAC
TGGGAGCCTGATGATGCTCCCATCCCGAGGAGAAATGTCACCGCCGCCGCCAGGGCTTCGGTTACAAGATCTTC
AGCGGCCTCCTGAAGGTGGCCGGCCTCCTGCCCTGCTTCGAGAGGCATCCCATAGGCCCTTCACAATGCTGTGG
CCCACAGACGCCGCCTTTCGAGCTCTGCCTCCGGATCGCCAGGCCTGGCTGTACCATGAGGACCACCGTGACAAG
CTAGCAGCCATTCTGCGGGGCCACATGATTGCAATGTGAGGCCTTGGCATCTGACCTGCCCCAACCTGGGCCCA
CTTCGAACCATGCATGGGACCCCCATCTCTTTCTCCTGCAGCCGAACGCGGGCCGGTGAGCTCATGGTGGGTGAG
GATGATGCTCGCATTGTGCGAGCGGCACTTGCCCTTTGAGGGTGGCCTGGCCTATGGCATCGACCAGCTGCTGGAG
CCACCTGGCCTTGGTGCTCGCTGTGACCACCTTGAGACCCGGCCCCCTGCGACTGAACACCTGCAGCATCTGTGGG
CTGGAGCCACCCTGTCTGAGGGGTACAGGAGCAGGGCAGCCCTGAGGCCTGCTGGCGCTTCTACCCGAAGTTC
TGGACGTCCCCTCCGCTGCACTCTTTGGGATTACGCAGCGTCTGGGTCCACCCAGCCTTTGGGGTAGGCCCCAA
GGCCTGGGCAGGGGCTGCCACCGCAATTGTGTACCAACACCTGGAAGCCCAGCTGCTGCCCTGGTCACTATGGC
AGTGAGTGCCAAGCTTGCCCTGGCGGCCCCAGCAGCCCTTGAGTGACCGTGGCGTGTGCATGGACGGCATGAGT
GGCAGTGGGCAGTGTCTGTGCCGTTCAGGTTTTGCTGGGACAGCCTGTGAACTCTGTGCTCCTGGTGCCTTTGGG
CCCCATTGTCAAGCCTGCCGCTGCACTGTGCATGGCCGCTGTGATGAGGGCCTTGGGGGCTCTGGCTCCTGCTTC
TGTGATGAAGGCTGGAAGTGGGCCACGCTGTGAGGTGCAACTGGAGCTGCAGCCTGTGTGTACCCACCCCTGTGCA
CCCGAGGCTGTGTGCCGTGCAGGCAACAGCTGTGAGTGCAGCCTGGGCTATGAAGGGGATGGCCGTGTGTGTACA
GTGGCAGACCTGTGCCAGGACGGGCATGGTGGCTGCAGTGAACACGCCAACTGTAGCCAGGTAGGAACAATGGTC
ACTTGTACCTGCCTGCCGACTACGAGGGTGTGAGTGGCTGGAGCTGCCGGGCCGCAACCCCTGCACAGATGGCCAC
CGCGGGGGCTGCAGCGAGCACGCCAACTGCTTGAGCACCGGCCTGAACACACGGCGCTGTGAGTGCCACGCAGGC
TACGTAGGCGATGGAAGTGCAGTGTCTGGAGGAGTGGGAACACCTGTGGACCGCTGCTTGGGCCAGCCACCGCCC
TGCCACTCAGATGCCATGTGCACTGACCTGCACTTCCAGGAGAAACGGGCTGGCGTTTTCCACCTCCAGGCCACC
AGCGGCCCTTATGGTCTGAACTTTTCGGAGGCTGAGGCGGCATGCCAAGCACAGGGAGCCGTCTTGGCTTCATTC
CCTCAGCTCTCTGCTGCCAGCAGCTGGGCTTCCACCTGTGCCTCATGGGCTGGCTGGCCAATGGCTCCACTGCC
CACCTGTGGTTTTCCCTGTGGCGGACTGTGGCAATGGTTCGGGTGGGCATAGTCAGCCTGGGTGCCCGCAAGAAC
CTCTCAGAACGCTGGGATGCCTACTGCTTCCGTGTGCAAGATGTGGCCTGCCGATGCCGAAATGGCTTCGTGGGT
GACGGGATCAGCACGTGCAATGGGAAGCTGCTGGATGTGCTGGCTGCCACTGCCAACTTCTCCACCTTCTATGGG
ATGCTATTGGGCTATGCCAATGCCACCCAGCGGGGTCTCGACTTCTTGGACTTCTTGGATGATGAGCTCACGTAT
AAGACACTCTTCGTCCCTGTCAATGAAGGCTTTGTGGACAACATGACGCTGAGTGGCCAGACTTGGAGCTGCAT

1251/6881
FIGURE 1163C

GCCTCCAACGCCACCCTCCTAAGTGCCAACGCCAGCCAGGGGAAGTTGCTTCCGGCCCACTCAGGCCTCAGCCTC
ATCATCAGTGACGCAGGCCCTGACAACAGTTCCCTGGGCCCCCTGTGGCCCCAGGGACAGTTGTGGTTAGCCGTATC
ATTGTGTGGGACATCATGGCCTTCAATGGCATCATCCATGCTCTGGCCAGCCCCCTCCTGGCACCCCCACAGCCC
CAGGCAGTGCTGGCGCCTGAAGCCCCACCTGTGGCGGCAGGCGTGGGGGCTGTGCTTGCCGCTGGAGCACTGCTT
GGCTTGGTGGCCGGAGCTCTCTACCTCCGTGCCCCAGGCAAGCCCCATGGGCTTTGGCTTCTCTGCCTTCCAGGCG
GAAGATGATGCTGATGACGACTTCTCACCGTGGCAAGAAGGGACCAACCCACCCTGGTCTCTGTCCCCAACCT
GTCTTTGGCAGCGACACCTTTTGTGAACCCTTCGATGACTCACTGCTGGAGGAGGACTTCCCTGACACCCAGAGG
ATCCTCACAGTCAAGTGACGAGGCTGGGGCTGAAAGCAGAAAGCATGCACAGGGAGGAGACCACCTTTTATTGCTTG
TCTGGGTGGATGGGGCAGGAGGGGCTGAGGGCCTGTCCCAGACAATAAAGGTGCCCTCAGCGGATGTGGGC

1252/6881
FIGURE 1164

MAGPRGLLP LCLLAFCLAGFSFVRGQVLFKGC DVKTT FVTHVPCTSCAAIKKQTCPSGWLREL PDQITQDCRYEV
QLGGSMVSMMSGCRRKCRKQVVQKACCPGYWGSRCHECPGGAETPCNGHGTCLDGM DRNGTCVCQENFRGSACQEC
QDPNRF GPDCQSVCS CVHGV CNHGPRGDG SCLCFAGYTGP HCDQELPVCQELRCPQNTQCSAEAPSCRCLPGYTQ
QGSECRAPNPCWPSPCSLLAQCSVSPKGQAQCHCPENYHGDGMVCLPKDPCTDNLGGCPSNSTLCVYQKPGQAFC
TCRPGLV SINSNASAGCFAFCSPFSCDRSATCQVTADGKTS CVCRESEVGDGRACYG HLLHEVQKATQTGRVFLQ
LRVAVAMMDQGC REILT TAGPFTVLVPSVSSFS SRTMNASLAQQ LCRQHIIAGQHILEDTRTQQTRRWWTLAGQE
ITVTFNQFTKYSYKYKDQ PQQTFNIYKANNIAANGVFHVVTGLRWQAPSGTPGDPKRTIGQILASTEAFSRFETI
LENCGLPSILDGPGPFTVFAPSNEAVDSL RDGR LIYLF TAGLSKLQELVRYHIYNHGQLTVEKLISKGRILTMAN
QVLAVNISEEGRILLGPEGVPLQRVDVMAANGVIHMLD GILLPPTILPILPKHCSEEQHKIVAGSCVDCQALNTS
TCPPNSVKLDIFPKECVYIHDPTGLNVLKKG CASYCNQTIMEQGCKGFFGPDCTQCPGGFSNPCYKGNCSDGI
QNGACLCFPDYKGIACHICSNPNKHGEQCQEDCGCVHGLCDNRPGSGGVCQQGT CAPGFSGRFCNESMGDCGPT
GLAQHCHLHARCVSQEGVARCRCLDGFEGDGF SCTPSNPCSHPDRGGCSENAECVPGSLGTHHCTCHKGWSGDGR
VCVAIDECELDMRGGCHTDALCSYVGPGQSRCTCKLGFAGDGYQCSPIDPCRAGNGGCHGLATCRAVGGGQRVCT
CPPGFGG DGFSCYGDIFRELEANAHFSIFYQWLKSAGITLPADRRVTALVPSEAAVRQLSPEDRAFWLQ PRTL PN
LVRAHFLQ G ALFEEELARLGGQEVATLNPTTRWEIRNISGRVWVQNASVDVADLLATNGVLHILSQVLLP PRGDV
PGGQGLLQQLDLVPAFSLFRELLQHHGLVPQIEAATAYTIFVPTNRSLAQGNSSHL DADTVRHHVVLGEALSME
TLRKGGRHNSLLGPAHWIVFYNHSGQPEVNVHPLEGPMLEAPGRSLIGLSGVLTVGSSRCLHSHAEALREKCVNC
TRRFRCTQGFQLQDTPRKSCVYRSGFSF SRGCSYTC AKKIQVPDCCPGFFGTLCEPCPGGLGGVCSGHGQCQDRF
LGSGECHCHEGFHGTACEVCELGRYGP NCTGVCDCAHGLCQEG LQGDGSCVCNVGWQGLRCDQKITSPQCPRKCD
PNANCVQDSAGASTCACAAGYSGNGIFCSEVDPCA HGHGGCSPHANCTKVAPGQRTCTCQDGYMGD GELCQEINS
CLIHGGCHIHAECIPTGPQQVSCSCREGYSGDGIRTCELLDPCSKNNGGCSPYATCKSTGDGQRTCTCDTAHTV
GDGLTCRARVGLELLRDKHASFFSLRLLEYKELKGDGPFTIFVPHADLMSNLSQDELARIRAH RQLVFRYHV VGC
RRLRSED LLEQGYATALS GHPLRF SEREGSIYLNDFARVVSSDHEAVNGILHFIDRVLLPPEALHWE PDDAP IPR
RNVTA AAQGF GYKIFSGLLKVAGLLP LLREASHRPFTMLWPTDAAFRALPPDRQAWLYHEDHRDKLAA IILRGHMI
RNVEALASDLPNLGPLRTMHGTPISFSCSRTRAGELMVGEDDARIVQRHLPFEGGLAYGIDQLLEPPGLGARCDH
FETRPLRLNTCSICGLEPPCPEGSQE QGSPEACWRFY PKFWTSPPLHSLGLRSVWVHPSLWGRPQGLGRGCH RNC
VTTTWKPSCCPGHYGSECQACPGGPSSPCSDRGVCM DGMMSGQCLCRSGFAGTACELCAPGAFGPHCQACRCTV
HGRCDEGLGGSGSCFCDEGWTGPRCEVQLELQP VCTPPCAPEAVCRAGNSCECSLGYEGDGRVCTVADLCQDGHG
GCSEHANCSQVGTMTCTCLPDYEGDGWSCRARNPCTDGHRRGGCSEHANCLSTGLNTRRCECHAGYVGDGLQCLE
ESEPPVDRCLGQPPPCHSDAMCTDLHFQEK RAGVFHLQATSGPYGLNFSEAEACEAQGAVLASFPQLSAAQQLG
FHLCLMGWLANGSTAHPVVFPVADCGN GRVGI VSLGARKNLSERWDAYCFRVQDVACRCRNGFVGDGISTCNGKL
LDVLAATANFSTFYGMLLGYANATQRGLDFLDFLDDELTYKTLFVPVNEGFVDNMTLSGPDLELHASNATLLSAN
ASQGKLLPAHSGLSLIISDAGPDNSSWAPVAPGTVVVSRIIVWDIMAFNGIIHALASPLLAPPQPQAVLAPEAPP
VAAGVGAVLAAGALLGLVAGALYLRARGKPMGFGFSAFQAEDDADDDFSPWQEGTNPTLVSVPNPVFGSDTFCEP
FDDSLLEEDFPDTQRILTVK

1253/6881
FIGURE 1165A

GC GGCGGTGGCGGCGGAGACCCGAACATGGCGACCGCGCGCACCTTCGGGCCCCGAGCGGGAAGCCGAGCCGGCCA
AGGAAGCGCGCGTCTGTGGGCTCGGAGCTTGTGGACACTTATACGGTTTACATCATCCAGGTCACTGATGGCAGCC
ATGAGTGGACAGTAAAGCACCGCTACAGCGACTTCCATGACCTGCATGAAAAGCTCGTTGCAGAGAGAAAGATTG
ATAAAAACTGCTTCCGCCCAAAAAGATAATTGGGAAAAACTCAAGAAGCTTGGTGGAGAAGAGGGAGAAGGATC
TGGAGGTCTACCTCCAGAAGCTCCTGGCTGCCTTCCCTGGCGTGACCCCCAGAGTACTGGCCCACTTCTTGCAATT
TTCACTTCTATGAGATAAATGGCATCACCGCGGCACTGGCTGAAGAGCTCTTTGAGAAAGGAGAACAGCTCCTGG
GGGCCGCGGAGGTCTTTGCCATTGGACCCCTGCAGCTGTATGCCGTACGGAGCAGCTGCAGCAGGGAAAGCCCA
CGTGCGCCAGTGGGGATGCCAAGACCGACCTCGGGGCACATCCTGGACTTCACCTGTGCCTTAAGTACCTTAAGG
TTTCTGGCACAGAAGGACCTTTTGGGACCAGCAACATTACAGGAGCAGCTCCTGCCGTTGCACCTATCAATATTCA
AGTCCCTGCATCAGGTGGAGATAAGTCACTGTGATGCTAAGCACATCAGAGGGCTGGTTCGCATCGAAGCCACCT
TAGCCACGCTGAGTGTCCGCTTCTCAGCAACCTCGATGAAGGAAGTCTTGTTCCTGAAGCCTCAGAATTTGATG
AGTGGGAGCCTGAAGGCACAACCCTAGAAGGCCCTGTGACTGCCGTACATCCCACTTGGCAGGCATTGACCACGC
TTGACCTGAGCCACAACAGCATCTCCGAGATCGACGAGTCTGTGAAACTGATCCCAAAGATTGAGTTCCTGGACC
TGAGTCACAATGGATTGCTGGTTGTGGACAATCTGCAGCACCTGTATAACCTTGTGCATCTGGACCTGTCTTACA
ACAAGCTCTCCTCCTTGAAGGGCTTCACACCAAGCTGGGGAACATCAAGACCTTAAACCTGGCAGGCAACCTCC
TAGAGAGTCTGAGTGGCCTGCACAAGCTCTACTCACTGGTCAACCTGGATCTCCGGGACAACAGGATCGAACAGA
TGGAGGAGGTCCGGAGCATAGGCAGCCTCCCGTGTCTGGAGCACGTGTCTCTGCTGAACAACCCCTCTGAGCATCA
TCCCCGACTACCGGACCAAGGTGCTGGCTCAGTTCGGAGAGAGGGCCTCAGAGGTCTGTCTGGATGACACAGTGA
CCACAGAGAAGGAGCTGGACACTGTGGAAGTGTGAAAGCAATTAGAAAAGCCAAGGAGGTCAAGTCCAAACTGA
GCAACCCAGAGAAGAAGGGTGGTGAAGACTCCCGGCTCTCAGCTGCCCCCTGCATCAGACCCAGCAGCTCCCCCTC
CCACTGTGGCTCCCGCATCTGCCTCCCTGCCCCAGCCATCCTCTCTAACCAAGGAATCATGTTCTCGTTCAGGAGG
AGGCCCTGGCCAGCAGCCTCTCGTCCACTGACAGTCTGACTCCCGAGCACCCAGCCATTGCCAGGGATGTTCTG
ATTCTTGGAGTCCATCCCTGCGGGACAGGCAGCTTCCGATGATTTAAGGGACGTGCCAGGAGCTGTTGGTGGTG
CAAGCCAGAACATGCCGAGCCGGAGGTCCAGGTGGTGGCGGGGTCTGGCCAGATCATCTTCTGCCCTTACCT
GCATTGGCTACACGGCCACCAATCAGGACTTCATCCAGCGCCTGAGCACACTGATCCGGCAGGCCATCGAGCGGC
AGCTGCCTGCCTGGATCGAGGTGCCAACCAGCGGGAGGAGGGCCAGGGTGAACAGGGCGAGGAGGAGGATGAGG
AGGAGGAAGAAGAGGAGGACGTGGCTGAGAACCGCTACTTTGAAATGGGGCCCCCAGACGTGGAGGAGGAGGAGG
GAGGAGGCCAGGGGGAGGAAGAGGAGGAGGAAGAGGAGGATGAAGAGGCCGAGGAGGAGCGCCTGGCTCTGGAAT
GGGCCCTGGGCGCGGACGAGGACTTCTGTCTGGAGCACATCCGCATCCTCAAGGTGCTGTGGTGTCTTCTGATCC
ATGTGCAGGGCAGTATCCGCCAGTTCGCCGCCTGCCTTGTGCTCACCAGCTTCGGCATCGCAGTCTTCGAGATCC
CGCACCAGGAGTCTCGGGGCAGCAGCCAGCACATCCTCTCCTCCCTGCGCTTTGTCTTTTGTCTCCCGCATGGCG
ACCTCACCAGATTTGGCTTCTCATGCCGAGCTGTGTCTGGTGTCAAGGTACGGCACAGTGAGAACACGCTCT
TCATTATCTCGGACGCCGCCAACCTGCACGAGTTCCACGCGGACCTGCGCTCATGCTTTGCACCCACGACATGG
CCATGCTGTGTAGCCCCATCCTCTACGGCAGCCACACCAGCCTGCAGGAGTTCCTGCGCCAGCTGCTCACCTTCT
ACAAGGTGGCTGGCGGCTGCCAGGAGCGCAGCCAGGGCTGCTTCCCCGTCTACCTGGTCTACAGTGACAAGCGCA
TGGTGCAGACGGCCGCCGGGACTACTCAGGCAACATCGAGTGGGCCAGCTGCACACTCTGTTTCAGCCGTGCGGC
GCTCCTGTCTGCGCGCCCTCTGAGGCCGTCAAGTCCGCGGCCATCCCCCTACTGGCTGTTGCTCACGCCCCAGCACC
TCAACGTATCAAGGCCGACTTCAACCCCATGCCAACCGTGGCACCCACAACCTGTGCAACCGCAACAGCTTCA
AGCTCAGCCGTGTGCCGCTCTCCACCGTGTCTGAGACCCACACGCAGCTGTACCCAGCCTCGGGGCGCCTTTG
CTGATGGCCACGTGCTAGAGCTGCTCGTGGGGTACCGCTTTGTCACTGCCATCTTCGTGCTGCCCCACGAGAAGT
TCCACTTCTGCGCGTCTACAACCAGCTGCGGGCCTCGCTGCAGGACCTGAAGACTGTGGTTCATCGCCAAGACCC
CCGGGACGGGAGGCAGCCCCCAGGGCTCCTTTGCGGATGGCCAGCCTGCCGAGCGCAGGGCCAGCAATGACCAGC
GTCCCCAGGAGGTCCCAGCAGAGGCTCTGGCCCCGGCCCCAGTGGAAAGTCCCAGCTCCAGCCCCCTGCAGCAGCCT
CAGCCTCAGGCCCCAGCGAAGACTCCGGCCCCAGCAGAGGCCTCAACTTCAGCTTTGGTCCCAGAGGAGACGCCAG
TGGAAGCTCCAGCCCCACCCCAAGCCGAGGCCCCCTGCCAGTACCCGAGTGAGCACCTCATCCAGGCCACCTCGG
AGGAGAATCAGATCCCCCTCGCACTTGCCTGCCTGCCCCGTGCTCCGGCACGTGCGCAGCCTGCGGGGACGCGCCA
TCATCGAGCTCTTCCACAGCAGCATTGCTGAGGTTGAAAACGAGGAGCTGAGGCACCTCATGTGGTCTCTCGGTGG
TGTTCTACCAGACCCAGGGCTGGAGGTGACTGCCTGCGTGTCTCTCCACCAAGGCTGTGTACTTTGTGCTCC

1254/6881
FIGURE 1165B

ACGACGGCCTCCGCCGCTACTTCTCAGAGCCACTGCAGGATTTCTGGCATCAGAAAAACACCGACTACAACAACA
GCCCTTTCCACATCTCCAGTGCTTCGTGCTAAAGCTTAGTGACCTGCAGTCAGTCAATGTGGGGCTTTTCGACC
AGCATTTCCGGCTGACGGGTTCACCCCGATGCAGGTGGTCACGTGCTTGACGCGGGACAGCTACCTGACGCACT
GCTTCTCCAGCACCTCATGGTCGTGCTGTCCTCTCTGGAACGCACGCCCTCGCCGGAGCCTGTTGACAAGGACT
TCTACTCCGAGTTTGGGAACAAGACCACAGGGAAGATGGAGAACTACGAGCTGATCCACTCTAGTCGCGTCAAGT
TTACCTACCCCACTGAGGAGGAGATTGGGGACCTGACGTTCACTGTGGCCCAAAGATGGCTGAGCCAGAGAAGG
CCCCAGCCCTCAGCATCCTGCTGTACGTGCAGGCCTTCCAGGTGGGCATGCCACCCCTGGGTGCTGCAGGGGCC
CCCTGCGCCCCAAGACACTCCTGCTCACCAGCTCCGAGATCTTCTCTGGATGAGGACTGTGTCCACTACCCAC
TGCCCGAGTTTGCCAAAGAGCCGCCGCAGAGAGACAGGTACCGGCTGGACGATGGCCGCCGCGTCCGGGACCTGG
ACCGAGTGCTCATGGGCTACCAGACCTACCCGCAGGCCCTCACCTCTCGTCTTCGATGACGTGCAAGGTCATGACC
TCATGGGCAGTGTCACCCTGGACCACITTTGGGGAGGTGCCAGGTGGCCCGGCTAGAGCCAGCCAGGGCCGTGAAG
TCCAGTGGCAGGTGTTTGTCCCACTGCTGAGAGCAGAGAGAAGCTCATCTCGCTGTTGGCTCGCCAGTGGGAGG
CCCTGTGTGGCCGTGAGCTGCCTGTGAGCTCACCGGCTAGCCAGGCCACAGCCAGCCTGTGCTGTCCAGCCTG
ACGCCTACTGGGGCAGGGCAGCAGGCTTTTGTGTTCTCTAAAAATGTTTTATCCTCCCTTTGGTACCTTAATTTG
ACTGTCCTCGCAGAGAATGTGAACATGTGTGTGTGTTGTGTTAATTCTTTCTCATGTTGGGAGTGAGAATGCCGG
GCCCCTCAGGGCTGTCGGTGTGCTGTCAGCCTCCCACAGGTGGTACAGCCGTGCACACCAGTGTCGTGTCTGCTG
TTGTGGGACCGTTGTAAACACGTGACACTGTGGGTCTGACTTCTCTTCTACACGTCCTTTCTGAAGTGTGAG
TCCAGTCCTTTGTTGCTGTTGCTGTTGCTGTTGCTGTTGGCATCTTGCTGCTAATCCTGAGGCTGGTAG
CAGAATGCACATTGGAAGCTCCCACCCCATATTGTTCTTCAAAGTGGAGGTCTCCCCTGATCCAGACAAGTGGGA
GAGCCCGTGGGGGCAGGGGACCTGGAGCTGCCAGCACCAAGCGTGATTCTGCTGCCTGTATTCTCTATTCCAAT
AAAGCAGAGTTTGACACCGTCTTAAAAA

1255/6881
FIGURE 1166

MATARTFGPEREAEPAKEARVVGSELVDITYTVYIIQVTDGSHEWTVKHRYSDFHDLHEKLV AERKIDKNLLPPKK
IIGKNSRSLVEKREKDLEVYLQKLLAAFPGVTPRVLAHFLHFHFYEINGITAALAEELFEKGEQLLGAGEVFAIG
PLQLYAVTEQLQQGKPTCASGDAKTDLGHILDFTCRLKYLKVSGETEGPFGTSNIEQLLPFDLSIFKSLHQVEIS
HCDAKHIRGLVASKPTLATLSVRFSATSMKEVLVPEASEFDEWEPEGTTLEGPVTAVIPTWQALTTDLSDHNSIS
EIDESVKLIPKIEFLDLSHNGLLVVDNLQHLVNLVHLDLSYNKLSLEGLHTKLGNIKTNLNLAGNLESLSGLHK
LYSLVNLDLRDNRIEQMEEVRSIGSLPCLEHVSLNNPLSIIPDYRTKVLAQFGERASEVCLDDTVTTEKELDTV
EVLKAIQKAKEVKSKLSNPEKKGGEDSRLSAAPCIRPSSSPPTVAPASASLPQPILSNQGIMFVQEEALASSLSS
TDSLTPEHQPIAQGCSDSLESIPAGQAASDDL RDVPGAVGGASPEHAEPVQVVP GSGQIIIFLPFTCIGYTATNQ
DFIQRLSTLIRQAIERQLPAWIEAANQREEGQGEQGEEDDEEEEEEDVAENRYFEMGPPDVEEEGGGQGEED
EEEEDEEAEERLALWALGADEDFLLEHIRILKVLWCFLIHVQGSIRQFAACLVLTDFGIAVFEIPHQESRGSS
QHILSSLRFVFCFPHGDLTEFGFLMPELCLVLKVRHSENTLFIISDAANLHEFHADLRSCFAPQHMAMLCSPILY
GSHTSLQEFRLRQLLTFYKVAGGCQERSQGCFFVYLVYSDKRMVQTAAGDYSGNIEWASCTLCSAVRRSCCAPSEA
VKSAAIPYWLLLTTPQHNLVIKADFNPMPNRRGTHNCRNRNSFKLSRVPLSTVLLDPTRSCTQPRGAFADGHVLELL
VGYRFVTAIFVLPHEKFHFLRVYNQLRASLQDLKTVVIAKTPGTGGSPQGSFADGQPAERRASNDQRPQEVPAEA
LAPAPVEVPAPAPAAASASGPAKTPAPAEASTSALVPEETPVEAPAPPPAEAPAQYPSEHLIQATSEENQIPSHL
PACPSLRHVASLRGSAIIELFHSSIAEVENEEELRHLMWSSVVFYQTPGLEVTACVLLSTKAVYFVLHDGLRRYFS
EPLQDFWHQKNTDYNNSPFHISQCFVLKLSDLQSVNVGLFDQHFRLTGSTPMQVVTCLTRDSYLTCHFLQHLMVV
LSSLERTPSPEPVDKDFYSEFGNKTTGKMENYELIHSSRVKFTYPSEEEIGDLTFTVAQKMAEPEKAPALSILLY
VQAFQVGMPPPGCCRGPLRPKTLTLLTSSEIFLLDEDCVHYPLPEFAKEPPQRDRYRLDDGRRVRDLDRVLMGYQT
YPQALT LVFDDVQGHDLMGSVTL DHFGEVPGGPASQGREVQWQVFVPSAESREKLISLLARQWEALCGREL PV
ELTG

1256/6881
FIGURE 1167

GGCACGAGGAGCGTTTCGTTTGGACTTCTCGACTTGAGTGCCCGCCTCCTTCGCCGCCGCCCTCTGCAGTCCTCAG
CGCAGTTATGCCCAGTTCTTCCCGCTGTGGGGACACGACCACGGAGGAATCCTTGCTTCAGGGACTCGGGACCCT
GCTGGACCCCTTCTTCGGGTTTAGGGGATGTGGGGACCAGGAGAAAGTCAGGATCCCTAAGAGTCTTCCCTGCCT
GGATGGATGAGTGGCTTCTTCTCCACCTAGATTCTTTCCACAGGAGCCAGCATACTTCTGAACTGAGAGAGTGT
TGTTCCGCCGCTGCCCATTTCTTATCCCGAGTCCCCCAGGCCTTTCTGCAGAAAGCAGGCAAATCTCTGTTGTTCTA
TGCCCCAAACTGCCCAAGATGATGGAAGTTGGGGCCAAGCCAGCCCCTCGGGCATTGTCCACTGCAGCAGTACA
CTACCAACAGATCAAAGAAACCCCTCCGGCCAGTGAGAAAGACAAAAGTCTAAGGCCAAGGTCCAACAGACTCC
TGATGGATCCCAGCAGAGTCCAGATGGCACACAGCTTCCGTCTGGACACCCCTTGCTGCCACAAGCCAGGGCAC
TGCAAGCAAATGCCCTTTCTTGGCAGCACAGATGAATCAGAGAGGCAGCAGTGTCTTCTGCAAAGCCAGTCTTGA
GCTTCAGGAGGATGTGCAGGAAATGAATGCCGTGAGGAAAGAGGTTGCTGAAACCTCAGCAGGCCCCAGTGTGGT
TAGTGTGAAAACCGATGGAGGGGATCCCAGTGGACTGCTGAAGAACTTCCAGGACATTATGCAAAAGCAAAGACC
AGAAAGAGTGTCTCATCTTCTTCAAGATAACTTGCCAAAATCTGTTTCCACTTTTCAGTATGATCGTTTCTTTGA
GAAAAAATTGATGAGAAAAAGAATGACCACACCTATCGAGTTTTTAAAGTGTGAACCGGCGAGCACACATCTT
CCCCATGGCAGATGACTATTGAGACTCCCTCATCACCAAAAGCAAGTGTGAGTCTGGTGCAGTAATGACTACCT
AGGAATGAGTCGCCACCCACGGGTGTGTGGGGCAGTTATGGACACTTTGAAACAACATGGTGTGGGGCAGGTGG
TACTAGAAATATTTCTGGAAGTGTAAATTCATGTGGACTTAGAGCGGGAGCTGGCAGACCTCCATGGGAAAGA
TGCCGCACTCTTGTCTTCTCGTGCTTTGTGGCCAATGACTCAACCCCTCTTACCCTGGCTAAGATGATGCCAGG
CTGTGAGATTTACTCTGATTCTGGGAACCATGCCTCCATGATCCAAGGGATTGAAACAGCCGAGTGCCAAAGTA
CATCTTCCGCCACAATGATGTCAGCCACCTCAGAGAACTGCTGCAAAGATCTGACCCCTCAGTCCCCAAGATTGT
GGCATTGTGAACTGTCCATTCAATGGATGGGGCGGTGTGCCCACTGGAAGAGCTGTGTGATGTGGCCCATGAGTT
TGGAGCAATCACCTTCGTGGATGAGGTCCACGCAGTGGGGCTTTATGGGGCTCGAGGCGGAGGGATTGGGGATCG
GGATGGAGTCATGCCAAAATGGACATCATTTCTGGAACACTTGGCAAAGCCTTTGGTTGTGTTGGAGGGTACAT
CGCCAGCACGAGTTCTCTGATTGACACCGTACGGTCTATGCTGCTGGCTTCATCTTACCACCTCTCTGCCACC
CATGCTGCTGGCTGGAGCCCTGGAGTCTGTGCGGATCCTGAAGAGCGCTGAGGGACGGGTGCTTCGCCGCCAGCA
CCAGCGCAACGTCAAACCTCATGAGACAGATGCTAATGGATGCCGGCCTCCCTGTTGTCCACTGCCCCAGCCACAT
CATCCCTGTGCGGGTTGCAGATGCTGCTAAAAACACAGAAGTCTGTGATGAACTAATGAGCAGACATAACATCTA
CGTGCAAGCAATCAATTACCCTACGGTGCCCCGGGGAGAAGAGCTCCTACGGATTGCCCCACCCCTCACCACAC
ACCCAGATGATGAACTACTTCCCTTGAGAATCTGCTAGTCACATGGAAGCAAGTGGGGCTGGAAGTGAAGCCTCA
TTCCTCAGCTGAGTGCAACTTCTGCAGGAGGCCACTGCATTTTGAAGTGTGAGTGAAAGAGAGAAGTCTATTT
CTCAGGCTTGAGCAAGTTGGTATCTGCTCAGGCCCTGAGCATGACCTCAATTATTTCACTTAACCCAGGCCATTA
TCATATCCAGATGGTCTTCAGAGTTGTCTTTATATGTGAATTAAGTTATATTAAATTTTAATCTATAGTAAAAAC
ATAGTCCTGGAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

1257/6881
FIGURE 1168

MESVVRRCPFILSRVPQAFLOKAGKSLIFYAQNCPKMMEVGAKPAPRALSTAAVHYQQIKETPPASEKDKTAKAKV
QQTPDGSQQSPDGTQLPSGHPLPATSQGTASKCPFLAAQMNQRGSSVFCKASLELQEDVQEMNAVRKEVAETSAG
PSVVSVKTDGGDPSGLLKNFQDIMQQRPERVSHLLQDNLPKSVSTFQYDRFFEKKIDEKKNDHTYRVFKTVNRR
AHIFPMADDYSDSLITKKQVSVWCSNDYLGMSRHRVCGAVMDTLKQHGAGAGGTRNISGTSKFHVDLERELADL
HGKDAALLFSSCFVANDSTLFTLAKMMPGCEIYSDSGNHASMIQGIIRNSRVPKYIFRHNDVSHLRELLQRSDPSV
PKIVAFETVHSMGDGAVCPLEELCDVAHEFGAITFVDEVHAVGLYGARGGGIGDRDGVMPKMDIISGTLGKAFGCV
GGYIASTSSSLIDTVRSYAAGFIFTTSLPPMLLAGALESVRILKSAEGRVLRQHQNRNVKLMRQMLMDAGLPVVHC
PSHIIPVRVADAANKNTEVCDELMSRHNIYVQAINYPTVPRGEELLRIAPTPHHTPQMMNYFLENLLVTWKQVGLE
LKPHSSAECNFCRRPLHFVMSEREKSYFSGLSKLVSAQA

1258/6881
FIGURE 1169

ATGCCCTACCAATATCCATTGCTGACCCCGGAGCAGAAGGAGCTGTCTGACATGACTCATCGCATCGTAGCTCTG
GGCAAGGGCATCCCGGCTGCAGATGAGTCCACTGGGAGCACTGCCAAGTGGCTGCAGTCCATTGGCACCGAGAAT
ACCGAGGAGAACCGGTGCTTCTACCGCCAGCTGTGGCTGACAGCTGACAACCGCGTGAACCCCTGCATCAAGGGT
GTCATCCTCTTCCATGAGACGCTGTACCAAAAGGCGGATGATGGGCGTCCCTTCCCCCAAGTTATCAAATCCAAG
GGCAATGTTGTGAGCATCAAGTGTGTCAATGTCCTGGCCCACTATGCCAGCATCTGCCAGCAGAATGGCATTGTG
CTCTTCTACTGCCAGTATGTAACCGAGAAGGTGTGGCTGCTCTACAAGGCTCTGAGTGACCATGACATCTACCTG
GAAGGCACCTTGCTGAAGTCCAATATGGTCACCCCAGGCCATGCCTGCATCCAGAAGTTTTCTCATGAGGAGATT
GCCATGGCAACTGTCACAAGCACTACACTCTGGGGAATAAGCGGCCTAGAAGGATCACAACCTGGGCCAGAACAGG
GCCACCCAGACTCATCACTGAGGCAGAGCAAGGAAGTGTCCATCAACCTCAATGCCATTAACAAGTGCCCCCTC
CTGAAGCCCTGGGGCCTGACCTTCTCATATAGCTGA

1259/6881
FIGURE 1170

TTCCGGCGTTGTTGACCCTATTTCCCGTGCTGCACCGCAGCCCCTTTCTCTTCCGGTTCTAGGCGCTTCGGGAGC
CGCGGCTTATGGTGCAGACATGGCCAAGTCCAAGAACCACACCACACACAACCAGTCCCGAAAATGGCACAGAAA
TGGTATCAAGAAACCCCGATCACAAAGATACGAATCTCTTAAGGGGGTGGACCCCAAGTTCCTGAGGAACATGCG
CTTTGCCAAGAAGCACAAACAAAAGGGCCTAAAGAAGATGCAGGCCAACAATGCCAAGGCCATGAGTGCACGTGC
CGAGGCTATCAAGGCCCTCGTAAAGCCCAAGGAGGTTAAGCCCAAGATCCCAAAGGGTGTGAGCCGCAAGCTCGA
TCGACTTGCCCTACATTGCCCACCCCAAGCTTGGGAAGCGTGCTCGTGCCCGTATTGCCAAGGGGCTCAGGCTGTG
CCGGCCAAAGGCCAAGGCCAAGGCCAAGGCCAAGGATCAAACCAAGGCCCAGGCTGCAGCCCCAGCTTCAGTTCC
AGCTCAGGCTCCCAAACGTACCCAGGCCCTACAAAGGCTTCAGAGTAGATATCTCTGCCAACATGAGGACAGAA
GGACTGGTGCGACCCCCCACCCTGGGCTACCATCTGCATGGGGCTGGGGTCCTCCTGTGCTATTTGTA
CAAATAAACCTGAGGCAGGAAA

1260/6881
FIGURE 1171

MAKSKNHTTHNQSRKWHRNGIKKPRSQRYESLKGVDPKFLRNMRFKKHNKKGLKKMQANNAKAMSARAEAIKAL
VKPKEVKPKIPKGVSRKLDRLAYIAHPKLGKRARARIAKGLRLCRPKAKAKAKAKDQTKAQAAAPASVPAQAPKR
TQAPTKASE

1261/6881
FIGURE 1172

GGGCGCTGAGAGGCGAGCGTGAGCCAGCGACAGGAGAGTGAGCTCACCACGCGCAGCGCCATGAACCAGCAAGGG
TCCCGAGGAGGAGCACCCATCGGTGACGCTCTTCCGCCAGTACCTGCGTATCCGCACTGTCCAGCCCAAGCCTGA
CTATGGAGCTGCTGTGGCTTTCTTTGAGGAGACAGCCGCCAGCTGGGCCTGGGCTGTCAGAAAGTAGAGGTGGC
ACCTGGCTATGTGGTGACCGTGTTGACCTGGCCAGGCACCAACCCTACACTCTCCTCCATCTTGCTCAACTCCCA
CACGGATGTGGTGCCCTGTCTTCAAGGAACATTGGAGTCACGACCCCTTTGAGGCCTTCAAGGATTCTGAGGGCTA
CATCTATGCCAGGGGTGCCCAGGACATGAAGTGCCTCAGCATCCAGTACCTGGAAGCTGTGAGGAGGCTGAAGGT
GGAGGGCCACCGGTTCCCCAGAACCATCCACATGACCTTTGTGCCTGATGAGGAGGTTGGGGGTACCAAGGCAT
GGAGCTGTTTCGTGCAGCGGCCTGAGTTCCACGCCCTGAGGGCAGGCTTTGCCCTGGATGAGGGCATAGCCAATCC
CACTGATGCCTTCACTGTCTTTTATAGTGAGCGGAGTCCCTGGTGGGTGCGGGTTACCAGCACTGGGAGGCCAGG
CCATGCCTCACGCTTCATGGAGGACACAGCAGCAGAGAAGCTGCACAAGGTTGTAAACTCCATCCTGGCATTCCG
GGAGAAGGAATGGCAGAGGCTGCAGTCAAACCCCCACCTGAAAGAGGGGTCCGTGACCTCCGTGAACCTGACTAA
GCTAGAGGGTGGCGTGGCCTATAACGTGATACCTGCCACCATGAGCGCCAGCTTTGACTTCCGTGTGGCACCGGA
TGTGGACTTCAAGGCTTTTGGAGGAGCAGCTGCAGAGCTGGTGCCAGGCAGCTGGCGAGGGGGTCACCCTAGAGTT
TGCTCAGAAGTGGATGCACCCCCAAGTGACACCTACTGATGACTCAAACCCCTGGTGGGCAGCTTTTAGCCGGGT
CTGCAAGGATATGAACCTCACTCTGGAGCCTGAGATCATGCCTGCTGCCACTGACAACCGCTATATCCGCGCGGT
GGGGGTCCCAGCTCTAGGCTTCTCACCCATGAACCGCACACCTGTGCTGCTGCACGACCACGATGAACGGCTGCA
TGAGGCTGTGTTCCCTCCGTGGGGTGGACATATATACAGCCTGCTGCCTGCCCTTGCCAGTGTGCCTGCCCTGCC
CAGTGACAGCTTGAGCCCTGGAACCTCTAAACCTTTGCCCCTGGGGCTTCCATCCCAACCAGTGCCAAGGACCTCC
TCTTCCCCCTTCAAATAATAAAGTCTATGGACAGGGCTGTCTCTGAAGTACTAACACAAGGACA

1262/6881
FIGURE 1173

MTSKGP EEEHPSVTLFRQYLRI RTVQPKPDYGA AVAF FEETARQLGLGCQKVEVAPGYVVTVLTWPGTNPTLSSI
LLNSHTDVVPVFKEHWSHDPFEAFKDSEGYIYARGAQDMKCVSIQYLEAVRRLKVEGHRFPRTIHMTFVPDEEVG
GHQGMELFVQRPEFHALRAGFALDEGIANPTDAFTVFYSESPWWVRVTSTGRPGHASRFMEDTAAEKLHKVVNS
ILAFREKEWQRLQSNPHLKEGSVTSVNLTKLEGGVAYNVIPATMSASFDFRVAPDVDFKAFEEQLQSWCQAAGEG
VTLEFAQKWMHPQVTPDDSNPWAAFSRVCKDMNLTLEPEIMPAATDNRYIRAVGV PALGFSPMNRTPVLLHDH
DERLHEAVFLRGVDIYTRL LPALASVPALPSDS

1263/6881
FIGURE 1174

CGCCAGCACGCGCCTGCTTCCCGTCTGCGGAGTCCACGCAGCTCCCCAGATCAAGAAGCTGAGGCCCCAGGTTA
CACACTAAAGTAAATGGCAGAGGCAGAAATAACACCTATGTCCTCCTGACCCCAAGGCATGTTCTTAAAGTTCTG
GAAACCTCCTGGAGGCTTCCTTGCTGCTCCTCTGGGACTGCCACCCTGGGCAGGGTGTTCTGTGGCCCCCTCATCA
TCGTGGTTTTTGAACCACAGGCCCTTACCAGCACAGCAGCAGCAGGCATGGCAGCAAGCGTGAGCAGCGCGAGG
GCACCATCCAGGTGCAGGGCCAGGCCCTCTTCTTCCGAGAGGCCCTGCCCCGCAGTGGGCAGGCTCGCTTCTCTG
TACTGCTGCTGCATGGTATTCTGCTTCTCCTCCGAGACCTGGCAGAACCTGGGTACACTGCACAGGCTGGCCCAGG
CTGGCTACCGGGCTGTGGCCATTGACCTGCCAGGTCTGGGGCACTCCAAGGAAGCAGCAGCCCCCTGCCCTATTG
GGGAGCTGGCCCCCTGGCAGCTTCCTGGCGGCTGTGGTGGAATGCCTTGGAGCTGGGCCCCCGGTTGTGATCAGTC
CATCACTGAGTGGCATGTACTCCCTGCCCTTCTCACGGCCCCCTGGCTCCCAGCTCCCGGGCTTTGTGCCAGTGG
CCCCCATCTGCACTGACAAAATCAATGCTGCCAACTATGCCAGTGTGAAGACTCCAGCTCTGATTGTATATGGAG
ACCAGGACCCCATGGGTGAGACCAGCTTTGAGCACCTGAAGCAGCTGCCCAACCACCGGGTGCTGATCATGAAGG
GGGCGGGGCACCCCTGTTACCTGGACAAACCAGAGGAGTGGCATAACAGGGCTGCTGGACTTCCTGCAGGGGCTCC
AGTGAAGCCCAGCACTGCTGCAGGGGGTGGGCTGCCTGCCTGCTCTGAGCTCTCTCTTGCACGCTCTCTCTTCTC
TCCCAGGCTCTGGCTCATGCACATGCAACAGGTGCGTCTGTCTATATGTCTGGGTTCTTGTCTTTTGTGGTCTGT
TTGTCTTTTCTACCTCTTTCTCTTGCAGTGATAGACTGAGGGGGTAAATCAAGAGAAAAAACTCTCAGGAATCA
AGGAACATAATCCTGTGGAGGGTAATCCATTACATGAGCTTCTCCTGTTCTTCCACTTTCCTGCCTGGCTTTTAC
TCCTTCCCCTGCTCTGCCAGCCTTTCCTCCCACCCACTCCTCCTTCTGCAAATGCCCTGAAGGCCAGCCCTTA
CCCCAACACCCACTTCCCCACCTCCTTAGGCCCCAGATACATACATGCCACATGCACGCTTACATGTTTAGAGC
CATCCTTGTTTCCAAATATGACCTTCGCTTGAGGGCAACTGCATAGGTACATCTAACTCTGGACTGGCATGCAC
ATTGTATGTGCAGCTTTGCATATACACACATGCATACATGAGCCTCCACACAAGCACTTGCACACATGTGGACT
CCTAACCATGCTAACCTCACTGGCTGGGAAGGTGGGGACCCCATGGGCCAGCCCTTGCAGGAGGCCCTTTTGCAA
GGCTTAGGGTGTGGCCAGCCCTGAAAGCTACTTGGACACAGGTTTCAGCTGGCCCCAGCCAGAGTGACCCCCA
GAAAGGGAGGGCCACCGCTTTGCCCCCTGCTTTTACCCTTCTTCTGGGTGCTCTACACCTCAGGTTACCAGGCC
TGAGGCATCTCAGCCAAGCTTGTTTCTGCTCTGAGGCTTGTGGGGTGGGAGCCAGAGTGGAGGTCGGTGAAATA
AAGTGATGCAATTAGAAAAAAAAAAAAAAAAAAAAA

1264/6881
FIGURE 1175

MAASVEQREGTIQVQGQALFFREALPGSGQARFSVLLHGHGIRFSSETWQNLGTLHRLAQAGYRAVAIDLPGLGHS
KEAAAPAPIGELAPGSFLAAVDALELGPPVVISPSLSGMYSLPFLTAPGSQLPGFVPVAPICTDKINAANYASV
KTPALIVYGDQDFMGQTSFEHLKQLPNHRVLMKGAGHPCYLDKPEEWHTGLLDFLQGLQ

1265/6881
FIGURE 1176

ATAACCCCTCATTGTTTCGCAGCTGATGTCACTCGCAGTTGTGAGCGGCCGCTCTCCCGGGGACAATGTGGGACT
GAGCGGGCCAGCCGCCGTGCCGCCGCCGCCGCCGCCGAGGACAGCCCCAGCGAGAGCCGGCCAGGTTGCAGCGC
GGACACACTCGCAGGTCGCTGTGGCCCCAGCCTCGCCTGACAGAATGAGCGGCTCGGACGGGGGACTGGAGGAGG
AGCCAGAGCTCAGCATCACCTCAGCTGCGGATGCTGATGCACGGGAAGGAAGTGGGCAGCATCATCGGGAAGA
AGGGCGAGACTGTAAAGCGAATCCGGGAGCAGAGCAGTGCCCGGATCACCATCTCCGAGGGCTCCTGCCCTGAAC
GCATCACCACCATCACCGGGTCTACAGCAGCTGTCTTCCATGCAGTCTCCATGATTGCTTTCAAACCTGGATGAGG
ACCTTTGTGCTGCTCCTGCAAATGGTGGAAATGTCTCCAGGCCTCCAGTGACCCTGCGCCTTGTTCATCCCTGCCA
GTCAGTGTGGCTCACTGATTGGGAAGGCTGGCACCAAGATCAAGGAGATCCGAGAGACTACGGGTGCCCAGGTAC
AGGTGGCAGGGGACCTGCTCCCCAACTCCACAGAGCGAGCTGTTACGGTATCTGGGGTGCTGATGCCATCATCC
TGTGTGTGCGCCAGATCTGCGCTGTTATCCTGGAGTCCCCACCCAAAGGAGCCACTATCCCCTACCATCCGAGCC
TCTCCCTAGGTACTGTTCTTCTCTCTGCCAACAGGGCTTCTCTGTCCAGGGTCAGTATGGGGCTGTGACCCAG
CTGAGGTACCAAGCTCCAGCAGCTCTCAAGCCATGCGGTCCCCTTTGCCACACCCAGCGTGGTGCCAGGACTGG
ATCCCGGCACACAGACCAGCTCACAGGAGTTCTTGGTTCCCAACGATTTGATTGGCTGTGTGATCGGGCGCCAGG
GCAGCAAGATCAGCGAGATCCGGCAGATGTCAGGGGCACATATCAAGATCGGGAACCAAGCAGAGGGCGCTGGGG
AGCGGCATGTACCATCACTGGCTCTCCGGTCTCCATCGCCCTGGCCCAGTACCTCATCACTGCCTGTCTAGAGA
CGGCCAAGTCTACCTCTGGGGGGACGCCCAGCTCGGCCCCCGCAGACCTGCCTGCCCCCTTCTCGCCACCCCTGA
CGGCCCTGCCACAGCTCCCCCTGGCCTGCTGGGCACACCCTATGCCATCTCCCTCTCCAACCTTCATCGGCCTCA
AGCCCATGCCCTTCTTGGCTTTACCACCTGCTTCCCCAGGGCCGCCGCCGGCTTGGCGGCCTACACTGCCAAGA
TGGCAGCAGCTAATGGGAGCAAGAAGGCTGAGCGGCAGAAATTCTCCCCCTACTGAGGCCAGCTGAGGTACAGGC
AGGGGCAGGCAGGACCACCAGCAGGGGGCTGCCTCTGCACCCTACCCGCCCAAGGAGACTCCACCCTGGGGTCCC
AAACGCCGCTAACGCCCAGACGCATGGATGCACCCCTACCCTGCCTCCATCTATGGGAGTTCTTTCTCTCAGAG
TGGGGGCAGTTTCTGGCCAGGGGTCTGAGCTGCGGCAGCCCCAGGGCAGGGGGCCCTACCTCCTCAGCTCTGTG
CTTGATACAGGGAGCAGCCAGGAGACTCCCTAGTGCCCCCACCATGGCGGGTGTCACTCACGCACTCCCCATCC
CTTAGGGCTTCTGGCCTACTGCATCCTTGTGGGAGTCAGGGAGGAGGGCCCGTTGGGTAGCTGGGGCCAGGCTT
CTCTCCCCACCACCTGCAGATTTCTTGCTGCTTCCACTGATAACCCTTTTGACTGGAATGAACTGGCTGGGCTTGT
CAGGGGGCACCCCAAAGAGGGGGCACTGCCAGGTAGCTGGGGGAGTGGCATGGGGCAGGGGCCAGTTCTCAGCA
GCAGACACTCTGTACAGTTTTTTCAATCCCTGTTTTTTGAATAAATATTCTCAGCGACCAAAAAAAAAAAAAAAAAA
AAAAAAA

1266/6881
FIGURE 1177

MSGSDGGLEEEPELSITLTLRMLMHGKEVGSIIIGKKGETVKRIREQSSARITISEGSCPERITTTITGSTAAVFHA
VSMIAFKLDEDLCAAPANGGNVSRPPVTLRLVIPASQCGSLIGKAGTKIKEIRETTGAQVQVAGDLLPNSTERAV
TVSGVPDAIILCVRQICAVILESPPKGATIPYHPSLSLGTVLLSANQGF SVQGQYGAVTPAEVTKLQQLSSHAVP
FATPSVVPGLDPGTQTSSQEF LVPNDLIGCVIGRQGSKISEIRQMSGAHIKIGNQAEGAGERHVTITGSPVSIAL
AQYLITACLETAKSTSGGTPSSAPADLPAPFSPPLTALPTAPPGLLGTPY AISLSNFIGLKMPMPFLALPPASPGP
PPGLAAYTAKMAAANGSKKAERQKFSPY

1267/6881
FIGURE 1178

CCTCTGGAGTCCCTGTGGCAGAACTCAAATGGAAGGAGGAGCAGCTGCACCCAGGGGAGCAGGGTGTACCTCCG
TTGGATAGAGCCGGCCAGGTTGCAGCGCGGACACACTCGCAGGTCGCTGTGGCCCCAGCCTCGCCTGACAGAATG

AGCGGCTCGGACGGGGGACTGGAGGAGGAGCCAGAGCTCAGCATCACCTCACGCTGCGGATGCTGATGCACGGG
AAGGAAGTGGGCAGCATCATCGGGAAGAAGGGCGAGACTGTAAAGCGAATCCGGGAGCAGAGCAGTCCCCGGATC
ACCATCTCCGAGGGCTCCTGCCCTGAACGCATCACCAACATCACCGGGTCTACAGCAGCTGTCTTCCATGCAGTC
TCCATGATTGCTTTCAAACCTGGATGAGGACCTTTGTGCTGCTCCTGCAAATGGTGGAAATGTCTCCAGGCCTCCA
GTGACCCTGCGCCTTGTCATCCCTGCCAGTCAGTGTGGCTCACTGATTGGGAAGGCTGGCACCAAGATCAAGGAG
ATCCGAGAGACTACGGGTGCCCAGGTACAGGTGGCAGGGGACCTGCTCCCCAACTCCACAGAGCGAGCTGTTACG
GTATCTGGGGTGCTGATGCCATCATCCTGTGTGTGCGCCAGATCTGCGCTGTTATCCTGGAGTCCCCACCCAAA
GGAGCCACTATCCCCTACCATCCGAGCCTCTCCCTAGGTACTGTTCTTCTCTCTGCCAACCAGGGCTTCTCTGTC
CAGGGTCAGTATGGGGCTGTGACCCAGCTGAGGTACCAAGCTCCAGCAGCTCTCAAGCCATGCGGTCCCCTTT
GCCACACCCAGCGTGGTGCCAGGACTGGATCCCGGCACACAGACCAGCTCACAGGAGTTCTTGGTTCCCAACGAT
TTGATTGGCTGTGTGATCGGGCGCCAGGGCAGCAAGATCAGCGAGATCCGGCAGATGTGAGGGGCACATATCAAG
ATCGGGAACCAAGCAGAGGGCGCTGGGGAGCGGCATGTCACCATCACTGGCTCTCCGGTCTCCATCGCCCTGGCC
CAGTACCTCATCACTGCCTGTCTAGAGACGGCCAAGTCTACCTCTGGGGGGACGCCAGCTCGGGCCCCGCAGAC
CTGCCTGCCCCCTTCTCGCCACCCCTGACGGCCCTGCCCACAGCTCCCCCTGGCCTGCTGGGCACACCCTATGCC
ATCTCCCTCTCCAACCTTCATCGGCCTCAAGCCCATGCCCTTCTTGGCTTTACCACCTGCTTCCCCAGGGCCGCCG
CCGGGCTTGGCGGCCTACACTGCCAAGATGGCAGCAGCTAATGGGAGCAAGAAGGCTGAGCGGCAGAAATTCTCC
CCCTACTAGAGGCCAGCTGAGGTACAGGCAGGGGCAGGCAGGACCACCAGCAGGGGGCTGCCTCTGCACCCTACCC
GCCCAAGGAGACTCCACCCTGGGGTCCCAAACGCCGCTAACGCCACAGCGCATGGATGCACCCCCCTACCCTGCCT
CCATCTATGGGAGTTCTTTCTCTCAGAGTGGGGCAGTTTCTGGCCCAGGGGTCTGAGCTGCGGCAGCCCCAGGG
CAGGGGGCCCTACCTCCTCAGCTCTGTGCTTGGATACAGGGAGCAGCCAGGAGACTCCCTAGTGCCCCCACCATG
GCGGGTGTCACTCACGCACTCCCCATCCCTTAGGGCTTCTTGGCCTACTGCATCCTTGTGGGAGTCAGGGAGGAG
GGCCCGTTGGGTAGCTGGGGCCAGGCTTCTCTCCCCACCACCTGCAGATTTCTTGCTGCTTCCACTGATACCCTT
TTGACTGGAATGAACTGGCTGGGCTTGTGAGGGGGCACCCCAAAGAGGGGGCACTGCCAGGTAGCTGGGGGAGTG
GCATGGGGCAGGGGCCAGTTCTCAGCAGCAGACACTCTGTACAGTTTTTTCAATCCCTGTTTTTGAATAAATAT
TCTCAGCGACCA

1268/6881
FIGURE 1179

MSGSDGGLEEEPELSITLTLRMLMHGKEVGSIIIGKKGETVKRIREQSSARITISEGSCPERITTITGSTAAVFHA
VSMIAFKLDEDLCAAPANGGNVSRPPVTLRLVIPASQCGSLIGKAGTKIKEIRETTGAQVQVAGDLLPNSTERA
TVSGVPDAIILCVRQICAVILESPPKGATIPYHPSLSLGTVLLSANQGF SVQGQYGAVTPAEVTKLQQLSSHAVE
FATPSVVPGLDPGTQTSSQEF LVPNDLIGCVIGRQGSKISEIRQMSGAHIKIGNQAEGAGERHVTITGSPVSIAL
AQYLITACLETAKSTSGGTPSSAPADLPAPFSPPLTALPTAPPGLLGTPY AISLSNFIGLKPM PFLALPPASPGP
PPGLAAYTAKMAAANGSKKAERQKFSPY

1269/6881
FIGURE 1180

ATTTCCTTTTAGTGTCTCAGGGTAAGGGAAAGGCTAGGTACCTACCATGTATGTGCTTATTGTTTTAATTCTCATC
ACTCTTTGGAGATGGGAATTTGTATCCCCCTTCTACAGATGGAGAAGCTGAGGCTCAGAGGGTTGAATGGGCTCCC
CAGGCTTACACAGCTCGTGAGACACACATAAGCACCCCTGGTCAGAGTGATGTGTGGCGCTCAAGGTCCATGCAGT
CTCTTTCTCTGAGGAGTTTACTAGCCCAGCTCTGGGGTCCCCATGTAAGGGCAGGGGCAGGGTGGACTGGGCTC
CTCTCGAACCCCTCTTTGGCTGCCCCAGCGAGAGCCGGCCAGGTTGCAGCGCGGACACACTCGCAGGTCGCTGTG
GCCCCAGCCTCGCCTGACAGAATGAGCGGCTCGGACGGGGGACTGGAGGAGGAGCCAGAGCTCAACATCACCCCTC
ACGCTGCGGATGCTGATGCACGGGAAGGAAGTGGGCAGCATCATCGGGAAGAAGGGCGAGACTGTAAAGCGAATC
CGGGAGCAGGTGAGGATGGAGTTTGGGGGAGGAGCCAGGGCACCTGATGTGGAGGGGAGATCCCTGCCCCACTT
TCTCTCTGAACCACTCCTTCTGGGCTGACCAGTGAGTCCCCAGAGGGTGGCAGTTTTGAGCCTTGCCCTCAGGCC
TGGTGAGTGGGGCAGGCAGACAAGTTCCGGCAAGGGAGCAGGGAAGATGCCCCGCTGCCCCGGCGCTCATTCTATA
TCTGCAGAGCAGTGCCCGGATCACCATCTCCGAGGGCTCCTGCCCTGAACGCATCACCAACATCACCGGTCTAC
AGCAGCTGTCTTCCATGCAGTCTCCATGATTGCTTTCAAAGTGGATGAGGACCTTTGTGCTGCTCCTGCAAATGG
TGGAAATGTCTCCAGGCCTCCAGTGACCCTGCGCCTTGTCTATCCCTGCCAGTCAGTGTGGCTCACTGATTGGGAA
GGCTGGCACCAAGATCAAGGAGATCCGAGAGGTGAGGGGCGAGATATACCAACACAGGGGAATCCGGGGCAAGGG
AGCAGTTGTAAGAGGGGTGTTGGGCTTATGGCGTCTCCCCACCTAGAGAGCTCTGAGCCTGGGCAGCCCTTTTC
TGGGTTATGGGAGCAGCCAGAAGTGGCCCCGTCTCTGTTTGCAGACTACGGGTGCCAGGTACAGGTGGCAGG
GGACCTGCTCCCCAACTCCACAGAGCGAGCTGTTACGGTATCTGGGGTGCCTGATGCCATCATCCTGTGTGTGCG
CCAGATCTGCGCTGTTATCCTGGAGTCCCCACCAAAGGAGCCACTATCCCCTACCATCCGAGCCTCTCCCTAGG
TACTGTCTTCTCTCTGCCAACAGGGCTTCTCTGTCCAGGGTCAGTATGGGGCTGTGACCCCAGCTGAGGTAC
CAAGCTCCAGCAGCTCTCAAGCCATGCGGTCCCCTTTGCCACACCCAGCGTGGTGCCAGGACTGGATCCCGGCAC
ACAGACCAGCTCACAGGAGTTCTTGGTTCCCAACGATTTGATTGGCTGTGTGATCGGGCGCCAGGGCAGCAAGAT
CAGCGAGATCCGGCAGATGTCAGGGGCACATATCAAGATCGGGAACCAAGCAGAGGGCGCTGGGGAGCGGCATGT
CACCATCACTGGCTCTCCGGTCTCCATCGCCCTGGCCAGTACCTCATCACTGCCTGTCTAGAGACGGCCAAGTC
TACCTCTGGGGGGACGCCCAGCTCGGCCCCCGCAGACCTGCCTGCCCCCTTCTCGCCACCCCTGACGGCCCTGCC
CACAGCTCCCCCTGGCCTGCTGGGCACACCCTATGCCATCTCCCTCTCCAACCTTCATCGGCCTCAAGCCCATGCC
CTTCTTGGCTTTTACCACCTGCTTCCCCAGGGCCGCCGCGGGCTTGGCGGCCTACACTGCCAAGATGGCAGCAGC
TAATGGGAGCAAGAAGGCTGAGCGGCAGAAATTTCTCCCCCTACTGAGGCCAGCTGAGGTACAGGCAGGGGCAGGC
AGGACCACCAGCAGGGGGCTGCCTCTGCACCCCTACCCGCCCAAGGAGACTCCACCCTGGGGTCCCAAACGCCGCT
AACGCCCAGACGCATGGATGCACCCCCCTACCCTGCCTCCATCTATGGGAGTTCTTTCTCTCAGAGTGGGGGCAGT
TTCTGGCCCCAGGGGTCTGAGCTGCGGCAGCCCCAGGGCAGGGGGCCCTACCTCCTCAGCTCTGTGCTTGGATACA
GGGAGCAGCCAGGAGACTCCCTAGTGCCCCCACCATGGCGGGTGTCACTCACGCACTCCCCATCCCTTAGGGCTT
CCTGGCCTACTGCATCCTTGTGGGAGTCAGGGAGGAGGGCCCGTTGGGTAGCTGGGGCCAGGCTTCTCTCCCCAC
CACCTGCAGATTTCTTGCTGCTTCCACTGATACCCTTTTGAAGTGAATGAAGTGGCTGGGCTTGTGAGGGGCAC
CCCAAAGAGGGGGCACTGCCAGGTAGCTGGGGGAGTGGCATGGGGCAGGGGCCAGTTCTCAGCAGCAGACACTC
TGTACAGTTTTTTCAATCCCTGTTTTTGAATAAATATTCTCAGCGACCAAAAAAAAAAAAAAAAAAAAAA

1270/6881
FIGURE 1181

MPRCPALILYLQSSARITISEGSCPERITTTITGSTAAVFHAVSMIAFKLDEDLCAAPANGGNVSRPPVTLRLVIP
ASQCGSLIGKAGTKIKEIREVRGEIYHPQGIRGKGAVVRGVLGLWRPPHLESSEPGQPFSGLWEQPEVAPVLCLO
TTGAQVQVAGDLLPNSTERAVTVSGVPDAIILCVRQICAVILESPPKGATIPYHPSLSLGTVLLSANQGFVQGG
YGAVTPAEVTKLQQLSSHAVPFATPSVVPGLDPGTQTSSQEFLVPNDLIGCVIGRQGSKISEIRQMSGAHIKIGN
QAEGAGERHVTITGSPVSIALAQYLITACLETAKSTSGGTPSSAPADLPAPFSPPLTALPTAPPGLLGTPYAISL
SNFIGLKPMFPLALPPASPGPPPGLAAYTAKMAAANGSKKAERQKFSPY

1271/6881
FIGURE 1182

GAATTCCGCCGCTGCTACACGCCTGGTGGGCAGCATGTCGGCAACAGCGGCTGCTCGTAAGCGGGGAAAAGCCGGC
CTCTGGGGCCGGGGCTGGCGCGGGGGCCGGCAAGCGGCGGCGAAAGGCCGACTCTGCGGGGGACAGGGGCAAATC
CAAGGGTGGCGGCAAGATGAATGAGGAGATCTCCAGCGACTCTGAGAGCGAGAGCCTAGCTCCAAGGAAGCCTGA
GGAGGAGGAGGAGGAGGAGCTGGAGGAACTGCACAGGAAAAGAAGCTGCGCTTGGCCAAGCTCTACCTAGAGCA
GCTCCGTCAGCAAGAGGAGGAGAAGGCTGAGGCCCCGTGCATTTGAGGAGGACCAGGTGGCGGGGCGCCTGAAGGA
GGATGTGCTTGAGCAGAGGGGCAGGCTGCAGAAGTTGGTGGCAAAAGAGATCCAGGCCCCAGCCTCAGCTGACAT
TCGCGTTTTACGGGGGCACCAGCTCTCTATCACATGTTTGGTCGTCACCCCCGATGACTCAGCCATCTTCTCTGC
TGCCAAAGACTGCAGCATCATTAAAGTGGAGCGTGGAGAGTGGACGGAAGCTGCATGTGATTCTCTCGAGCCAAGAA
GGGTGCCGAGGGAAAAGCCCCCTGGCCACAGCAGCCACGTCTCTGCATGGCCATCTCTCTCCGACGGCAAGTACCT
TGCCTCTGGTGACCGCAGCAAGCTCATTCTCATTTGGGAGGCCCAGAGCTGCCAGCACTTGTACACCTTCACAGG
ACACCGGGATGCAGTGTTCGGTCTGGCATTCCGCAGAGGCACCCACCAGCTCTACAGCACATCCCACGATCGCTC
CGTGAAGGTGTGGAATGTGGCAGAGAACTCCTACGTGGAGACGCTCTTCGGACACCAGGACGCTGTGGCTGCACT
GGATGCCTTGAGCCGGGAGTGCTGTGTGACGGCTGGGGGCCGGGATGGGACTGTACGTGTGTGGAAGATCCCCGA
GGAGTCCCAGCTTGTCTTCTATGGCCACCAGGGCTCCATCGACTGCATCCACCTAATCAATGAGGAGCACATGGT
GTCCGGCGCGGACGATGGCTCTGTGGCCTTGTGGGGTCTCTCCAAGAAGCGACCACTTGCCCTGCAGCGTGAAGC
TCACGGGCTGCGGGGAGAGCCAGGCCTGGAGCAGCCCTTCTGGATATCGTCGGTGGCAGCCCTCCTCAACACAGA
CCTTGTGGCCACAGGCTCCCACAGCTCCTGTGTGCGGCTTTGGCAGTGTGGGGAAGGCTTCCGGCAGCTTGACCT
TCTCTGTGACATCCCCCTGGTGGGTTTTATCAACAGCCTCAAGTTCTCCAGCTCTGGGGACTTCCCTGGTGGCTGG
GGTAGGGCAGGAGCACAGGCTTGGCCGATGGTGGAGAATCAAAGAGGCTCGGAATTCTGTCTGCATCATCCCCT
CCGCAGGGTCCCTGTACCCCCAGCTGCTGGTTCCTGACACTCTTATCCTCCTTATTTAAGTCCTTCCCAGGCTAT
GCCCCACCTCTTTGAAGCTT

1272/6881
FIGURE 1183

MSATAAARKRGKPPASGAGAGAGAGKRRRKADSAGDRGKSKGGGKMNEEISSDSESESLAPRKPEEEEEEELEETA
QEKKLRLAKLYLEQLRQQEEEEKAEARAFEEEDQVAGRLKEDVLEQRGRLOKLVAKEIQAPASADIRVLRGHQLSIT
CLVVTPDDSAIFSAAKDCSIIKWSVESGRKLHVIPRAKKGAEGKPPGHSSHVLCMAISSDGKYLASGDRSKLILI
WEAQSCQHLYTFTGHRDAVSGLAFFRRGTHQLYSTSHDRSVKVWNVAENSYVETLFGHQDAVAALDALSRECCVTA
GGRDGTVRVWVKIPEESQLVFYGHQGSIDCIHLINEEHVMVSGADDGSVALWGLSKKRPLALQREAHGLRGEPGLEQ
PFWISSVAALLNTDLVATGSHSSCVRLWQCGEGFRQLDLLCDIPLVGFINSLKFSSSGDFLVAGVGQEHRLGRWW
RIKEARNSVCIIPLRRVPVPPAAGS

1273/6881
FIGURE 1184A

GCAGCTTAGGCGCCACCAAGGCAAGAACCTAGCCTCCGAGGACCCCAAAAAGAAGAGAGCTCAGAAGCCCTCCCA
CATGAGAAGAAACATACGAAAGCTACTCCGGGAGGATCAATTGGAGCCTGTTACCAAAGCAGCACAGCAAGAAGA
GTTGGAAAGAAGGAAGCGCCTGGAGCAGCAGAGGAAAGATTATGCAGCCCCCTATTCTACTGTTCCGCTGGAGTT
CCTCCCTGAGGAAATTGCTTTAAGGGCAAGTGACGGTCCCCAACTGCCTCCTCGGGTCTTGGCCCAGGAAGTCAT
TTGTTTGGACAGTAGCAGTGGCAGTGAGGATGAAAAAGCAGTCGAGATGAGGTGATTGAACTGAGCTCTGGAGA
GGAGGACACTCTGCACATTGTGGACAGCAGTGAATCTGTTCAGTGAAAGATGATGAGGAAGAAGAGAAGGGTGGCAC
CCATGTCAATGATGTCTTAACCAGCGTGACGCCCTTGGGCGGGTCCCTTGTC AACCTAAACCACCTCCAGAGGA
GGAAATGTCTTCCTTGCCCCACAGTTGGCACGGGCTGTGAAACCTCATCAGATTGGCGGGATCCGGTTCCCTTTA
CGATAACCTAGTGGAGTCTCTGGAGAGGTTTAAGACCAGCAGTGGCTTTGGCTGTATTCTGGCCCACAGCATGGG
TCTGGGGAAAACCTTGCAAGTGATCTCTTTCATCGACGTCTCTTCCGCCACACGCCAGCCAAAACAGTCCTTGC
CATTGTGCCGTTAATACTCTTCAGAATTGGCTGGCAGAGTTCAACATGTGGCTTCCACCTCCTGAAGCCCTCCC
GGCTGACAACAAGCCTGAAGAAGTCCAGCCTCGGTTCTTTAAAGTTCACATCTTGAATGATGAGCACAAGACGAT
GGCATCTCGTGCTAAAGTGATGGCTGATTGGGTGTGAGAGGGTGGCGTGCTGCTGATGGGGTACGAGATGTACAG
ACTCCTCACTCTGAAGAAATCATTGGCCACAGGTAGACCGAAGAAAACCAAGAAGCGTTCTCACCCAGTCATCAT
TGATCTAGATGAGGAAGATCGGCAGCAGGAGTTTCGGAGAGAGTTTGAGAAGGCTTTATGCCGCCCTGGCCCTGA
TGTAAGTAATCTGTGATGAGGGACACCGCATCAAAAACCTGCCAGGCCAGCACCTCACAGGCTCTGAAGAATATCCG
CTCTCGCCGCCGGGTGGTGCTGACTGGGTACCCTCTGCAAAAACACCTCATTGAGTACTGGTGCATGGTGGACTT
TGTGCGCCAGACTTCCTTGGCACCCGGCAGGAGTTTCAGCAACATGTTTGAACGCCCTATCCTGAATGGGCAATG
TATTGACAGCACACCTCAGGACGTCCGCCTCATGCGGTACCGGAGCCATGTCTGCACAGTCTTCTGGAGGGCTT
TGTGCAGAGGAGAGGCCACACTGTGCTGAAGATTTCATCTCCCTGCCAAGGAAGAAAATGTGATCCTTGTGCGGCT
CTCCAAGATCCAGCGAGATTTGTATACACAGTTTCATGGATCGCTTCCGGGACTGTGGTAGCAGCGGTTGGCTGGG
GCTGAACCCCTTAAAGGCATTCTGTGTGTGTGCAAGATCTGGAATCACCTGATGTGCTGTATGAAGCCCTTCA
GAAGGAGAGCTTGGCCAAAGAGCAGGACCTAGACGTGGAAGAACTTGGCTCTGCAGGGACCAGTGCCCCGTGTCC
ACCACAGGGAACAAAAGGCAAGGGAGAGGATAGCACCTTGGCTTCCTCGATGGGAGAGGCAACCAATAGCAAGTT
CCTACAGGGCGTTGGCTTCAACCCTTTCCAGGAGCGAGGCAACAACATTGTCACATATGAATGGGCCAAGGACCT
TCTGACTAATTACCAGACTGGAGTCTAGAAAACCTCTCCCAAGATGGTACTGCTTTTCCACCTGATTGAGGAAAG
TGTGAAGCTTGGGGACAAGATCCTTGTGTTTAGCCAGAGTCTTTCCACCTTGGCTCTCATCGAGGAATTCCTTGG
AAAACGAGAAGTACCTGTCCACCTGGTACCGAGGGGCAAGGAGCACAGAAGTGGGTTGAAACATCAGCTACTT
CCGGCTAGATGGTAGCACCCCTGCCTTTGAGAGGGAGCGGCTTATTAATCAGTTCAATGATCCCAGCAACCTCAC
CACCTGGCTGTTCCTTCTCTTACAAGGGCCGGATGCTTGGGTGTGAATCTGATTGGTGCCAACCGAGTGGTGGT
GTTTGATGCTTCCTGGAACCTTGCCATGATGCCAGGCAGTATGTGCGGTATACCGTTATGGCCAGAAAAAGCC
CTGTTACATCTATCGCCTTGTGGCTGATTACACTCTAGAAAAGAAGATCTATGACCGTCAGATTTCCAAGCAGGG
CATGTGATCGGGTGGTGGATGATCTAAATCCAATGCTGAACTTCACACGGAAAGAGGTGGAAAACCTACTGCA
CTTTGTTGAGAAGGAGCCAGCTCCCCAAGTTTCTTGAACGTAAAGGGGATCAAGGAGTCAGTCCTGCAACTGGC
CTGTCTGAAGTACCTTCACCTCATCACCAGGAGCCTTTCGAGCATGAGTCATTGCTCTTGAACCGAAAGGATCA
CAAGCTAACCAAGGCTGAGAAAAAGCAGCAAGAAAAAGCTATGAGGAAGACAAACGCACATCAGTCCCCATATAC
CCGCCATCGTATGCGCAGTATTACCCTGCCAGCGATCAGAGCCTGACCAGCATCCCCGCCTTCAGCCAGAGAAA
CTGGCAGCCAACTTTGAAGGGTGTGAAAAGCCTGTGGCCAGTGTTCGTCCTGTGCAGTCCACCCCCATCCCCAT
GATGCCCCGGCATGTCCCATTTGGGAGGAAGTGTAAGCTCTGCCTCCAGCACAAATCCATCCATGAACTTTCCCAT
CAACTACTTGCAGCGTGCAGGAGTCCTTGTGCGAAGGTGGTCACCACGACAGATATTGTTATTCTGGACTCAA
CAGCTCCACAGATGTACAGGCAAGAATTAATGCTGGTGAGAGCATCCACATCATCCGTGGGACAAAAGGGACGTA
CATCCGTACCAGTGATGGACGGATCTTTGCTGTCCGGGCAACTGGCAAACCAAGGTTCTGAAGATGGTCCGGAT
GGCTGCCTCAGGTTCCAGGGACCTTCTTGCGAGTCCACAAGCAACGGCAGACACAGTGCCTCATACCCAAAGC
CCCCGACCCTGAGGGGGCTGGCCAGGCCCGTCTCTCCTGACAGCCCAGAGATCATCAGTGAGCTTCAGCAGTATGC
AGATGTGGCTGCTGCCCCGGGAATCCCGTCAGAGCTCCCCAAGCACCAATGCCGCCCTGCCTGGCCCCCGGCCCA
ACTTATGGACAGCAGTGCTGTTCCCGGGACAGCTCTCGGAACTGAGCCTCGACTAGGGGGTTCATTGCCTCAATAG
TTCCCTCTTGGTGACTGGCCAGCCCTGTGGTGACAGGCACCCAGTGCTGGACTTAAGGGGGCCACAAGCGAAAGTT
GGCCACACCACCTGCTGCCAGGAGTCATCCCGCCGGCGGTCCAGGAAGGGTCATCTGCCAGCCCCCGTGCAGCC

1274/6881
FIGURE 1184B

GTATGAACACGGGTATCCAGTCTCTGGCGGGTTTGCCATGCCACCCGTCTCCTTAAACCATAACCTCACCACCCC
CTTCACCTCCCAGGCTGGGGAGAACTCCCTGTTTATGGGCAGTACCCCTCCTACTACCAGCTGTCCAATTTGCT
GGCAGATGCCCCGCTGGTGTTTCCAGTGACTACTGACCCTCTGGTGCCAGCAGGCCCCGTCAGTTCCTCTTCCAC
GGCTACCTCAGTCACTGCCAGCAACCCCTCCTTCATGCTCAACCCTTCTGTGCCAGGGATACTACCCAGCTATT
ACTCCCATTCTCACAGCCACTCCTGTCCGAGCCGAGGATGTTTGCGCCTTTTCCTTCCCCTGTCTTGCCCAGCAA
CCTTTCGCGGGGCATGTCTATCTATCCAGGCTACATGTCCCCACATGCAGGCTACCCAGCTGGTGGCCTCCTACG
GTCCCAGGTGCCTCCATTTGACTCTCATGAGGTTGCCGAGGTTGGGTTTCAGCTCCAATGATGATGAGGATAAAGA
CGATGATGTGATAGAGGTCAGTGGGAAATAGCTAGGGAGCCCCCTCCCCACCTCACTTGGGGCCCCCAGCAGGTTG
CCCACCAAGCTGAAAGGCAGTGATTTAGACCTTTTGAGAATAGGACACTTGGCAGGAGGGAAAAGGAAGAGGACA
AAGGAGGGTGTTGGCCAAAGTGGCAGAGCTCTGTTGCTGTTTAACAAAAGAGGC

1275/6881
FIGURE 1185

MRRNIRKLLREDQLEPVTKAAQQEELERRKRLEQQRKDYAAP IPTVPLEFLPEEIALRASDGPQLPPRVLAQEVI
CLDSSSGSEDEKSSRDEVIELSSGEEDTLHIVDSSESVSSEDDEEEKGGTHVNDVLNQDALGRVLVNLNHPPEE
ENVFLAPQLARAVKPHQIGGIRFLYDNLVESLERFKTSSGFGCILAHSMGLGKTLQVISFIDVLFRTHTPAKTVLA
IVPVNTLQNLWLAEFNMWLPPEALPADNKPEEVQPRFFKVHILNDEHKTMASSRAKVMADWVSEGGVLLMGYEMYR
LLTLKKSFATGRPKTKKRSHPVII DLDEEDRQQEFRRFEKALCRPGPDVVICDEGHRIKNCQASTSQALKNIR
SRRRVVLTGYPLQNNLIEYWCMVDFVRPDLGTRQEF SNMFERPILNGQCIDSTPQDVRLMRYRSHVLHSLLEGF
VQRRGHTVLKIHLPKEENVILVRLSKIQRDLTYQFMDRFRDCGSSGWLGLNPLKAFCVCCCKIWNHPDVLYEALQ
KESLANEQDL DVEELGSAGTSARCPPQGTKGKGEDSTLASSMGEATNSKFLQGVGFNPFQFERGNNIVTYEWAKDL
LTNYQTGVLENSPKMVLLFHLIEESVKLGDKILVFSQSLSTLALIEEFLGKREVPCPPGTEGQGAQKWVRNISYF
RLDGSTPAFERERLINQFNDPSNLTTWLFLLSTRAGCLGVNLIGANRVVVFDA SWNPCHDAQVCRVYRYGQKKP
CYIYRLVADYTLEKKIYDRQISKQGMSDRVVDDLNPMLNFTRKEVENLLHFVEKEPAPQVSLNVKGIKESVLQLA
CLKYPHLITKEPFEHESLLLNRKDHKLTKAEKKAACKSYEEDKRTSVPYTRPSYAQYYPASDQSLTSIPAFSQRN
WQPTLKGDEKPVASVRPVQSTP IPMPRHVPLGGSVSSASSTNPSMNFP INYLQ RAGVLVQKVVT TTDIVIPGLN
SSTDVQARINAGESIHI IRGTKGTIIRTSDGRIFAVRATGKPKVPEDGRMAASGSQGPSCESTSNGRHSASSPKA
PDPEGLARPVSPDSPEII SELQQYADVAAAARESRQSSPSTNAALPGPPAQLMDSSAVPGTALGTEPRLGGHCLNS
SLLVTGQPCGDRHPVLDLRGHKRKLATPPAAQESSRRRSRKGHLPAPVQPYEHGYPVSGGFAMPFVSLNHNLTTP
FTSQAGENSLFMGSTPSYYQLSNLLADARLVFPVTTDPLVPAGPVSSSSTATSVTASNPSFMLNPSVP GILPSYS
LPFSQPLLSEPRMFAPFPSPVLP SNLSRGMSIYPGYMSPHAGYPAGGLLRSQVPPFDSHEVAEVGFSSNDDDEDKD
DDVIEVTGK

1276/6881
FIGURE 1186

GCCACCGCCGCGCCGAGTCCTTTTGTCCAAGATGGCGGCGCCGGGGGCGCTGCCTCCTCGGCCGCCGCCTCCGCC
GCCGCCGCTGTGAGAAACCTACGGGCCGCCCGCCCGCCGCGCCAGCGCCATGAAGCGGCAGAGCGAGCGAGACTC
TAGCCCGAGCGGGCGCGGCTCGTCATCGTCCGCCAAGCGTCCGCGGGAGCGCGAACGGGAGGCGGAGGCGGGCGG
GCGGCGGGCGGCGCACAAAGGCCTCTGGCGGCGCCAAGCACCCGGTTCCAGCGCGGGGCCCGCGACAAACCCGCGG
CAGCGGAAGCGGCGGGGGCGGGCATCGCGACGGCGCGGCACCGGGGACGCGAATCACCGCGCGAGTAGCGGGCG
CTCCTCGGGCTCCGGCGCTGGCGGCGGGGGACGCGGCGGCAAGGCCTCGGGGGACCCGGGCGCCTCCGGCATGTC
GCCCCGCGCGTCTCCTCTGCCGCCGCCCTCCGCCACCGCCTGGGGCCGAGCCCGCGTGTCCCGGCTCATCCGCGGC
CGCGCCTGAGTACAAGACGTTGCTCATCAGCAGCTTGAGCCCCGCGCTGCCCGCCGAGCACCTCGAGGACCGGCT
CTTCCACAGTTCAAGCGCTTCGGCGAGATCAGCCTCCGCTGTGCGACACGCCTGAGCTGGGCCGTGTGGCCTA
CGTGAATTTCCGGCACCCACAGGACGCGACGCGAGGCCCGCCAGCACGCCCTGGCCCGGAGCTGCTGCTCTACGA
CCGCCCGCTCAAGGTAGAGCCCGTGTACCTGCGTGGCGGCGGCGGGAGCAGTCGGCGAAGTAGCAGCAGCAGCGC
CGCCGCTTCCACGCCTCCCCAGGGCCGCCCGCGCCCGCCGACCCGCTCGGCTACCTCCCGCTACACGGAGGCTA
CCAGTACAAGCAGCGCTCGCTGTCCCCGTGCTGCCCGCCCCCTGCGGGAGCCCCGTGCCCGTACAGCCGCCGC
AGCCTTCGCCCTGGATGCCGCTGCTGCCGCCGCCGTGGGACTGTCCCGGAGCGGGCCCTGGACTACTACGGGCT
GTACGACGACCGTGGGCGCCCCATAGGCTACCCAGCTGTGTGTGAGGAGGACCTGATGCCCGAGGATGACCAGCG
GGCCACGCGCAACCTCTTCATTGGTAACCTGGACCACAGCGTATCTGAGGTGGAGCTGCGAAGGGCCTTCGAGAA
ATATGGCATCATCGAGGAGGTGGTCATCAAGAGGCCTGCCCGTGGCCAGGGCGGTGCCTATGCCTTCCTCAAGTT
CCAGAACCTGGACATGGCCCATAGGGCTAAGGTGGCCATGTGCGGCCGAGTGATTGGTCGCAACCCCATTAAGAT
AGGCTATGGCAAGGCCAACCCACCACTCGTCTCTGGGTGGGTGGCCTGGGACCTAACACGTCACTGGCGGCTCT
GGCCCGAGAGTTTGACCGCTTTGGGAGCATTCGGACCATTGATCACGTCAAAGGAGATAGCTTTGCCTATATTCA
GTACGAGAGCTTGGACGCGAGCCAGGCCGCTGTGCTAAAATGAGGGGTTTTCCCTTGGGTGGACCAGACCGCAG
GCTCCGCGTGGATTTTGCCAAAGCAGAGGAGACTCGGTACCCCCAGCAGTACCAGCCCTCGCCACTCCCTGTGCA
TTATGAGCTGCTCAGAGATGGATACACCGGCACCGCAACCTGGACGCCGACCTGGTGCGGGACAGGACGCCCCC
ACACCTTCTGTACTCAGACCGAGACCGGACTTTTTTTGGAAGGGGACTGGACCAGCCCCAGTAAAAGCTCTGACCG
CCGAAACAGCCTTGAGGGCTACAGTCGCTCAGTGCGCAGCCGGAGTGGTGAGCGTTGGGGGGCAGATGGAGACCG
TGGTTTTGCCAAAGCCCTGGGAAGAGAGGGCGGAAACGGAGAAGCCTTTCCAGTGACCGTGGGAGGACAACCCATTC
ACCATATGAGGAACGGAGTAGGACCAAGGGCAGTGGGCAGCAGTCAGAGCGGGGCTCCGACCGCACCCCTGAGCG
CAGCCGCAAGGAGAACCCTCCAGTGAAGGGACCAAGGAGTCCAGCAGCAACTCCCTCAGCAACAGCAGACATGG
GGCTGAGGAACGGGGCCACCACCACCACCACGAGGCTGCAGACTCTTCCCACGGGAAGAAGGCAAGAGACAG
CGAGCGCAATCACCGGACCACAGAGGCCGAGCCCAAGCCTCTGGAAGAGCCAAAACACGAGACCAAAAAGCTGAA
GAATCTTTCAGAGTACGCTCAGACACTACAGCTGGGTTGGAATGGGCTTCTGGTGTTGAAAAACAGCTGCTTCCC
CACGTCTATGCATATCCTAGAGGGGGACCAGGGGGTGATCAGCAGTCTCCTCAAAGACCACACTTCTGGGAGCAA
GCTGACCCAGCTGAAGATCGCCAGCGCCTTCGACTGGACCAGCCCAAGCTTGACGAGGTACACGACGCATCAA
GCAGGGGAGCCCCAACGGCTATGCGGTCTCTTAGCCACCCAGGCAACCCCCAGTGGGCTTGGCACTGAGGGGAT
GCCACAGTAGAGCCCGGTCTGCAGAGGCGGCTTCTCAGGAACCTGGTCTCCTACTTGAAACAGAAGCAGGCCGC
AGGGGTGATCAGCTTGCCAGTGGGGGGGTCCAAGGGCAGAGACGGCACAGGCATGCTCTACGCCTTCCCACCCCTG
CGACTTTTCCCAGCAGTACCTCCAGTCAGCACTAAGGACATTGGGCAAGCTAGAAGAAGAACACATGGTGATAGT
CATCGTCAGAGACACTGCCTAGCCCAAGCCTGTCTTTCCAGCGTCATGTTGTGTACAAAAGCAGTTATTTTA
AAATCTGATCCCCTCTCTACCTACCCTTTGGTTTGAATTATCTCCTGGGTATTTTGGTTTCAATTTGGGTGGGG
ATCAAAGTCCTGTCCACCACCAAACTAAGTTCTTAGATTTTGGGGGATTTTTTTTTTAAACGATGAGAAGGGA
ATCCGGTTATGTTGATTTCTAGTGTACAAGATACTGTCTGCTGTGGTTCTGTATTTTTTTTATTTTTTGACCACT
GTATGGAAAGTTGTCTAGTAAAACCTTTGACAGAGGATGGATTTTTTAAACCTG

1277/6881
FIGURE 1187

CTTCCGTCGCTGCTGTAGTCGCTTCCTGCGGCCAGCCCGGGTTCAATCAGCGGCCGACAACGTCTAGGGCTCAG
ACACCACCAGCCAATGAGGGAGGGCAGCGTGGAGCCGCCCGTCTGGGCTCGCGGCTCCTGGACCAATGGGGAAGT
GGCATGTGGGAGGGCGCCGGGGGGCCCCCGCCAATGGGGAGCTACGGCGCGCGGCCGGGACTTGGAGGCGGTGC
GGCGCGGGCGGGTGCGGTTTCAGTCGGTCGGCGGGCGGCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATGA
GGAGGATGTGGGCCACGCAGGGGCTGGCGGTGGCGCTGGCTCTGAGCGTGCTGCCGGGCAGCCGGGCGCTGCGGC
CGGGCGACTGCGAAGTTTGTATTTCTTATCTGGGAAGATTTTACCAGGACCTCAAAGACAGAGATGTCACATTCT
CACCAGCCACTATTGAAAACGAACCTATAAAGTTCTGCCGGAAGCAAGAGGCAAAGAGAATCGGTTGTGCTACT
ATATCGGGGCCACAGATGATGCAGCCACCAAATCATCAATGAGGTATCAAAGCCTCTGGCCCACCACATCCCTG
TGGAGAAGATCTGTGAGAAGCTTAAGAAGAAGGACAGCCAGATATGTGAGCTTAAGTATGACAAGCAGATCGACC
TGAGCACAGTGGACCTGAAGAAGCTCCGAGTTAAAGAGCTGAAGAAGATTCTGGATGACTGGGGGGAGACATGCA
AAGGCTGTGCAGAAAAGTCTGACTACATCCGGAAGATAAATGAACTGATGCCTAAATATGCCCCAAGGCAGCCA
GTGCACGGACCGATTTGTAGTCTGCTCAATCTCTGTTGCACCTGAGGGGGAAAAACAGTTCAACTGCTTACTCC
CAAAACAGCCTTTTTGTAAATTTATTTTAAAGTGGGCTCCTGACAATACTGTATCAGATGTGAAGCCTGGAGCTT
TCCTGATGATGCTGGCCCTACAGTACCCCATGAGGGGATTCCCTTCCTTCTGTTGCTGGTGTACTCTAGGACTT
CAAAGTGTGTCTGGGATTTTTTTTATTAAAGAAAAAAATTTCTAGCTGTC

1278/6881

FIGURE 1188

ACCAGCCCAGCCTTTTCAGTGCAGGCTCCAGCCCTCCACCCCCACCCGAGTTGCAGGATGTCGATGACAGACTTGC
TGAACGCTGAGGACATCAAGAAGGCGGTGGGAGCCTTTAGCGCTACCGACTCCTTCGACCACAAAAAGTTCTTCC
AAATGGTCGGCCTGAAGAAAAAGAGTGC GGATGATGTGAAGAAGGTGTTTCACATGCTGGACAAGGACAAAAGTG
GCTTCATCGAGGAGGATGAGCTGGGATTCATCCTAAAAGGCTTCTCCCCAGATGCCAGAGACCTGTCTGCTAAAG
AAACCAAGATGCTGATGGCTGCTGGAGACAAAGATGGGGACGGCAAAATTGGGGTTGACGAATTCTCCACTCTGG
TGGCTGAAAGCTAAGAAGCACTGACTGCCCCTGGTCTTCCACCTCTCTG

1279/6881
FIGURE 1189

MSMTDLLNAEDIKKAVGAFSATDSFDHKKFFQMVGLKKKSADDVKKVFHMLDKDKSGFIEEDELGFILKGFSPDA
RDLSAKETKMLMAAGDKDGDGKIGVDEFSTLVAES

1280/6881
FIGURE 1190

CCGCGCCAGTCGCCTAGCAGGTCCTCTACCGGCTTATTCTGTGCCGGATCTTCATCGGCACAGGGGCCACTGAG
ACGTTTCTGCCCTCCCTCTTTCTTCCTCCGCTCTTTCTCTTCCCTCTCGTTTAGTTTGCCTGGGAGCTTGAAAGGA
GAAAGCACGGGGTCGCCCCAAACCCCTTCTGCTTCTGCCCATCACAAAGTGCCACTACCGCCATGGGCCTCACTAT
CTCCTCCCTCTTCTCCCGACTATTTGGCAAGAAGCAGATGCGCATTGATGGTTGGATTGGATGCTGCTGGCAA
GACAACCATTCTGTATAAACTGAAGTTAGGGGAGATAGTCACCACCATTCTACCATTGGTTTTAATGTGGAAAC
AGTAGAATATAAGAACATTTGTTTCACAGTATGGGATGTTGGTGGTCAAGATAGAATTAGGCCTCTCTGGAAGCA
TTACTTCCAGAATACCCAGGGTCTTATTTTTGTGGTAGATAGCAACGATCGTGAAAGAATTCAGGAAGTAGCAGA
TGAGCTGCAGAAAATGCTTCTGGTAGATGAATTGAGAGATGCAGTGCTGCTACTTTTTGCAAACAAACAGGATTT
GCCAAATGCTATGGCCATCAGTGAAATGACAGATAAACTAGGGCTTCAGTCTCTTCGTAACAGAACATGGTATGT
TCAAGCCACTTGTGCAACACAAGGAAGTGGTCTGTATGAAGGACTTGACTGGCTGTCAAATGAGCTTTCAAAACG
TAAATGAAATTGGATATCTAACCAAGGACATGTTTGATAAAATGGTCTAGGCTTGTTACAACAAAATTAGTTT
GTATCTTGGTTATTAAACAGTATCTGGGACTGGTTTGGGCAGAAATATTAACTTATTTTGTTGCCAATTATTGTT
TACCGAGTATAATGTTGCTATTTAGCAATGTGCTTGGTTTTAAAGAAATTCTCCTTGGGAAAAAAGTATCCTCTT
TTAATTTTACTTCCCATAAGCGTAAATGCCTGGACATAGCTCTTGTGCAACCTTTAAATAAATTGTTTTGAGTGT
TTTTTGAGCCCCAGACAAATAATGTTTTAAAGTTATCCCCTTGCTACTTTACTGATACCTTTATCATTCCCTGAGA
CAGTTTGCTAATTTAAAAATGTAGCATTCCATTTGTATTTATTTCTCTCCCTTGCCAAAAAGATTTTCTAATACT
GCTTGTACCAGCCAGAGAAAGATCCAAAACACTACTCAGCTCTCTTGCACTGAGGAAATTTTTCCCCCTACATTG
ACTCCTGGCCTACATCAGCCAACTTAACCTTGGTGGGGTTTGGATTTGATAGCCAATTAGTTCTGTGCTGGTTG
CAAAGAATTGATATTTAGATGGTTTTTAATACTCAGCAGATTGTCTTCCTTTATATTGTGTCTTTTTTATGTTGC
ATGTTGCTTTTTGTTATCAGCCTGATTTTTTGTCTAGTATATGATAGTTCTGCTGATGTTTTGTTTATTGGGCAGA
CATATCTTCATTAAGAGTTTTTGGAAACTCACCAAATTCGATGAATACATTTTCTTCTTAACCCATTTCGGAATT
ATTCCTAATAAAATGATAAAATACGT

1281/6881
FIGURE 1191

MGLTISSLFSRLFGKKQMRILMVGLDAAGKTTILYKLLGEIVTTIPTIGFNVETVEYKNICFTVWDVGGQDRIR
PLWKHYFQNTQGLIFVVDSDNRERIQEVADELQKMLLVDEL RDAVLLLFANKQDLPNAMAI SEMTDKLG LQSLRN
RTWYVQATCATQGTGLYEGLDWLSNELSKR

1282/6881
FIGURE 1192

TCAGGAATCGGGATTAAAAGTTAACCAGCCAGCATCCTTTGCTATAAGGTTGAATGGCGCAAAAGGCAAGATTGA
TGTATAGGTGCACAGCCCCTCTGGAGCCGTGGAGGAGTGCCACGTGTCTGAGCTGGAGCCAGATAAGTATGCTGT
TCGCTTCATCCCTCATGAGAATGGTGTCCACACCATCGATGTCAAGTTCAATGGGAGCCACGTGGTTGGAAGCCC
CTTCAAAGTGCGCGTTGGGGAGCCTGGACAAGCGGGGAACCCTGCCCTGGTGTCCGCCTATGGCACGGGACTCGA
AGGGGGCACCACAGGTATCCAGTCGGAATTCTTTATTAACACCACCCGAGCAGGTCCAGGGACATTATCCGTAC
CATCGAAGGCCCATCCAAGGTTAAAATGGATTGCCAGGAAACACCTGAAGGGTACAAAGTCATGTACACCCCAT
GGCTCCTGGTAACTACCTGATCAGCGTCAAATACGGTGGGCCAACACATCGTGGGCAGTCCCTTCAAGGCCAA
GGTGACAGGCCAGCGTCTAGTTAGCCCTGGCTCAGCCAACGAGACCTCATCCATCCTGGTGGAGTCAGTGACCAG
GTGCTCTACAGAGACCTGCTATAGCGCCATTCCCAAGGCATCCTCGGACGCCAGCAAGGTGACCTCTAAGGGGGC
AGGGCTCTCAAAGGCCCTTTGTGGGCCAGAAAGATTCTTCTGGTGGACTGCAGCAAGCTGGCTCCAACATGC
TGCTGATCGGGGTCCATGGGGCCACCACCCCTGCGAGGAGGTCTCCATGAAGCATGTAGGCAACCAGCAATACA
ACGTCACATACGTGCTCAAGGAGAGGGGCGATTATGTGCTGGCTGTGAAGTGGGGGGAGGAACACATCCCTGGCA
GCCCTTTTCATGTACAGTGCCTTAAACAGTTTTCTCAAATCCTGGAGAGAGTTCTTGTGGTTGCTTTTGTTC
TTGTTTGTAAATTCATTTTATACAAAGCCCTCCAGCCTGTTTGTGGGGCTGAAACCCCATCCCTAAAATATTGCTG
TTGTAAGTGCCTTCAGAAATAAGTCCTAGACTGGACTCTTGAGGGACATATTGGAGAATCTTAAGAAATGCAAG
CTTGTTCAGGGGGCTGAGAAGATCCTGAGTACACTAGGTGCAAACCAGAACTCTTGGTGGAAACAGACCAGCCACT
GCAGCAGACAGACCAGGAACACAATGAGACTGACATTTCAAAAAAACAACAACTGGCTAGCCTGAGCTGCTGGTTC
ACTCTTCAGCATTTATGAAACAAGGCTAGGGGAAGATGGGCAGAGAAAAAGGGGACACCTAGTTTGGTTGTCATT
TGGCAAAGGAGATGACTTAAATCCGCTTAATCTCTTCCAGTGTCCGTGTTAATGTATTGGCTATTAGATCACT
AGCACTGCTTTACCGCTCCTCATCGCCAACACCCCATGCTCTGTGGCCTTCTTACACTTCTCAGAGGGCAGAGT
GGCAGCCGGGCACCCTACAGAACTCAGAGGGCAGAGTGGCAGCCAGGCCACATGTCTCTCAAGTACCTGTCCC
CTCGCTCTGGTGATTATTTCTTGCAAGATCACCACACGAGACCATCCCGGCAGTCATGGTTTTGCTTTAGTTTTTC
CAAGTCCGTTTTAGTCCCTTCTTGGTCTGAAGAAATTCTGCAGTGGCGAGCAGTTTCCCACTTGCCAAAGATCC
CTTTTAACCAACACTAGCCCTTGTTTTTAACACACGCTCCAGCCCTTCATCAGCCTGGGCAGTCTTACCAAAATG
TTTAAAGTGATCTCAGAGGGGCCCATGGATTAAACGCCCTCATCCCAAGGTCCGTCCCATGACATAACACTCCACA
CCCGCCCCAGCCAACCTTCATGGGTCACTTTTTCTGGAAAATAATGATCTGTACAGACAGGACAGAATGAACTCC
TGCGGGTCTTTGGCCTGAAAGTTGGGAATGGTTGGGGGAGAGAAGGGCAGCAGCTTATTGGTGGTCTTTTACCA
TTGGCAGAAACAGTGAGAGCTGTGTGGTGCAGAAATCCAGAAATGAGGTGTAGGGAATTTTGCCTGCCTTCTGC
AGACCTGAGCTGGCTTTGGAATGAGGTTAAAGTGTGAGGGACGTTGCCTGAGCCCAAATGTGTAGTGTGGTCTGG
GCAGGCAGACCTTTAGGTTTTGCTGCTTAGTCCTGAGGAAGTGCCACTCTTGTGGCAGGTGTAGTATCTGGGGC
GAGTGTGGGGGTAAAAGCCACCCCTACAGAAAGTGGAACAGCCCGGAGCCTGATGTGAAAGGACCACGGGTGTT
GTAAGCTGG

1283/6881
FIGURE 1193

ATAGAGGACACGACCAAGATGGCGGCGGTGTCTGGCTTGGTGCGGAGACCCCTTCGGGAGGTCTCCGGGCTGCTG
AAGAGGCGCTTTCACTGGACCGCGCCGGCTGCGCTGCAGGTGACAGTTTCGTGATGCTATAAATCAGGGTATGGAT
GAGGAGCTGGAAAGAGATGAGAAGGTATTTCTGCTTGGAGAAGAAGTTGCCAGTATGATGGGGCATACAAGGTT
AGTCGAGGGCTGTGGAAGAAATATGGAGACAAGAGGATTATTGACACTCCCATATCAGAGATGGGCTTTGCTGGA
ATTGCTGTAGGTGCAGCTATGGCTGGGTGCGGCCCATTTGTGAATTTATGACCTTCAATTTCTCCATGCAAGCC
ATTGACCAGGTTATAAACTCAGCTGCCAAGACCTACTACATGTCTGGTGGCCTTCAGCCTGTGCCTATAGTCTTC
AGAGGGCCCAATGGTGCCTCAGCAGGTGTAGCTGCCAGCACTCACAGTGCTTTGCTGCCTGGTATGGGCACTGC
CCAGGCTTAAAGGTGGTCAGTCCCTGGAATTCAGAGGATGCTAAAGGACTTATTAAATCAGCCATTCGGGATAAC
AATCCAGTGGTGGTGTCTAGAGAATGAATTGATGTATGGGGTTCCTTTTGAATTCCTCCGGAAGCTCAGTCAAAA
GATTTTCTGATTCTATTGGAAGCCAAAATAGAAAGGCAAGGAACACATATAACTGTGGTTTCCCATTCAGA
CCTGTGGGCCACTGCTTAGAAGCTGCAGCAGTGCTATCTAAAGAAGGAGTTGAATGTGAGGTGATAAATATGCGT
ACCATTAGACCAATGGACATGGAAACCATAGAAGCCAGTGTCATGAAGACAAATCATCTTGTAAGTGTGGAAGGA
GGCTGGCCACAGTTTGGAGTAGGAGCTGAAATCTGTGCCAGGATCATGGAAGGTCCTGCGTTCAATTTCTGGAT
GCTCCTGCTGTTTCGTGTCACTGGTGTGATGTCCCTATGCCTTATGCAAAGATTCTAGAGGACAACCTCTATACCT
CAGGTCAAAGACATCATATTTGCAATAAAGAAAACATTAAATATTTAGTTTGGACTTGAATATCAAGTCGTTGAA
ATTTATTTGAAATACTTGCTGGCACTGCACCTGGATTTGTACTGCAAGACCTGACTATTCATAACGGAAAACGAT
TTCTAAAGCAACAGCAGGTATTTTGTACAGGGAAGTTTAAATGTGTTTGTGTATGGAAAACCTCTCCACTCTCCT
CCCCTAGATGCCATGCTTCCTTTTGTCTGTTACGGTTGCCATGTTCTTTGAATAACAAATTATATAACATTTTAT
CCTCTCTACCAACAAGGACAAAGTATGGATGTGGCAGAGTCCTCATGAAAGATGTATCCAACAAGATAACTTAT
ATGTATAAAATTAAAGCATATAATATACATTTACTGTTAGTTTGTGTTTGGATAAGGAATAAAGGAATTTCTAACAT
G

1284/6881
FIGURE 1194

MAAVSGLVRRPLREVSGLLKRRFHWTAPAALQVTVRDAINQGMDEELERDEKVFLLGEEVAQYDGAYKVSRLWK
KYGDKRIIDTPISEMFGAGIAVGAAMAGLRPICEFMTFNFMSQAIDQVINSAAKTYYSGLQPVPVFRGPNGA
SAGVAAQHSQCFAAWYGHCPGLKVVSPWNSEDAKGLIKSAIRDNNPVVLENELMYGVPFEPPEAQSKDFLIPI
GKAKIERQGTHITVSHSRPVGHCLEAAAVLSKEGVECEVINMRTIRPMDMETIEASVMKTNHLVTVEGGWPQFG
VGAEICARIMEGPAFNFLDAPAVRVTGADVPMPLYAKILEDNSIPQVKDIIFAIKKTLNI

1285/6881
FIGURE 1195

GTCAGCCGCTGTCCCCTTAGCCGCGATGCCGCTGGAGAACCTGGAGGAGGAGGGTCTGCCCAAGAACCCCGACTT
GCGTATCGCGCAGCTGCGCTTCCTGCTCAGCCTGCCCGAGCACCGCGGAGACGCTGCCGTGCGCGACGAGCTGAT
GGCGGCCGTCCGCGATAACAACATGGCTCCTTACTATGAAGCCTTGTGCAAATCCCTCGACTGGCAGATAGACGT
GGACCTACTCAATAAAATGAAGAAGGCAAATGAAGATGAGTTGAAGCGTTTGGATGAGGAGCTGGAAGATGCAGA
GAAGAATCTAGGAGAGAGCGAAATTCGCGATGCAATGATGGCAAAGGCCGAGTACCTCTGCCGGATAGGTGACAA
AGAGGGAGCTCTGACAGCCTTTTCGCAAGACATATGACAAAACCTGTGGCCCTGGGTCACCGATTGGATATTGTATT
CTATCTCCTTAGGATTGGCTTATTTTATATGGATAATGATCTCATCACAGAAACACAGAAAAGGCCAAAAGCTT
AATAGAAGAAGGAGGAGACTGGGACAGGAGAAACCGCCTAAAAGTGTATCAGGGTCTTTATTGTGTGGCTATTTCG
TGATTTCAAACAGGCAGCTGAACTCTTCCTTGACACTGTTTCAACATTTACATCCTATGAACTCATGGATTATAA
AACATTTGTGACTTATACTGTCTATGTCAGTATGATTGCCTTAGAAAGACCAGATCTCAGGGAAAAGGTCATTAA
AGGAGCAGAGATTCTTGAAGTGTTGCACAGTCTTCCAGCAGTTCGGCAGTATCTGTTTTCACTCTATGAATGCCG
TTACTCTGTTTTCTTCCAATCATTAGCGGTTGTGGAACAGGAAATGAAAAAGGACTGGCTTTTTTGCCCCCTCATT
TCGATACTATGTAAGAGAAATGAGAATTCATGCATACAGTCAGCTGCTGGAATCATATAGGTCATTAAACCCTTGG
CTATATGGCAGAAGCGTTTGGTGTTGGTGTTGGAATTCATTGATCAGGAACGTCCAGGTTTATTGCTGCCGGGAG
ACTACACTGCAAAATAGATAAAGTGAATGAAATAGTAGAAACCAACAGACCTGATAGCAAGAACTGGCAGTACCA
AGAACTATCAAGAAAGGAGATCTGCTACTAAACAGAGTTCAAAAACCTTCCAGAGTAATTAATATGTAAAGCCA
TGTAACATAACAAAGGATTTGCTTTAGAGATAATTATTTGGAATTTTATAGCTTACTTCACAATGTGCCCAGGTC
AGCTGTATAAAATAAATACTGCATTGTTGTTTC

1286/6881
FIGURE 1196

MPLENLEEEGLPKNPDLRIAQLRFLSLPEHRGDAAVRDELMAAVRDNNMAPYYEALCKSLDWQIDVDLLNKMKK
ANEDELKRLDEELED AEKNLGESEIRDAMMAKAEYLCRIGDKEGALTAFRKTYDKTVALGHRLDIVFYLLRIGLF
YMDNDLITRNTEKAKSLIEEGDWDRRNRLKVYQGLYCVAIRDFKQAAELFLDTVSTFTSYELMDYKTFVITYTVY
VSMIALERPDLREKVIKGAEILEVLHSLPAVRQYLFSLYECRYSVFFQSLAVVEQEMKKDWLFAPHYRYVREMR
IHAYSQLLSYRSLTLGYMAEAFGVGVFEFIDQELSRFIAAGRLHCKIDKVNEIVETNRPDSKNWQYQETIKKGD
LLNRVQKLSRVINM

1287/6881
FIGURE 1197

GAGAAGCCATGAGCAGCAGTCTCTCGCAACACCCCTGTACGAGGCGGTGCGGGAAGTCCTGCACCGGAACCAGCGC
AAGCGCCGCAAGTTCCTGGAGACGGTGGAGTTGCAGATCAGCTTGAAGAACTATGACCCCCAGAAGGACAAGTGC
TTCTCGGGCACCCTCAGACTTAAGTCCACTCCCCGCCCTAAGTTGTGTGTGTGTGTCTCTGGGGGACCAGCAGCAC
TGTGACGAGGCTAAGGCCGTGGATATCCCCACATGGACATCGAGGCGCTGAAAAAACTCAAAAAGAATAAAAAA
CTGGTCAAGAAGCTGGCCAAGAAGTATGATGCGTTTTTGGCCTCAGAGTCTCTGATCAAGCAGATTCCACGAATC
CTCGGCCCAGGTCTAAATAAGGCAGGAAAGTTCCCTTCCCTGCTCACACACAACGAAAACATGGTGGCCAAAGTG
GGTGAGGTGAAGTCCACAATCAAGTTCCAAATGAAGAAGGTGTTATGTCTGGCTGTAGCTGTTGGTCACGTGAAG
ATGACAGCCGATGAGCTTGTGTATAACATTACCTGGCTGTCAACTTCTTGGTGTCAATTGCTCAAGAAAACTGG
CAGAATGTCCGGGCCTTATATATCGAGAGCACCATGGGCAAGCCCCAGCGCCTATATTAAGGCACATTTGAATAA
ATTCTATTACCAGTTCAAAAAAAAAAAAAAAAAAAAAACAAAAAAAAA

1288/6881
FIGURE 1198

GCTCAAGTGGCCAAGGCAAGATGGGTCAAAGTCAGAGTGGTGGTCATGGTCCTGGAGGTGGCAAGAAGGATGACA
AGGACAAGAAAAAGAAATATGAACCTCCTGTACCAACTAGAGTGGGGAAAAAGAAGAAAAACAAAGGGACCAG
ATGCTGCCAGCAAACCTGCCACTGGTGACACCTCACACTCAGTGCCGGTTAAAATTACTGAAGTTAGAGAGAATTA
AAGACTATCTTCTCATGGAGGAAGAATTCATTAGAAAATCAGGAACAAATGAAACCATTAGAAGAAAAAGCAAGAGG
AGGAAAGATCAAAAGTGGATGATCTGAGGGGGACCCCGATGTCAGTAGGAACCTTGGAAAGAGATCATTGATGACA
ATCATGCCATCGTGTCTACATCTGTGGGGCTCAGAACACTACGTCAGCATTCTTTTCATTTGTAGACAAGGATCTGC
TGGAACTTGGCTGCTCGGTCTGCTCAACCACAAGGTGCATGCCGTGATAGGGGTGCTGATGGATGACACGGATC
CCCTGGTCACAGTGATGAAGGTAGAAAAGGCCCCCCCAGGAGACCTATGCAGATATTGGGGGGTTGGACAACCAA
TTCAGGAAATTAAGGAATCTGTGGAGCTTCCTCTCACCCATCCTGAATATTATGAAGAGATGGGTATAAAGCCTC
CTAAGGGGGTCATTCTCTATGGTCCACCTGGCACAGGTAAAACCTTGTTAGCCAAAGCAGTAGCAAACCAAACCT
CAGCCACTTTCTTGAGAGTGGTTGGCTCTGAACTTATTGAGAAGTACCTAGGTGATGGGGCCAAACTCGTACGGG
AATTGTTCCGAGTTGCTGAAGAACATGCACCGTCCATCGTGTATTATTGATGAAATTGACGCCATTGGGACAAAA
GATAAGACTCCAATTCTGGTGGTGAGAGAGAAAATTCAGCGAACAATGTTGGAAGTCTGAACCAGTTGGATGGAT
TTGATTCTAGGGGAGATGTGAAAGTTATCATGGCCACAAACCGAATAGAACTTTGGATCCAGCACTTATCAGAC
CAGGCCGCATTGACAGGAAGATTGAGTTCCCCCTGCCTGATGAAAAGACGAAGAAGCGCATCTTTCAGATTCA
CAAGCAGGATGACGCTGGCTGATGATGTAACCCTGGACGACCTGATCATGGCTAAAGATGACCTCTCTGGTGCTG
ACATCAAGGCAATCTGTACAGAAGCTGGTCTGATGGCCTTAAGAGAACGTAGAATGAAAGTAACAAATGAAGACT
TCAAAAAATCTAAAGAAAATGTTCTTTATAAGAAACAGGAAGGCACCCCTGAGGGGCTGTATCTCTAATGAACCA
TGGCTGTCATCAGGAAAATGGTTGGGAGATTTCTCAGTCCCTGAAAGGGATGAGGCTGGGGGAGTTGCCAGAGG
AATCCCTGTTCCCACTGATTTTTATTAGCAAAACATCCTGTGTCTTTTGGAGTACGATGTGTAAGTGCCCATTGG
GTGGCCTGTTGGTCACTGTGCAGCAGTCTGCTTCCCAATAAAGCGTGCTCTTTCACAA

1289/6881
FIGURE 1199

ATGCCTTCAAAGGAAAAGCAAGGGACACTCACCTTGCAAAACCATCAAACTATTCCACAGACGCCACATGAGC
CCCCATTTATCTGACTTAAAAGAAGCAGGGTCTGCTGGGATTGCAATCCTCTGGTTCCAGAGAGAGAAGCTCTTT
CAAAGACTGGATTCTGGCCACAAAAGAAGGTTCTGCTTACTGGAATCAAGAGGTCAAAGATTTTTCTGAATCA
TGCATCCACGGAGAAGAGCCCATTAGGGCTATTCCAGCAGACAGCAGTAAGGATGTCCATGAGCTTTATGTTGTT
GTTGGGAGCTGGGATTCTACTCTTCCAGAAGAATATGACCTCAAAAGGAGCCACCACAGAACGAGCTCGGCACCC
ATCTACGAATGTATTGCTAAGGATCATTGGGGATGGGGTGACCCAGAAGTGAAGTGGCTCCATGATCCATTAAAC
AATCACCTGAAATCCACAGTGCCAGTCAACTAATGGGGCTTGGAGCCATCATTAGGTCACTGGAAAATGATATC
TTCCTGGAGGTTGATACTGGCTTCACCATCCTGAGAGCAGAAGGCTTGAGGGAGGAACAGCCTCCTGGGCATGGA
GGCACCTGCCATCCCACATCAAATCACAGAGCCATGCTTAAAAGGGCCAGGTGGATGACTTATGTGGAAGAAGTG
AGCCGGGTGAGGATTTCTACTTCGAGAAACCTTGCTCGAAGCGCTTTCATCATTCTCTCCTACACAACAAACCCCT
GAACTCTTAGAAGCAGCTCTTGGCACAGGAGCCTCCAACCCGTTTTTCAGCCGGCTTTCTCTACTTGTTCAT
TCCATGATCACAGAAAACAGCTCCATTAAGACTCTTTTCAGGTCTACCAAAGAGCTAGTGATTGCACTCAATCGA
TGTTTCTTCGGCATTACTCAAAGTGCAGCTACACTCAGCCACAGCTTCACATCAGATTTATCAGCAGAGAACAA
AAGAAGTACTTGAAATTGCCACTTACAACGTTTATGAGTAAACTGGAATCCAAAGTCTGGCCTCTAGCCAAGCGG
TTACGCCAGTGGCCTGACTCATATACAAAGAAGTTTGAGCACAGAATCTACCCCATCACATTTTCTGTGGAAAC
CCTCAGGAGTGGAAGAAATTGTTCAAACCCTGTGCTGCCCAGAGACTCTTTCTTCCGATCAACCTGGAGCTCTAC
GCCTCCTACGTTTACCTGTCCATGTCTTACTACTTTGACCGCGATGATGTGGCTTTGAAGAAGTTTGCCAAATAC
TTTCTTCACCAATCTCATGAGGAGAGGGAACATGCCGAGAACTGATGACGTTGCAGAACCAACGAGGTGGCCGA
ATCTTCCTTCAGGATATCAAGAAACCAGACTGTGACGACTGGGAGAGCGGGCTGAATGCGATGGATGACAAAAAT
GACCCCCATTTGTGTGACTTCATTGAGACACATTACCTGAATGAGCAGGTGAAAGCCATCAAAGAATTGGGTGGC
CACGTGACCAACTTGTGCAAGATGGGAGCACCCGAATCTGGCTCGGCAGAATATCTCTTTGACAAGCACACGCTG
GGAGACAGTGATAACGAAAGCTAA

1290/6881
FIGURE 1200

MPSKEKQGTLTLQNHQNYSHRRHMSPHLSDLKEAGSAGIRILWFQREKLFQRLDSGPQKKVPAYWNQEVKDFSES
CIHGEEP IRAIPADSSKDVHELIVVVGSWDSTLPEEYDLKRSHHRTSSAPIYECIAKDHGWGDP EVNWLHDPLN
NHPEIHSASQLMGLGAIIRSLENDIFLEVDTGFTILRAEGLREEQPPGHGGTCHPTSNHRAMLKRARWMTYVEEV
SRVRISTSRNLARSAFIILSYTTNPELLEAALGTGASNPFPSRLSLLVSHSMITENSSIKTLFRSTKELVIGPKD
ARRDFQVVSRRGSADFWRKCLASSDGSICLLSIGKPELIRLIQLIK

1291/6881
FIGURE 1201

ATGATCTTTAATTTTGCCCTGAATACCTTGGTTGCAATCACTGTGCTTGTTTATCCAAACGGCATTTCAGGAATAC
ATACGACAACTGCCTCCGAATTTTCCCTACAGAGATGATGTCATGAGGCCTGGAGAACCCAGGAGTTTCCAAGCT
GTGCTGCCACCCGAGCTCTGGATCCACCTGGCTGTGGTGGCCTGTGGCAATCGGCTGGAGGAGACGCTGGTCATG
CTCAAATCAGCTGTGCTTTTGTAGCCACAGGAAGATCCAATTCCACATCTTCACTGAAGACTCTCTGAAGCCCGAG
TTTGATAAGCAGTTACGCCAGTGGCCTGACTCATATACAAAGAAGTTTGAGCACAGAATCTACCCCATCACATTT
TCTGTTGGAAACCCTCAGGAGTGGAAGAAATTGTTCAAACCCTGTGCTGCCAGAGACTCTTCTTCCGATCAAC
CTGGAGCTCTACGCCTCCTACGTTTACCTGTCCATGTCTTACTACTTTGACCGCGATGATGTGGCTTTGAAGAAC
TTTGCCAAATACTTTCTTACCAATCTCATGAGGAGAGGGAACATGCCGAGAACTGATGACGTTGCAGAACC
CGAGGTGGCCGAATCTTCTTTCAGGATATCAAGAAACCAGACTGTGACGACTGGGAGAGCGGGCTGAATGCGATG
GATGACAAAAATGACCCCATTTGTGTGACTTCATTGAGACACATTACCTGAATGAGCAGGTGAAAGCCATCAAA
GAATTGGGTGGCCACGTGACCAACTTGTGCAAGATGGGAGCACCCGAATCTGGCTCGGCAGAATATCTCTTTGAC
AAGCACACGCTGGGAGACAGTGATAACGAAAGCTAA

1292/6881
FIGURE 1202

GTCGGCGTGTCGAGTGGCTCTTCCTGGCTGCTGAGGCGGGTTAAGGTCTGAGGGTCTTGTGGGGCCACGGCGCTG
ATCACCAGGTGTTTGGCTTGGTCGGTTCCTATTTCTCGCCTGGCAATGGCGACGTACACCTGCATAACTTGCCGG
GTGGCGTTCGCGACGCGGACATGCAGCGGGCCCACTATAAGACGGACTGGCACCGCTACAACCTGCGGCGGAAG
GTGGCCAGCATGGCCCCAGTGACCGCCGAGGGCTTCCAGGAGCGAGTGCGGGCGCAGCGGGCCGTCGCGGAGGAG
GAGAGCAAGGGCTCGGCCACCTACTGCACCGTTTGAGTAAGAAGTTTGCTCTTTCAACGCCTACGAGAACCAC
CTCAAGTCCCGGCGTCACGTTGAGCTGGAGAAGAAGGCCGTGCAGGCAGTGAATCGGAAAGTGGAGATGATGAAT
GAAAAGAACTTGGAGAAAGGACTGGGCGTGGACAGTGTGGACAAGGATGCCATGAACGCGGCCATCCAGCAGGCC
ATCAAGGCCCAGCCGTCCATGTCTCCCAAGAAGGCGCCCCCAGCGCCTGCAAAGGAGGCCAGGAATGTCGTGGCC
GTGGGTACTGGTGGCCGTGGGACCCACGACCGAGACCCGAGTGAGAAACCACCCCGCTCCAGTGGTTTGAACAG
CAGGCGAAGAAGTTGGCAAAGCAGCAGGAGGAGGACAGCGAGGAGGAGGAAGAGGACCTGGATGGAGACGATTGG
GAAGATATTGATTCTGATGAAGAATTGGAATGTGAGGATACTGAAGCAATGGACGATGTGGTGGAGCAGGATGCA
GAGGAGGAAGAGGCTGAGGAAGGCCACCCCTTGGTGCCATCCCTATCACGGACTGCTTATTTTGTTCCTCATCAT
TCCAGCTCGCTGATGAAGAATGTGGCTCACATGACCAAAGACCACAGTTTCTTTATTCCTGATATAGAATATCTT
TCAGATATTAAGGGACTGATTAAATACTTGGGAGAGAAAGTTGGTGTGGCAAGATTTGCTTGTGGTGCAACGAG
AAAGGGAAGTCCTTCTACTCCACAGAAGCTGTACAGGCACATATGAATGACAAAAGCCACTGTAAGCTCTTCACA
GATGGCGATGCTGCTTTGGAATTTGCAGACTTCTATGATTTTAGGAGTAGCTATCCAGATCACAAGGAAGGGGAG
GACCCCAATAAGGCTGAGGAGTTGCCCTCAGAAAAGAACTTGGAAATATGATGATGAAACCATGGAATTGATTCTG
CCTTCTGGTGCCAGAGTGGGTGATCGCTCCTTGATGAGATACTACAAACAGCGATTTGGCTTGTCAAGAGCTGTG
GCAGTTGCCAAAAATCGGAAGGCCGTGGGCCGAGTACTTCAGCAGTACAGAGCCCTGGGATGGACTGGCAGCACA
GGAGCGGCTCTTATGCGAGAGCGAGACATGCAGTATGTCCAAAGGATGAAATCAAAATGGATGCTGAAGACAGGA
ATGAAGAACAATGCCACCAAGCAGATGCACTTTCGGGTCCAAGTGAGATTCTGAGAGTCTGCTGGGATTGAGCAA
TCATCTCCTGCCAAGTTTCCTCCTTGCCCTGAGGACCAGTGAAAGACAGATCATAGGAGAGACCCTTTTGCTGC
TACTTCATTCTGCTTGACCTAATAATAAAAGTTAGAACCAT

1293/6881
FIGURE 1203

GCAGACGCCATTATCCTCTGTTTCTCTGCTGCACCGACCTCGACGCCTTGCCTGTGGCCCACTTGTTCACTGACT
ATAGGCTACTGCAGCACTGGGGTGTCTAGTTGTTGGTCCCACCCAGAACGCTTCAGTTCTGCTCTGCAAGGATATA
TAATAACTGATTGGTGTGCCCATTTAATAAAAAGAATATGTAACTGAACAGCCGGAAGAAACCTTCCCGAACACT
GAAACCAATGGTGAATTTGGTAAACACCCTGCAGAAGATATGGAAGAGTAACAAGCATTTAAAAGATCTAGAAAC
ACTGATGAGATGGTTGAATTACGCATTCTGCTTCAGACCAAGAATGCTGGGGCAGTGATTGGAAAAGGAGGCAAG
AATATCAAGGCTCTCCGTACAGACTACAATGCCAGTGTTTCAGTCCCAGACAGCAGTGGCCCCGAGCACATATTG
AGTATCAGTGCTGGTATTGACACAATTGGAGAAATTCTGAAGAAAATCATCCCTACCTTGGAAGAGTACCAACAC
TATAAAGGAAGTGACTTTGACTGCGAGTTGAGGCTGTTGATTATCAGAGTCTAGCAGGAGGAATTATTGGGGTC
GAAGGTGCTAAAATCAAAGAACTTCGAGAGAACTCAAACCACCATCAAGCTTTTCCAGGAATGCTGTCCTTAT
TCCACTGACAAGAGTTGTTCTTATTGGAGGAAAACCCGATAGGGTTGTAGAGTGCATAAAGATCATCCTTGATCT
TATATATGAGTCTCCCATCAAAGGACGTGCACAGCCTTATGATCCCAATTTTTATGATGAAACCTATGATTATGG
TGGTTTTACAATTATGTTTGATGACCGCTGTGGACGCCAGTGGGATTTCCCATGCGGGGAAGAGGTGGTTTTGA
CAGAATGCCTCCTGGTCAGGGTGGGCGTCCCATGCCTCCATCTAGAAGAGATTATGATGATATGAGCCCTCGTCA
AGGACCACCTCCACCTCCTCCAGGACAAGTGGTGAGGGTGGTAGCAGAGCTCGGAATCTTCCTCTTCCTCCTCC
ACCACCACCTAGAGGGGGAGACCTCATGGCCTATGACAGAAGAGGGAGACCTGGAGACTGTTACCATGGCATGGT
TGGTTTCAGTGCTGATGAACTTGGGACTCTGCAATAGATACATGGAGCCCATCAGAATGGCAGATGGCTTATGA
ACCACAGGGTGGCTCCAGATATGATTATTCCTATGCAGGGGGTCGTGGCTCATATGGTAATCTTGGTGGACTTAT
TATTACTACACAAGTAACGATTCCCAAAGATTTGGCTGGATCTATTATTG

1294/6881
FIGURE 1204

ATGAATAAGGAGAATCACTCCTTGATAGCTGAGTTCATCCTCACAGGATTTACATATCATCCAAAGCTGAAGACT
GTTCTGTTTGTGGTGTTCTTTGCCATCTATCTGATCACCATGGTGGGGAACATTGGTTTGGTGGCATTGATTTAT
ATAGAGCAACGTCTTCACACACCAATGTACATATTTTAGGCAACCTAGTTCTGATGGATTCTGCTGTTCTCTCT
GCTATTACTCCCAAGATGTTAGAGAACTTCTTTTCTGAGGACAAAAGGATTACCCTGTATGAATGTATGGCACA
TTTTATTTTCTCTGTCTTGCTGAAACTACAGACTGCTTTCTTCTGGCGGCAATGGCCTATGACTGCTATGTGGCC
ATATGCAACCCACTGCAGTACCACACCATGATGTCCAAGACACTCTGCATTGAGATGACTGCAGGAGCCTACCTA
GCTGGCAACCTGCATCCCATGATTGAAAACCTTTTGCCCAGAGTAGCAGCCAAACTTGAGGTTGCCCCGATTTCT
GACATCATTTGCAATCAAGTCACCTGACACATTTGTGAGAACTATTTATGCAGGAAATGCTCTATGTACAGTGAAG
TGTGATGAGAAAGTGAAAGTGTTTTCTGTCCGTGGAACATCCTTTGATGCTGCAGCAACAAGTGGCGGTAGTGCC
AGTTCAGAAAAGGCATCAAGTACTTCACCAGTGGAATATCAGAGTGGCTTGACCAGAAATTAACAAAAAGTGAT
CGACCAGAGCTAACAGGTGCCAAAGTGGTGGTATCTGGTGACTGCTATCCATCTTATAACACACTCATTCTTCAG
ACACATCACAATGCACATGATCAGATTACAGCTTTCTTTACCTTAAGGATGTCTTCAACCACCACAAGCCCTTTC
CAAATTCCTACGTAGATAAAATTTGGCTTTTCTAG

1295/6881
FIGURE 1205

ATGATCAGGTGTGATAAGTGCTGTAATGAAGGCAATTACAAGGAGAGGATATTTGAAATCATTGCTGTGGAGGGT
GAGAGTGCGAACAAGGAAGTTGTGGTAGCATTGCTAGACAGTTTTGAGAGCCCAGCTCCAGAGCTTAAGGTTATT
GCTGAATTAAGCCACGCCTCATTGCTACGATTCAGAGTACCCTGGTAATAGCTGAGCATGCAAATGATTCCCTA
GCACCCATTACTTTAAATACCATTACTGCAGCCACACGCCTTGGAGGTGAAGTGTCTGCTTAGTAGCTGGAACC
AAATGTGACAAGGTGGCACAAGATCTCTGTAAAGTAGCAGGCATAGCAAAAGTTCTGGTGGCTCAGCATGATGTG
TACAAAGGCCTACTTCCAGGTGAGGTTTTCCAGTAG

1296/6881
FIGURE 1206

TCTTTTCGCCATCTTTTGTCTTTCCGTGGAGCTGTCGCC~~ATGA~~AAGGTCGAGCTGTGCAGTTTTAGCGGGTACAAG
ATCTACCCCGGACACGGGAGGCGCTACGCCAGGACCGACGGGAAGGTTTTCCAGTTTCTTAATGCGAAATGCGAG
TCGGCTTTCTTTCCAAGAGGAATCCTCGGCAGATAAACTGGACTGTCCTCTACAGAAGGAAGCACAAAAAGGGA
CAGTCGGAAGAAATTCAAAAGAAAAGAACCCGCCGAGCAGTCAAATTCAGAGGGCCATTACTGGTGCATCTCTT
GCTGATATAATGGCCAAGAGGAATCAGAAACCTGAAGTTAGAAAGGCTCAACGAGAACAAGCTATCAGGGCTGCT
AAGGAAGCAAAAAAGGCTAAGCAAGCATCTAAAAAGACTGCAATGGCTGCTGCTAAGGCACCTACAAAGGCAGCA
CCTAAGCAAAAGATTGTGAAGCCTGTGAAAGTTTCAGCTCCCCGAGTTGGTGGAACGCT~~TAA~~ACTGGCAGATTA
GATTTTTAAATAAAGATTGGATTATAACTCT

1297/6881
FIGURE 1207

MKVELCSFSGYKIYPGHGRRYARTDGKVFQFLNAKCESAFLSKRNPRQINWTVLYRRKHKKGQSEEIQKKRTRRÄ
VKFQRAITGASLADIMAKRNQKPEVRKAQREQAIRAAKEAKKAKQASKKTAMAAKAPTKAAPKQKIVKPKVSA
PRVGGKR

1298/6881
FIGURE 1208

GCTCCTCCACAGGAGGCCTACACGCCGCCGCTTGTGCTGCCGCCATGTCGCTAGTGATCCCTGAAAAGTTCCAGC
ATATTTTGCAGTACTCAACACCAACATCGATGGGCAGCGGAAAATAGCCTTTGCCATCACTGCCATTAAGGGTG
TGGGCCGAAGATATGCTCATGTGGTGTTGAGGAAAGCAGACACTGACCTCACCAAGAGGGCGGGAGAACTCACTG
ATGATGAGGTGGAACGTGTGATCACCGTTATGCAGAATCCACGCCAGTACAAGATCCCAGACTGGTTCTTGAACA
GACAGAAGGATGTAAAGGATGGAAAATATAGCCAGGTCCTAGCCAATGGTCTGGACAACAAGCTCCGTGAAGACC
TGGAGCGACTGAAGAAGATTCTGGGCCCATAGAGGGCTGCGTCACTTCTGGGGCCTTCGTGTCCGAGGCCAGCACA
CCAAGACCACTGGCCGCCGTGGCCGCACCGTGGGTGTGTCCAAGAAGAAATAAGTCTGTAGGCCTTGTCTGTAA
TAAATAGTTTATATACC

1299/6881
FIGURE 1209

ACCGCGGGGCTGGGTCCCAGCCGGCAGCAGAGAGCTGGTCGCCCACCACCCCAAGCTACTGCTGCCGCCTGGCT
ATTTCCCGGGCGGGGCGGTACGTGGTGGTGGCTGAGAGCCCCCTGCCGCCTGGCGAGTGGGAGCTGTGCCGCGCAG
TCCCGGGCCCTGCTTACGAGGAGGAGGGCACTCCCTGCGCTACCAGCGTCTGGTGCCCTCTCGCAGCCGCATCG
TGCGGACGCCCTCCCTGAAGGACAGCCCGGCAGGCCGGGGGCTCAGCAAGGCCGCCGTGTCCGAGGAGCTCAAGT
GGTGGCACGAGCGTGCACGCCTCCGGAGCACCCGCCCCCACTCACTGGACCGCCAAGGAGCTTTCCGGGTCAGGA
GCCTGCCCCCTTGGGAGAGAGGGCTTCGGGCGAGCCCTGGGACCCCGGGCACAGGTGCCACAGTGTGTGTGCTGC
GGAGATCGCCTGACGGGGCCCTGTGCAAGTCTTTGTACCTGAAAAAGGAGAGATCATCAGCCAGGTGTAACTCT
GCGCCCCACGCTGGAAAAAACTGTTTCATAGAGGGGCTGGGCTGAGACCCCCCACCCTGAGTGCCCTCTTTCAG
CTTCCCCATCCCCATCGCAGGCCGATGACCTGGAGCTGAGACCTTTTATTATTTTTTTTTTACACGACTTTTTTC
AGAAGCCCTGACCTAAGGATTTATATATGTGGATTGTCCTCAATACCCCTGTGATATGATTATGTTTTATCCCCC
AGAGTTTGGCCTACTGGACTTAAGGCCTTGCCGTCTGACTGACAGCCTCTATCTCCTTATATAAGACAAGTGGC
AGGGGACGAGTGAAGCAGAGTGGGCCACCTTGGGAGTTCTCCAACACTCTGTGCTCTGGTTCTAAGAAATTCCCT
GGGGAAGTGGCCCTGGCCCTCCTGTCCCACTATTGTGAGGCTGGACATGGTACATACTCATGCACATGACTCT
CCCCATTTCCAGGTCTCTGGGTACCCAGCCTGGGCTGGGGGAGAATCTCTTCCCCCTTTCTAATGTGCTCTG
TGATGCACACACCAAGTGGTAGGTCAAAGGTCAGTATATCCCGGTGGTGTATTGTCTTGCTAGACCCTGCTATTT
TCCTGACCCCTAAATCCTCTTTAGGGACCCAGTCACTATAACCCTGTCTATGCCCTGTGGGCTCCAGACCCCTG
AGCTTTGAGTCAGTGGCATCACGGTTTGTAGCCTCAGGGGTCCGGCTGGGGGCTGATCCATGCTTGTGGTTAGT
GGACAGCAGCCACCCTTTGACAGCTACCTCTGGGCATCTCAAGGGCTTGAGCCCCACTGCTCCTTCTAACATTT
TGTTTGTGTTGTTTTGAGATGGAGTCTCGCTCTGTGCGCCAGGCTGGAATGCAGTAGCAAGATTTGGGCTCACTG
CAACCCCGTCTCCCGGTTCAAGCGAATCTCCTGCCTCAGCCTTCCGAGTAGCTGGGATTACAGGCAAGCACCA
CCATGCCTGCTAATTTTTTATTTTTTAGTAGAGATGGGGTTTCATCATGTTGGCCAGGCTGGTCTCGAACTCCTGA
CCTCAAGTGATCCACCTGCCTTGGCCTTTCAAAGTGCTGGGATTACAGGCATGAGCCACCGCACCTGGCCCTTCT
AACGTTTTTTCATCATAGTCCCAAAAACCAATACTTTACAAGTGGTTTTTGAAAGGCACCACTTTTGTGGCATGT
TCTGGTTGGGAGAGGGAGTCAAGTTCCTACTCCCCCACCAGCTATGCTTCTGCTCTGAGAAGGTGGTTATTTA
TACAAACATGGACATACTCACTCCCAAGGGCTGATGAGATGCTGAATTTTCTTTGGGGGCATTATTAATTGTCC
CAGCTGCAGCGACTGGAGCAAGTCTGGAAGCTGCCTGTGCTAAGACCACCCAGCTGTCCCTGGGTTCTCATCCTA
GGGCCCTTCTTTGCTTCCAGGTCAAGGGGACCTGCTTCAATGAGAAAGCAACTGAATTGAGGCTAGGAGAGGTAGGG
AGAGCTGAGTTCTGACTTCACCTGTGCAGAACTCTCTGCCCCCATGTTACCTGGACTGGAACAGACTGTGAATAT
AGCAGAAGGTTCCAAGAAGTCTGGTGTCTGACCTAGAAGAGGCACAGTTCTCTCTACTGGAAAGAAAACGATGTA
GCCGATTGCACAAGGGTGCCAAGGGAAGACCCAGGATGGCCCATCAAAGGAACCTGGGGGAGGATGCAGGAGGCT
GAAGGGATGCACCTGGCATTCTCTCACTGTGCTCTTACCGCATCAGCAACCCCCAACTTTTGGGCCTACTCTGC
CCCCATGCGTGAATACCCTGCTTGGATGCTGTGCTTTTCCGGTTTGTCTCTAAGCCCCCTTCTCCAGGGCATGT
TGGTTTCCCTGGCCTCTCAGTGTCTTAAGTGGAGCCAGAGTGCCTTGTACTGAGCCAGGAGACGGCTGAGCACT
GGCCCTCCACACCTAAGCGTCCTTTACATTAAGTTATTGGTCTTGTATAACACCTGGTGCCATTGCCAAGTGGCT
GTGTCCTCAGCTACAGAGCTGGAATTGTGTGGGGTTTAGTGCTAAATACTTCAATAAAGTCTGTTTTTTGTGATT
GGCTG

1300/6881
FIGURE 1210

MFWLGEVTVPTPPTSYASALRRWLF IQTWYSLPRADEMLN FLWGHSLIVPAAATGASLEAACAKTTQLSLGSH
PRAFFASRSGDLLQ

1301/6881
FIGURE 1211

ATGAAACTCTTCTACGAATGTGGGAAATGCAAAAAGGAATTGAAGGAAGGGAAAAAACTGAAGCCTGGAAAACAT
ATTAATCCCAGTGCTTTTACGCCCCGAAACAAAGAGACTAAGCCAGACTATGGGGGAAAGGGAGATAAGAAGGAT
CCTGGAACCTTTAAAGAGGGGAAAGAGTGAGATTTCAGAAATCGCCAGGACTGGACTTTAAGGGACGTCTGTGTTCAG
CACAAGGGGACTGGCACACACAGACACACGAGACCGAGGAGAACTGCAGACAAATGGAGATACAAAGACTTAGAA
GGACAGCTCCTTTACCTCATCCTACTTTGTCCAGAAGTGTGTGGATCAGAACCCCAACCCCATGCCACTATTAGA
GGCAGCCACGGAGGACGGAAAGTGCCTTTGGTTTCTCCGGACAGCAGTAGGCCAGCTCGGTTTCTGAGGCACACT
GGGAGGTCTCGCGGAATTGAGAGATCCACTCTGGAGGAACCAACCTTCAGCCTCTCCAGAGAAGGAGGAGTGTG
CCCGTGTGAGACTAGCTCGCCCAACAGAGCCGCCAGCCCGCTCGGACATCAATGGGGCCGCGGTGAGACCTGAG
CAAAGACCAGCAGCCAGGGGCTCTCCGCGTGAGATGATCAGAGATGAGGGGTCTCTAGCTCGGTCAAGAATGTTG
CGTTTCCCTTCGGGGTCCAGCTCTCCCAACATCCTTGCCAGCTTTGCAGGGAAGAACAGAGTATGGGTCACTCTCA
GCCCCCTCATGCCTCGGAAGGCTACTACCGCCTCATGATGAGCCTGCTGAAGGACGATGTGTACTGTGAGCTGGCG
GAGAGGCACATCCAACAGATTGTGCTCTTCCACCAGGCAGGTGAGGAAGGAGGCAAGGTGAGAAGGATCACCAGC
GAGGGCCAGATCCTGGAGCAGCCCCTGGACCCTAGCCTCATCCCTAAGCTGATGAGCTTCCTGAAGCTGGAGAAG
GGCAAGTTTGGCATGGTGTCTGCTGAAGAAGACGCTGCAGGTGGAGGAGCGCTATCCATATCCCGTTAGGCTGGAA
GCCATGTACGAGGTCATCGACCAAGGCCCATCCGTAGGATCGAGAAGATCAGGCAGAAGGGCTTTGTCCAGAAA
TGTAAGGCCTCTGGTGTAGAGGGCCAGGTGGTGGCGGAGGGGAATGACGGTGGAGGGGGAGCAGGAAGGCCAAGC
CTGGGCAGCGAGAAGAAGAAAGAGGACCCAAGGAGAGCACAAGTCCCACCAACCAGAGAGAGTCGGGTGAAGGTC
CTGAGAAAACTGGCCGCCACTGCACCAGCTTTGCCCAACCTCCCTCAACCCCCAGAGCCACCACCTTCCTCCT
GCCCCAGCCACAACAGTGAAGTGGTCCACGTCCCGGGCGGTAACAGTTGCTGCAAGACCTATGACCACCACTGCC
TTTCCCAACCACGCAGAGGCCCTGGACCCCCCTACCCCTCCCACAGGCCCCCTACAACCACTGAGGTGATCACTGCC
AGGAGACCTCAGTTTCAGAGAATCTTTACCCTCCATCCCGGAAGGATCAGCACAGGGAGAGGCCACAGACAACC
AGGAGGCCCAGCAAGGCCACCAGCTTGGAGAGCTTCACAAATGCCCTCCCACCACCATCTCAGAACCCAGCACA
AGGGCTGCTGGCCCAGGCCGTTTCCGGGACAACCGCATGGACAGGCGGGAACATGGCCACCAGACCCAAATGTG
GTGCCAGGTCTCCCAAGCCAGCAAAGGAGAAAACCTCCCAAAAAGAAGGCCCAGGACAAAATCTTAGTAATGAG
TATGAGGAGAAGTATGACCTCAGCCGGCCTACTGCCTCTCAGCTGGAGGACGAGCTGCAGAGTCCCAAGAAGTCA
GTGGCCGACCTGCTGGGGTCTTTGAAGGCAAAACGAAGACTCCTTCTGATCACTGCTCCCAAGGCTGAGAACAAT
ATGTATGTGCAACAACGTGATGAATATCTGAAAAGTTTCTGCAAGATGGCTACCAGGAAAAATCTCTGTGATCACC
ATCTTCGGCCCTGTCAACAACAGCACCATGAAAAATCGACCCTTTAGCTAGATAATGAGAAGCCCATGCGAGTG
GTGGATGATGAAGACTTGGTAGACCAGCGTCTCATCAGCGAGCTGAGGAAAGAGTACGGAATGACCTACAATGAC
TTCTTCATGGTGCTAACAGATGTGGATCTGAGAGTCAAGCAATACTATGAGGTACCAATAACAATGAAGTCTGTG
TTTGATCTGATCGATACTTTCCAGTCCCGAATCAAAGATATGGAGAAGCAGAAGAAGGAGGGCATTGTTTGCAA
GAGGACAAAAAGCAGTCCCTGGAGAACTTCCTATCCAGGTTCCGGTGGAGGAGGAGGTTGCTGGTGTCTCTGCT
CCTAACGATGAAGACTGGGCCTATTACAGCAGCTCTCTGCCCTCAGTGGTCAGGCGTGCAATTTTGGTCTGCGC
CACATAACCATTTCTGAAGCTTTTAGGCGTTGGAGAGGAAGTTGGGGGAGTGTTAGAAGTGTTCCTCAATTAATGGG
AGCTCTGTTGTTGAGCGAGAAGACGTACCAGCCCATTTGGTGAAAGACATTTCGTAACATTTTCAAGTGAGCCCG
GAGTACTTCTCCATGCTTCTAGTCGGAAAAGACGGAAATGTCAAATCCTGGTATCCTTCCCCAATGTGGTCCATG
GTGATTGTGTACGATTTAATTGATTGATGCAACTTCGGAGACAGGAAATGGCGATTTCAGCAGTCACTGGGGATG
CGCTGCCCAGAAGATGAGTATGCAGGCTATGGTTACCATAGTTACCACCAAGGATACCAGGATGGTTACCAGGAT
GACTACCGTCATCATGAGAGTTATCACCATGGATACCTTACTGA

1302/6881
FIGURE 1212

MTWRMGPRFTMLLAMWLVCGSEPHPHATIRGSHGGRKVPLVSPDSSRPARFLRHTGRSRGIERSTLEEPNLQPLQ
RRRSVPVLRRLARPTEPPARSDINGAAVRPEQRPAARGSPREMIRDEGSSARSRLRFPSSSSPNILASFAGKNR
VWVISAPHASEGYRLMMSLLKDDVYCELAERHIQQIVLFHQAGEEGGKVRITSEGQILEQFLDPSLIPKLMSF
LKLEKGKFGMVLLKKTQVEERYPPVRL EAMYEVIDQGP IRRIEKIRQKGFVQKCKASGVEGQVVAEGNDGGGG
AGRPSLGSEKKKEDPRAQVPPTRESRVKVLRLKLAATAPALPQPPSTPRATTLPPAPATTVTRSTSRAVTVAARP
MTTAFPTTQRPWTPSPSHRPPTTTEVITARRPSVSENLYPSPRKDQHRERPQTTTRPSKATSLESFTNAPPTTI
SEPSTRAAGPGRFRDNMRDRREHGHRDPNVVPGPPKPAKEKPPKKAQDKILSNEYEEKYDLSRPTASQLEDELQ
VGNVPLKKAKESKKHEKLEKPEKEKKKKMKKNENADKLLKSEKQMKKSEKSKQEKEKSKKKKGGKTEQDGYQKPT
NKHFTQSPKKS VADLLGSFEGKRRLLLITAPKAENMYVQQRDEYLESFCKMATRKISVITIFGPVNNSTMKIDH
FQLDNEKPMRVVDDLDLVDQRLISELRKEYGMTYNDFMVLTDVLDLRVKQYYEVPITMKS VFDLIDTFQSRIKDM
EKQKKEGIVCKEDKKQSLENFLSRFRWRRRLLVISAPNDEDWAYSQQLSALSGQACNFGRLRHITILKLLGVGEEV
GGVLELFPINGSSVVEREDVPAHLVKDIRNYFQVSPEYFSMLLVGKDGNVKS WYSPMWSMVIVYDLIDSMQLRR
QEMAIQQSLGMRCPEDEYAGYGYHSYHQGYQDGYQDDYRH HESYHHGYPY

1303/6881
FIGURE 1213

TTCTGGGAAGGGAGAATGGCGGCGCCCGGGCTGCGGCTGGGAGCGGGAAGACTCTTTGAAATGCCTGCGGTGCTA
GAGCGACTGAGCCGCTATAATAGCACGTCCCAAGCTTTTGCTGAGGTGCTGCGGCTGCCGAAGCAGCAGCTGAGG
AAGCTGCTGTACCCGCTGCAGGAAGTAGAGCGGTTCTCGCCCCCTACGGGAGGCAAGACCTTCACCTGCGTATC
TTTGACCCAAGCCCGGAGGACATAGCCAGGGCGGACAACATCTTCACGGCCACTGAACGGAACCGCATCGACTAC
GTCAGCTCCGCCGTCCGTATCGACCACGCCCCGGACCTTCCGCGGCCAGAGGTGTGTTTTATAGGCAGAAGCAAT
GTTGGAATAATCATCTCTAATCAAGGCTTTATTTTCACTGGCCCCTGAGGTTGAAGTCAGAGTCTCCAAAAAACCA
GGACACACAAAAGAAAATGAATTTTTTCAAAGTTGGAAAAACATTTTACAGTGGTGGACATGCCAGGTTATGGCTTT
AGAGCACCTGAAGATTTTGTGACATGGTAGAGACCTATCTAAAAGAACGAAGGAAGTTGAAGAGAACATTTTTTA
TTAGTGGATAGCGTTGTGGAATTCAAAAACAGACAATATTGCCATAGAAATGTGTGAAGAATTTGCATTACCT
TATGTGATTGTATTAACAAAAATTGACAAATCTTCCAAGGGACATCTTTTAAACAAGTGCTTCAGATCCAGAAA
TTTGTTAACATGAAAACCTCAAGGATGTTTTCTCAGTTGTTTCTGTAAGTGCTGTGACCTTTTCTGGAATCCAC
CTGTTGAGATGCTTTATAGCCAGTGTAACAGGAAGTCTTGACTAATGGTTCCCGGTTTAGCTGAAGATTCAAAAA
AAAAAAAAAAGCTTTATGCTAACTGGAGTTAAATACCTAGAAGAATTTCAACATTGTTTTAAATGTTGTGCATC
TGTAACCTCAGGAGGATCACTTGAGCTTTAAACCTGTGCCTTCTCGAAACAAGAATTTGTGCCTGAGGTGAAAA
AAGTTTGTAAGTTATTGAATTATGGTGTTCATTAGAACAGCTACTAGCTGATTCCCCTATTTTAACAACTGACA
AGAGCACATCCATAAAATGAAAACCTGTTACAACATATGTACAGAAGGGTTTGACGTTTTATTGGGCTTTTGTCTT
TTAAAGAATATGTCTACTATGGGTATTTTTTTTTTTAAATGTTAAATGGGCTAGGTAAAAGGGGGCTGCTTTTCT
GTTAAGCATCGATAGGTAAGTTGATGGATAAAAGTTACTATGTAAGCCTATTTTTTTGAGTCCTTATTGAATAT
TGAAAACATTCTTGATAAAATGTGTTAGTCCATGTTGGAAACAACCGAAAGAACAGAATTCAAGTTCTAGTTCTG
ATGTTTATTATATATGTTGGATCTTGGGCAACTTACTTGATTTCTCGGAAATTCATTTGTTACTGTAAACGTGAA
AGCTATTAAGATTCAAATGAATGGTTTTACAGCAGGTAACATGTGAGAAGACAGCTACATATTTGTAAAGCCAAA
CCAACAAAGAAATATAGCAAAATTCACAGGTAGATTTATTACAAGAAATGTCCTTTTCATGGGGGAAGTAACATTT
TCACTAGTGAAAAAGCAAAAAACAAAAATAGCTTTAAGTGAGAAAACATAATTT

[illegible]

1305/6881
FIGURE 1215

MLTGVLLANGTLNASILNSLYNENLVKEGVSAFAVKLFKSWINEKDINAVAASLRKVSMDNRLMELFPANKQSV
EHFTKYFTEAGLKEELSEYVRNQQTIGARKELQKELQEQMSRGDPFKDIILYVKEEMKKNNIPEPVVIGIVWSSVM
STVEWNNKEELVAEQAIKHLKQYSPLLAFTTQGQSELTLLKIQEYCYDNIHFMKAFQKIVVLFYKAEVLSEEP
ILKWKYKDAHVAKGKSVFLEQMKKFVEWLKNAEEEESESEAEED

1306/6881
FIGURE 1216A

GGCACGAGGGATCGGCGGAGCTCCACCTCCGCTTACAGCTCGCTGCCGCCGTCTTGCCCCGCGCCCCCAGGAGA
CCTGGACCAGACCACGATGTGGAAACGCTGGCTCGCGCTCGCGCTCGCGCTGGTGGCGGTGCGCTGGGTCCGCGC
CGAGGAAGAGCTAAGGAGCAAATCCAAGATCTGTGCCAATGTGTTTTGTGGAGCCGGCCGGGAATGTGCAGTCAC
AGAGAAAGGGGAACCCACCTGTCTCTGCATTGAGCAATGCAAACCTCACAAAGAGGCCTGTGTGTGGCAGTAATGG
CAAGACCTACCTCAACCCTGTGAAGTGCATCGAGATGCCTGCCTCACTGGATCCAAAATCCAGGTTGATTACGA
TGGACACTGCAAAGAGAAGAAATCCGTAAGTCCATCTGCCAGCCCAGTTGTTTGCTATCAGTCCAACCGTGATGA
GCTCCGACGTCGCATCATCCAGTGGCTGGAAGCTGAGATCATTCCAGATGGCTGGTTCTCTAAAGGCAGCAACTA
CAGTGAAATCCTAGACAAGTATTTTAAGAACTTTGATAATGGTGATTCTCGCTGGACTCCAGTGAATTCCTGAA
GTTTGTGGAACAGAATGAAACTGCCATCAATATTACAACGTATCCAGACCAGGAGAACAACAAGTTGCTTAGGGG
ACTCTGTGTTGATGCTCTCATTGAAGTGTCTGATGAAAATGCTGATTGGAAACTCAGCTTCCAAGAGTTTCTCAA
GTGCCTCAACCCATCTTTCAACCTCCTGAGAAGAAGTGTGCCCTGGAGGATGAAACGTATGCAGATGGAGCTGA
GACCGAGGTGGACTGTAACCGCTGTGTCTGTGCCCTGTGGAATTTGGGTCTGTACAGCCATGACCTGTGACGGAAA
GAATCAGAAGGGGGGCCAGACCCAGACAGAGGAGGAGATGACCAGATATGTCCAGGAGCTCCAAAAGCATCAGGA
AACAGCTGAAAAGACCAAGAGAGTGAGCACCAAAGAGATCTAATGAGGAGGCACAGACCAGTGTCTGGATCCAG
CATCTTCTCCACTTCAGCGCTGAGTTCAGTATACACAAGTGTCTGCTACAGTCGCCAAATCACCAGTATTTGCTT
ATATAGCAATGAGTTTTATTTTGTATTTGTTTTGCAATAAAGGATATGAAGGTGGCTGGCTAGGAAGGGAAGG
GCCACAGCCTTCATTTCTAGGAGTGCTTTAAGAGAACTGTAAATGGTGCTCTGGGGCTGGAGGCTAGTAAGGAA
ACTGCATCAGATTGAAAGAGGAACAGACCCAAATCTGAACCTCTTTTGAGTTTACTGCATCTGTGACGAGGCTG
CAGGGAGTGCACACGATGCCAGAGAGAACTTAGCAGGGTGTCCCCGGAGGAGAGGTTTGGGAAGCTCCACGGAGA
GGAACGCTCTCTGCTTCCAGCCTCTTTCCATTGCCGTGAGCATGACAGACCTCCAGCATCCACGCATCTCTTGGT
CCCAATAACTGCCTCTAGATACATAGCCATACTGCTAGTTAACCCAGTGTCCCTCAGACTTGGATGGAGTTTCTG
GGAGGGTACACCCAAATGATGCAGATACTTGTATACTTTGAGCCCCTTAGCGACCTAACCAAATTTTAAAAATAC
TTTTTACCAAAGTGCTATTTCTCTGTAAAACACTTTTTTTTTTGGCAAGTTGACTTTATTCTTCAATTATTATCA
TTATATTATTGTTTTTTAATATTTTATTTTCTTGACTAGGTATTAAGCTTTTGTAATTATTTTTCAGTAGTCCCA
CCACTTCATAGGTGGAAGGAGTTTGGGGTCTTCTGCTGAGGGGCTGAAATAACCCAGATGCCCCCACCCTGC
CACATACTAGATGCAGCCCATAGTTGGCCCCCTAGCTTCCAGCAGTCCACTATCTGCCAGAGGAGCAAGGGTGC
CTTAGACCGAAGCCAGGGGAAGAAGCATCTTCATAAAAACTTTCAAGATCCAAACATTAATTTGTTTTTATTTA
TTCTGAGAAGTTGAGGCAAATCAGTATTCCCAAGGATGGCGACAAGGGCAGCCAAGCAGGGCTTAGGATATCCCA
GCCTACCAATATGCTCATTGCTACTAAGTGGAGGGTGTGTTGGCCCTGTCTCTTTCTTTTCTGGACCTCAGTTT
CCTCAGTGAGCTGGTAAGAATGCACTAACCTTTTGATTGATAAGTTATAAATTCTGTGGTTCTGATCATTGGTC
CAGAGGGGAGATAGGTTTCTGTGATTTTTCTTCTTCTCTATAGAATAAATGAAATCTTGTTACTAGAACAAGAA
ATGTCAGATGGCCAAAAACAAGATGACCAGATTTGATCTCAGCCTGATGACCTACAGGTCGTGCTATGATATGG
AGTCCCTCATGGGTAAAGCAGGAAGAGAGTGGGAAAGAGAACCACCCCACTCTGTCTTCATATTTGCATTTATGT
TTAACCTCCGGCTGGAAATAGAAAGCATTCCCTTAGAGATGAGGATAAAAGAAAGTTTCAGATTCAACAGGGGGA
AGAAAATGGAGATTTAATCCTAAAACTGTGACTTGGGGAGGTCAGTCATTTACAGTTAGTCCTGTGTCTTTTCGAC
TTCTGTGATTATTAACCCCACTCACTACCCTGTTTCAGATGCATTTGGAATACCAAAGATTAAATCCTTGACATA
AGATCTCATTTGCAGAAAGCAGATTAAAGACCATCAGAAGGAAATTATTTAGGTTGTAATGCACAGGCAACTGTG
AGAACTGTTGTGCCAAAAATAGAATTCCTTCTAGTTTTTCTTGTCTCATTGAAAGGAGAAAATCCACTTTG
TTTAGCATTTCAAGCTTTTATGTATCCATCCCATCTAAAACTCTTCAAACCTCCACTGTTCAGTCTGAAATGCA
GCTCCCTGTCCAAGTGCTTGGAGAACTCACAGCAGCACGCCTTAATCAAAGGTTTACCAGCCCTTGGACACTA
TGGGAGGAGGGCAAGAGTACACCAATTTGTTAAAAGCAAGAAACCACAGTGTCTCTTCACTAGTCATTTAGAACA
TGGTTATCATCCAAGACTACTCTACCCTGCAACATTGAACTCCCAAGAGCAAATCCACATTCCTCTTGAGTTCTG
CAGCTTCTGTGTAAATAGGGCAGCTGTGCTCTATGCCGTAGAATCACATGATCTGAGGACCATTATGGAAGCTG
CTAAATAGCCTAGTCTGGGAGTCTTCCATAAAGTTTTGCATGGAGCAAACAAACAGGATTAACTAGGTTTGGT
TCCTTCAGCCCTCTAAAGCATAGGGCTTAGCCTGCAGGCTTCCTTGGGCTTTCTCTGTGTGTGTAGTTTTGTAA
ACACTATAGCATCTGTTAAGATCCAGTGTCCATGGAAACATTCACATGCCGTGACTCTGGACTATATCAGTTT
TTGGAAAGCAGGGTTCTCTGCCTGCTAAACAAGCCACGTGGACCAGTCTGAATGTCTTTTCTTTACACCTATGT
TTTTAAGTAGTCAAACCTCAAGAAACAATCTAAACAAGTTTCTGTTGCATATGTGTTTGTGAACCTGTATTGTGA

1307/6881
FIGURE 1216B

TTTAGTAGGCTTCTATATTGCATTAACTTGTTTTGTAACTCCTGATTCTTCCTTTTCGGATACTATTGATGAA
TAAAGAAATTAAAGTGAIAAAAAAAAAAAAAAAAAAAAAA

1308/6881
FIGURE 1217

MWKRWLALALVAVAVRAEEELRSKSKICANVFCGAGRECAVTEKGEP TCLCIEQCKPHKRPVCGSNGKTYLN
HCELHRDACL TGSKIQVDYDGHCKEKKS VSPSASPVCYQSNRDELRRRIIQWLEAEIIPDGWFSKGSNYSEILD
KYFKNFDNGDSRLDSSEFLKFVEQNETAINIT TYPDQENNKLLRGLCVDALIELSDENADWKLSFQEFKCLNPS
FNPPEKKCALEDETYADGAETEVD CNRCVCACGNWVCTAMTCDGKNQKGAQTQTEEMTRYVQELQKHQETAECT
KRVSTKEI

1309/6881
FIGURE 1218

CTCCCAAGATGTCGTTCCCAAAGTATAAGCCGTCGAGCCTGCGCACTCTGCCTGAGACCCTCGACCCAGCCGAAT
ACAACATATCTCCGGAACCCGGCGGGCGCAAGCCGAGCGTTGGCCATAAGAGCCCAGCTGAAACGAGAGTACC
TGCTTCAGTACAACGATCCCAACCGCCGAGGGCTCATCGAAAATCCTGCCTTGCTTCGTTGGGCCTATGCAAGAA
CAATAAATGTCTATCCTAATTTTCAGACCCACTCCTAAAACTCACTCATGGGAGCTCTGTGTGGATTGTTGGGCCCC
TCATCTTCATTTATTATATTATCAAACTGAGAGGGATAGGAAAGAAAACTTATCCAGGAAGGAAAAATTGGATC
GAACATTTACCTCTCATATTAAGTCTGGCAATGATGACTATATGTATTCTGCCTAAATAAATCATCTATTAAT
CATTAAAAAAAAA

1310/6881
FIGURE 1219

MSFPKYKPSSLRTLPELDPAEYNISPETTRAQAERLAIRAQLKREYLLQYNDPNRRGLIENFALLRWAYARTIN
VYPNFRPTPKNSLMGALCGFGPLIFIYYIIKTERDRKEKLIQEGKLDRTFHLST

1311/6881
FIGURE 1220

GATGACACACAATAATTTTTGGTTGAAGAAGATAGAAATCAGTGTTTCAGAAGCAGAAAAACGAACTGGAAGAAA
TGCCATGAACATGCAAGAAACATATACTGCTTACCTCATTGAAACAAGGTCAGTTGAACATACCGATGGTCAGAG
TGTCTAACAGACTCACTATGGCGGCGATATAGTGAATTTGAGTTGTTGAGAAGCTACCTTTTAGTTTACTATCC
ACATATTGTTGTGCCACCTCTGCCAGAAAAACGGGCAGAAATTTGTTTGGCATAAACTCTCTGCTGACAACATGGA
TCCAGATTTTGTGGAGAGGCGACGGATTGGTTTAGAAAACTTTCTCTTGAGGATTGCTTCACATCCCATCCTTTG
TAGAGACAAAATCTTCTATCTGTTTTTAACACAGGAAGGTAAGTGAAGGAGACTGTGAATGAAACTGGGTTTCA
GCTGAAGGCAGACTCCAGGTTAAAAGCGCTTAATGCAACATTCAGAGTGAAAAACCCAGACAAGAGATTTACTGA
CCTTAAGCACTATAGTGATGAACTGCAGTCTGTCATCTCACATCTTCTTCGAGTCAGAGCTAGAGTAGCAGATCG
ACTCTATGGTGTATATAAAGTACATGGGAATTATGGTCGAGTTTTTCAGTGAATGGAGTGCCATAGAAAAAGAAAT
GGGTGATGGACTGCAGAGTGGTGCATCATATGGATGTGTATGCATCTTCTATTGATGATATTTTGGGAAGATGA
AGAACATTATGCAGATCAGTTAAAAGAGTATCTTTTTTATGCAGAAGCATTGCGGGCTGTGTGCAGGAAACATGA
ACTTATGCAGTATGACTTGGAGATGGCTGCTCAGGACTTAGCATCCAAGAAGCAGCAGTGTGAGGAACTGGTAAC
TGGGACTGTGAGAACATTCTCTTTGAAGGGAATGACTACCAAGCTCTTTGGTCAAGAAACTCCAGAGCAGAGAGA
AGCCAGAATAAAGGTGCTAGAAGAACAATAAATGAAGGAGAACAACAGCTAAAGTCTAAAAATCTGGAAGGCAG
AGAATTTGTGAAAAACGCATGGGCTGATATTGAACGCTTCAAAGAACAAAAGAACCGAGACTTAAAGGAGGCCCT
CATAAGCTATGCAGTCATGCAGATCAGTATGTGCAAAAAGAGTCTCACCTGTCAACCCAGGCTGGAGTGCAATGG
CATGATCTCAGCTCACTACAACCTCCGCCTCCCGTGTTCAGCAATTCTACCTCATCCAGCCGAGTAGATGGGAT
TACAGGGAATTCAAGTTTGGACCAATGCTAAGGAATGCTTTAGCAAGATGTAATCCTGTGAATTGAATTTCTCTT
CAATCAAAGTGCCCCAAAACAGAAGCACAAGTAAATAAAAAGAAATTTAAGTCACTACCTAGTATACATAAACATA
TACAATAAGTTAAATAAATTCAGCTTTCTTTAACTTAATTGTGGTCGTGTTAATGTAGCACAAAAAATATATTTT
AATGAAGATTAAATATTATAATTTGAGGTTTTGGGGACTGGTGTGATTCCAAAAGTTAATTTAATAATATATA
CCAACAGATTGTTTGTACGCTTCTGAACCAATGACTGAATGTCAAGATGTTTCGTTAATTTCTAGATGTTTGT
CAAGACCAGCTGTTTCAGATCTATTAATGTAGGGAATTTTCCCTAAGATTGAATTCCTATATTTACTTGGTAAG
ATCCACTAATCTGTTATAGGGAGTTGTTTTCTCTTGCCCTTAGTTGAGCTATTTGGTTTGACAAAGCTCAGCAG
AAACTTGATGTGAAAAATCTACGATTTTCTTCTACATTCATTGATGCCCTTGTAATGTTTGCATACACTAGAAA
ATGCCTTCAATTTGTGTTTTACCAGAATTTTGATACTGGTCAGAAATTTTATACTGCCAACAAAGAACTCAAC
TTCTCAGATCTATAATGGGATACATTGTCATCCTCTAGCAACTCCTATATAGAAAGTTTTAACTGAATATGTTAC
ATATAAGAATTAAATTCCTCTCAAATAATTCTTAACCTCAGTAATGAGCCTAAATTTACTCTGCTTGGCTCTCTA
CACATGGCATTTCAGGGTATAAGATGTAGCATTTCATGTGTAAGATATATGTACTAAACATATGTGTTGCTATC
TTCAATCATTAACATCCTTCTTTTCTATTGCTTGGCTGTAATTTTTGTAAAGATAAATTATATTGTTTTTTGTAT
GTGTGTTTGTAGTATATGTTTCAGAAGGCAAGCATCTTCATTTTGCTAGCTTTGCAGAATCTTAAAAATGTGTACTC
GTTATTTCTAATGATGTAAAAAAAATCCCTAGTCCTGTTTAGCATTTGACTTTTTTATATGTTTTAAATGTTGC
TGGATTTTTGTGCTGTTTGCCAACTTATACAATAAATAAATGAAATATTGTGCTG

1312/6881
FIGURE 1221A

GCAATTTTAGAATGTGCTGGACAAAATGTAGAAAGGGAATGTTCTCAGCAAGCTCAGCAGCGCAAAAATGATTAT
ATAATCACCGGAGGTGGATTTTTGAGGTGCAAGAATATCATTTCATGTAATTGGTGGAATGATGTCAAGAGTTCA
GTTTCCTCTGTTTTGCAGGAGTGTGAAAAAAAAAATTACTCATCCATTTGCCTCCCAGCCATTGGGACAGGAAAT
GCCAAACAACACCCAGATAAGGTTGCTGAAGCCATAATTGATGCCATTGAAGACTTTGTCCAGAAAGGATCAGCC
CAGTCTGTGAAAAAAGTTAAAGTTGTTATCTTTCTGCCTCAAGTACTGGATGTGTTTTATGCCAACATGAAGAAA
AGAGAAGGGACTCAGCTTTCTTCCCAACAGTCTGTGATGTCTAACTTGCATCATTTTTTGGGCTTTTCAAAGCAA
TCTCCCCAAAAAAGAATCATTTGGTTTTTGAAAAAGAAAACAGAATCAGCAACTTTTCGGGTGTGTGGTGAAAAT
GTCACGTGTGTGGAATATGCTATCTCCTGGCTACAAGACCTGATTGAAAAAGAACAGTGTCTTACACCAGTGAA
GATGAGTGCATCAAAGACTTTGATGAAAAGGAGTATCAGGAGTTGAATGAGCTGCAGAAGAAAGTTAAATATTAAC
ATTTCCCTGGACCATAAGAGACCTTTGATTAAGGTTTTGGAATTAGCAGAGATGTGATGCAGGCTAGAGATGAA
ATGAGGCGATGATCAAGAGAGGTTGATTGGGCAAAGAACAGGAATCCCGGCAGATTGTATCAGTGAGTTTATA
GAATGGCAGTATAATCGACAATAACACTTCTCATGTGTTTTAACAAAATGACCAATCTGAAATTAGAGGATGCAA
GGAGAGAAAAAGAAAAAACAGTTGATGTCAAATTAATCATCGGCACTACACAGTGAACCTTGAACACATACACTG
CCACAGACACAAAGGGCCACAGTTTATCTGTTTCAGCGCCTCAGGAAATCCAAAGTTGACATCCCTGCACACTGGA
GTGATATGAAGCAGCAGAATTTCTGTGTGGTGGAGCTGCTGCCTAGTGATCCTGAGTACAACACGGTGGCAAGCA
AGTTTAATCAGACCTGCTCACACTTCAGAATAGAGAAGATTGAGAGGATCCAGAATCCAGATCTCTGGAATAGCT
ACCAGGCAAAGAAAAAACTATGGATGCCAAGAATGGCCAGACAATGAATGAGAAGCAACTCTTCCATGGGACAG
ATGCCGGCTCCGTGCCACACGTCAATCGAAATGGCTTTAACCGCAGCTATGCCGGAAGAATGCTGTGGCATATG
GAAAGGGAACCTATTTTGCTGTCAATGCCAATTATTCTGCCAATGATACGTACTCCAGACCAGATGCAAATGGGA
GAAAGCATGTGTATTATGTGCGAGTACTTACTGGAATCTATACACATGGAAATCATTCATTAATTGTGCCTCCTT
CAAAGAACCCTCAAATCCTACTGACCTGTATGACACTGTCACAGATAATGTGCACCATCCAAGTTTATTTGTGG
CATTTTATGACTACCAAGCATACCCAGAGTACCTTATTACGTTTAGAAAATAACACTTTGGTATCCTTCCCACAA
AATTATTCTCCATTTGTACATATCTAGTTGTAAAACAAGTTTTAGCTTTTTTTTTTAATTCCTCTTAACAGATTT
TTCTAATATCCAAGGATCATTCTTTGTGCTGAAAGTCAGTCTTTCTTCAGCTTCCCTTTTATAATGGAAATGAAC
TTATTATCTTGAGAGCAAATAAAGTTGAAAAATTTAAATGAGATAATGCAGTTGCAACTGTGTGTCCACAAGTATG
GACATCAAATCTGTGGGAAAAGAACAGGTTTGTATTTTTCAGGAAGGAGAGAATAACAGTCTTATAGACAGAGGGC
ACAGCTAAGCACAGCTGCCACTGCAGGAGACAGGCCCCATGTCAGGATGCCATAGTGCTGTGGGGAGCACAGTAT
TACCCAGTGGGTAGGGCTTCTGTCTTCCCTGGGAGCAGGGATGGTATCTTAGTCAATTTTTTCCCTTGAGATGA
GGTCTGTGCCTGATGTACAACGGATACTCCATAAATGTTTGACAAACCAACGAAGAATGAAAAAAGCCTAGTCA
GACTCCCATCCAAAGTAGGAATCTCTTTAACATTCTTGACTCACTATCACTTTACCTCAAATTGAACAGATT
CCATGACGGAACCTTCATTCTTCACAACTAGCCAGTGACATGTGGGACAGCTCTGGCCAGGGCTCTGGGACTGCA
GTGTAATGCGCTCTGCACGGTCCAGGAGCTGTGATGTGGCTGTGGTCTAGGGGAATCCTGCCTGCCCATGGAG
TTGCGCAGCACAAACCCTGGCTCCAATTGCCAGAAGGCTCTTTTTAATGCTGAACCAAAATGTGCCTTTTTTTTT
TTTTTTTGAGATGGAGTTTCACTCTTGTGCCCAGGCTGGAGTGCAATGGCGCGATCTCAGCTCACTGCAGCCAC
TGCTCCAGGTTCAAGTGATTCTCCTGCCTCAGCTCCCGAGTAGCTGGGATTACAGGCATGCGCTAACACACC
CAGCTAATTTTGATTTTTTAGTAGAGACGAGGTTTCTCCATGTTTCGACAGGCTGGTCTCGAACTCCACCTCAGC
CTCCCAAACCTGCTGGGATTACAGGTGTGAGCCACCGTGACCAGCCAATGTGCCTTCTTATAGTGTCTACTCATTG
GTCTTTGTTCTGCCAGTGATAACAATGGGATAACGCCCTGTACACATCTTCATTGTGAAACCCTTCCCCTGTGC
TGAGATTAAATGAACTCTAAGATTATTAAATAGTATATTTTCCCTTGACAGCCTAGCGTTTGATGATTTTAAAGCC
TTATGTATAAATAAACCAAGGAAGTAAGCAGTCATATTGCTAATTTGCTAACTCCTATCTATTGAATGGTGAAG
TTTTAAAAATTTCCCAGGTAAGTTTAAAGATTCAAACACCATCTATTGAGCACCTACATTGTGTGCCAGGTAGTA
AAATAGGTGCTTTCATACACATTGTCTCAATTCCGTGTGAGGTGAGAATTATCTCTGCATTTGAACTTGAGGAAA
CATGCTCAGAGTGCAAGAAGCTTCCTTGCTGAGATCACCTAGAAAGGAACCTCAGAGCCGGCAACTGAATCTT
GGTCCCTGTGATGTCAAGCCATTGCTCTCCCACTGCAGAACATGGCCTCTAGATTAATGCCACCGATTACAGGAA
CACCTCCGACAGTCTTGAAATACCCCCATGTTGCCTTGTTTGTGTTTTTCTTCTGCTTCTTCTATTACAGTCTC
TTCATTGGAAGCTCTGTAGGCCAAGGCCAGAGCTGATACTGACACGGAGCCAATGCAGATAGCACATCAGATGCT
AGGGGTGCTGGGAGGATTAAGGGACTTAATCTGCTAGGAACACCTGTACTTGAAGTGAGGAGGCTAGGGGGCC
ACAGTTGCTGCTTCATTAACATAGAGTTTTTGGATTTTTTCTCTGTGGTTTTGTTTTTAAAGTGAGTTGGCAGA

1313/6881
FIGURE 1221B

CTCCTTGTTGCTTAAGAGTGGCTTTCTAGGCAGGCCACTGGCATCTGAATTCATCATTGACAATAAATGTAAGAA
ATTGGAATAAAAAAGAGAGACCTGCTGTTATTTCGCTTTTGTTCTCCAGTGATTTGATTAATCAGGGCAAGGCTG
AATATCAGAGTGTATCGCACTGAAGAATAATAATCCATTCAGTAATGTTATAGTTATCCTCAATCTAAATATGTC
AACTGTCATTTTGCTACTTTTCAAATAAAATACTTGAAAACCTGTC

1314/6881
FIGURE 1222

MKKREGTQLSSQQSVMSKSLASFLGFSKQSPQKKNHLVLEKKTESATFRVCGENVTCVEYAIISWLQDLIEKEQCPY
TSEDECIKDFDEKEYQELNELQKKLNINISLDHKRPLIKVLGISRDVMQARDEIEAMIKRVRLAKEQESRADCIS
EFIEWQYNDNNTSHCFNKMTNLKLEDARREKKKTVDVKINHRHYTVNLNTYTATDTKGHSLSVQRLTKSKVDIPA
HWSMDKQQNFCVVELLPSDPEYNTVASKFNQTCSHFRIEKIERIQNPDLWNSYQAKKKTMDAKNGQTMNEKQLFH
GTDAGSVPHVNRNGFNRSYAGKNAVAYGKGTYFAVNANYSANDTYSRPDANGRKHVYYVRVLTGIYTHGNHSLIV
PPSKNPQNPTDLYDTVTDNVHHPSLFVAFYDYQAYPEYLITFRK

1315/6881
FIGURE 1223

GAATTCGGGGGGCGCCGGAGTGGAGAAAGGAGCCAGCGGTGGGCAGCGCTGCTGGGATGGCGCGGGCCGGGCCGG
CGTGGCTGCTGCTGGCAATCTGGGTGGTCCTGCCATCATGGCTGTCCTCTGCAAAGGTCTCCTCGCTCATTGAGA
GAATCTCTGACCCCAAGGACTTGAAAAAACTGCTCAGAAACCGGAATAATGTACTGGTGCTTTACTCCAAATCTG
AGGTGGCAGCTGAAAATCATCTCAGGTTACTGTCCACAGTGGCCCAGGCGGTGAAAGGACAAGGGACCATCTGCT
GGGTGGACTGTGGTGATGCAGAGAGTAGAAAATTGTGCAAGAAGATGAAAGTTGACCTGAGCCCGAAGGACAAAA
AGGTTGAATTATTCCATTACCAGGATGGTGCATTTTCATACTGAATATAACCGAGCTGTGACATTTAAGTCCATAG
TGGCCTTTTTTGAAGGATCCAAAAGGGCCCCCACTGTGGGAGGAAGATCCTGGAGCCAAAGATGTTGTCCACCTTG
ACAGTGAAAAGGACTTCAGACGGCTCCTGAAGAAGGAAGAGAAGCCGCTCCTGATCATGTTTTATGCCCCCTGGT
GCAGCATGTGCAAGAGGATGATGCCGCATTTCCAGAAGGCTGCGACTCAGCTGCGAGGCCACGCCGTGCTGGCCG
GGATGAATGTCTACTCCTCTGAATTTGAAAACATCAAGGAGGAGTACAGCGTGCGCGGCTTCCCCACCATCTGCT
ATTTTGAGAAAGGACGGTTCTTGTTCCAGTATGACAACTATGGGTCCACAGCTGAGGACATTGTGGAGTGGCTGA
AGAATCCGCAGCCGCCACAGCCCCAGGTCCCTGAGACTCCCTGGGCAGATGAGGGCGGCTCCGTTTATCACCTGA
CCGATGAAGACTTTGACCAGTTTGTGAAGGAACACTCCTCTGTCTCGTCATGTTCCACGCCCCATGGTGTGGCC
ACTGTAAGAAAATGAAGCCGGAGTTTGAGAAGGCAGCAGAAGCCCTCCATGGAGAAGCGGATAGCTCTGGTGTCC
TTGCAGCTGTGATGCCACTGTCAACAAGGCCCTGGCAGAAAGATTCCACATCTCAGAGTTTCTACGTTGAAGT
ATTTTAAGAATGGAGAGAAATACGCAGTGCCTGTGCTCAGGACAAAGAAGAAGTTTCTCGAGTGGATGCAAAACC
CTGAGGCCCCCCCCGCCCCCAGAGCCACGTGGGAAGAGCAGCAGACAAGCGTGTGACCTGGTGGGGGACAACT
TCCGGGAGACCCTGAAGAAGAAGAAACACACCTTGGTCATGTTCTACGCCCCCTGGTGCCACACTGTAAGAAGG
TCATTCCGCACTTTACTGCTACTGCTGATGCCTTCAAAGATGACCGAAAAGATTGCCTGTGCCGCTGTTGACTGTG
TCAAAGACAAGAACCAAGACCTGTGCCAGCAGGAGGCGGTCAAGGGCTACCCCACTTTCCACTACTACCACTATG
GGAAGTTCGCAGAAAAGTATGACAGCGACCGCACAGAATTGGGATTTACCAATTATATTCGAGCCCTCCGGGAGG
GAGACCATGAAAGACTAGGGAAAAAGAAGGAAGAGTTATAATTCCTGCCTCAGAAAAAGCTTTTCCATTACACTG
TGAATGATACCTGTTTTGTTGTTTCTGAATTTCCCCCGAATTC

1316/6881
FIGURE 1224

MARAGPAWLLLLAIWVVLPSWLSSAKVSSLIERISDPKDLKKLLRTRNNVLVLYSKSEVAAENHLRLLSTVAQAVK
GQGTICWVDCGDAESRKLCKKMKVDLSPKDKKVELFHYQDGAFHTEYNRAVTFKSIVAFLKDPKGPPLWEEDPGA
KDVVHLDSEKDFRRLKKKEEKPLLIMFYAPWCSMCKRMMPHFQKAATQLRGHAVLAGMNVYSSEFENIKEEYSVR
GFPTICYFEKGRFLFQYDNYGSTAEDIVEWLKNPQPPQPQVPETPWADGGSVYHLTDEDQFVKEHSSVLVMF
HAPWCGHCKKMKPEFEKAAEALHGEADSSGVLAAVDATVNKALAERFHISEFPTLKYFKNGEKYAVPVLRTKKKF
LEWMQNPEAPPPPEPTWEEQQTSLHLVGDNFRETLLKKKKHTLVMFYAPWCPHCKKVIPHFTATADAFKDDRKIA
CAAVDCVKDKNQDLCQQEAVKGYPTFHYYHYGKFAEKYDSRTELGFTNYIRALREGDHERLGKKKEEL

1317/6881
FIGURE 1225

CTCAGACTGCTGTGCTAGCAATCAGTGAGACTCCGTGGGCGTAGGACCCTCTGAGCCAGGTGCGGGATATAATCT
TGTGGTGCGCCGTTTTTTAAGCCGGTCCGAAAAGCGCAATATTCGGGTGGGAGTGACCCGATTTCAGGGCTGT
GACCATCTATGACAAGCCGGCATCTTTCTTTAAAGAGACACCTCTGGACCTGCTGCACCGGCTCTTCATGAAGCT
GGGTGGCACTCACTCTCTGTTCAGGGCCTGCTCAGAACCTGAGGACGCAGCCATGGAGCGGTTCGGCCTTCATGGA
GCTGGATGCTGGGAGCAGGCTGGTGATGCATCTCCGCGAGTGGCCAGCCCTGCTGGTCAGCAGCACGGGCTGGAC
AGAGTTTGAACAACCTTACTCTTGATGGACACAACCTTCCTTCTCTTGTCTGTGTGATAACAGGGTCGGTGGACCT
GGGTGTCTGTCTGCACATGTCTCCAGTGGCCTGGACCTGCCCATGAAGGTGGTGGACATGTTCCGGGTGCTGTTT
GCCGTGTGTGTGCCGTGAACCTCAAGTGTTTACATGAGCTGGTGAAACATGAAGAAAATGGCCTGGTCTTTGAGGA
CTCAGAGGAACCTGGCAGCTCTGCAGATGCTTTTCTCAAACCTTCCTGATCCTGCAGGCAAGCTAAACCAGTTTTG
GAAGAACCCTGCGGGAGTCGCAGCAGCTCCGATGGGATGAGAGCTGGGTGCAGACTGTGCTCCCTTTGGTTATGGA
CATACAACCTCCTGGGCCAGAGGCTAAAACCCCGGGACCCCTGCTGTCCTTCCCGCAGCTTCTTCTCGGAGTCTCA
GGGCAAACCCCTTTTGAGCAGCGCCTCCCAGTGGCCAGAAGCTGAAATGACGGCAGTGGTGCCGCCTGGTGAATGA
ATTGGTTCTGTGACCCGG

1318/6881
FIGURE 1226

MKLGGTHSPFRACSEPEDAAMERSAFMELDAGSRLVMHLREWPALLVSSTGWTEFEQLTLDGHNLP SLVCVITGS
VDLGVCCLHMSSSSGLDLP MKVVDMFGCCLPVC AVNFKCLHEL VKHEENGLVFEDSEELAALQMLFSNFPDPAGKLN
QFWKNLRESQQLRWDESWVQTVLPLVMDIQLLGQRLKPRDPCCPSRSFFSESQGKPF

1319/6881
FIGURE 1227

GCAGACACGTGATGCGGGGGAGGGGGGGGGGGCGTGCCAGGAGCAAGCGTCTGCCGCGGTGGCCGGGTGCCGGTA
AGGGTTTTCCAGCGCCCCCGGCCTAGGTTTTGGAGGCGCGGGAATGCGTTCGTTGCTCAGTGTGCGACTTCCCCCT
ATTCCCATCGGCGGAGGCTGTCACTTTACGCTCATAACCGTTTTTCTTTACTGCACTCGTGTGCGGAGGAAAGGG
ACTTGCGTGGCACCCCCAGACCTCCCCGCTCTCCGCTTCCACGTTTGGTACATCCTGCCTGAGGCAGGAAGCCGCA
GCTTGAGGGACGGCCTGTCGTACGGTGC GGATGGTGGTGGCCTGCGAGGCTCATTCTAGCAAGGAACAAGGCTTT
CCCGCTTTGATTTTATAAATATTATGTTTACAAAGCTGTAATATATAGAAATTGATAAGACGTGTCCCTGTCCCT
GGAAACGCAGGCACCGCGTGTGGAAAGACATTCTGCGGTGTTTGACAGACTCCCCAGTTGGTGCCATGCT
CTGTGCTTAGGGAAGTGTGAGACCCCTGGAGGGGTGGGTACCGGGACCGCACTCAGCCTGGGGTTTGGAGGCGGC
CTCCTATAGGAAGCGACCTGGGACCTAAGATTTTACTGACTGACTGTGGGTTCAGTGAATAAAAAGGAAGAAACA
AAGAGCATTGCAGGCATCGGGACTGTCACATTTGACAAGATCAAAGCTGCAGGAAAATGGACAGTGAGGTTTCTAGA
GAGATGGAAGGATCTTGATTTGATTGATGATGCTTGGCGAGAAGACAAGCTGCCTTATGAGGATGTCGCAATAC
CACTGAATGAGCTTCCTGAACCTGAACAAGACAATGGTGGCACCACAGAATCTGTCAAAGAACAAGAAATGAAGT
GGACAGACTTAGCCTTACAGTACCTCCATGAGAATGTTCCCCCATTTGGAAACTGACGCTTGGCTCCTTTCTTGT
GGATGGATTTTCTCAAAGTACACAGATAAAGCATGGTTTGTTCAGTCTCCAAATTCAAACCTTTGAGTAATAAA
TCAGCACTCAAAAATGTACACCCATTTAGTTTGTGGTAGCAAAGTGCAATGCGAAATTGAATGAGAACTGAGAT
TTCTCAGTAATGGTGAATATTTGCTCTTTAAACCTAAAACCTTTTATTGAGTAGCTTATATTTGAACATGATTG
GTTAAACATTTGCCTCTACCTCTGATTTTGCTTTGCTGTCAAAGTTTAAACACCTTCCAACCTTATGTGTGTCC
TGTAACACAGGTGATTGAACGTATGAGAGGGAAAGGCAAAGAAAAAGGAAGCCAGACACTAGGAGAATTATTAAC
TTCTCATACTTCCCCACATTGAGAAGCATTCGGAGTGTATTTAGCCTGTAGATGTTGTGATATGCAATATCCCA
TTCCCTGGTTACTGGCATTCCCTAAGATTCTTCATGGTATTTTCAAACCTTTGGATAAATTTACAGATTAGAAAGAT
ATCTGACAGTTAATCTCTGTTCTCCTTACAAATTCCTTTGTGCTGCTGGAAAGGATCTTTGGCTAGGTGGATGA
CTAGTTTTATTCAAAGCCTTTTCTCAAAGCCCTTTTCAAGTTACAACCACCCCACTATGGAATCAGTATTTAGTTAT
ACATTTGTATAAGAACCTGTATTTTGAAAAACACATTCATGTATATTTATTCCTGGAATTATTTGCCTGTAAAC
AGTGTCTTTTATGTTCTCTCCCCAGATTGTAAACTCTGTAAGAAGCTGCTTGTATCTGTATCCCTTGTGAAACT
CTGAAAACACTGAATAACTAAAATCTCTTCTCATCCTTTT

1320/6881
FIGURE 1228

MRGRGGGRGRSKRLPRWPGAGKGFQRPRPRFWRRGNAFVAQCRTSPYSHRPRLSLYAHNRFSLLHSCREERDLRG
TPRPPRLRFHVWYILPEAGSRS

1321/6881
FIGURE 1229

AGTGGCGGAGAGGATCGTGGTACTGCTATGGCGGAATCATCGGAATCCTTCACCATGGCATCCAGCCCGGCCAG
CGTCGGCGAGGCAATGATCCTCTCACCTCCAGCCCTGGCCGAAGCTCCCGGCGTACTGATGCCCTCACCTCCAGC
CCTGGCCGTGACCTTCCACCATTGAGGATGAGTCCGAGGGGCTCCTAGGCACAGAGGGGCCCCCTGGAGGAAGAA
GAGGATGGAGAGGAGCTCATTGGAGATGGCATGGAAAGGGACTACCGCGCCATCCAGAGCTGGACGCCTATGAG
GCCGAGGGACTGGCTCTGGATGATGAGGACGTAGAGGAGCTGACGGCCAGTCAGAGGGAGGCAGCAGAGCGGGCC
ATGCGGCAGCGTGACCGGGAGGCTGGCCGGGGCTGGGCCGCGATGCGCCGTGGGCTCCTGTATGACAGCGATGAG
GAGGACGAGGAGCGCCCTGCCCCGAAGCGCCGCCAGGTGGAGCGGGCCACGGAGGACGGCGAGGAGGACGAGGAG
ATGATTGAGAGCATCGAGAACCTGGAGGATCTCAAAGGCCACTCTGTGCGCGAGTGGGTGAGCATGGCGGGCCCC
CGGCTGGAGATCCACCACCGCTTCAAGAACTTCCTGCGCACTCACGTGACAGCCACGGCCACAACGTCTTCAAG
GAGCGCATCAGCGACATGTGCAAAGAGAACCCTGAGAGCCTGGTGGTGAAGTATGAGGACTTGGCAGCCAGGGAG
CACGTGCTGGCCTACTTCTGCTGAGGCACCGGCGGAGCTGCTGCAGATCTTTGATGAGGCTGCCCTGGAGGTG
GTACTGGCCATGTACCCCAAGTACGACCGCATACCAACCACATCCATGTCCGCATCTCCACCTGCCTCTGGTG
GAGGAGCTGCGCTCGCTGAGGCAGCTGCATCTGAACCAGCTGATCCGCACCAGTGGGGTGGTGACCAGCTGCACT
GGCGTCTGCCCCAGCTCAGCATGGTCAAGTACAAGTCAACAAGTGCAATTCGTCTCTGGGTCTTTCTGCCAG
TCCCAGAACCAGGAGGTGAAACCAGGCTCCTGTCTGAGTGCCAGTGGCCCGGCCCTTTGAGGTCAACATGGAG
GAGACCATCTATCAGAACTACCAGCGTATCCGAATCCAGGAGAGTCCAGGCAAAGTGGCGGCTGGCCGGCTGCCC
CGCTCCAAGGACGCCATTCTCCTCGCAGATCTGGTGGACAGCTGCAAGCCAGGAGACGAGATAGAGCTGACTGGC
ATCTATCACAACAATATGATGGCTCCCTCAACACTGCCAATGGCTTCCCTGTCTTTGCCACTGTATCTTAGCC
AACCACGTGGCCAAGAAGGACAACAAGTTGCTGTAGGGGAAGTACCGATGAAGATGTGAAGATGATCACTAGC
CTCTCCAAGGATCAGCAGATCGGAGAGAAGATCTTTGCCAGCATTGCTCCTTCCATCTATGGTCATGAAGACATC
AAGAGAGGCCTGGCTCTGGCCCTGTTCTGGAGGGGAGCCCCAAAACCCAGGTGGCAAGCACAAGGTACGTGGTGAT
ATCAACGTGCTCTTGTGCGGAGACCTGGCACAGCGAAGTGCAGTTTCTCAAGTATATTGAGAAAGTGTCCAGC
CGAGCCATCTTACCACCTGGCCAGGGGGCGTGGCTGTGGGCTCACGGCGTATGTCCAGCGGCACCCTGTGAGC
AGGGAGTGGACCTTGGAGGCTGGGGCCCTGGTTCTGGCTGACCGAGGAGTGTGTCTCATTGATGAATTTGACAAG
ATGAATGACCAGGACAGAACCAGCATCCATGAGGCCATGGAGCAACAGAGCATCTCCATCTCGAAGGCTGGCATC
GTCACCTCCCTGCAGGCTCGCTGCACGGTCATTGCTGCCGCCAACCCCATAGGAGGGCGCTACGACCCCTCGCTG
ACTTTCTCTGAGAACGTGGACCTCACAGAGCCCATCATCTCACGCTTTGACATCCTGTGTGTGGTGAGGGACACC
GTGGACCCAGTCCAGGACGAGATGCTGGCCCGCTTCTGTGGTGGGCAGCCACGTGAGACACCACCCAGCAACAAG
GAGGAGGAGGGGCTGGCCAATGGCAGCGCTGCTGAGCCCGCCATGCCCAACACGTATGGCGTGGAGCCCTGCCC
CAGGAGGTCTGAAGAAGTACATCATCTACGCCAAGGAGAGGGTCCACCCGAAGCTCAACCAGATGGACCAGGAC
AAGGTGGCCAAGATGTACAGTGACCTGAGGAAAGAATCTATGGCGACAGGCAGCATCCCCATTACGGTGCGGCAC
ATCGAGTCCATGATCCGCATGGCGGAGGCCACGCGCGCATCCATCTGCGGGACTATGTGATCGAAGACGACGTC
AACATGGCCATCCGCGTATGCTGGAGAGCTTCATAGACACACAGAAGTTCAGCGTCATGCGCAGCATGCGCAAG
ACTTTTGCCCGCTACCTTTTCACTCCGGCGTGACAACAATGAGCTGTTGCTCTTCATACTGAAGCAGTTAGTGGA
GAGCAGGTGACATATCAGCGCAACCGCTTTGGGGCCCAGCAGGACACTATTGAGGTCCCTGAGAAGGACTTGGTG
GATAAGGCTCGTCAGATCAACATCCACAACCTCTCTGCATTTTATGACAGTGAGCTCTTCAGGATGAACAAGTTC
AGCCACGACCTGAAAAGGAAAATGATCCTGCAGCAGTTCTGAGGCCCTATGCCATCCATAAGGATTCTTTGGGAT
TCTGGTTTGGGGTGGTCAGTGCCCTCTGTGCTTTATGGACACAAAACCAGAGCACTTGATGAACTCGGGGTACTA
GGGTGAGGGCTTATAGCAGGATGTCTGGCTGCACCTGGCATGACTGTTTGTCTTCCAAGCCTGCTTTGTGCTTC
TCACCTTTGGGTGGGATGCCTTGCCAGTGTGTCTTACTTGGTTGCTGAACATCTTGCCACCTCCGAGTGCTTTGT
CTCCACTCAGTACCTTGGATCAGAGCTGCTGAGTTCAGGATGCCTGCGTGTGGTTTAGGTGTTAGCCTTCTTACA
TGGATGTGAGGAGAGCTGCTGCCCTCTTGGCGTGAGTTGCGTATTCAGGCTGCTTTTGCTGCCTTTGGCCAGAGA
GCTGGTTGAAGATGTTTGTAAATCGTTTTAGTCTCCTGCAGGTTTCTGTGCCCTGTGGTGAAGAGGGCACGAC
AGTGCCAGCGCAGCGTTCTGGGCTCCTCAGTCGCAGGGGTGGGATGTGAGTCATGCGGATTATCCACTCGCCACA
GTTATCAGCTGCCATTGCTCCCTGTCTGTTTCCCCACTCTCTTATTTGTGCATTGCGTTTGGTTTCTGTAGTTTT
AATTTTTAATAAAGTTGAATAAAATAT

1322/6881
FIGURE 1230

MAESSESFTMASSPAQRRRGNDPLTSSPGRSSRRTDALTSSPGRDLPPFEDESEGLLGTEGPLEEEEDGEELIGD
GMYDYRAIPELDAIEAEGLALDDEDVEELTASQREAAERAMRQRDREAGRGLGRMRRLLYDSDEEDEERPARK
RRQVERATEDGEEDEEMIESIENLEDLKGHSVREWVSMAGPRLEIHHRFKNFLRTHVDSHGHNVFKERISDMCKE
NRESLVVNYEDLAAREHVLAYFLPEAPAEELLQIFDEAALEVVLMYPKYDRITNHIHVRISHLPLVEELRSLRQL
HLNQLIRTSGVVTSTGTGVLPLQLSMVKYCNKCNFVLGPFQSQNQEVKPGSCPECQSAGPFVEVNMEETIYQNYQR
IRIQESPGKVAAGRLPRSKDAILLADLVDSCKPGDEIELTGIYHNNDGSLNTANGFPVFATVILANHVAKKDNK
VAVGELTDEDVKMITSLSKDQQIGEKIFASIAPSIYGHEDIKRLALALFGGEPKNPGGKHKVRGDINVLLCGDP
GTAKSQFLKYIEKVSSRAIFTTGQASAVGLTAYVQRHPVSREWLEAGALVLADRGVCLIDFDMNDQDRISI
HEAMEQQSISISKAGIVTSLQARCTVIAAANPIGGRYDPSLTFSENVDLTEPIISRFDILCVVRDTPVQDEML
ARFVVGSHVRHHPNKEEEGLANGSAAEPAMPNTYGVEPLPQEVLLKKYIIYAKERVHPKLNQMDQDKVAKMYSDL
RKESMATGSIPITVRHIESMIRMAEAHARIHLRDYVIEDDVNMAIRVMLESFIDTQKFSVMRSMRKTTFARYLSFR
RDNNELLLFILKQLVAEQVITYQRNRFGAQQDTIEVPEKDLVDKARQINIHNLSAFYDSELFMRMNKFSHDLKRKMI
LQQF

1323/6881
FIGURE 1231

ACCATGGGCCGGCTGCTGCGGGCCGCCGGCTGCCGCCGCTGCTTTCGCCGCTGCTGCTTCTGCTGGTTGGGGGA
GCGTTCCTGGGTGCCTGTGTGGCTGGGTCTGATGAGCCTGGCCCAGAGGGCCTCACCTCCACCTCCCTGCTAGAC
CTCCTGCTGCCCCTGGCTCAGGCTTCCCCAGCGAAGAGAATGAAGAGTCTCGGATTCTGCAGCCACCACAGTACTTCTGG
GAAGAGGAGGAAGAGCTGAATGACTCAAGTCTGGACCTGGGACCCACTGCAGATTATGTTTTCTGACTTAACT
GAGAAGGCAGGTTCCATTGAAGACACCAGCCAGGCTCAAGAGCTGCCAAACCTCCCCCTCTCCCTTGCCCAAGATG
AATCTGGTTGAGCCTCCCTGGCATATGCCTCCAGAGAGGAGGAAGAAGAGGAAGAGGAAGAGGAGGAGAGGGAG
AAGGAAGAGGTAGAGAAACAAGAGGAGGAGGAAGAGGAGGAGCTGCTCCCTGTGAATGGATCCCAAGAAGAAGCC
AAGCCTCAGGTCCGTGACTTTTTCTCTCACCAGCAGCAGCCAGACCCCAGGGGCCACCAAAAGCAGGCATGAAGAC
TCCGGGGACCAGGCCTCATCAGGTGTGGAGGTGGAGAGCAGCATGGGGCCCAGCTTGCTGCTGCCTTCAGTCACC
CCAACTACAGTGACTCCGGGGGACCAGGACTCCACCAGCCAAGAGGCAGAGGCCACAGTGCTGCCAGCTGCAGGG
CTTGGGGTAGAGTTCGAGGCTCCTCAGGAAGCAAGCGAGGAAGCCACTGCAGGAGCAGCTGGTTTGTCTGGCCAG
CACGAGGAGGTGCCGGCCTTGCCCTTCAATCCCTCAAACCACAGCTCCAGTGGGGCCGAGCACCCAGATGAAGAT
CCCCCTGGCTCTAGAACCTCAGCCTCTTCCCCACTGGCCCTGGAGACATGGAAGTACACCTTCTCTGCTACC
TTGGGACAAGAAGATCTCAACCAGCAGCTCCTAGAAGGGCAGGCAGCTGAAGCTCAATCCAGGATACCCCTGGGAT
TCTACGCAGGTGATCTGCAAGGACTGGAGCAATCTGGCTGGGAAAACTACATCATTCTGAACATGACAGAGAAC
ATAGACTGTGAGGTGTTCCGGCAGCACCGGGGGCCACAGCTCCTGGCCCTGGTGGAAGAGGTGCTGCCCCGCCAT
GGCAGTGGCCACCATGGGGCCTGGCACATCTCTCTGAGCAAGCCCAGCGAGAAGGAGCAGCACCTTCTCATGACA
CTGGTGGGCGAGCAGGGGGTGGTGCCCACTCAAGATGTCCTTTCCATGCTGGGTGACATCCGCAGGAGCCTGGAG
GAGATTGGCATCCAGAACTATTCCACAACCAGCAGCTGCCAGGCGCGGGCCAGCCAGGTGCGCAGCGACTACGGC
ACGCTCTTCGTGGTGCTGGTGGTCATTGGGGCCATCTGCATCATCATCATTGCGCTTGGCCTGCTCTACAACTGC
TGGCAGCGCCGGCTGCCCAAGCTCAAGCACGTGTCGCACGGCGAGGAGCTGCGCTTCGTGGAGAACGGCTGCCAC
GACAACCCACGCTGGACGTGGCCAGCGACAGCCAGTCGGAGATGCAGGAGAAGCACCCACGCTGAACGGCGGC
GGGGCCCTCAACGGCCCGGGGAGCTGGGGGGCGCTCATGGGGGGCAAGCGGGACCCCGAGGACTCGGACGTGTTC
GAGGAGGACACGCACCTGTGAGCGCAGCCGAGGCGCAGGCCGAGTGGGCGGCCAGGACCAAGCGAGGTGGACCCC
GAAACGGACGGCCCGGAGCCCGCACCAGCCCCGCGCCTACCCGGGGCCGCCCCGCGGCCTGGCCCTCGGCGCGGG
CTCCTTCCCGCTTCCCCCGACTTCACACGGCGGCTTCGACCAACTCCCTCACTCCCCGCCGAGGGGCAGGCCTC
AAAGCCCGCCTTGCCCCCGCTTTCCCGCCCTGAACCCCGGCCCGCGGGCGGGCGGCGCTTCTGCGCCCC
GGGACTCAATTAAACCCGCCCGGAGACCACGCCGGGCCAGCG

1324/6881
FIGURE 1232

ATTTTACCTGATGCTATGAGAGAATCATATTGAAGATGAAATGTCTAATATATAATGTATATTTTAAAGCAGAGA
CTATTTTGGTGGATAGGTGGGAGGGAGCAAGGGGAGTTTGAGGGAATCAGAGCTTGATGCTACTGTACAGAACTG
GACAGGTTGGGCCGGCAGTGGTGGGGCCAGAGGGCTCTGTGCTCTAGGAGCTAAGCCAGCAGCCCCGAGAGGGG
ACTTGGCTGGGCCTTTTCTATGGGCAAGGCCAGTGCTCTTCTGCCCCACCAGGGACCATGGAGCAGTGGCACCC
TATGGGGCTATGATCCCTAGGCCTGGGCCTGGGCCTGCCT**ATG**GGCCAGAGCTACCCTGGGAGTGTCAGTGCTAG
CAGCACAGCTACCTCTGGTGGCAGGAGAAGAGAGGGCCAGCACAGCAGCAGGCCAGGCCTTCTGTCCAGGTCTG
CATGGAGCACTCGGTGACCCAGAGCAGGGACTGGAGGCACCCCCAGCCCTGCCCCAGGCCACAGCAGGACAGGCC
GGGACAGGCCTCACCCAAGGCCAAGGCTGGCATCAGCCAATCATTAGAGCTGAGGCCCTGGGCCTAGCCTGCCC
TTCTCAGGTGCCAATACCACCCCAGCCCTGCCCTTGGCCTCACTTTTTCCCAGCAATAAGTGGGGTTTACCAACC
GCCTCGGGAATACTTTCCCTTCTAAATGGGACTTGCTGTTACCTCAGGAGGCTCCTTAGTGCAATATGACCCCT
GGTCAGGGCTTTGCCACCGTTGAAGCCCTGCAGAAGGTGCAATGTAGGGGTTCTGGGGCCACAGAGGAGAGGCCA
CTTCCCACAGGACCCCCAACAT**TGA**AGTCTAGGCCTCAGGGGCTCCCGCCCTTCTTCTCCAGCAGCGGGAAGT
CCACTGCTCTCCAGGCCCTGTTCTGGAGGCTAACCTTGGTTTCTGGAGAGTGTGCCCTCCACCCTCCCTCCAG
CAGCCCTGATCACACCATGAGAGCCAGGAACGGGTACCCCTGCTGAAGATCACTCTGTGCCCTGGGGGAGGAGCC
AAGCCCTCACCCACAAGGGGCAGGTGGGGGCTTGTTGCTGACCCGGCCCAAGTCCCCACAGAGCACCTTCTGT
AGCTCCAGCTTGCTCCTGG

1325/6881
FIGURE 1233

MAQSYPGSVSASSTATSGGRRREAQHSSRPGLPVQVCMEHSVTQSRDWRHPQPCPRPQQDRPGQASPKAKAGISQ
SFRAEALGLACPSQVPIPPQPCPWPFFPAISGVHHPPREYFLLNGTCCYLRRLLSANMTLVRALPPLKPCRRC
NVGVLGPQRRGHFPPGPPT

1326/6881
FIGURE 1234

CTGCAGACGAGGCAGGCGGAAGAGGCGGGACTTCGCGGGTGACGTCATCGGGGCGCCGGAGGCCCGGGGCGCCTG
GGAATTTGAAGCAAACAGGCAGCGCGGACAATGGCGGTCGCTCGTGACGCTTTGGGGCCATTGGTGACGGGTCT
GTACGACGTGCAGGCTTTCAAGTTTGGGGACTTCGTGCTGAAGAGCGGGCTTTCTCCCCATCTACATCGATCT
GCGGGGCATCGTGTCTCGACCGGTCTTCGTGAGTCAGGTTGCAGATATTTTATTCCAACTGCCCAAATGCAGG
CATCAGTTTTGACACCGTGTGTGGAGTGCCTTATACAGCTTTGCCATTGGCTACAGTTATCTGTTCAACCAATCA
AATCCAATGCTTATTAGAAGGAAAGAAACAAAGGATTATGGAAC TAAGCGTCTTGTAGAAGGAATATTAATCC
AGGAGAAACCTGTTTAAATCATTGAAGATGTTGTACCAGTGGATCTAGTGTTTTGGAACTGTTGAGGTTCTTCA
GAAGGAGGGCTTGAAGGTCAGTGATGCCATAGTGCTGTTGGACAGAGAGCAGGGAGGCAAGGACAAGTTGCAGGC
GCACGGGATCCGCCTCCACTCAGTGCTGTACATTGTCCAAATGCTGGAGATTCTCGAGCAGCAGAAAAAGTTGA
TGCTGAGACAGTTGGGAGAGTGAAGAGGTTTATTACAGGAGAATGTCTTTGTGGCAGCGAATCATAATGGTTCTCC
CCTTTCTATAAAGGAAGCACCCAAAGAACTCAGCTTCGGTGACGTGCAGAGCTGCCCAGGATCCACCCAGTTGC
ATCGAAGCTTCTCAGGCTTATGCAAAAGAAAGGAGACCAATCTGTGTCTATCTGCTGATGTTTCACTGGCCAGAGA
GCTGTTGCAGCTAGCAGATGCTTTAGGACCTAGTATCTGCATGCTGAAGACTCATGTAGATATTTTGAATGATTT
TACTCTGGATGTGATGAAGGAGTTGATAACTCTGGCAAATGCCATGAGTTCTTGATATTTGAAGACCGGAAGTT
TGCAGATATAGGAAACACAGTGAAAAAGCAGTATGAAGGAGGTATCTTTAAATAGCTTCCTGGGCAGATCTAGT
AAATGCTCACGTGGTGCCAGGCTCAGGAGTTGTGAAGGCCTGCAAGAAGTGGGCCTGCCTTTGCATCGGGGGTG
CCTCCTTATTGCGGAAATGAGCTCCACCGGCTCCCTGGCCACTGGGGACTACACTAGAGCAGCGGTTAGAATGGC
TGAGGAGCACTCTGAATTTGTTGTTGGTTTTATTTCTGGCTCCCGAGTAAGCATGAAACCAGAATTTCTTCACTT
GACTCCAGGAGTTCAGTTGGAAGCAGGAGGAGATAATCTTGGCCAACAGTACAATAGCCCACAAGAAGTTATTGG
CAAACGAGGTTCCGATATCATCATTTGTAGGTCGTGGCATAATCTCAGCAGCTGATCGTCTGGAAGCAGCAGAGAT
GTACAGAAAAGCTGCTTGGGAAGCGTATTTGAGTAGACTTGGTGTTTGAGTGCTTCAGATACATTTTTCAGATAC
AATGTGAAGACATTGAAGATATGTGGTCCTCCTGAAAGTCACTGGCTGGAAATAATCCAATTATTCCTGCTTGGA
TTCTTCCACAGGGCCTGTGTAAGAATGGGTTCTGGAGTTCTCATGGTCTTTAGGAAATATTGAGTAATTTGTAAT
CACCGCATTGATACTATAATAAGTTCATTCTTAAGCTTGCTTTTTTTGAGACTGGTGTTTGTTAGACAGCCACAG
TCCTGTCTGGGTTAGGGTCTTCCACATTGAGGATCCTTCTATCTCTCCATGGGACTAGACTGCTTTGTTATTC
TATTTATTTTTTAAATTTTTTTTCGAGACAGGATCTCACTCTGTTGCCAGGATGGAGTGCAGTGGTGAGATCACGG
CTCATTGCAGCCTCGACCTCCAGGTGATCCTCCACCTCAGCTTCCAGATTAGCTGGTGCTATAGGCATGCACC
ACCACGTCCATCTAAATTTCTTTATTATTTGTAGAGATGAGGTCTTGCCATGTTACCCAGGCTGGTCTCAACTCC
TGGGCTCAAGCGATCCTCCTGCCTCAGTCTCTCAAAGTGCTGGGATTACAGGTGTGAGCCACTGTGCCAGCCTA
ATTGCAGTAAGACAAAAATTTCTAGGGCACCAAGAGGCTAAAGTCAGCACAGCTTTTCTTGTCCTGTATT

1327/6881
FIGURE 1235

CTCGGGTCTGGTGGCTGCCGGCCCTGCGGCATCTCGCC**ATC**GGGAGCACGGAGAGCAGCGAGGGCCGCAGGGTGT
CCTTCGGAGTGGACGAGGAGGAGCGGGTCCGGGTGCTGCAGGGTGTCCGGCTGTCTGAAAACGTGGTGAACCGCA
TGAAGGAGCCCAGCTCTCCACCCCTGCTCCACATCTTCTACCTTTGGCCTTCAAGATGGCAACTTGAGAGCCC
CTCACAAAGAATCCCACTGCCCAGGTGCGGGGAGCAGTGGTGGCCAGCAGCCCTCAGGGATGAAGGAGGGTGTCA
AGAGGTATGAACAGGAGCATGCTGCTATCCAGGATAAGCTCTTCCAGGTGGCAAAGAGGGAAAGAGAGGCTGCCA
CCAAGCACTCCAAGGCATCCCTGCCCACGGGCGAAGGCAGCATCAGCCATGAGGAGCAGAAGTCAGTCCGGCTGG
CCAGGGAGCTGGAGAGCAGAGAGGCAGAGCTAAGACGCCGTGACACCTTCTACAAGGAGCAGCTGGAGCGTATTG
AGAGGAAGAATGCTGAGATGTATAAACTGTCTTCAGAGCAATTCCATGAGGCAGCCTCAAAGATGGAGAGCACAA
TAAAGCCCCGCAGGGTGGAGCCCGTCTGCTCAGGGTTGCAGGCCCAGATTCTCCACTGCTACCGAGATCGCCCGC
ATGAGGTGCTGCTGTGCTCGGACCTGGTCAAGGCATACCAGCGCTGCGTGAGCGCCGCCACAAGGGCT**TG**AGGAG
CAGACATCATTCCCTGCCCTGGCAGTGAAGTGGAGCCCTGAAGAAGGGACCAATCATGGGACCACAGCCACTGTG
CCCTGCCGTTTCTGCTGGGCCCCTGCATATGCCCTGAGCCTGGGGCTGCCACGTGTTTAGGAAACAAAGTATG
CGCTACTGTCTGAAAACAAATAAAGCAGATGCCTTTGTTTTTCAGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAA

1328/6881
FIGURE 1236

MGSTESSEGRRVSEFGVDEEERVRLQGVRLSENVVNRMKPSSPPPAPTSSTFGLQDGNLRAPHKESTLPRSGSS
GGQQPSGMKEGVKRYEQEHAAIQDKLFQVAKREREAATKHSKASLPTGEGSISHEEQKSVRLARELESREAELRR
RDTFYKEQLERIERKNAEMYKLSSEQFHEAASKMESTIKPRRVEPVCSGLQAQILHCYRDRPHEVLLCSDLVKAY
QRCVSAAHKG

1329/6881
FIGURE 1237

GAGAGTGGCCAGCGAGGGCAGCGTTTCGCCGCCCTCAGGCCCCGTCCCGGCCCGCAGCCGCCTGCGTTTCGGTT
TGTGAGCAGGCCCCGGCCGGGCCAGGAGCGAGAGCGAGACTCTGGAGCGGTCCCGCCGCAGTCGCCCGGGCCGGG
AAAGGCGGGCGATGCCCCCAACCGCCGCTCGGGCCATGTCCGAGGGGCGCGCTGTTGTGCGCCGCCGGGGCGCCG
TGCCCCGCTGTGCTCCCCCGGGCCCAGCCGCTCGTCCGAGGCGCGAGGAGCTGCGCCGCCACCTCGTGGGCCT
CATCGAGCGCAGCCGGGTGGTGATCTTCAGCAAGAGCTACTGTCCCCATAGTACTCGGGTGAAAGAACTCTTTTC
TTCTTTGGGAGTCTGAATGTAATGTCTTGGAACTTGATCAAGTTGATGATGGGGCCAGGGTTCAAGAAGTGCTGTC
AGAAATCACTAATCAGAAAACCTGTGCCCAATATTTTCGTGAATAAAGTGCATGTAGGTGGATGTGACCAAACCTTT
CCAGGCATATCAGAGTGGTTTTGTTACAGAAGCTCCTTCAGGAAGATTTGGCATATGATTATGATCTCATCATCAT
CGGTGGTGGTTCTGGAGGCCCTTTCATGTGCGAAGGAAGCTGCCATTTTGGGAAAGAAAGTTATGGTGCTAGACTT
TGTTGTCCCGTCACCTCAGGGCACATCCTGGGGTCTTGGTGGCACTTGTGTAAATGTAGGTTGTATTCTTAAGAA
ATTGATGCATCAGGCTGCCCTTTTGGGGCAGGCATTATGTGACTCAAGGAAATTTGGCTGGGAATATAATCAACA
AGTGAGGCACAACCTGGGAGACAATGACAAAAGCGATTGAGAACCACATCAGCTCTCTAAACTGGGGCTACAGGTT
GTCTCTGAGGGAAAAGGCTGTGGCCTATGTCAATTCCTATGGAGAATTTGTTGAACATCATAAAAATAAGGCAAC
CAATAAAAAAGGACAGGAGACTTATTACTGTCTGCACAGTTTGTCTATAGCAACGGGTGAAAGGCCACGGTATTT
AGGAATCCAAGGAGATAAAGAATACTGTATTACTAGTGATGACCTTTTTTCTCTGCCTTATTGCCCTGGCAAAAC
ATTAGTGGTGGGTGCCTCTTATGTTGCCCTGGAGTGTGCAGGGTTTCTGGCTGGCTTTGGCCTAGATGTCACAGT
TATGGTACGCTCAATCCTTCTCCGTGGCTTCGACCAAGAAATGGCAGAAAAAGTGGGTTCCTACATGGAGCAGCA
TGGTGTGAAGTTCCTACGGAAATTCATACCTGTGATGGTTCAACAGTTGGAGAAAGGTTACCTGGAAAGCTGAA
AGTGTGGCTAAATCCACTGAAGGAACAGAAACAATTGAAGGAGTCTATAACACAGTTTTGTTAGCTATTGGTTCG
TGACTCCTGTACAAGGAAAATAGGCTTGGAGAAGATTGGTGTCAAAATTAATGAGAAGAGTGGAAAAATACCTGT
AAATGATGTGGAACAGACCAATGTGCCATATGTCTATGCTGTTGGTGATATTTTGGAGGATAAGCCAGAGCTCAC
TCCTGTGCGCCATACAGTCAGGCAAGCTGCTAGCTCAGAGACTTTTTGGGGCCTCTTTAGAAAAGTGTGATTATAT
TAATGTTCCGACTACAGTGTTTACTCCTCTGGAGTATGGTTGCTGTGGATTATCTGAAGAGAAAGCTATTGAAGT
ATATAAAAAAGAGAATCTAGAAAATATATCATACTTTGTTCTGGCCTCTTGAATGGACAGTAGCTGGCAGAGAGAA
CAACACTTGTTATGCAAAGATAATCTGCAATAAATTCGACCATGATCGGGTGATAGGATTTTCATATTCTTGGACC
AAACGCCCGGTGAGGTTACCCCAAGGATTTGCAGCTGCAATGAAATGTGGGCTCACAAAACAGCTACTTGATGACAC
CATTGGAATTCACCCACATGTGGGGAGGTGTTACGACTTTGGAAATCACAAAGTCGTCAGGACTAGACATCAC
TCAGAAAGGCTGCTGAGGCTAGGCCTGCTGCTGTTTAGTTCTCCTTGTTCATATTCTCATTCTCTCAAAGATAAG
AATGCTCTCGGATAAAATGAGCCTGTGCTCATGACAGCTGCTCTGTTACTCAGGGACCAGTGCAGGGCTGTCTTA
CGACACTTAGATGAGAAAGTAGACAAGGAAAGAGGACAGCAGTGGGCATCTGCCTTGTGGTCTTGCTGACAGCGA
GAAGCAGTGGGACTGCTTCCCTGACGCCTTAGCTTGGAGCCCCGTTATGAGGTGAGCCAAGGCTGACTCTCGCAA
GCCAGGACTGAGCTTCCCTCGGAAAGACCTTTGAGTGGCACCATTACCTAAGTTAGCTTTTCTGGTCGCTATTG
TTTTTATCCCCTTTGCTTTGTTGTTTCTGTGAAAATATATTTTCAGTTAAGAAATGCTATAAAGTAGTGGTTTTTC
TAGTGCGTGGGCCTAGAATTCACACATGCTCACTGGTGAACAGTGTCTGTGGGCTGCTGTGGGCTGCATTTGGAT
AGCTGTCTGCATTAGCAGGAAGCTGTACACACTGTGTAGGGTTAGTCATCTCTTTTCTTTTTTGAGGCACATTTA
ACCTACTGTCAAAACGCTGACTCATGCTTCACCTCACACTCACTACTTGGTGGTGATAACCTTGAAGCTATTCT
CCCCTAATTAATATCTCGAGACTGAGCAAAATATCTCATGTAAGATAAAAGTACTTGAATTGCTTTTTTCATGTTT
ATCTTAATAGTATTATTTCCAAAAGTTTTTAATACTGTATTATGTGAAATCTAACTAATTTATCTGTGAAATAAT
TCCATCACAGTCTGTTTAAATGATGATAAAGTTCATAAATGAATACAGGT

1330/6881
FIGURE 1238A

AGCGATCCGAGGCCCGGCCCGGCCCGGCCCGGCCCGGCCCGCTTGCCGCCGGGCTAGCACTGACGTGT
CTCTCGGCGGAGCTGCTGTGCAGTGGAACGCGCTGGGCCGCGGGCAGCGTCGCCTCACGCGGAGCAGAGCTGAGC
TGAAGCGGGACCCGGAGCCCGAGCAGCCGCGGCC**ATCG**CAATCAAATTTCTGGAAGTCATCAAGCCCTTCTGTGT
CATCCTGCCGGAATTCAGAAGCCAGAGAGGAAGATTAGTTTAAGGAGAAAGTGCTGTGGACCGCTATCACCCCT
CTTTATCTTCTTAGTGTGCTGCCAGATTCCCCTGTTTGGGATCATGTCTTCAGATTACAGCTGACCCCTTCTATTG
GATGAGAGTGATTCTAGCCTCTAACAGAGGCACATTGATGGAGCTAGGGATCTCTCCTATTGTACGTCTGGCCT
TATAATGCAACTCTTGGCTGGCGCCAAGATAATTGAAGTTGGTGACACCCCAAAGACCGAGCTCTCTTCAACGG
AGCCCAAAGTTATTTGGCATGATCATTACTATCGGCCAGTCTATCGTGTATGTGATGACCGGGATGTATGGGA
CCCTTCTGAAATGGGTGCTGGAATTTGCCTGCTAATCACCATTACAGCTCTTTGTTGCTGGCTTAATTGTCCTACT
TTTGGATGAACTCCTGCAAAAAGGATATGGCCTTGGCTCTGGTATTTCTCTCTTCATTGCAACTAACATCTGTGA
AACCATCGTATGGAAGGCATTACAGCCCCACTACTGTCAACACTGGCCGAGGAATGGAATTTGAAGGTGCTATCAT
CGCACTTTTCCATCTGCTGGCCACACGCACAGACAAGGTCCGAGCCCTTCGGGAGGCGTTCTACCGCCAGAATCT
TCCCAACCTCATGAATCTCATCGCCACCATCTTTGTCTTTGCAGTGGTCATCTATTTCCAGGGCTTCCGAGTGGA
CCTGCCAATCAAGTCGGCCCCGCTACCGTGGCCAGTACAACACCTATCCCATCAAGCTCTTCTATACGTCCAACAT
CCCCATCATCCTGCAGTCTGCCCTGGTGTCCAACCTTTATGTCTCTCCCAAATGCTCTCAGCTCGCTTCAGTGG
CAACTTGCTGGTCAGCCTGCTGGGCACCTGGTCCGACACGTCTTCTGGGGGCCAGCACGTGCTTATCCAGTTGG
TGGCCTTTGCTATTACCTGTCCCTCCAGAATCTTTTGGCTCCGTGTTAGAAGACCCGGTCCATGCAGTTGTATA
CATAGTGTTTCATGCTGGGCTCCTGTGCATTCTTCTCCAAAACGTGGATTGAGGTCTCAGGTTCTCTGCCAAAGA
TGTTGCAAAGCAGCTGAAGGAGCAGCAGATGGTGATGAGAGGCCACCGAGAGACCTCCATGGTCCATGAACTCAA
CCGGTACATCCCCACAGCCGCGGCCCTTTGGTGGGCTGTGCATCGGGGCCCTCTCGGTCTGGCTGACTTCCTAGG
CGCCATTGGGTCTGGAACCGGGATCCTGCTCGCAGTCACAATCATCTACCAGTACTTTGAGATCTTCGTAAAGGA
GCAAAGCGAGGTTGGCAGCATGGGGGCCCTGCTCTTCT**TGAG**CCCGTCTCCCGGACAGGTTGAGGAAGCTGCTCCA
GAAGCGCTCGGAAGGGGAGCTCTCATCATGGCGCGTGCTGCTGCGGCATATGGACTTTTAATAATGTTTTTGAA
TTTCGTATTCTTTTCACTTCCACTGTGTAAAGTGCTAGACATTTTCCAATTTAAAATTTTGCTTTTTATCCTGGCAC
TGGCAAAAAGAACTGTGAAAGTGAAATTTTATTACAGCCGACTGCCAGAGAAGTGGAATGGTATAGGATTGTCCC
CAAGTGTCATGTAACCTTTTGTTTTAACTTTGCACCTTCTCAGTGCTGTATGCGGCTGCAGCCGTCTCACCTGT
TTCCCCACAAAGGGAATTTCTCACTCTGGTTGGAAGCACAAACACTGAAATGTCTACGTTTCATTTTGGCAGTAG
GGTGTGAAGCTGGGAGCAGATCATGTATTTCCCGGAGACGTGGGACCTTGCTGGCATGTCTCCTTACAAATCAGG
CGTGGGAATATCTGGCTTAGGACTGTTTCTCTCTAAGACACCATTTGTTTTCCCTTATTTTAAAAGTGATTTTTTT
AAGGACAGAATCTTCTCCAAAAGAGAGGGATGGCTTTCCAGAAGACACTCCTGGCCATCTGTGGATTGTCTGT
GCACCTATTGGCTCTTCTAGCTGACTCTTCTGGTTGGGCTTAGAGTCTGCCTGTTTCTGCTAGCTCCGTGTTTAG
TCCACTTGGGTATCATGACTCTGCCAAGCTGAGCCTGGCCAAGCTAGGTGGACAGACCCCTGCAGTGATGTCCGTT
TGTCCAGATTCTGCCAGTCATCACTGGACACGTCTCCTCGCAGCTGCCCTAGCAAGGGGAGACATTGTGGTAGCT
ATCAGACATGGACAGAACTGACTTAGTGCTCACAAGCCCTACACCTTCTGGGCTGAAGATCACCCAGCTGTGT
TCAGAATTTTCTTACTGTGCTTAGGACTGCACGCAAGTGAGCAGACACCACCGACTTCCTTTCTGCGTCACCAGT
GTCGTACGACAGAGAGAGGACAGCACAGGCTCAAGGTTGGTAGTGAAGTCAGGTTCCGGGTGCATGGGCTGTGGTG
GTGTTGATCAGTTGCTCCAGTGTTTGAAATAAGAAGACTCATGTTTATGTCTGGAATAAGTTCTGTTTGTGCTGA
CAGGTGGCCTAGGTCTGGAGATGAGCACCTCTCTTGGCCTTTAGGGAGTCCCCTCTTAGGACAGGCACCTGCC
CAGCAGCAAGGGCAGCAGAGTTGGGTGCTAAGATCCTGAGGAGCTCGAGGTTTCGAGCTGGCTTTAGACATTGGT
GGGACCAAGGATGTTTTGCAGGATGCCCTGATCCTAAGAAGGGGGCCTGGGGGTGCGTGACGCTGTCTGGGGAGA
CCCCACTCTGACAGTGGGCACACGGCAGCCTGCAAAGCACAGGGCCACCGCCACAGCCCGGCAGAGGGGGCACACT
CTGGAGACCTTGCTGGCAGTGCTAGCCAGGAAACAGAGTGACCAAGGGACAAGAAGGGACTTGCCATAAGCCACC
CAGCAACTCAGCAGCAGAACCAAGATGGGCCCCAGGCTCCTCCATATGGCCCAGGGCTTACCACCCCTATCACAG
TGGCCTTGCTTAGACCCAGTCTGAGCAGGGGAGAGGCTCTTGAGACCTGATGCCCTCCTACCCACATGGTTCTC
CCACTGCCCTGTCTGCTCTGCTGCTACAGAGGGGCAGGGCCTCCCCAGCCACGCTTAGGAATGCTTGCTCTG
GCAGGCAGGCAGCTGTACCAAGCTGGTGGGCAGGGGGCTGGAAGGCACCAGGCCTCAGGAGGAGCCCCATAGTC
CCGCTGACGCTGTAAACATCGGCTGGGCCCTGCAAGGCCACACTCACGCCCTGTGGGTGATGGTCACGGTGG
GTGGGTGGGGGCTGACCCAGCTTCCAGGGGACTGTCACTGTGGACGCCAAAATGGCATAACTGAGATAAGGTGA

1331/6881
FIGURE 1238B

ATAAGTGACAAATAAGCCAGTTTTTTACAAGGTAAAAAAAAAAAAAAAAAAAAA

1332/6881
FIGURE 1239

MAIKFLEVIKPFVCVILPEIQKPERKIQFKEKVLWTAITLFI FLVCCQIPLFGIMSSDSADPFYWMRVILASNRGT
LMELGISP I VTSGLIMQLLAGAKIIEVGDTPKDRALFNGAQLFGMIITIGQSIVYVMTGMYGDPSEMGAGICLL
ITIQLFVAGLIVLLLLDELLQKGYGLGSGISLFIATNICETIVWKAFSPTTVNTGRGMEFEGAIIALFHLLATRTD
KVRALREAFYRQNLPLNMNLIATIFVFAVVIYFQGFRVDLPIKSARYRGQYNTYPIKLFYTSNIP I ILQSALVSN
LYVISQMLSARFSGNLLVSL LGTWSDTSSGGPARAYPVGGLCY YLSPPESFGSVLEDPVHAVVYIVFMLGSCAFF
SKTWIEVSGSSAKDVAKQLKEQQMV MRGHR ETS MVHELNR YIPTAAAFGGLCIGALSVLADFLGAIGSGTGILLA
VTIIYQYFEIFVKEQSEVGSMGALLF

1333/6881
FIGURE 1240

ATGAAAGATTGAGGAGGTGAAGAGCACTACGAAGACGCAGCGCATCGCCTCCCACAGCCACGTGAAAGGGCTGGGG
CTGGACGAGAGCGGCTTGGCCAAGCAGGCGGCCTCAGGGCTTGTGGGCCAGGAGAACGCGCGAGAGGTGTGGCCA
GTGGACCAGGGAGTTGGGGGCTGCAAGCAGGGCTGCTGCGGCGAGAGAGCTGCTGAAGTCGGGCCTGCAGGTGCT
CCAGGTCAGCGGGCGACTTTGGCCGCTGCAGAGACCGAGATACGCGGGGTAACAGCCCGTTCCGGAGCCGGTCAT
CAGGCGCCAAGCCCCGCTGGGCTCCTCGCAGCCGCGGGACCTTTCTCCGCCCTTCCCGAGGCTGAGTTTCCTGAA
CGGGAAGCTGCCGGCCCGCGGGGCAGCCGGGAGCAGCCAGGGCGTGAGGACGTGGGTTCCCGTCACCCCCGGCTT
GGAACAGCAGCGCCGCAACAACCGCTGGCGTTTCATCGAGCCTCTCAGCAGCCCTGCGAGGCGATCCCGGGGAGAA
TCCCACGCCACAGCCGAGGAAACTGAGGCAGGCAGGGTGACACACAGCCCAGTAGTGGCGGGCGGGCGCCCAGGC
TGCCACCGCGCTGAGGACCGGCCCTCTGCCAGCCGGGAGGCGTGGGGCAGGACAGCCGCGCTCTCGCCAGGGCC
CAGAGCCCCACTTTGCCAAGGAGCTGTCGCTGGAGCGGTGACTTTGTTTCAGGGCCGAGAACCGGAGGAGGAGGCC
AGACTTGCTGCTGGGCAGCTGGCACATGGGACATGGGGTGTATGACTCCAGCATTTATGGAGCGCCTGCTGTGT
GCTCTGCAGGTGAGCAATGTGAGGCTCAGAGAAGAGAAACAGAAAGCCCGGAGGCTTGAGTGGGTCAGACACCCA
TCAGGAGCTTGGCATGAGTATGACAGCTCCTTGACGCAAAGTCCAGGGGGCATGAGTGCTGGGGCCATTGCAGGC
ACCAGGACCCAAGCCTAG

1334/6881
FIGURE 1241

MVDRLRPVKFPLL MGQPEAQGPAGAPGORATLAAAETEIRGVTARSGAGHQAPSPAGLLAAAGPFSALPEAE
FPEREAAGPRGSREQPGREDVGSRHPRLGTAAPQQPLAFIEPLSSPARRSRGESHATAEETEAGRVTHSPVVAGG
RPGCHRAEDRPLCQPGGVGQDSRALARAQSPTLPRSCRWSGDFVQGREPEEEARLAAGQLAHGTWGVMTPAFMER
LLCALQVSNVRLREEKQKARRLEWVRHPSGAWHEYDSSLTQSPGGMSAGAIAGTRTQA

1335/6881
FIGURE 1242

AGGTAAAGGGAGAAGATGAGGAAGAGAACAATTTGGAAGTACGTGAAACCAAATTAAGGGTAAAAGTGGGAGAT
TCTTCACAGTCAAGCTCCCAGTTGCTCTTGATCCTGGGGCCAAGATTTTCAGTCATTGTGGAAACAGTCTACACCC
ATGTGCTTCATCCATATCCAACCCAGATCACCCAGTCAGAGAAACAGTTTGTGGTGTGTTGAGGGGAACCATTATT
TCTACTCTCCCTATCCAACGAAGACACAAACCATGCGTGTGAAGCTTGCCTCTCGAAATGTGGAGAGCTACACCA
AGCTGGGGAACCCACGCGCTCTGAGGACCTACTGGATTATGGGCCTTTTCAGAGATGTGCCTGCCTATAGTCAGG
ATACTTTTAAAGTACATTATGAGAACAACAGCCCTTTCTGACCATCACCCAGCATGACCCGAGTCATTGAAGTCT
CTCACTGGGGTAATATTGCTGTGGAAGAAAATGTGGACTTAAAGCACACAGGAGCTGTGCTTAAGGGGCCTTTCT
CACGCTATGATTACCAGAGACAGCCAGATAGTGGAATATCCTCCATCCGTTCTTTAAGACCATCCTTCCTGCTG
CTGCCCAGGATGTTTATTACCGGGATGAGATTGGCAATGTTTCTACCAGCCACCTCCTTATTTTGGATGACTCTG
TAGAGATGGAAATCCGGCCTCGCTTCCCTCTCTTTGGCGGGTGGGAAGACCCATTACATCGTTGGCTACAACCTCC
CAAGCTATGAGTACCTCTATAATTTGGGTGACCAGTATGCACTGAAGATGAGGTTTGTGGACCATGTGTTTGATG
AACAAGTGATAGATTCTCTGACTGTGAAGATCATCCTGCCTGAAGGAGCCAAGAACATTGAAATTGATAGTCCCT
ATGAAATCAGCCGTGCCCCAGATGAGCTGCACTACACCTATCTGGATACATTTGGCCGCCCTGTGATTGTTGCCCT
ACAAGAAAAATCTGGTAGAACAGCACATTTCAGGACATTGTGGTCCACTACACGTTCAACAAGGTGCTCATGCTGC
AGGAGCCCCCTGCTGGTGGTGGCGGCCTTCTACATCCTGTTCTTCACCGTTATCATCTATGTTCCGGCTGGACTTCT
CCATCACCAAGGATCCAGCCGCAGAAGCCAGGATGAAGGTAGCCTGCATCACAGAGCAGGTCTTGACCCTGGTCA
ACAAGAGAATAGGCCTTTACCGTCACTTTGACGAGACCGTCAATAGGTACAAGCAATCCCGGGACATCTCCACCC
TCAACAGTGGCAAGAAGAGCCTGGAGACTGAACACAAGGCCTTGACCAGTGAGATTGCACTGCTGCAGTCCAGGC
TGAAGACAGAGGGCTCTGATCTGTGCGACAGAGTGAGCGAAATGCAGAAGCTGGATGCACAGGTCAAGGAGCTGG
TGCTGAAGTCGGCGGTGGAGGCTGAGCGCCTGGTGGCTGGCAAGCTCAAGAAAGACACGTACATTGAGAATGAGA
AGCTCATCTCAGGAAAGCGCCAGGAGCTGGTCACCAAGATCGACCACATCCTGGATGCCCTGTAGCCCCTGCCCCG
CATCCTCCAGGGGGCCAGGGTGCCTGCACCTTGTCTGTGGCAGGCAGATTGGGTGGTAGTGGGAGGTTGTGCATG
GAGGCCAGTGAAAGCTGACATCTGTAAAAGGCCTTCAAGGAAGAGAAACCAGGCCCTGCGTCAGGCAGTGTGAGT
TTGCCGTTTGTCTTAACTTTCTTTTTTTTTTTTTTTTTTAAAAAAGAAAACCTTTAAAAAACTCCCATTA AAAACA
AAACATCTTTGTGTTTTGAACAAAGGAATTTTCAATATTTGATTGGTATTCTGTTCTGAAGTCTAGGATATTTTT
CAGCCTATAAAGCCCCCTGTTTTATGCCCTTCTAATTCTGATGTTTGGGTATTGTGTGAGTGCATGTGTTTTTTT
TTTTTTTTTTTTTAAAGCGTGTGTGAACAAATGGAAATAAAGCAGGGACTGTG

1336/6881
FIGURE 1243

CTGCTCTTCCCGGTCATGGAGGCGCCAGCCGCCGGCTTGTTTCTGCTCCTGTTGCTTGGGACTTGGGCCCCGGCG
CCGGGCAGCGCCTCCTCCGAGGCACCGCCGCTGATCAATGAGGACGTGAAGCGCACAGTGGACCTAAGCAGCCAC
CTGGCTAAGGTGACGGCCGAGGTGGTCCTGGCGCACCTGGGCGGCGGCTCCACGTCCCAGCTACCTCTTTCCTG
CTGGCTTTGGAGCCTGAGCTCGAGGCCCGGCTGGCGCACCTGGGCGTGCAGGTAAAGGGAGAAGATGAGGAAGAG
AACAATTTGGAAGTACGTGAAACCAAATTAAGGGTAAAAGTGGGAGATTCTTCACAGTCAAGCTCCCAGTTGCT
CTTGATCCTGGGGCCAAGATTTTCAGTCATTGTGGAAACAGTCTACACCCATGTGCTTCATCCGTATCCAACCCAG
ATCACCCAGTCAGAGAAACAGTTTGTGGTGTGTTGAGGGGAACCATTTTCTACTCTCCCTATCCAACGAAGACA
CAAACCATGCGTGTGAAGCTTGCCTCTCGAAATGTGGAGAGCTACACCAAGCTGGGGAACCCACGCGCTCTGAG
GACCTACTGGATTATGGGCCTTTTCAGAGATGTGCCTGCCTATAGTCAGGATACTTTTAAAGTACATTATGAGAAC
AACAGCCCTTTTCCTGACCATCACCAGCATGACCCGAGTCATTGAAGTCTCTCACTGGGGTAATATTGCTGTGGAA
GAAAATGTGGACTTAAAGCACACAGGAGCTGTGCTTAAGGGGCCTTTCTCACGCTATGATTACCAGAGACAGCCA
GATAGTGAATATCCTCCATCCGTTCTTTTAAGACCATCCTTCCTGCTGCTGCCAGGATGTTTATTACCGGGAT
GAGATTGGCAATGTTTCTACCAGCCACCTCCTTATTTTGGATGACTCTGTAGAGATGGAAATCCGGCCTCGCTTC
CCTCTCTTTGGCGGGTGAAGACCCATTACATCGTTGGCTACAACCTCCCAAGCTATGAGTACCTCTATAATTTG
GGTGACCAGTATGCACTGAAGATGAGGTTTGTGGACCATGTGTTTGATGAACAAGTGATAGATTCTCTGACTGTG
AAGATCATCCTGCCTGAAGGAGCCAAGAACATTGAAATTGATAGTCCCTATGAAATCAGCCGTGCCCCAGATGAG
CTGCACTACACCTATCTGGACACATTTGGCCGCCCTGTGATTGTTGCCTACAAGAAAAATCTGGTAGAACAGCAC
ATTAGGACATTGTGGTCCACTACACGTTCAACAAGGTGCTCATGCTGCAGGAGCCCCTGCTGGTGGTGGCGGCC
TTCTACATCCTGTTCTTCACCGTTATCATCTATGTTTCGGCTGGACTTCTCCATCACCAAGGATCCAGCCGCAGAA
GCCAGGATGAAGGTAGCCTGCATCACAGAGCAGGTCTTGACCCCTGGTCAACAAGAGAATAGGCCTTTACCGTCAC
TTTGACGAGACCGTCAATAGGTACAAGCAATCCCGGGACATCTCCACCCCTCAACAGTGGCAAGAAGAGCCTGGAG
ACTGAACACAAGGCCTTGACCAGTGAGATTGCACTGCTGCAGTCCAGGCTGAAGACAGAGGGCTCTGATCTGTGC
GACAGAGTGAGCGAAATGCAGAAGCTGGATGCACAGGTCAAGGAGCTGGTGCTGAAGTCGGCGGTGGAGGCTGAG
CGCCTGGTGGCTGGCAAGCTCAAGAAAGACACGTACATTGAGAATGAGAAGCTCATCTCAGGAAAGCGCCAGGAG
CTGGTCACCAAGATCGACCACATCCTGGATGCCCTGTAGCCCCCTGCCCGCATCCTCCAGGGGGCCCAGGGTGCCT
GCACTTTGCTGTGGCAGGCAGATTGGGTGGTAGTGGGAGGTTGTGCATGGAGGCCAGTGAAAGCTGACATCTGTA
AAAGGCCTTCAAGGAAGAGAAACCAGGCCCTGCGTCAGGCAGTGTGAGTTTGCCGTTTGTCTTAACCTTTCTTTT
TTTTTTTTTTTTAAAAAAGAAAACCTTTAAAAAACTCCCATTA AAAACAAAACATCTTTGTGTTTTGAACAAAGG
AATTTTCAATATTTGATTGTTATTCTGTTCTGAAGTCTAAGATATTTTTCAGCCTATAAAGCCCCCTGTTTTATG
CCCTTCTAATTCTGATGTTTGGGTATTGTGTGAGTGCATGTGTTTTTTTTTTTTTTTTTAAAGCGTGTGTGAACA
AATGAAATAAAGCAGGGACTGTG

1337/6881
FIGURE 1244

GTGAGCGCCAGGAAGGTAGCGAGGCCAGCGTCGCCCCGGGACTCGCTGCTCAAGTCTGTCTATTGCCTGCCGCCA
CATCCATCCTAGCAGGGCCCCGTCGCCCCACCAGGCGGACAAAAGCGGTCCGCTGAACACCATGCGGCCGCTCGGC
GTGCCGCCCAGGCTCTGCTGGTGAGCGCCGCCACCCCGCGCCAGGTCCCGCGAGCCCGCCTGCCGCGCACCTCG
CCCTGCTCCAGCTCTACTCCAGGCCCCGTCGCCCCGGGGCGCCGCCACCGCGCCTCGCTCGGGCCGTTGCCG
TCTGCACCCAGACCCTGAGCCGCCGCCGCCGGCCATGGAGGTGGCGCCCGAGCAGCCGCGCTGGATGGCGCACCC
GGCCGTGCTGAATGCGCAGCACCCCGACTCACACCACCCGGGCCTGGCGCACAACTACATGGAACCCGCGCAGCT
GCTGCCTCCAGACGAGGTGGACGTCTTCTTCAATCACCTCGACTCGCAGGGCAACCCCTACTATGCCAACCCCGC
TCACGCGCGGGCGCGCGTCTCCTACAGCCCCGCGCAGCCCGCCTGACCGGAGGCCAGATGTGCCGCCACACTTG
TTGCACAGCCCCGGGTTTGCCCTGGCTGGACGGGGGCAAAGCAGCCCTCTCTGCCGCTGCGGGCCACCACCACAAC
CCCTGGACCGTGAGCCCCCTTCTCCAAGACGCCACTGCACCCCTCAGCTGCTGGAGGCCCTGGAGGCCACTCTCT
GTGTACCCAGGGGCTGGGGGTGGGAGCGGGGGAGGCAGCGGGAGCTCAGTGGCCTCCCTCACCCCTACAGCAGCC
CACTCTGGCTCCACCTTTTCGGCTTCCACCCACGCCACCCAAAGAAGTGTCTCCTGACCCCTAGCACCACGGGG
GCTGCGTCTCCAGCCTCATCTTCCGCGGGGGGTAGTGCAGCCCCGAGGAGAGGACAAGGACGGCGTCAAGTACCAG
GTGTCACTGACGGAGAGCATGAAGATGGAAAGTGGCAGTCCCCTGCGCCAGGCCTAGCTACTATGGGCACCCAG
CCTGCTACACACCACCCCATCCCCACCTACCCCTCCTATGTGCCGGCGGCTGCCACGACTACAGCAGCGGACTC
TTCCACCCCGGAGGCTTCTTGGGGGGACCGGCCTCCAGCTTACCCCTAAGCAGCGCAGCAAGGCTCGTTCCTGT
TCAGAAGGCCGGGAGTGTGTCAACTGTGGGGCCACAGCCACCCCTCTCTGGCGGGGGACGGCACCGGCCACTAC
CTGTGCAATGCCTGTGGCCTCTACCACAAGATGAATGGGCAGAACCGACCACTCATCAAGCCCAAGCGAAGACTG
TCGGCCGCCAGAAGAGCCGGCACCTGTTGTGCAAATTGTGACGACAACCACCACCTTATGGCGCCGAAACGCC
AACGGGGACCCTGTCTGCAACGCCTGTGGCCTCTACTACAAGCTGCACAATGTTAACAGGCCACTGACCATGAAG
AAGGAAGGGATCCAGACTCGGAACCGGAAGATGTCCAACAAGTCCAAGAAGAGCAAGAAAGGGGCGGAGTGCTTC
GAGGAGCTGTCAAAGTGCATGCAGGAGAAGTCATCCCCCTTCAGTGCAGCTGCCCTGGCTGGACACATGGCACCT
GTGGGCCACCTCCCGCCCTTCAGCCACTCCGGACACATCCTGCCCACTCCGACGCCCATCCACCCCTCCTCCAGC
CTCTCCTTCGGCCACCCCAACCCGTCCAGCATGGTGACCGCCATGGGCTAGGGAACAGATGGACGTCGAGGACCG
GGCACTCCCGGGATGGGTGGACCAAACCCCTTAGCAGCCCAGCATTTCCCGAAGGCCGACACCACTCCTGCCAGCC
CGGCTCGGCCCAGCACCCCTCTCCTGGAGGGCGCCCAGCAGCCTGCCAGCAGTTACTGTGAATGTTCCCCACCG
CTGAGAGGCTGCCTCCGCACCTGACCGCTGCCCAGGTGGGGTTTCTGTCATGGACAGTTGTTTGGAGAACAACAA
GGACAACCTTATGTAGAGAAAAGGAGGGGACGGGACAGACGAAGGCAACCATTTTTAGAAAGGAAAAAGGATTAGG
CAAAAATAATTTATTTTGTCTCTTGTCTTAACAAGGACTTGGAGACTTGGTGGTCTGAGCTGTCCCAAGTCCTCC
GGTTCTTCTCGGGATTGGCGGGTCCACTTGCCAGGGCTCTGGGGGCAGATTTGTGGGGACCTCAGCCTGCACCC
TCTTCTCCTCTGGCTTCCCTCTCTGAAAATAGCCGAACTCCAGGCTGGGCTGAGCCAAAAGCCAGAGTGGCCACGGC
CCAGGGAGGGTGAGCTGGTGCCTGCTTTGACGGGGCCAGGCCCTGGAGGGCAGAGACAATCACGGGCGGTCTGCA
CAGATTCCCAGGCCAGGGCTGGGTACAGGAAGGAAACAACATTTTCTTGAAAGGGGAAACGTCTCCAGATCGC
TCCCTTGGCTTTGAGGCCGAAGCTGCTGTGACTGTGTCCCTTACTGAGCGCAAGCCACAGCCTGTCTTGTGAGG
TGGACCTGTAAATACATCCTTTTTCTGTTAACCTTCAACCCCTCGCCTACTACTCTGAGAC

1338/6881
FIGURE 1245

GTCAAAGTGCATGCAGGAGAAGTCATCCCCCTTCAGTGCAGCTGCCCTGGCTGGACACATGGCACCTGTGGGCCA
CCTCCCGCCCTTCAGCCACTCCGGACACATCCTGCCCCTCCGACGCCCATCCACCCCTCCTCCAGCCTCTCCTT
CGGCCACCCCAACCGTCCAGCATGGTGACCGCCATGGGCTAGGGAACAGATGGACGTCGAGGACCGGGCACTCC
CGGGATGGGTGGACCAAACCTTAGCAGCCCAGCATTTCCCGAAGGCCGACACCACTCCTGCCAGCCCGGCTCGA
CCCAGGGAGAGGCTGTGTCCCTGCTGGGGTCTCAGGTCCAGCTTTACTGTGGCTGTCTGGATCCTTCCCAAGGTA
CAGCTGTATATAAACGTGTCCCGAGCTTAGATTCTGTATGCGGTGACGGCGGGGTGTGGTGGCCTGTGAGGGGCC
CCTGGCCCAGGAGGAGGATTGTGCTGATGTAGTGACCAAGTGCAATATGGGCGGGCAGTCGCTGCAGGGAGCACC
ACGGCCAGAAGTAACTTATTTTGTACTAGTGTCCGCATAAGAAAAAGAATCGGCAGTAT

1339/6881
FIGURE 1246

GGCACGAGGATAAAGCCTGAGGCGGCGGCAGCGGCGGAGTTGGCGGCTTGGAGAGCTCGGGAGAGTTCCCTGGAA
CCAGAACTTGGACCTTCTCGCTTCTGTCTCCGTTTAGTCTCCTCCTCGGCGGGAGCCCTCGCGACGCGCCCGGC
CCGGAGCCCCCAGCGCAGCGGCCGCGTTTGAAGGATGACCTCTAGGAAGAAAGTGTTGCTGAAGGTTATCATCCT
GGGAGATTCTGGAGTCGGGAAGACATCACTCATGAACCAGTATGTGAATAAGAAATTCAGCAATCAGTACAAAGC
CACAATAGGAGCTGACTTTCTGACCAAGGAGGTGATGGTGGATGACAGGCTAGTCACAATGCAGATATGGGACAC
AGCAGGACAGGAACGGTTCCAGTCTCTCGGTGTGGCCTTCTACAGAGGTGCAGACTGCTGCGTTCTGGTATTTGA
TGTGACTGCCCCCAACACATTCAAAACCCTAGATAGCTGGAGAGATGAGTTTCTCATCCAGGCCAGTCCCCGAGA
TCCTGAAAACCTTCCCATTTGTTGTGTTGGGAAACAAGATTGACCTCGAAAACAGACAAGTGGCCACAAAGCGGGC
ACAGGCCTGGTGCTACAGCAAAAACAACATTCCCTACTTTGAGACCAGTGCCAAGGAGGCCATCAACGTGGAGCA
GGCGTTCCAGACGATTGCACGGAATGCACCTTAAGCAGGAAACGGAGGTGGAGCTGTACAACGAATTTCTGAACC
TATCAAACTGGACAAGAATGACCGGGCCAAGGCCTCGGCAGAAAGCTGCAGTTGCTGAGGGGGCAGTGAGAGTTG
AGCACAGAGTCCTTCACAAACCAAGAACACACGTAGGCCTTCAACACAATTCCCCTCTCCTCTTCCAAACAAAAC
ATACATTGATCTCTCACATCCAGCTGCCAAAAGAAAACCCCATCAACACAGTTACACCCACATATCTCGCACA
CACACACACACACGCACACACACACACACAGATCTGACGTAATCAAACCTCCAGCCCTTGCCCGTGATGGCTCCTT
GGGGTCTGCCTGCCACCCACATGAGCCCGCAGTATGGCAGCAGGACAAGCCAGCGGTGGAAGTCATTCTGATA
TGGAGTTGGCATTGGAAGCTTATTCTTTTGTTCACCTGGAGAGAGAGAGAACTGTTTACAGTTAATCTGTGTCTA
ATTATCTGATTTTTTTTTATTGGTCTTGTGGTCTTTTTACCCCCCTTTCCCCTCCCTCCTTGAAGGCTACCCCTT
GGGAAGGCTGGTGCCCATGCCCCATTACAGGCTCACACCCAGTCTGATCAGGCTGAGTTTGTATGTATCTATC
TGTTAATGCTTGTTACTTTTAACTAATCAGATCTTTTTACAGTATCCATTTATTATGTAATGCTTCTTAGAAAAG
AATCTTATAGTACATGTTAATATATGCAACCAATTAAAATGTATAAATTAGTGTAACAAAAAAAAAAAAAAAAAAAA

1340/6881
FIGURE 1247

MSFSSRPVPEILKTSHLLCWETRLTSKTDKWPQSGHRPGATAKTTFPTLRPVPRRPSTWSRRSRRLHGMHLSRKR
RWSCCTNFLNLSNWTRMTGPRPRQKAABAEGAVRVEHRVLHKPRTHVGLQHNSPLLFTKHTLISHIQLPKENPI
KHSYTPHISHTHHTHTHTHRSDVIKLQPLPVMAPWGLPAHPHEPASMAAGQASGGSHSDMELALEAYSFCSLER
ERTVYS

1341/6881
FIGURE 1248

AGAATCTTCAGTTTCTGTGAGCGTCCGCTTCGTCTGGGCACTTCCGGTACTCCCATTTCAGTTCCGGTCCCTGTCT
TTTACGTTTCCGGCAAACATCAGTGTCTGTGGGTAGTTGGAATCTTCAGTTCCCTGTGAGCGTCGGCGTCTTCTG
GGCCTGTGGAGTTTCTTGGACAGGGGCCGCGGGGCTCCAGGACGGCGCCCTTAGCGACACCATGCCCCGAAATGC
AGAAAAGGCCATGACGGCCTTAGCAAGATTTCCGCCAGGCTCAGCTGGAAGAGGGAAAAGTGAAGGAACGAAGACC
CTTCTGGCCTCAGAATGTACTGAACTGCCTAAAAGCTGAGAAGTGGAGACGACAGATCATTGGAGAGATCTCTAA
AAAAGTGGCTCAGATTCAGAATGCTGGTTTAGGTGAATTTTCAATTTCGTGACCTGAATGATGAAATTAACAAGCT
GCTAAGGGAGAAAAGGACACTGGGAGGTCCGGATAAAGGAGCTGGGAGGTCCTGATTATGGAAAAGTTGGCCCTAA
AATGCTGGATCATGAAGGAAAAGAAGTCCCAGGAAACCGAGGTTACAAGTACTTTGGAGCAGCAAAAAGATTGCC
TGGTGTTAGAGAGCTGTTTGAAAAAGAACCTCTTCCTCCTCCCAGAAAGACACGTGCTGAGCTCATGAAGGCAAT
CGATTTTGAGTACTATGGTTACCTAGATGAAGATGATGGTGTATTGTGCCTTTGGAACAGGAATATGAAAAGAA
ACTCAGAGCCGAGTTAGTGGAAGAGTGGAAAGCAGAGAGAGAGGCTCGGCTGGCAAGAGGAGAAAAGGAAGAGGA
GGAGGAAGAGGAGGAAGAGATCAACATCTATGCAGTCACCGAGGAGGAGTCCGACGAGGAAGGCAGCCAGGAGAA
AGGAGGGGACGACAGCCAGCAGAAGTTTATTGCTCACGTCCCTGTTCCCTCGCAGCAAGAGATTGAGGAGGCACT
GGTGCGAAGGAAGAAAATGGAATCCTCCAGAAGTATGCAAGCGAGACCCTGCAGGCCCCAAAGTGAAGAAGCCAG
AAGGCTCCTGGGGTATTAGGACCCAGCTGGGGCTCTCCTTGGAGTTCTTCCATCCCCCAGTGGTACCTCAGGACC
CAGGGCTGCAGACACAGGCTGGTGCTGCAAGGGCTCCTGCCCCATTCTCAGCCTTCCTTCCCTCTCCTTGCTCA
TGTTGACCGGAGGGTAGGGGTCTGTCCCTGGTCTTCTGGTAGGTTTTGTACACATATTTTGCTACTGTGTGGAT
CCATTTATTTTTATTGTGGAGTGTATACAACAGGTTGCGAACTGGCTGCCTGTGTCTTATTTTGACTTGCACTGC
CATTTTGAGGGGAGAAGAATCAATTAGTGGAACATTTAAAAATGCAATTTTTTGACAGACCAAAGTATAATTTT
AAAAAATGCAATTTTCTAAAAGACACATCTCTTGA AAAATGAGATGATGTGGCCAGGCGCAGTGGCTCACGCCT
GTAACCCCAGCACTTTGGGAGGCCGAGGCGGGCGGGTCACGAGGTCAAGAGATGGAGACCATCCTGGCCAACATG
GTGAAACCCCATGTCTACTAAAAATACAAAAAATTAGCTGGGCGTACTGGCATGCACCTGTAGTCCCAGCTGCT
TGGGAGGCTGAGGCAGGAGAATCACTTGAACCCGAGAGGTGGAGGTTGAAGTGAGCCAAGATCGTGCCATTGCAC
TCCAGCCTGGCGACAGAGTGAGACTCTGTCCCACAAAAAAAAAAAAAAAAA

1342/6881
FIGURE 1249

MARNAEKAMTALARFRQAQLEEGKVKERRPFLASECTELPKAEKWRRQIIGEISKKVAQIQNAGLGEFRIRDIND
EINKLLREKGHWEVRIKELGGPDYGKVGPKMLDHEGKEVPGNRGYKYFGAAKDLPGVRELFEKEPLPPPRKTRAE
LMKAIDFEYYGYLDEDDGVIVPLEQEYEKKLRAELVEKWKAEREARLARGEKEEEEEEEEEINIYAVTEESDEE
GSQEKGGDSQQKFIAHVPVPSQQEIEEALVRRKKMELLQKYASETLQAQSEEARRLLGY

1343/6881
FIGURE 1250

GAATTCCAAACAGCCTCTACCTTGCGAGCCGTCTTCCCCAGGCCTGCGTCCGAGTCTCCGCCGCTGCGGGCCCCGC
TCCGACGCGGAAGATCTGACTGCAGCC**ATG**AGCAGCAATGAGTGCTTCAAGTGTGGACGATCTGGCCACTGGGCC
CGGGAATGTCCTACTGGTGGAGGCCGTGGTTCGTGGAATGAGAAGCCGTGGCAGAGGTGGTTTTACCTCGGATAGA
GGTTTCCAGTTTGTTTCCTCGTCTCTTCCAGATATTTGTTATCGCTGTGGTGAGTCTGGTCATCTTGCCAAGGAT
TGTGATCTTCAGGAGGATGCCTGCTATAACTGCGGTAGAGGTGGCCACATTGCCAAGGACTGCAAGGAGCCCAAG
AGAGAGCGAGAGCAATGCTGCTACAACTGTGGCAAACCAGGCCATCTGGCTCGTGAATGCGACCATGCAGATGAG
CAGAAATGCTATTCTTGTGGAGAATTTCGGACACATTCAAAAAGACTGCACCAAAGTGAAGTGCTATAGGTGTGGT
GAAACTGGTCATGTAGCCATCAACTGCAGCAAGACAAGTGAAGTCAACTGTTACCGCTGTGGCGAGTCAGGGCAC
CTTGACCGGAATGCACAATTGAGGCTACAGCC**TAA**TTATTTTCCCTTTGTCGCCCCCTCCTTTTTCTGATTGATGG
TTGTATTATTTTCTCTGAATCCTCTTCACTGGCCAAAGGTTGGCAGATAGAGGCAACTCCCAGGCCAGTGAGCTT
TACTTGCCGTGTAAAAGGAGGAAAGGGGTGGAAAAAACCAGACTTTCTGCATTTAACTACAAAAAAGTTTATGT
TTAGTTTGGTAGAGGTGTTATGTATAATGCTTTGTTAAAGAACCCCTTTCCGTGCCACTGGTGAATAGGGATTG
ATGAATGGGAAGAGTTGAGTCAGACCAGTAAGCCCGTCCTGGGTTCCTTGAACATGTTCCCATGTAGGAGGTAAA
ACCAATTCTGGAAGTGTCTATGAACCTTCATAAATAACTTTAATTTTAGTATAATGATGGTCTTGGATTGTCTGA
CCTCAGTAGCTATTAAATAACATCAAGTAACATCTGTATCAGGCCCTACATAGAACATACAGTTGAGTGGGAGTA
AACAAAAAGATAAACATGCGTGTTAATGGCTGTTTCGAGAGAAATCGGAATAAAAGCCTAAACAGGAACAACCTCA
TCACAGTGTGATGTTGGACACATAGATGGTGATGGCAAAGGTTAGAACACATTATTTTCAAAGACTAAATCTA
AAACCCAGAGTAAACATCAATGCTCAGAGTTAGCATAATTTGGAGCTATTCAGGAATTGCAGAGAAATGCATTTT
CACAGAAATCAAGATGTTATTTTTGTATACTATATCACTTAGACAACGTGTGTTTCATTTGCTGTAATCAGTTTTT
AAAAGTCAGATGGAAAGAGCAACTGAAGTCCTAGAAAATAGAAATGTAATTTTAACTATTCCAATAAAGCTGGA

1344/6881
FIGURE 1251

MSSNECFKCGRSGHWARECPTGGGRGRGMRSRGRGGFTSDRGFQFVSSSLPDICYRCGESGHLAKDCDLQEDACY
NCGRGGHIAKDCKEFKREREQCCYNCGKPGHLARDCDHADEQKCYSCGEFGHIQKDCTKVVCYRCGETGHVAINC
SKTSEVNCYRCGESGHLARECTIEATA

1345/6881
FIGURE 1252

CATGGCTGCCCTCAGATCCCTTGTGAAGCCCAAGATCGTCAAAAAGAGAACCAAGAAATTCATCCGGCACCAGTC
AGACCGATATGTCAAAATCAAGATGAGAAGAATAATGTCTGGGGTGAAGGTGAAGCACCCAGCCCAAGACTCAGC
AGCCAGGAAGTGGCCCAGCGCTCTTTATACCACGGGTGCAGGAATTCACACAGAAAAGTGGAGGCCAAGGCGTGA
GAATTCCTCAATGACTGCCCTCTAAAGGAAGAGGACCAGGCTTCCTGTCAGAGACTGAGGACCCAGGAAGAAACA
TGTCTCGGCCCCCTGTCCCCCTCCACAATTCAGAGGCCACATTCTAACAGGGGAGGCTGACCAATTAAACAGATAA
TGACACCTCCTAGAGCTAAGAGCTCTCCGACTATGAACCAGATGCCTGGAGAACACGGATGAATGGTCTGAGCAT
GAGCAGGGGTGGGAGGCAGCGTTAAGGGAGGCATCAGAGTCAGAACCTAGCAAACAAGTGTTTGTGAAGAAGAAT
TCATAGAAAAGGGCAATGCGGGCATCACATGGGCTAAGGAACAGAGGGGTAGCAGTAGCTGTTGTGCCAAGCTGC
AGGTGTTATACACTACCCTCTAGATCTGGGTTTCCTTAAAACACCTTGAGAGGACAACCCTGCAAAGCACGGCAC
AGTGGCCGAGAGGGAAAGGAGCATTGAGGCTCTCAGTCCTCGCTCTGAGCCTACTTCTCTGCTTCTGGGCTCCAG
CCATCTTTGTGGAAAGGGGGCTGCTAGTGACACCCCTCTCAAGGGTCTTTCCAGCTCTAGGTCGGCTGTGCTGGAG
TCTAGGATTTGCCCACTGAGAAATCTGTTTCCAAGTTCCTTCAACCTGATGCATCCTGCAGCATCACGGCAGCTG
TTCAGAGTGGTCAGAAGGCCCCCTGAATGAGCTCAGTAGAGGGAAGCCTGGGAACAGGGAGGCACCTGCAGCTCTA
CTCATGGCCTGGCCAGAGCTCAGCAGCTCTTCTCTGCCATCTAGTGGGGATGGCATAACCATCACTGGGGACCACC
CTGTGCAAACCTGGTGAGCCTGAGTGCCTGTACAGAGGGAAAGAAAGGGGGGGGATAACAGGATTTAGATGAAATA
GCAACTCCTACCCTATTGTCAAAATCATCCAGCTTTTTCAAAACATCATATTGTAAGTATTTTTTGTGTTTTTG
ACAGAGTCTTGCTGTGTACCAAGGCTGGAATGCAGTGGCATGATCTCGGCTCACTGTAGCCTCTGTCTCCCTGG
TTCAAGCAATTCTGCCCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGCGCCACCACACCCAGCTAAGTTTTGT
ATTTTTTTTAGTAGAGTCAGGGTTTTACTTTGGCCAGGCTGGTCTTAAACTCCTGGCCTCAACTGATCTGCCTGTC
TCGGCCTCCCAAAGAACTGGGATTACAGGCATGAGGCACCGTGCCTGTCCCATGTTGTACTTAATAGATATTTAC
CATATACAATTATTTTTTAATTTAAATAAATCAATGAACAGTGTTATTTTTT

1346/6881
FIGURE 1253

MHPAASRQLFRVVRRLNELSRGKPGNREAPAALLMAWPESLSSSSLPSSGDGIPSLGTTLCKLVSLSACHRGKER
GGIQDLDEIATPTLLSKSSSFKTSYCTDFFVFLTESCCVTKAGMQWHDLGSL

1347/6881
FIGURE 1254

GGTGGCGTGGGGACTCCCTGAAAGCAGAGCGGCAGGGCGCCCGGAAGTCGTGAGTCGAGTCTTCCCGGGCTAATC
CATGCCGGGTGGGAGGCTGCTGACGCAGGTCCGGCGCCAGGTGCTGGGTGCGACTCGGGGACGGCCTGGGTGCTGC
CCTGGGCCCCGGGGAACAGAACACACATCTGGCTTTTTGTTAGAGGTCTTCATGGAAAGAGTGGTACATGGTGGGA
TGAGCATCTTTCTGAAGAAAATGTCCCATTCATTAAGCAGTTGGTCTCTGATGAAGATAAAGCCCAATTAGCAAG
TAAACTGTGTCCTCTGAAAGATGAACCATGGCCTATACATCCTTGGGAACCAGGTTCCCTTTAGAGTTGGTCTTAT
TGCCCTTGAAGCTGGGCATGATGCCTTTATGGACCAAGGATGGTCAAAAGCATGTGGTCACATTACTTCAGGTACA
AGACTGTGTCATGTCCTTAAATATACGTCAAAGGAAAACTGTAATGGAAAATGGCAACCCTGTCTGTAGGAGGAAA
AACTGTATCACGTTTTTCGTAAAGCTACATCCATATTGGAATTTTACCGGGAACCTTGGATTGCCGCCGAAACAGAC
AGTTAAAATCTTTAATATAACAGATAATGCTGCAATTAAACCAGGCACCTCCTCTTTATGCTGCTCACTTTCGTCC
TCGACAGTATGTGGATGTCACAGCCAAATCGTAGTGGTAAAGGTTTTCAAGGTGTCATGAAAAGATGGGGATTTA
AAGGCCAGCCTGCTACGCATGGTCAAACGAAAACCCACAGGAGACCTGGAGCTGTTGCAACTGGTGATATTGGCA
GAGTCTGGCCTGGAACATAAATGCCTGGAAAAATGGGAAACATATACAGGACAGAATATGGACTGAAAGTGTGGA
GAATAAACACAAAGCACAAACATAATCTATGTAATGGCTCTGTACCTGGACATAAAAAATTGCTTAGTAAAGGTCA
AAGATTCTAAACTGCCTGCATATAAGGATCTCGGTAAAAATCTACCATTCCCTACATATTTTCTGATGGAGATG
AAGAGGAAGTCCAGAAAGATTTGTATGATGAAAACGTGTGTGAGCCCGGTGCGCCTTCTATTACATTTGCCTAAC
ATCTTTGGACGTGGCAGAACCTTACATATTCTGTGAGCTTCGATGAGCCAGAGTGATATCATAACCACCAGAAAT
CATACTCTCCTTTCTTAGTCACAACAAAATCACACATGTCATCTTTGTCAAGGGCATAAATATATCATTTCATACC
CCCATTAAATTTTGTAGAAAAATTACCACATTAAATATATGAGTTAAGTAGATTGGATTGTGCTGAAATTGGTGT
TGGGCATATTAGCAAAATATTCTTAATTTGTGGACTCGATTCTTTTTTACTACATAATTTCCCAAGTTATCTTAAG
ATGTCTGTAAATTTAACTTTTATTAAAGTTTGTCAATCTTTGTGAATAGTGGTTGTGGAACAGTAGAAAACCAT
ATGGGGACTATAGTGCAACCTATTTGGGTAAAGAAACCATTTGCTAAAATGGAGAAAGTAAATAGATTTTTTATT
AAATTACAGAAACATGTTAAAGGCCGGACAAAGGAAAGACAATAAAATCATAAATTATC

1348/6881
FIGURE 1255

ATGATGACAGTAGGAGTTGAGTGGAGGAGATGGCAAGTTGAGCGGAGGAGGTGGCAGTGGGGCCCCAGATCAGGT
GCCTCCATGGCAGGCTCTGAAGAGCTGGGGCTCCGGGAAGACACGCTGAGGGTCCTAGCTGCCTTCCTTAGGCGT
GGTGAGGCTGCTGGGTCTCCTGTTCCAAATCCACCTAGAAGCCATGCCCCAAGAAGAGCCAACAGACTTCCTGAGC
CGCCTTCGAAGATGTCTTCCCTGCTCCCTGGGGCGAGGAGCAGCCCCCTCTGAGTCCCCCTCGGCCTTGGTCTCTG
CCCATCCGCCCCCTGCTATGGAGCCCCTGGCCCTGGCCATGGAGCTGAGCCGGCGCGTGGCCGAGCTGGGGGACAC
CCGGGCCGGA CT CAGCGTAGAGCACGCGCACAGCCTCACGCCCTGGATCCAGGCCCACGGGGGGCCGGCTCCACTG
CGTTCGTTCTGTGGTGAGCCCTTGCTGTATGCCCCGACTGCAGCCATGAGTGTGGACGCTATGCCTGGCGTCAAT
GACTGGGTACGCTAA

1349/6881
FIGURE 1256A

GAGGTCAGACCGGTTGCTTTCCCGGGAGTTTCGGCGTTTGCTGCGGGCTGCAGCAGCTGAAGTGTAGTGTTCCTTG
GGACTGGCGGTCTGCACTTCTCTCCCGGGTTCCATCTCCCCCGCCCGGTGGTGAGGCCCTCGAGGAGGGCTCGG
ACGGGTGTAGCGATCCGCGCTAGAGGAAGACGAGGCCCGGAACGCATGTCCCCAGGGCAGGTTAGGGGGCTGG
AGGGGTCAAATCCCGGGGTACTTGTGGAGACTCTTTAGCGTGGCTTCTTCTCTCTGCTGAGACCCCCGAGAGCTTT
CCCAGTTCTCCTCCCAGGACCACCGGGGTTCTGAAGATCGGGACTTTTCTGCGCCCCCTCCACCAACAGCCCATC
TCCTGTCTATGAAGAAAGACCCTTCGTAGAAACAACCTTCCCCGCTGCTGACGCGTTTTCCCGTCCCGTCCCCGAA
GTAGTCTACTATGACCTCGTTGTGAGCCTCTGAACGATTTTGACACTTTCCCGAGGCCTAGGGTATTATATCCTA
ACCTTACTAAAGACCACAGAGGTGCTTGCCATTATGCGGAAATCAGCTTGCTGGCATTGCTCCCTCCCAGATCCTT
TCTGTAGAGAGTTATTTTTCAGATATTCATGACTTTGAATATGATAAAAGCCTGGGGAGTACTCGGTTTTTTAA
GTTGCTCGAGCCAAGCACCGAGAAGGCCTGGTCTGTTGTGAAGGTTTTTGCAATTCAGGATCCCACATTGCCTTTA
ACCAGCTATAAAACAAGAGCTGGAGGAACCTGAAAATCAGGCTTAATCTGCACAGAATTGTCTACCTTTCCAGAAA
GCATCAGAAAAAGCATCTGAGAAAGCAGCTATGCTCTTTAGGCAGTATGTGCGAGACAATCTCTATGATCGCATC
AGTACCCGTCATTCTTGAATAACATTGAGAAGCGCTGGATTGCTTTCCAGATCCTGACAGCTGTGGACCAAGCA
CACAAATCTGGAGTTTCGTATGGGGACATCAAGACTGAGAATGTGATGGTCACCAGTTGGAATTGGGGTTCTTCTA
ACTGATTTTGCCAGTTTTTAAGCCCACTTATCTTCCAGAAGACAACCCGGCAGATTTCAATTATTTCTTTGACACA
TCACGGAGGAGAACTTGCTATATTGCTCCTGAACGTTTTGTTGATGGTGGGATGTTTGCCACTGAGTTAGAATAT
ATGAGAGATCCTTCAACTCCGCTTGTAGACTTAAATAGCAATCAGAGAACAAGAGGAGAGTTGAAGAGAGCAATG
GACATCTTTTTCAGCAGGTTGTGTGATAGCTGAGCTTTTTACAGAAGGTGTACCATTATTTGATCTCTCTCAACTT
TTGGCTTATAGAAATGGACATTTTTTCCCTGAACAAGTGCTAAATAAAATGAAGATCACAGTATCAGAGAATTG
GTAACCTCAGATGATTACCGTGAGCCAGATAAACGTTTAGAGGCAGAAGATTACTTAAACAGCAGCGTGGCAAT
GCCTTTCTGAAATATTTTACACTTTTTCTTCAGCCCTACATGGCCAGTTTGCCAAGGAAACGTTTCTTTCTGCA
GATGAGCGTATTCTGGTTATACGGAAGGATTTGGGCAACATTATTCACAATCTCTGTGGACATGATCTGCCAGAA
AAAGCCGAAGGAGAGCCTAAGGAAAATGGGCTGGTTATCTTGGTATCTGTTATAACATCCTGCCTACAGACCCTT
AAATACTGTGATTCCAACTAGCTGCTTTGGAAGTATTCTTCATTTGGCTCCAAGATTAAGTGTGAAATCCTT
TTGGATCGTATTACTCCATATCTTTTGCAATTCAGCAATGACTCTGTTCTTAGGGTGAGGGCTGAAGCCTTGAGG
ACGTTGACCAAAGTTCTTGCTCTCGTCAAAGAGGTTCTCGTAATGATATCAATATTTATCCGGAATACATTCTG
CCAGGCATAGCCCACTTAGCCCAAGATGATGCTACTATCGTTAGACTAGCCTATGCTGAAAACATAGCTCTGCTG
GCAGAAACAGCTCTGAGATTCTTGGAATTAGTACAGTTAAAAAATCTTAATATGGAAAATGACCCCAATAATGAA
GAAATAGATGAGGTTACACATCCAAATGGAATTTATGACACAGAGCTCCAAGCCTTACATGAAATGGTCCAGCAG
AAAGTTGTTACTTTGCTAAGTGACCCTGAAAATATTGTAAAACAAACCTTGATGGAAAATGGAATAACACGGCTG
TGTGTATTCTTTGGACGTGAGAAAGCCAACGATGTTTTGTTGTCCACATGATTACTTTCTTAAATGATAAGAAT
GATTGGCATCTACGTGGAGCATTTTTTGTATAGTATAGTTGGTGTGCTGCCTATGTTGGCTGGCAAAGCTCCTCA
ATTCTCAAGCCTCTGCTGCAACAAGGTCCTTAGTGATGCTGAGGAATTTGTCAATTGIGAAAGCTCTTTATGCCCTT
ACTTGTATGTGCCAGTTAGGACTGCTACAAAAACCCCATGTTTACGAATTTGCCAGTGATATTGCCCCCTTCCTG
TGTCATCCCAATTTATGGATACGTTATGGTGCCGTGGGATTTATCACAGTGGTAGCTCGTCAAATAAGTACAGCT
GATGTCTACTGTAACTGATGCCTTATCTTGACCCATATATTACCCAACCAATAATACAGATTGAAAGAAAACCTT
GTTCTGCTCAGTGTTTTAAAGGAACCAGTAAGTCGTTCTATATTTGATTATGCTTTGAGGTCTAAAGATATTACT
AGCTTGTTCAGACATCTTCACATGCGTCAGAAGAAACGAAATGGTTCTCTTCCCGACTGCCCTCCGCCAGAGGAT
CCTGCCATAGCACAGCTTCTGAAGAAGTTGCTCTCACAGGGAATGACAGAGGAAGAGGAAGACAAACTTCTGGCA
CTGAAAGACTTCATGATGAAATCTAATAAAGCAAAGGCCAATATAGTGGACCAGAGCCATCTTCATGATAGTAGT
CAGAAAGGTGTAATTGACTTGGCAGCTTTAGGCATAACTGGGAGACAAGTTGATCTTGTTAAAACCAACAAGAA
CCAGATGACAAACGGGCCAGAAAACATGTAAAACAAGACTCAAATGTAAATGAAGAATGGAAAAGCATGTTTGGG
TCACTGGACCCACCAACATGCCACAGGCCCTACCTAAAGGGAGTGATCAGGAGGTGATTACAGCTGGGAAACCT
CCTCGTTCCGAGTCTCTGCTGGCATTGTGTCCCTTTGTCAACTTCTTCACAGGTTCCAGAAGTGACAACCTGTC
CAAAATAAAAAACAGTAATACCGGTTTTAAGTAGTACAATCTTACCATCCACCTATCAGATTGCAATTACAAC
TGTAAAACTGAACTTCAGCAACTCATCCAGCAAAAGCGGGAGCAGTGCAATGCTGAGAGAATAGCTAAGCAGATG
ATGGAAAATGCTGAATGGGAGAGTAAACCACCACCCTGGATGGCGTCCTAAAGGGCTGTTAGTTGCCCATCTT
CATGAGCATAAATCTGCTGTGAATCGAATTAGAGTCTCTGATGAACACTCACTTTTTGCAACATGTTCAAATGAT

1350/6881
FIGURE 1256B

GGCACAGTGAAAATCTGGAACAGTCAAAAGATGGAGGGGAAGACCACCACTACCAGATCTATTCTTACATACAGC
CGAATTGGAGGACGAGTCAAGACGCTCACATTCTGCCAAGGCTCCCACTATTTAGCCATAGCATCTGATAATGGT
GCTGTCCAGCTTCTTGGAATTGAGGCTTCTAAGCTGCCCAAGTCTCCTAAAATCCATCCTCTACAAAGCAGAATT
CTAGATCAGAAGGAGGACGGTTGTGTTGTGGATATGCATCACTTCAACTCTGGAGCACAGTCTGTTCTTGCCTAT
GCCACTGTGAATGGCTCTCTGGTTGGCTGGGACCTTAGGTCTTCAAGCAATGCGTGGACTTTAAAGCATGATTTA
AAGTCGGGCCCTCATCACTTCCTTTGCTGTGGACATCCACCAATGCTGGCTCTGCATTGGTACAAGCAGTGGTACC
ATGGCTTGTGTTGGGACATGAGGTTCCAGTTGCCAATTTCAAGTCACTGTTCATCCTTCCAGGGCTCGAATCAGACGC
CTCTCAATGCACCCTCTGTATCAGTCCTGGGTGATTGCAGCTGTTTCAAGGCAACAACGAAGTGTCCATGTGGGAC
ATGGAGACTGGTGACAGAAGATTTACTCTCTGGGCCAGCAGTGCACCACCACTTTCTGAATTACAGCCTTCTCCT
CATAGCGTCCATGGTATCTACTGTAGTCCTGCAGATGGAAATCCTATCCTACTAACAGCTGGCTCAGATATGAAA
ATAAGGTTTTTGGGACTTGGCTTACCCAGAAAGGTCCATATGTTGTTGCAGGAAGTACTAGTTCCCCATCTGTGTCC
TACTACAGGAAAATAATTGAAGGCACTGAAGTTGTCCAGGAAATTCAGAATAAGCAGAAAGTAGGACCAAGTGAT
GACACCCCTCGAAGGGGCCAGAGTCCCTGCCCGTGGGACATCATGACATCATCACTGATGTCGCCACATTCCAG
ACCACACAGGGCTTCATCGTAACTGCTTCTAGAGATGGGATTGTGAAGGTGTGGAATTAAAACCTACTGATTTGT
ATAAATTTTAATAGTTATAAATATAATACTATAACTCGAGAAAAGGCATTTCTAGAGAACAGATTCATTTGCTTA
ATTTTCAAATTATGTCTCCATATTACTGTTTCATGACTGACTGACTAAATGACACCCAAAATGGTTAAGATGTA
CTTGACTAGTTTACTTATGCATCTCTTTGCAAGAATCAGCCAGCCAACAATGTCTGGGATTTTTATTGTATATGT
TATAGAGGTGAGAAATGTAAATATGAAAATGAATATGTTTATTTTGTATTGAAAAAGATGGTTGAAAAGATGGT
TGTAAGCTATTATAGTATAAACACATTTTTTGCTATTAAAAATGCTATTCAAAGCAGTTAAACTGT

1351/6881
FIGURE 1257

MGNQLAGIAPSQILSVESYFSDIHDFEYDKSLGSTRFFKVARAKHREGLVVVKVFQIDPTLPLTSYKQEELEELK
IRLNSAQNCPLPFQKASEKASEKAAMLFRQYVRDNLVDRISTRPFLNNIEKRWIAFQILTAVDQAHKSGVRHGDIK
TENVMVTSWNWVLLTDFASFKPTYLPEDNPADFNFFDTSRRRTCYIAPERFVDGGMFATELEYMRDPSTPIVLDL
NSNQRTRGELKRAMDIFSAGCVIAELFTEGVPLFDLSQLLAYRNGHFFPEQVLNKIEDHSIRELVTQMIHREPDK
RLEAEDYLKQQRGNAPPEIFYTFLQPYMAQFAKETFLSADERILVIRKDLGNIHNLCGHDLPEKAEGEPKENGL
VILVSVITSCLQTLKYCDSKLALELILHLAPRLSVEILLDRITPYLLHFSNDSVPRVRAEALRTLTKVLALVKE
VPRNDINIYPEYILPGIAHLAQDDATIVRLAYAENIALLAETALRFLELVQLKNLNMENDPNNEEIDEVTHPNGN
YDTELQALHEMVQQKVVTLLSDPENIVKQTLMEGITRLCVFFGRQKANDVLLSHMITFLNDKNDWHLRGAFFDS
IVGVAAYVGWQSSSILKPLLQQGLSDAEFEVIVKALYALTCMCQLGLLQKPHVYEFASDIAPFLCHPNLWIRYGA
VGFITVVARQISTADVCKLMPYLDPYITQPIIQIERKLVLLSVLKEPVSRISFDYALRSKDITSLEFRHLHMRQK
KRNGSLPDCPPPEDPAIAQLLKKLLSQGMTEEEEDKLLALKDFMMKSNKAKANIVDQSHLHDSSQKGVIDLAALG
ITGRQVDLVKTKQEPDDKRARKHVKQDSNVNEEWKSMFGSLDPPNMPQALPKGSDQEVQITGKPPRSESSAGICV
PLSTSSQVPEVTTVQNKKPVIPVLSSTILPSTYQIRITTCKTELQQLIQKREQCNAERIAKQMMENAEWESKPP
PPGWRPKGLLVAHLHEHKS AVNRIRVSDEHSLFATCSNDGTVKIWN SQMEGKTTTTRSILTYSRIGGRVKTLTF
CQGSHYLAIASDNGAVQLLGIEASKLPKSPKIHPLQSRILDQKEDGCVVDMHHFN SGAQSVLAYATVNGSLVGWD
LRSSNAWTLKHDLKSLITSFAVDIHQCWLCIGTSSGTMACWDMRFQLPIS SHCHPSRARIRRLSMHPLYQSWV
IAAVQGNNEVSMWDMETGDRRFTLWASSAPPLSELQSPH SVHG IYCSPADGNPILLTAGSDMKIRFWDLAYPER
SYVVAGSTSSPSVSYRKIIEGTEVVQEIQNKQKVGPSDDTPRRGPESLPVGHHDIIITDVATFQTTQGFIVTASR
DGIVKVWK

GGGCCCTGCGCTTCTCCATCAGACACCTGGGAATCACAGCTGGGGCCCCCTGCTTTGGCCGTTTGTCTGCTGGAATC
 TGATGGAGGAAAGACGCTCTGAGAGAGTAATTAGACGCAGACAGAGATCTCTCTCCATAGTCAGAGGAGCCTAGC
 AGGGGCTGAAGGAAGTGCCTGAGGATGACAAAGAAGGGGATCCATGAACAAGGAGGTGCTAACAGGTTTCTGCT
 GATCTTGGCACTGACCGAAGCGCTGGCATTGCGCATCCAGGAACCATCTCCCAGGGAATCTCTTCAGGTCTCTCC
 TTCAGGCACTCCCCCGGGAACCATGGTGACAGCACCCACAGCTCTACCAGACATACTTCTGTGGTGATGCTGAC
 CCCCATCCCGATGGACCCCCCTCACAGGCTGCAGCTCCCATGGCAACACCGACACCCCGTGCAGAGGGGGCACCC
 TCCTACGCACACCATCTCCACCATCGCTGCGACAGTAACCGCCCCCATCTGAAAGCTCCCTGTCCACAGGGCC
 CGCTCCAGCAGCCATGGCAACCACATCTCTCCAAGCCAGAGGGCCGCCCTCGAGGGCAGGCTGCCCCACCATCT
 GCTGACAAAGCCACCGGGGGGCCACCAGCCGCCACCACAGCGCCCCCGCGACTACCACACGCAGGCCCCCAG
 GCCCCAGGCTCTTCCCGAAAAGGGGCTGGTAATTTCATCAGCCCTGTCCGCGCTGCACCTGGTGCCACTCCAG
 GAGTAAAGAAGGACAGCGAGGACGAAATCCAAGCTCCACACCTCTGGGGCAGAAGCGGCCCTGGGGAAAATCTT
 TCAGATCTACAAGGGCAACTTCACAGGCTGTGTGAACCGGAGCCCTCTACCCTCACCCCGAGGACCCACTCTG
 GGGCTACTCCTCTTCACCACAGCCCCAGACAGTGGCTGCGACCACAGTGCCAGCAATACCTCATGGGCACCCAC
 CACCACCTCCCTGGGGCCTGCAAAGGACAAGCCAGGCCTTCGCAGAGCAGCCAGGGGGGTGGTTCTACCTTCAC
 CAGCCAAGGAGGGACACCAGATGCCACAGCAGCCTCAGGTGCCCTGTCTAGTCCACAAGCTGCCCCAGTGCCTTC
 TCAGCGCCCCCACCACGGTGACCCACAGGATGGCCCCAGCCATAGTGACTCTTGGCTTACTGTTACCCCTGGCAC
 CAGCAGACCTCTGTCTACCAGCTCTGGGGTCTTCAGGCTGCCACGGGGCCACCCAGCTGCCTTCGATACCAG
 TGTCTCAGCCCCCTTCCAGGGGATTCTCAGGGAGCATCCACAACCCACAAGCTCCAACCCATCCCTCCAGGGT
 CTCAGAAAGCACTATTTCTGGAGCCAAGGAGGAGACTGTGGCCACCCTCACCATGACCGACCGGGTGCCAGTCC
 TCTCTCCACAGTGGTATCCACAGCCACAGGCAATTTCTCAACCGCCTGGTCCCCGCCGGGACCTGGAAGCCTGG
 GACAGCAGGGAACATCTCCCATGTGGCCGAGGGGGACAAACCGCAGCACAGAGCCACCATCTGCCTGAGCAAGAT
 GGATATCGCCTGGGTGATCCTGGCCATCAGCGTGCCCATCTCCTCCTGCTCTGTCTCTGCTGACGGTGTGCTGCAT
 GAAGAGGAAGAAGAAGACCGCCAACCCGGAGAACAACTGAGCTACTGGAACAACACCATCACCATGGACTACTT
 CAACAGGCATGCTGTGGAGCTGCCCAGGGAGATCCAGTCCCTTGAAACCTCTGAGGACCAGCTCTCAGAGCCCCG
 CTCCCCAGCCAATGGCGACTATAGAGACACTGGGATGGTCTTGTTAAACCCCTTCTGTCAAGAAACACTGTTTGT
 GGGAAACGATCAAGTATCTGAGATCTAACTACAGCAGGCATCACTTTGCCATTCCGTATTTTTCTGCTCTCTAAATT
 ATAAATATACAAATACATATATTATAAAATATAACCTTTGTGTAACCCCTGACTTAATGAGAAACATTTTTAGCTTT
 TTTTCTTATGAATTGTCAACATCTTTTTTACAAGTGTGGTTTAAAAAAAAAAAAAACTTTACAGAATGATCTGTG
 GCTTTATAAAATAAAGGTATTTCTAAGCAAAGCAGTTGCATTGATTGCTTCTCTTAATAACTATTCTTGAGCACC
 TGGGGATCCCAGGAACCCCTGGTCAAGGTGAGGTAAGAGACTGACCTCCTGTAGAAGCTGAATGTTACAGTGCAAGC
 GCACGATTCTTTGAGTGATTCTTAAAGCTCTGGTTCCCTCTGATTGGTGTGACCCATTTCTCCCTTCTCATA
 CGCACACCTGTAAAGGGAAGTGGACCGCCTCAGGGGAAGACGGCAGACTCATGCACAGAGAAGGAAAAGGGAACA
 TCTCATCACCTCTGAGGATGAGTACCCTGGAGCCTTATGACGGCACCATTTGGATGTCATGTTTAATTCCATCCAA
 GTTGTGGATGGCAGGCAGGAGCATGGAGCCCTCAGGAATCCATGGAGGACATCAAGGCATCCAAGGCCATATTC
 CCTAACATTACTTCCACTGCTAACAACAGGACTGCCTTTCCCTGGTGGGAAAATGCTCCCTTTATGCCCATTC
 TGTATCCCTCCAACACCCACATCTGCATTAAACACCCGTGCCTTTCTCTTGGAGAGGGTTTAGATGCAGATCCC
 GGCCCTGGAGCTTTAAATGCTTGCCCTTCTTCTTCAAGGATCAAATGTTTATTGGGGTTACGCTTTGTTTTCT
 CAAAAGGCCATGGTATCGTGCCCTGAGGAACATGTTTATCTAAGAAGCTTTGAGGTAGTAGAGCGATAATTTTT
 GAAACCTTCTCTGCAATCTTTAAAAAAGAAAAAAGATTGCCCAAACAATCATTGGGAGAAGACATCATT
 ATACTCTACTTGGCACTGCAAACCTGCTCGCAGCACCAGCCGGTGGACTTGCCATCCAGCTCTCAGCTTCCACT
 GCTCCCTTGTTCCTGGCGCGGCTGGCTGCCTCCCCGTGCTGTGTCCAGCACGGCCAACAACGTCAGACCCTCAGA
 GACGCCCAAGGGGCTTCCAGAGGTGGCCGCTTCTCTATTTTTTCTGATTGTGGCTGAGAGAGATGATTACTGCT
 TTGACACTTCTTTCTCTAAAAGAAAAATAGTTTGATAGTATATTTTGAATATAGATGCTCTTATAGTCAGATTG
 GGAATTGAACTTGAATATTGGGTCTATGTTTGTGTTGTTGCTGTAGTCTATCATGACTTTTTTCTTTCTGCATT
 TTCCTTAAAAAAAAAAAAAGATGGCCTTCAAAAGTGTGTTCTCAATGTTGTATGAACCTCCTTCACATGAGTTC
 GTTGTTGTCTCTCTTCAAAGACTCTTCAACCCACAAAGAAGCAACTAAATGTTTCTTAAGTTTAATTTCTAG
 CGTGTGTTGTCTTACCTTTTTTAACCTTACCATAATATTTCTGTTAACTGTTACATTTAATATACCAATGTGTGT
 AAGTATACAGAGAAAAATCTGTTTGTAAAGTAAATTTATATATAATATATGTAATCAAAGATACATATGTTATA

1353/6881

FIGURE 1258B

TATACATATGTGGATGTATGACTTATTTTTCCTTATCCACAGATTCAGCTACCATGTATATATAAATAAACTTA
TTTTATTAGCCAGAG

1354/6881
FIGURE 1259

MKRSLQALYCQLLSFLLILALTEALAFAIQEPSPRESLQVLPSGTPPGTMVTAPHSSSTRHTSVVMLTPNPDGPPS
QAAAPMATPTPRAEGHPPTHITISTIAATVTAPHSESSLSTGPAPAAMATTSSKPEGRPRGQAAPTILLTKPPGAT
SRPTTAPPRITTTTRRPPRPPGSSSRKGAGNSSRPVPPAPGGHSRSKEGQRGRNPSSTPLGQKRPLGKIFQIYKGNFT
GSVEPEPSTLTPTPLWGYSSSPQPQTVAATTVPSTNSWAPTTTSLGPAKDKPGLRRAAQGGGSTFTSQGGTPDA
TAASGAPVSPQAAPVPSQRPHHGDPQDGPSHSDSWLTVTPGTSRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGI
PQGASTTPQAPTHPSRVSESTISGAKEETVATLTMTDRVPSPLSTVVSTATGNFLNRLVPAGTWKPGTAGNISHV
AEGDKPQHRATICLSKMDIAWVILAI SVPISSCSVLLTVCCMKRKKKTANPENNL SYWNNTITMDYFN RHAVELP
REIQSLETSEDQLSEPRSPANGDYRDTGMVLVNPFCQETLFGNDQVSEI

1355/6881
FIGURE 1260

ATGGCGGCGGCATTACGGGTGGCGGCGGTGCGGGCAAGGCTCAGCGTTCTGGCGAGCGGTCTCCGCGCCGCGGT
CGCAGCCTTTGCAGCCAGGCCACCTCTGTTAACGAACGCATCGAAAACAAGCGCCGGACCGCGCTGCTGGGAGGG
GGCCAACGCCGTATTGACGCGCAGCACAAAGCGAGGAAAGCTAACAGCCAGGGAGAGGATCAGTCTCTTGCTGGAC
CCTGGCAGCTTTGTTGAGAGCGACATGTTTGTGGAACACAGATGTGCAGATTTTGGAATGGCTGCTGACAAGAAT
AAGTTTCCTGGAGACAGCGTGGTCACTGGACGAGGCCGAATCAATGGAAGATTGGTTTATGTCTTCAGTCAGGAT
TTTACAGTTTTTGGAGGCAGTCTGTCAGGAGCACATGCCAAAAGATCTGCAAAATCATGGACCAGGCCATAACG
GTGGGGGCTCCAGTGAATTGGGCTGAATGACTCTGGGGGAGCACGGATCCAAGAAGGAGTGGAGTCTTTGGCTGGC
TATGCAGACATCTTTCTGAGGAATGTTACGGCATCCGGAGTCATCCCTCAGATTTCTCTGATCATGGGCCCATGT
GCTGGTGGGGCCGCTACTCCCCAGCCCTAACAGACTTCACGTTTCATGGTAAAGGACACCTCCTACCTGTTTCATC
ACTGGCCCTGATGTTGTGAAGTCTGTCACCAATGAGGATGTTACCCAGGAGGAGCTCGGTGGTGCCAAGACCCAC
ACCACCATGTCAGGTGTGGCCACAGAGCTTTTGAAAATGATGTTGATGCCTTGTGTAATCTCCGGGATTTCTTC
AACTACCTGCCCTGAGCAGTCAGGACCCGGCTTCCGTCCGTGAGTGCCACGATCCCAGTGACCGTCTGGTTCCT
GAGCTTGACACAATTGTCCCTTTGGAATCAACCAAAGCCTACAACATGGTGGACATCATACACTCTGTTGTTGAT
GAGCGTGAATTTTTTGAGATCATGCCAATTATGCCAAGAACATCATTGTTGGTTTTTGCAAGAATGAATGGGAGG
ACTGTTGGAATTGTTGGCAACCAACCTAAGGTGGCTCAGGATGCTTGGATATTAATTCATCTGTGAAAGGGGCT
CGTTTTGTCAGATTCTGTGATGCATTCAATATTCCACTCATCACTTTTGTGATGTCCCTGGCTTTCTACCTGGC
ACAGCACAGGAATACGGGGGCATCATCCGGCATGGTGCCAAGCTTCTCTACGCATTTGCTGAGGCAACTGTACCC
AAAGTCACAGTCATCACCAGGAAGGCCTATGGAGGTGCCTATGATGTCATGAGCTCTAAGCACCTTTGTGGTGAT
ACCAACTATGCCTGGCCACCGCAGAGATTGCAGTCATGGGAGCAAAGGGCGCTGTGGAGATCATCTTCAAAGGG
CATGAGAATGTGGAAGCTGCTCAGGCAGAGTACATCGAGAAGTTTGCCAACCCTTTCCCTGCAGCAGTGCGAGGG
TTTGTGGATGACATCATCAACCTTCTTCCACACGTGCCGAATCTGCTGTGACCTGGATGTCTTGGCCAGCAAG
AAGGTACAACGTCCTTGAGAGAAACATGCAAAATATTCCATTGTAA

1356/6881
FIGURE 1261

MAAALRVAAVGARLSVLASGLRAAVRSLCSQATSVNERIENKRRTALLGGGQRRIDAQHKRGKLTARERISLLLD
PGSFVESDMEVEHRCADFGMAADKNKFPGDSVVTGRGRINGRLVYVFSQDFTVFGGSLSGAHAQKICKIMDQAIT
VGAPVIGLNDSSGGARIQEGVESLAGYADIFLRNVTASGVIPQISLIMGPCAGGAVYSPALTDFTFMVKDTSYLF
TGPDVVKSVTNEDVTQEELGGAKHTTTMSGVAHRAFENDVDALCNLRDFFNYLPLSSQDPASVRECHDPSDRLVP
ELDTIVPLESTKAYNMVDIIHSVVDEREFFEIMPNYAKNIIVGFARMNGRTVGIVGNQPKVASGCLDINSSVKGA
RFVRFCDAFNIPLITFVDVPGFLPGTAQEYGGIIRHGAKLLYAFAEATVPKVTVITRKAYGGAYDVMSSKHLCD
TNYAWPTAEIAVMGAKGAVEIIFKGHENVEAAQAEYIEKFANPFPAAVRGFVDDIIQPSSTRARICCDLDVLASK
KVQRPWRKHANIPL

1357/6881
FIGURE 1262

GAGGCTATGGCGCTCAACAAGAATCACTCGGAGGGCGGGGAGTGATCGTCAATAACACCGAGAGCATCCTAATG
TCCTATGATCACGTGGAACACATTCAATGACATGAAGAACGTGCCAGAAGCCTTCAAAGGGACCAAGAAAGGC
ACTGTCTACCTTACCCCTTACCGGGTCATCTTTCTGTCCAAGGGCAAGGATGCCATGCAGTCCTTCATGATGCCA
TTTTATCTCATGAAAGACTGTGAGATCAAGCAGCCCGTATTTGGTGCAAACCTACATCAAGGGAACAGTGAAGGCG
GAAGCGGGAGGTGGCTGGGAAGGCTCTGCTTCCTACAAGTTGACTTTCACGGCAGGGGGCGCCATTGAGTTCGGA
CAGCGGATGCTCCAGGTGGCATCTCAAGCCTCCAGAGGTGAAGTCCCCAGTGGAGCCTATGGCTACTCTTACATG
CCCAGCGGGGCTATGTCTATCCCCGCCAGTCGCCAATGGAATGTACCCCTGCCCTCCTGGCTACCCCTATCCA
CCGCCCCACCTGAGTTCTATCCAGGACCCCCATGATGGACGGGGCCATGGGATACGTGCAGCCCCACCACCG
CCCTACCCCTGGGCCCATGGAACCTCCGGTCAGCGGCCCCGATGTCCCCTCCACTCCTGCAGCCGAAGCCAAGGCC
GCAGAAGCAGCCGCCAGCGCCTATTACAACCCAGGCAATCCTCACAACGTCTACATGCCCACGAGCCAGCCGCCG
CCACCTCCCTACTACCCACCGGAAGATAAGAAGACCCAGTAGGCCCTCCTGCCTCCCTGCCCTCCACCCCTCATCT
CTCTACCCCTACCCCTCCCATCGGGGCTGTGCTGGGGCTTGGGGAGGGGAGGGGGCGCCTTGTTCTCCCTCCAGGT
CTGATCATAAAACAATTACCAGGAAGTAGCATTGTGGGACATTAGGGCCCCCGGCCTCGGGAGAGGTGCCGCCAG
CTTCCCATGCCAGCCCGGAGCCACAGTGCTGCCCAGCGTACCTCCCTCACCGTCTGGGGCTCTTCTGGGAGCAC
GGAGCATCCCCCTGTTCTGTTTCACTCTCAGCTTCTCCCCTCGAAGGGACTCTCTGGCCACCTCCTCCACCGCAG
TCCAGCTCCCTCAGTCTGGCACCCACTGCTACACTCAGCCTCATGAGCCACTTCAGACCAGCCAGGTGTCTTCCC
GGGCCCTGCCAGACCCTGCTCACATTCCCTCTGCTGGTCTGTGCTGGTCTCAGAAGGCCACCGCGCCCCGATTCC
ACTCAGCCAGGGTCCAGCTGCAGCCCCCGCCACCCCTTCCCTTCCCTTCCCTGTCTGGGTCTGTTGTTGCCACCC
TGTGTGACTTTTGAAGCTGTAAATGAGCTTCCAGGGCTTGGGTGGCGTCGGGGCAGGGCCGCCGAGGCTGGGAG
GAAGCCCTTCTGCCTTTTGCTGGTGTCTTCTGGAATTTGCTTTCCTCACCTCTCACTTCTTCTAGAAGGAGCTT
CCTGACTGGAACCAGAGAATGCATGTCTGTCCACTTGGTGGCTGCTGGGTGGGGCCGGGAACAAGGGCCCCCTGAC
CCTGTGTGCTGGCCGGGACCTGCCACCAGCCCCCAGCCTGCTTCTTCCCTTAAGCTTTGTGCCCTGGATGCG
CTAACATTCACCTCTTGTGTTGTCCCTGGACTGGCCATGAAGTGAGGAGATGGTTATTTAAAGAGAATTCCTATTT
ATTTGACAAAAAATCCAGTTAATATATTAATGTGAAATAAACCTGTTTGCCCCCTCG

1358/6881
FIGURE 1263

AGGCTCAGGATGAGATCCCAGCACTGTCCGTGTCCCGGCCCCAGACCGGCCTGTCCTTCCTGGGCCCTGAGCCTG
AGGACCTGGAGGACCTGTACAGCCGCTACAAGAAGCTGCAGCAAGAGCTGGAGTTCCTGGAGGTGCAGGAGGAAT
ACATCAAAGATGAGCAAAAGAACCTGAAAAAGGAATTTCTCCATGCCCAGGAGGAGGTGAAGCGAATCCAAAGCA
TCCCGCTGGTCATCGGACAATTTCTGGAGGCTGTGGATCAGAATACAGCCATCGTGGGCTCTACCACAGGCTCCA
ACTATTATGTGCGCATCCTGAGCACCATCGATCGGGAGCTGCTCAAGCCCAACGCCTCAGTGGCCCTCCACAAGC
ACAGCAATGCACTGGTGGACGTGCTGCCCCCGAAGCCGACAGCAGCATCATGATGCTCACCTCAGACCAGAAGC
CAGATGTGATGTACGCGGACATCGGAGGCATGGACATCCAGAAGCAGGAGGTGCGGGAGGCCGTGGAGCTCCCGC
TCACGCATTTTCGAGCTCTACAAGCAGATCGGCATCGATCCCCCGAGGCGTCCTCATGTATGGCCACCTGGCT
GTGGGAAGACCATGTTGGCAAAGGCGGTGGCACATCACACAACAGCTGCATTTCATCCGGGTCGTGGGCTCGGAGT
TTGTACAGAAAGTATCTGGGTGAGGGCCCCCGCATGGTCCGGGATGTGTTCCGCCTGGCCAAGGAGAATGCACCTG
CCATCATCTTCATAGACGAGATTGATGCCATCGCCACCAAGAGATTTCGATGCTCAGACAGGGGCCGACAGGGAGG
TTCAGAGGATCCTGCTGGAGCTGCTGAATCAGATGGATGGATTTGATCAGAATGTCAATGTCAAGGTAATCATGG
CCACAAACAGAGCAGACACCCTGGATCCGGCCCTGCTACGGCCAGGACGGCTGGACCGTAAAAATTGAATTTCCAC
TTCCTGACCGCCGCCAGAAGAGATTGATTTTCTCCACTATCACTAGCAAGATGAACCTCTCTGAGGAGGTTGACT
TGGAAGACTATGTGGCCCGGCCAGATAAGATTTTCAGGAGCTGATATTA ACTCCATCTGTCTCAGGAGAGTGGAATGT
TGGCTGTCCGTGAAAACCGCTACATTGTCTGGCCAAGGACTTCGAGAAAGCATAACAAGACTGTCTCATCAAGAAGG
ACGAGCAGGAGCATGAGTTTTACAAGTGACCTTCCCTTCCCTCCACCACCACTCAGGGGCTGGGGCTTCTCT
CGCACCCCCAGCACCTCTGTCCCAAACCTCATTCCCTTTTTTCTTTACCCAGGATTGGTTTCTTCAATAAATAG
ATAAGATCGAATCC

1359/6881
FIGURE 1264

CTGGAAGAATTTCGCGGCCGAAGTGGCTGGCTCATTTAAGATGAGGCTTCTGCTGCTTCTCCTAGTGGCGGCGTCT
GCGATGGTCCGGAGCGAGGCCTCGGCCAATCTGGGCGGCGTGCCCAGCAAGAGATTAAAGATGCAGTACGCCACG
GGGCCGCTGCTCAAGTTCCAGATTTGTGTTTCTGAGGTTATAGGCGGGTGTTTGAGGAGTACATGCGGGTTATT
AGCCAGCGGTACCCAGACATCCGCATTGAAGGAGAGAATTACCTCCCTCAACCAATATATAGACACATAGCATCT
TTCTGTGTCAGTCTTCAAAC TAGTATTAATAGGCTTAATAATTGTTGGCAAGGATCCTTTTGCTTCTTTGGCATG
CAAGCTCCTAGCATCTGGCAGTGGGGCCAAGAAAATAAGGTTTATGCATGTATGATGGTTTTCTTCTTGAGCAAC
ATGATTGAGAACCAGTGTATGTCAACAGGTGCATTTGAGATAACTTTAAATGATGTACCTGTGTGGTCTAAGCTG
GAATCTGGTCACTTCCATCCATGCAACAACCTGTTCAAATTCTTGACAATGAAATGAAGCTCAATGTGCATATG
GATTCAATCCCACACCATCGATCATAGCACCACCTATCAGCACTGAAAACCTCTTTTGCAATTAAGGGATCATTGCA
AGAGCAGCGTGACTGACATTATGAAGGCCTGTACTGAAGACAGCAAGCTGTTAGTACAGACCAGATGCTTCTTG
GCAGGCTCGTTGTACCTCTTGGAACCTCAATGCAAGATAGTGTTTCAGTGCTGGCATATTTTGGAATCTGCA
CATTCATGGAGTGCAATAATACTGTATAGCTTTCCCCACCTCCACAAAATCACCCAGTTAATGTGTGTGTGTGT
TTTTTTTTTAAGGTAAACATTACTACTTGTAACTTTTTTTCTTAGTCATATTTGAAAAAGTAGAAAATTGAGTTA
CAATTTGATTTTTTTTTTCCAAAGATGTCTGTAAATCTGTTGTGCTTTTATATGAATATTTGTTTTTATAGTTTA
AAATTGATCCTTTGGGAATCCAGTTGAAGTTCCCAAATACCTTTATAAGAGTTTATCAGACATCTCTAATTTGGCC
ATGTCCAGTTTATACAGTTTACAAAATATAGCAGATGCAAGATTATGGGGGAAATCCTATATTCAGAGTACTCTA
TAAATTTTTGTGTATGTGTGTATGTGCGTGTGATTACCAGAGAACTACTAAAAAACCAACTGCTTTTTTAAATCC
TATTGTGTAGTTAAAGTGTGCATGCCTTGACCAATCTAATGAATTGATTAATTAAGTGGCCTTTTACTTAACTA
AATAAAAAACTAAGCAGATATGA

1360/6881
FIGURE 1265

GCGGCCGAAGTGGCTGGCTCATTTAAGATGAGGCTTCTGCTGCTTCTCCTAGTGGCGGCGTCTGCGATGGTCCGG
AGCGAGGCCTCGGCCAATCTGGGCGGCGTGCCAGCAAGAGATTAGTGTTTCCTGAGGTTATAGGCGGGTGTTTG
AGGAGTACATGCGGGTTATTAGCCAGCGGTACCCAGACATCCGCATTGAAGGAGAGAATTACCTCCCTCAACCAA
TATATAGACACATAGCATCTTTCCTGTCAGTCTTCAAACCTAGTATTAATAGGCTTAATAATTGTTGGCAAGGATC
CTTTTGCTTTCTTTGGCATGCAAGCTCCTAGCATCTGGCAGTGGGGCCAAGAAAATAAGGTTTATGCATGTATGA
TGGTTTCTTCTTGAGCAACATGATTGAGAACCAGTGTATGTCAACAGGTGCATTTGAGATAACTTTAAATGATG
TACCTGTGTGGTCTAAGCTGGAATCTGGTCACCTTCCATCCATGCAACAACCTTGTTCAAATTCTTGACAATGAAA
TGAAGCTCAATGTGCATATGGATTCAATCCACACCATCGATCATAGCACCACTATCAGCACTGAAAACCTCTTT
TGCATTAAGGGATCATTGCAAGAGCAGCGTGACTGACATTATGAAGGCCTGTACTGAAGACAGCAAGCTGTTAGT
ACAGACCAGATG

1361/6881
FIGURE 1266

GCGGCCGAAGTGGCTGGCTCATTTAAGATGAGGCTTCTGCTGCTTCTCCTAGTGGCGGCGTCTGCGATGGTCCGG
AGCGAGGCCTCGGCCAATCTGGGCGGCGTGCCAGCAAGAGATTAAAGATGCAGTACGCCACGGGGCCGCTGCTC
AAGTTCCAGATTTGTGTTTCCTGAGGTTATAGGCGGGTGTTTGAGGAGTACATGCGGGTTATTAGCCAGCGGTAC
CCAGACATCCGCATTGAAGGAGAGAATTACCTCCCTCAACCAATATATAGACACATAGCATCTTTCCTGTCAGTC
TTCAAAC TAGTATTAATAGGCTTAATAATTGTTGGCAAGGATCCTTTTGCTTTCCTTGGCATGCAAGCTCCTAGC
ATCTGGCAGTGGGGCCAAGACCAGTGTATGTCAACAGGTGCATTTGAGATAACTTTAAATGATGTACCTGTGTGG
TCTAAGCTGGAATCTGGTCACCTTCCATCCATGCAACAAC TTGTTCAAATTC TTGACAATGAAATGAAGCTCAAT
GTGCATATGGATTCAATCCCACACCATCGATCATAGCACCACT

1362/6881
FIGURE 1267

CAATTAAGTTGCAGAGTTCTGATGGAGAGATATTTGAAGTTGATGTGGAAATTGCCAAACAATCTGTGACTATTA
AGACCATGTTGGAAGATTTGGGAATGGATGATGAAGGAGATGATGACCCAGTTCCTCTACCAAATGTGAATGCAG
CAATATTAAAAAAGGTCATTCAGTGGTGCACCCACCACAAGGATGACCCTCCTCCTCCTGAAGATGATGAGAACA
AAGAAAAGCGAACAGATGATATCCCTGTTTGGGACCAAGAATTCCTGAAAGTTGACCAAGGAACACTTTTGAAC
TCATTCTGGCTGCAAACTACTTAGACATCAAAGGTTTGCTTGATGTTACATGCAAGACTGTTGCCAATATGATCA
AGGGGAAAACTCCTGAGGAGATTCGCAAGACCTTCAATATCAAAAATGACTTTCCTCCTTTTTTGTAAAGCAATG
TCTGCCTAGTTTATTGTCCAGTTAACTTTAGTGACCTTTTAAAAGTTGGCATTGTAAATAAAACAACCTTGCAAAA
AAGTTTTCTGGAATAGAATTAACAAAATATTATCTTTATTCATGAGTTGGAACTGGAAAAAGGCTTCTTGAAGT
AAATGTTCTGAGTGGAGCTACTAGGATGTCTTCCAGCCTCCTGCAGTCAAGGAGTACCACTGTATTGATTAGCCT
GTATGTAGCAGGGCTCCCTTCATTGCATCTGAGGACTTGTTTTCTTTTCTTTATTTTTAATCCTCTTAGTTTTA
AATATATTGCCCTAGAGACTCAGTTACTACCCAGTTTGTGGTTTTTTGGGAGAAATGTAAGTGGACAGTTAGCTTT
TCAATTAAAAAGACACTTAACCCATGTGGGATGTCATCTTTTATAATTAGTGTTCCTCATGTGGAGAAAAATTATT
CACACTACTTGCAATGTAAAGAATAATTTAACTTTTAAACATTAAAAATATGTGGTAAAACCCAGAAAGCATCCATCA
TGAATGCAAGATACTTTCAATAAAAAGTAAGTTATATAGTAGGTAGTTAAGTTTGCTTTTGTGGACTTAAATGTG
TCTCTTCACTTAAATGGGTTGAATGTGTATATATTTGTTTCAGCTTGAAAAGACTTAGTTTATATCCTAGCTCACT
GGAGGCTGCTGACATAACCATAACTTCTGTCCCTTCTAATTGTCAATTTATATGCCTAACTGGAGCTAGTACTTTA
ATTCTTAACACAAAAATTACTCTGCCATTGTTTCCAGCTTCCCTCCTACAATAGAATGAAGTTTTTTTTGATGGCTT
GAGATGGCTCACAAATTTTGATTTTTTTTTTCTTCCTTGTGCTCCCTTTTTTTCTCCTTGCTTTTCCAGTTAACAT
CTATATTCACATGTAATCTTGTTTTCTTTACATTCAGTTGTTTCAGGCTCAGATCATCCCTTGACAGTAG
TTTGCCTTCATCTCACCTTTCATTTGTCCCAAATTCACCTTATTTAATAAAGTCCCATATGTTGTCTCACTTAA

1363/6881
FIGURE 1268

CAATTAAGTTGCAGAGTTCTGATGGAGAGATATTTGAAGTTGATGTGGAAATTGCCAAACAATCTGTGACTATTA
AGACCATGTTGGAAGATTTGGGAATGGATGATGAAGGAGATGATGACCCAGTTCCTCTACCAAATGTGAATGCAG
CAATATTAAAAAAGGTCATTCAGTGGTGCACCCACCACAAGGATGACCCTCCTCCTCTGAAGATGATGAGAACA
AAGAAAAGCGAACAGATGATATCCCTGTTTGGGACCAAGAATTCCTGAAAGTTGACCAAGGAACACTTTTTGAAC
TCATTCTGGCTGCAAACTACTTAGACATCAAAGGTTTGCTTGATGTTACATGCAAGACTGTTGCCAATATGATCA
AGGGGAAAACCTCCTGAGGAGATTCGCAAGACCTTCAATATCAAAAATGACTTTACTGAAGAGGAGGAAGCCCAGG
TACGCAAAGAGAACCAGTGGTGTGAAGAGAAAGTGAAATGTTGTGCCTGACACTGTAACACTGTAAGGATTGTTCC
AAATACTAGTTGCACTGCTCTGTTTATAATTGTTAATATTAGACAAACAGTAGACAAATGCAGCAGCAAGTCAAT
TGTATTAGCAGAATATTGTCCTCATTGCATGTGTAGTTTGAGCACAGATCCCAAACCTTACGGCCAAGTTTCTTC
TAGTATGATGGAAAGTTTCTTTTTTCTTTGCTCTGAATAAACTGAACTGTGGGTTCCTATAAGTGGCATTTTG
GGCTTTCCTCTTTTTTTGTAAAGCAATGTCTGCCTAGTTTATTGTCCAGTTAACTTTAGTGACCTTTTAAAGTT
GGCATTGTAAATAAAACAACCTTGCAAAAAAGTTTTCTGGAATAGAATTAACAAAATATTATCTTTATTCATGAGT
TGGAACTGGAAAAAGGCTTCTTGAAGTAAATGTTCTGAGTGGAGCTACTAGGATGTCTTCCAGCCTCCTGCAGT
CAAGGAGTACCACTGTATTGATTAGCCTGTATGTAGCAGGGCTCCCTTCATTGCATCTGAGGACTTGTTTTCTTT
TTCTTTATTTTTTAATCCTCTTAGTTTTTAAATATATTGCCTAGAGACTCAGTTACTACCCAGTTTGIGGTTTTTTG
GGAGAAATGTAACCTGGACAGTTAGCTTTTCAATTAAAAAGACACTTAACCCATGTGGGATGTCATCTTTTTATAA
TTAGTGTTCCTCATGTGGAGAAAATTATTCACACTACTTGATGTAAAGAATAATTTAACTTTTAAACATTAAATA
TGTGGTAAACCAGAAAGCATCCATCATGAATGCAAGATACTTTCAATAAAAAGTAAGTTATAT

1364/6881
FIGURE 1269

MPSIQLQSFIDGEIFAVDVEIAKQSVTIKTTLEDLGMDDEGDDPVPLPNVNAAVLKKVIQWCTHHKDDPPPPEDDE
NKEKQTDDIPVWDQEFLLKVAQGTLFELIRAANYLDIKGLLDVTCKTVANMIKGKTPEEIRKTFNIKNDFTAAAA
QVRKENQWCEEK

1365/6881
FIGURE 1270

GGTGGGTTTATCTCAAGGCCTGAGTAGCCGGTAACAAACGAGGGTTCCCGGGATTGGACCGACGCACCATGCCTC
TGCGACTTGATATCAAAAGAAAGCTAACTGCTAGATCTGATCGAGTTAAGAGTGTGGATCTGCATCCTACAGAGC
CATGGATGTTGGCAAGTCTTTACAATGGCAGTGTGTGTGTTTGAATCATGAAACACAGACACTGGTGAAGACAT
TTGAAGTATGTGATCTTCCTGTTTCGAGCTGCAAAGTTTGTGCAAGGAAGAATTGGGTTGTGACAGGAGCGGATG
ACATGCAGATTAGAGTGTTCATTACAATACTCTGGAGAGAGTTTCATATGTTTGAAGCACACTCAGACTACATTTC
GCTGTATTGCTGTTTCATCCAACCCAGCCTTTCATTCTAACTAGCAGTGATGACATGCTTATTAAGCTCTGGGACT
GGGATAAAAAATGGTCTTGCTCACAAGTGTGTTGAAGGACACACCCATTATGTTATGCAGATTGTGATCAACCCCA
AAGATAACAATCAGTTTGCCAGTGCCCTTTTGACAGGACTATCAAGGTGTGGCAGTTGGGCTCTTCGTCACCAA
ACTTCACTTTGGAAGGACATGAGAAAGGCGTGAATTGCATTGATTACTACAGTGGTGGGGACAAGCCATACCTCA
TTTCAGGTGCAGATGACCGTCTTGTAAAATATGGGATTATCAGAATAAAACATGTGTGCAGACACTGGAAGGAC
ATGCCCAAAATGTGTCTTGTGCCAGCTTTCATCCTGAGTTGCCAATCATTATCACAGGTTTCAAGATGGAACAG
TACGTATTTGGCATTCAAGCACCTACCGGCTTGAGAGCACACTGAATTATGGAATGGAGAGGGTATGGTGCCTGG
CCAGTCTAAGAGGGTCAAACAATGTGCTTTGGGCTATGATGAAGGGAGCATCATTGTTAAGCTTGGTCGGGAGG
AACCTGCCATGTCCATGGATGCCAATGGAAAGATAATTGGGCCAAGCATTTCAGAAAGTCCAGCAGGCCAACCTAA
AAGCAATGGGAGATGCTGAAATTAAAGATGGTGAAGATTGCCACTGGCAGTAAAGGATATGGGCAGTTGTGAAA
TATACCTCAGACTATTTCAGCACAATCCTAATGGGCGGTTTGTGGTGGTGTGTGGTGTATGGGGAGTATATCATCT
ACACAGCAATGGCATTGAGAAACAAGAGCTTTGGATCTGCTCAGGAGTTTGATGGGCCCCAGATTCTTCAGAGT
ATGCAATAAGAGAGAGCAACAGCATTGTAAAGATATTTAAGAACTTTAAGGAAAAAAATCATTAAACCAGATT
TTGGAGCAGAAAGTATCTACGGCGGCTTCTTATTGGGAGTCAGATCTGTAAATGGCTTAGCCTTCTATGACTGGG
ACAATACAGAACTCATACGAAGAATTGAAATTCAGCCCAAACATATTTTCTGGTCTGACTCTGGAGAGCTAGTCT
GTATTGCTACTGAGGAATCATTTTTTATCCTTAAGTATCTGTGCAAAAAGTCTTGGCTGCACAGGAAACACATG
AGGGAGTTACTGAAGATGGCATTGAAGATGCCCTTGAGGTTCTTGGTGTGATTCAGGAAATTTGTGAAAACAGGGC
TTTGGGTAGGCGATTGCTTCATTTACACAAGTTCTGTGAACAGATTAAATTATTATGTTGGAGGAGAAATAGTCA
CCATTGCCCACCTGGACAGGACGATGTATCTCCTAGGCTACATTCCTAAAGACAACAGGCTTTATCTGGGGGATA
AAGAATTGAACATCATTAGCTATTCCCTGCTGGTTTCAGTCCTGGAATACCAGACAGCTGTCTATGCGGAGGGACT
TTAGCATGGCTGATAAGGTCCTTCCCTACCATTCAAAAGAACAGAGGACCAGAGTTGCACACTTTTTGAAAAGC
AGGGCTTCAAGCAGCAAGCTCTTACAGTATCCACAGATCCTGAGCATCGTTTTGAGCTTGCTCTTCAGCTTGGAG
AGTTAAAAATTGCATACCAGTTAGCAGTGAAGCAGAGTCAGAACAGAAGTGGAAACAACCTTGCTGAACCTGCCA
TTAGTAAATGTCAGTTTGGCCTAGCCAGGAGTGCTGCATCATGCACAGGATTATGGGGGCTGCTGCTTTTGG
CCACTGCCTCTGAAATGCTAATATGGTGAACAAGCTAGCAGAGGGTGCGGAGAGAGATGGCAAAAATAATGTGG
CATTCATGAGCTACTTTTTACAGGGCAAGGTTGATGCCTGCCTAGAGCTCTTAATTAGAACTGGACGGCTGCCAG
AAGCTGCCTTCTTGGCCCGAACTTACTTACCCAGTCAGGTTTCAAGGGTAGTGAACTCTGGAGAGAGAATCTCT
CAAAAGTCAATCAGAAAGCAGCAGAATCCCTTGCTGACCCAACAGAGTATGAAAACCTGTTCCCTGGATTAAAG
AAGCCTTTGTTGTTGAAGAATGGGTGAAGGAAACACATGCTGATCTGTGGCCAGCCAAACAATACCCACTTGTCA
CGCCAAATGAAGAGAGAAATGTCATGGAAGAGGGGAAAAGACTTTCAGCCCTCAAGATCTACAGCTCAACAGGAAC
TTGATGGGAAAACCTGCTTCTCCTACTCCGGTTATTGTGGCCTCCACACAGCCAACAAAGAAGAAAAGAGTTTAC
TCGAACTAGAAGTAGATTTGGATAATTTGGAATTAGAAGATATTGACACAACAGATATCAATCTGGATGAAGATA
TTTTGGATGATGACTGTAATGCTTTCCATTTACCTGACTAAACAGATCATTATTATATATAGGTATTGATTGCT
ACCCTGACCACAGTGCTTTGGACTATGAGAACTTCTTAGATTTTTATATGTAAATGCTGTGGACCACTGGGAGC
ACAATGCCCACATCATCTTAAGAAGAGTTTATGTGCAGCATTTAAATCACTGTGTTTTCTTGTAACTAAAACA
GACATGGGCTTTGATTTTTTTCATACTATTAGACCATATCTCATAAACCTTTTGAATTAAAAAAA

1366/6881
FIGURE 1271

MPLRLDIKRKLTARSDRVKSVDLHPTWPMLASLYNGSVCVWNHETQTLVKTFEVCDLPVRAAKFVARKNWVVTG
ADDMQIRVFNYNTLERVHMFEAHSDYIRCIHVHTQPFILTSDDMLIKLWDWDKKWSCSQVFEGHTHYVMQIVI
NPKDNNQFASASLDRTIKVWQLGSSSPNFTLEGHEKGVNCIDYYSGGDKPYLISGADDRLVKIWDYQNKTCVQTL
EGHAQNVSCASFHELPIIITGSEDGTVRIWHSSTYRLESTLNYGMERVWCVASLRGSNNVALGYDEGSIIVKLG
REEPAMSDANGKI IWAKHSEVQQANLKAMGDAEIKDGERLPLAVKDMGSCEIYPQTIQHNPNGRFVVVCGDGEY
IIYTAMALRNKSFGSAQEFWAHDSSEYAIRESNSIVKIFKNFKEKKSFKPDFGAESIYGGFLLGVRSVNGLAFY
DWDNTELIIRRIEIQPKHIFWSDSGELVCIATEESFFILKYLSEKVLAAQETHGVTEGIEDAFEVLGEIQEIVK
TGLWVGDCFIYTSSVNRLNYYVGGEIVTIAHLDRTMYLLGYIPKDNRLYLGDKELNIISYSLLSVLEYQTAVMR
RDFSMADKVLPTIPKEQRTVAHFLEKQGFQKQALTVSTDPEHRFELALQLGELKIAYQLAVEAESEQKWKQLAE
LAISKQFGLAQECLHHAQDYGGLLLLATASGNANMVNKLAEAGAERDGNVAFMSYFLOGKVDACLELLIRTGR
LPEAAFLARTYLPQSQVSRVVKLWRENLSKVNQAAESLADPTEYENLFPGLKEAFVVEEWVKETHADLWPAKQYP
LVTPNEERNVMEEGKDFQPSRSTAQQELDGKPASPTPVIVASHTANKEEKSLELEVDLDNLELEDIDTTDINLD
EDILDD

1367/6881
FIGURE 1272

ATGCAGCGCTACAATTTTCATTATCTTAAGTACATTGTACATTTCTACAGAACCTGTGATTATTCTCGCATGATA
AGGATGGTACTTGCATATGGTGAATTACTACTGTTGACAGTTTCCGCAGAAATCCTATTTTCAGTGGACCAACATT
GTGGCATGGCAGCAAATGCCAACATTTTGTGGAATAGCAGCAAATCTACAAGAGACCCTGGTTGGTTTTTCGTTT
TGTTTTCTTTGTTTTTTCCCCCTTCTCCTGAATCAGCAGGGATGGAAGGAGGGTAGGGAAGTTATGAATTACTCC
TTCCAGTAG

1368/6881
FIGURE 1273

MQRYNFHYLKYIVHFYRTCDYSRMIRMVLAYGELLLLTVSAEILFQWTNIVAWQQMPTFCGIAANLQETLVGFSE
CFLCFFPLLLNQQGWKEGREVMNYSFQ

1369/6881
FIGURE 1274

AAAGCTCGCGCGGGGGAAGCGGGGCTGTAGCTGGGCAGGGAGAGGGCGGACGAAATCGGTAGCGATCTCGGCTGC
GGCGCTGCCGCGAGCTGCCCGGCCCGCGGGGCGCGCCCTGACCCCTTCATCTTTGGGCAGGCTCGAGGGCGCGCGCA
CGGTTGGCGTTCTGGGGCCTCAAACCTCTGGGCCTTGACCGGGCAGGCCGCGTCTCCCCGGGTGTGAGTCCACCG
GGACCCGGCCGCGCCTAAGCGCGGGCGCCACAGAAGCGGCGGCGCCGAAGACGCGCTCCTGGCTCGGCCCGAC
AGCCTCGCTTGGCCGCCAGTTCTTCTGCAGCCGAAGGCGGTTGTTCTTTTAAAGAATTATTGAAGACGAAGGTTT
TTTTCTTTTTATTTTTTTAATGGCTTTACAGAATCTTAAATAGAATACAGTTTGACATGACGGCAAAAAATGTTG
GTTTGACTTCCACAAATGCAGAAGTAAGAGGATTTATAGATCAGAATCTCAGTCCAACAAAAGGCAACATTTTCAT
TTGTTGCATTTCCAGTTTCCAATACCAACTCACCTACAAAGATTTTACCAAAAACCTTAGGACCAATAAATGTGA
ATGTTGGACCCCAAATGATTATAAGCACACCACAGAGACTAACCAGTTCAGGAAGTGTTCTGATTGGGAGTCCAT
ATACCCCTGCACCAGCAATGGTTACTCAGACACACATAGCAGAAGCTACTGGCTGGGTCCCTGGTGATAGAAAAC
GGGCTAGAAAATTTATAGACTCTGATTTTTCAGAAAGTAAACGAAGCAAAAAAGGAGATAAAAAATGGGAAAGGCT
TGAGACACTTTTCAATGAAAGTGTGTGAGAAAGTTCAACGAAAAGGTACAACATCGTACAATGAAGTCGCTGATG
AGCTGGTGTGAGAGTTACCAATTCAAATAACCATTTGGCTGCTGATTTCGGCTTATGATCAGAAGAACATTAGGC
GAAGAGTTTATGATGCTTTAAATGTGCTAATGGCAATGAACATAATTTCAAAGGAAAAAAGAAATCAAGTGGA
TTGGCCTGCCTACCAATTTCTGCTCAGGAATGTCAGAATCTGGAGATAGAGAAGCAGAGGCGGATAGAACGGATAA
AGCAGAAGCGGGCCAGCTGCAAGAACTTCTCCTACAGCAAATCGCTTTCAAAAACCTGGTACAGAGAAATCGAC
AAAATGAGCAGCAAAACCAGGGCCCGCGGCTCTGAACCTCTACCATTTCAGCTGCCATTTCATAATCATCAATACAA
GCAGAAAAACAGTCATAGATTGCAGCATCTCCAGTGACAAGTTTGAGTATCTTTTCAATTTTGACAACACCTTTG
AGATCCATGATGACATAGAAGTACTAAAGCGGATGGGAATGTCGTTTGGCCTGGAGTCAGGCAAAATGCTCTCTGG
AGGATCTGAACTTGCGAAATCCCTGGTGCCAAAGGCTTTAGAAGGTTATATCACAGATATCTCCACAGGACCTT
CTTGTTAAATCAGGGACTACTTCTGAACCTCTACCCAATCAGTTTCAAATTTAGACCTGACCACTGGTGCCACCT
TACCCAGTCAAGTGTAACCAAGGTTATGCTTGATGCAGAAGTGGCCTTAGCAACTGGGCAGTTTCTGGCCC
CAAACAGTCACCAGTCCAGCAGTGCAGCCTCTCACTGCTCCGAGTCCCGAGGCGAGACCCCTGTTCTGTTCAATG
ATGAAGATGAGGAAGATGATGAGGAGGATTCCTCCTCCCCAGAATAAAGACAAGAGAAAGCCTACGTTTCAATAT
GTGATGCTCATGTGTGTTTGTAGTGTGAGCTTTGTTTTTGAATGATTGCTTCAGTCTTTGCCTTTGTTTGCAC
TGTGTGTTTCAGTGAAAAC TAGAGAAACACAATAAGCAAATCACATGAAGGCTGAGATGATTGAGATGAAAGTTAA
CATAGTGTGAATGAAAGTCTGGCCAACAGAGCAGTAGATGATATAACAAAGAAAGCATGCTTTCTGAGGAGATAG
TGGGGATAATCCCTGAAGAGTTGGCAGTGTGAGTGCAACTCATTTATCTTCTGTGAGGTGGGATTTTTGTGTTCC
TCACACCCATGTAATTATTCTTAGAATTGAGATTGCTACACGGAGCAGTCTTGACGATCGTGTCTGACGTTT
CTCTTCCTTGCTGACTGCCTTTGACAAGGCAGAAATGAACATGAAAAGTCCCCAGGAGAGGGGAGCTGTGTAG
TGAGGGATACTGAGGGCAGTCTGTGGCTGAGGGGCACAGATTGAACTGCTGAACTAGTTGGAGGTCTAGATGAG
GTGCTTTACGCATCAGCTGCCTTAGACAGCTTCTAGAAAGGAGCGAGCGCTACTTCTTAAGTACTTAAGTGACAT
TTAGATAATTTATAGTAAAAC TGAATTTATTATTAGCCAATGCATTGGTGATAGAAATTTACTAGGGCTACTTCT
GGAAGCCAAAATAGAATAGCATTTCATGTGCATTAAATACTTTGCCAGCACTGCCTTTGCCAGCATCCTAAATC
TGGAGTTTTACAAAGAAGGAAAAC TGTATCTTTAGGTTAATCAAAGCTATGCATTTTCATATAGCTTTTTTCATTTAA
AACAAGACAAAGAAACAAATTCCTATGACCAAATTGCTTGCTACAGTTCCCTGCAGTAATTGTATGATCTCACC
CAGTGTGCAATTTGTGAAAATGAACCAAATGTCATTACTTTTGTCTTAAAGAAAAGTCTATTTCAAGAATATGAA
CAGCAGTG

1370/6881
FIGURE 1275

ACACACACTCCCGCTTGGGCCTCCTCTCTCTCTCCGGCTCCATTTTCTCCGCCGCCGGGGGCGGGGTCTCCTGT
GGGGGGCCAGCCGGTATCCAGGTCTCCCTTCAGTGCCGGGGTGAACCCCCGGGGGAGCCGAGAGCCGGGGGCA
GACGGGCGGGGGTTGGGGCGGAGGGAGCAGCGGCCCCAGCGAGTTTGTGGGGAGAAGTAACCAAGCGGGGGGAGG
GGCTGAGCAGGGAGGGGGCCTCAGGGCCCCCCCCCAGCTATGGAATAACGGCTACTGGGGCCGCCTCCTCCAGGC
GGGGCCCCGGGGGGGGCCTGGGATTGGTGAGTGGGGAGCCTGGGGGCCCTGGCGAGCCTCCTGGTGGCGGAGACCC
CGGTGGGGGTAGCGGGGGTTCCCGGGAGGCCGAGGGAAGCAAGACATCGGGGACATTCTGCAGCAGATAATGAC
CATCACCGACCAGAGCCTGGACGAGGCCAGGCCAAGAAACACGCCCTAAACTGCCACCGAATGAAGCCTGCTCT
CTTAGCGTCTGTGTGAAATCAAGGAGAAAACCGGCCTCAGCATTGCGAGCTCCAGGAGGAGGAGCCGGTGA
CCCACAGCTGATGCGCTTGGACAACATGCTTCTGGCAGAGGGTGTGGCTGGGCCCCGAGAAAGGGGGCGGCTCAGC
AGCAGCAGCTGCAGCCGCTGCAGCCTCTGGTGGTGGCGTGTCCCCTGACAACCTCCATCGAACACTCGGACTATCG
CAGCAAACCTTGCCAGATCCGTCACATATACCACTCGGAACCTGGAGAAGTATGAGCAGGCATGTAATGAGTTTAC
GACCCATGTTCATGAACCTGCTGAGGGAGCAGAGCCGACCCAGGCCCCGTTGGCCCCAAAGAGATGGAACGCATGGT
GAGCATCATCCATCGAAAGTTTACGCGCCATCCAGATGCAGCTGAAGCAGAGCACCTGCGAGGCTATGATGATGCT
GCGCTCCCGTTTTCTGGATGCCAGACGAAAGCGCCGTAACCTTACAGCAGACAGGCCACTGAGGTCTAAATGAGTA
TTTCTACTCCACCTGAGTAACCCATATCCTAGTGAGGAGGCCAAGGAGGAGCTTGCCAAGAAGTGTGGCATCAC
CGTGTCTCAGGTCTCCAACCGGTTTGGCAACAAGAAGATTGCGTATAAGAAAAACATCGGAAAGTTCCAAGAGGA
GGCAAACATCTATGCTGTCAAGACAGCCGTGTGAGTACCCAGGGGGGCCACAGCAGCACCAGCTCCCCGACACC
CCCTTCTCTGCAGGCTCTGGCGGCTCTTTCAATATCTCAGGATCTGGAGACATGTTTTCTGGGGATGCCTGGGCT
CAACGGAGATTCTATTCTGCTTCCCAGGTGGCATCACTCCGACGCTCGATGGGGCCAGGGGGCTATGGGGATAA
CCTCGGGGGAGGCCAGATGTACAGCCCACGGGAAATGAGGGCAAATGGCAGCTGGCAAGAGGCTGTGACCCCCCTC
TTCAGTGACATCCCCAACGGAGGGACCAGGGAGTGTTCACCTCTGATACCTCCAACCTGATCTTGCCCCCTCAGGGTC
ACAGGGGTGGGGGCTCTCACAAGGCGACTCTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCCAATACAGGAG
AAGCACAAGACAGAGAAGGGCCAATGGGGTCACTCCGCTCCCTAATGAGACTGTCTGTGCTGGGGGTGCTAATTAC
ATGGCAGGAAGAATGGGGCCCCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTTCCAACCTTTTTCTCTCTCG
CTTTCTTTCTTACACAGAAACATGCACATACCCAGAAACCTATTTTCTCAGACCCCTTTTTCTCCTCTGTCTTTC
TCTCTCCCTCTCCCACACCTCACACACATACTCCCACTTGCAACTATTCTGTTTTCTCTCTGGGCTCCCCAC
TTTCCCTTCCCCACCCCACTTGTAGGCTCTGGAATCTGGAGACGCCAGCCCTGCCCAATCAGAGATGCCAAAAAT
GGGGACATGACTTCTGGACAGAGGACATGGGACACGCCCCCATGCATCCCCACCCCTGCCCTCCAGACAGCTTA
CTTACCTCATACGCAGCTCATCTTAAACCAATAGAATCGCTTGGTGGACGAGAGTGTCTGACTCAGATATCTACC
TCGGAGGGAGTTTCTGCTACTTTAGGGAATTATTGACTGGGCTTTGGGGTTGAACTTTTTTTTTTTTTTTTTTT
AAAGAAAGAAAAAGAAACCTGGGATCCATCTGTTTTTGTGTTGTTGTTGTTTTTGTGTTGTTGTTGTTGTTGTTG
GTGGTGGTTCTTAATTTTTTAATTTAGTTTGGGGAAGTAGCTTGTTTTTTTTTTTTTTAAATAAATATGTTGATTCT
TGTCTTTTTTTTTATTCTTACTTTCCCATATTAGGGGTGATAGCCAAAGGGGTTCTGGTAAGAGAAAGGGGGACA
AACAGAACTGGTAAAGAGGCCCCCTGGCTCCAGGCCTGTCCATCAGGAAGTAAATTTTACAGGGCACCAAGCTT
TGCCCCCTAAATCCATTAGGTGTTCTTTGTTTCATGCAGGCAGGTTTCTGCCGCATTTGATGTGGAGGCAGTGAA
GGGCTTGCCCTGCTGGCCTCTCATCCCCCTTCTTCCCACAACCCCTGGGCAGGGCTGGACTCAGTAATTTTGAGG
AAATTGAAGATGCCATCTTCCCCTGTGAGTGACATGTCTTAATTTTTTAAAAAACTCTATTTGAAAAATTGGAGG
GGGAAGAATGGGAAGGGAGTTATTGCCAATATGTTAATTATGGGTGGGGTGCTTGTATATGTATCTTCCCTCAA
TTTCCGCATAAATGAGGTATCTTTTTGTACACCAAATCAAGGGGTAGGGAGAGGGAGGAGTTGCAAAAAGCC
AGATGTGGGGGAAAAGTAACATCAACACTGTCCCATCCTCAGCCCTGAACCTACCATCTGATCCCCCTCAGACAT
TCTCAGGATTTTACAAGACTGTGAGGTGGGGAACCCCTCCCATTAAGATCCGGGCAGGACTGGGGACAGGTTG
GAAATGTGATGGGTGGGGGGTGGGAGGCATGGGCCGGGGGCGAGTTCTCTCCTCACTTGTAACCTTGTGTAGTTT
CACAGAAAAAAAATGCAGTTTTAAATAAAGAAATTTCTTT

1371/6881
FIGURE 1276

[illegible]

1372/6881
FIGURE 1277

MRGANAWAPLCCLLLAAATQLSRQQSPERPVFCTCGGILTGESGFIGSEGFPGVYPPNSKCTWKITVPEGKVVLNF
RFIDLESDNLCRYDFVDVYNHANGQRIGRFCGTFRPGALVSSGNKMMVQMISDANTAGNGFMAMFSAAEPNERG
DQYCGGLDRPSGSFKTPNWPDRDYPAGVTCVWHIVAPKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDAR
RIGKYCGDSPAPIVSERNELLIQFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTTFFPVTGLKPTVALCQOK
CRRGTLEGNYCSSDFVLGTVITTTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRRGLN
YIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

1373/6881
FIGURE 1278

GAACCGCCATCTTCCAGTAATTCGCCAAAATGACAAACACAAAGGGAAAGAGGAGAGCCACCCGATATATGTTCT
CTAGGCCTTTTAGAAAACATGGAGCTGTTTCCTTTGGCGACGTATATGCGAATCTATAAGAAAGGTGATATTGTAG
ACATCAAGGGAATGGGTACTGTTCAAAAAGGAATGCCCCACAAGTGTTACCATGGCAAACTGGAAGAGTCTACA
ATGTTACCCAGCATGCTGTTGGCATTGTTGTAAACAAACAAGTTAAGGGCAAGATTCTTGCCAAGAGAATTAATG
TGCGTATTGAGCACATTTAGCACTCTAAGAGCCGAGATAGCTTCCTGAAATGCATGAAGGAAAATGATCAGAAAA
AGAAAGAAGCCAAAGAGAAAGGTACCTGGGTTCAACTAAAGTTCCAGCCTGCTCCACCCAGAGAAGCACACTTG
TGAGAACCAATGGGAAGGAGCCTGAGCTGCTGGAACTTATTCCTATGAATTCATGGCATAAATAGGTGTTAAAAA
AAATAAATAAAGGACCTCTGGGCTA

1374/6881
FIGURE 1279

MTNTKGKRRATRYMFSRPFRKHGAVPLATYMRIYKKGDIVDIKGMGTVQKGMPHKCYHGKTGRVYNVTQHAVGIV
VNKQVKGKILAKRINVRIEHISHSKSRDSFLKCMKENDQKKKEAKEKGTWVQLKFQPAPPREAHFVRTNGKEPEL
LELIPYEFMA

1375/6881
FIGURE 1280A

CCGCGGGCGGGGCGCGCTGGCGTTACAGTGACCCGGCGCTCATTGGCTCGCTCGCGGAAGTAGTCCTACATTTCGCG
GTCAGCGCGGGGTCTCCGGGCGCCCTGCAGGGCGGGCAGGCTGTGCCATCCCGCCGGACGTCGGGATGGTGCAGC
TGTACAACCTGCACCCGTTTCGGGTGCGCAGCAGGTGGTGCCCTGCAAGCTGGAGCCGGACCGGTTCTGTGGCGGGG
GGCGTGACGCGCTTTTCGTGGCGGGCGGGCTGCAAGGTGGAGGCGTTCGCGGTGGCCGGCCAGGAGCTGTGCCAGC
CGCGGTGCGCCTTCTCCACGCTGGGCGGGGTGTTGCGCCTGGCCTACAGCGAGGCTGGAGATTATTTGGTAGCAA
TTGAAGAGAAAAACAAAGCTACATTTCTACGTGCTTATGTGAAGTGGAGAAATAAAAGGACTGAAAACCTCTCGTG
TGTGTATCCGAATGATTGGGCATAATGTGGAGGGACCATTACAGCAAAGCCTTCAGAGACCAGATGTACATTATTG
AAATGCCGCTTTCGGAGGGCCCCCTTGTGCATTTCTGTGTCCTGTGAAAGGAGACCTTCTCGTTGGCTGCACAA
ATAAATTAGTCTTATTTAGTTTGAAGTACCAGATCAATTAATGAGGAATTCTCACTATTGGACTTTGAACGTTCTT
TAATTATACACATAGATAATATCACTCCTGTTGAGGTTTCTTTTTGTGTTGGATATGTTGCTGTCTATGTCAGACT
TAGAAGTCTTAATCGTAAACTGGAGTCAGGCCCTAAAAATGGAGAGAGAGTTACACCACCATCCACATAAGACCA
ACAATCGAATAAGACGGACAGAAGAAGGCATCAGTAATGAAATTTACAGCTTGAGTCAGATGATTTTGTCTATCT
GCCAGAAGCCCCCTGGAACCTTCTTGGTGAAAAAAGTGAACAGTCTGGATTATCTGTTACACTGGAGTCTACGGGAT
TAGCTGATGAAAAAAGAAAAATATTCCCACTTTACAGCACCTGCTCTATAGACGTTTTGCTCCTGATATTTCTGTCCT
ATGTCTTGTCTGATGACATCAAGCTACATTCCCTCCAGCTGCTACCCATTTACCAGACCGGTTCTCTTACATCTG
ATGGAAAAAATTTGTCTCAGGAAAAAGAATTGCTGAGTCTCTTTTGCTTTTTCTCCTTACCTCATGTGGGCTATC
TCTACATGGTTGTCAAATCTGTTGAATTGATGTCTAGTCTACCAAGTATCCTGAAAAGTCTCAGCAGGCAGTACTCA
CGCCACAATTTTTGCACGTCATTACAAGTAACAACCTGCAGTGTTTCACTGTGCGGTGCAGTGCGGCGGCAGCTC
GTGAGGAGGACCCGTACATGGACACCACCTGAAGGCTTGCCACCTGTCAGTATGGATGTCTGTGCTTTAAGAA
TACAGCTTTTTCATAGGCTTGAAAGCCATCTGTCACTTTAAAAACCACATCATACTTTTGACTAAAGCAGAACCTG
AAGCCATTCCAGAGAGAAGACAGTCACCCAAGAGGCTTCTTTCGAGAAAAGATAACAGTGTATAAATCAAAATAC
CTCCTGTAGCTGAGGCTGGGTGGAATTTGTATATTGTGAATACGATCTCACCAGTGCAGCTGTACAAAGAGATGG
TAGACTATAGCAATACCTATAAGACTGTCAAAACCCAGAGCTGCATTACCTTCTCAGTGAGGCTCATCTGTTAG
TGCGAGCTGCCCTGATGGATGCCAGTCAGCTGGAACCTGGAGAGAAGGCAGAGCTTTTGGAAGCATTTAAGGAAA
GCTGTGGGCACCTTGGGGACTGTTACAGCAGGCTTGACTCCAGCATTCTCATCTCACCTTGCCATACTATAAGA
TGTCTGGTTTGTCTATGGCTGAAGTTCTGGCCCGCACGGACTGGACAGTAGAGGATGGATTACAGAAATACGAGA
GAGGATTAATCTTTTACATTAATCATTCACTTTATGAAAACCTGGATGAAGAATTAAATGAAGAATTAGCAGCAA
AAGTGGTTCAGATGTTTTATGTGGCTGAGCCAAAGCAAGTGCCCATATTCTCTGTAGTCCTTCTATGAAGAATA
TTAATCCTTTAACTGCCATGAGCTATCTAAGGAAGCTGGATACTTCTGGGTTTTTCATCGATCTTAGTGACATTGA
CCAAGGCAGCAGTGCTCTGAAAATGGGAGATCTTGACATGCACAGAAATGAAATGAAAAGCCATTACAGAGATGA
AGTTGGTATGTGGCTTCATTCTGGAACCTCGGCTGTTGATTCAACAGAGAAAGGGACAGATTGTTCCAACCGAGC
TTGCACTTCACTTGAAGGAAACTCAGCCTGGATTGCTTGTGGCTTCAGTCTGGGCTTGCGAGAAGAACAACAAAA
TTGGAATTGAAGAAGCAGATTCTTTTTTAAAGGTGCTTTGTGCTAAGGATGAAGATACAATTCTCAGCTCTTGG
TAGACTTTTGGGAAGCTCAGCTAGTGGCATGTCTCCAGATGTGGTACTTCAGGAACCTTTTTTCAAACCTCACAT
CACAGTACATCTGGAGATTGTCTAAGAGGCAGCCTCTGACACCACACCATTCGGAACATCGGAGGATCTGATAA
ATGCCTGTAGTCATTATGGCTTAATTTATCCATGGGTTACAGTCGTAATATCATCTGATTCTTTAGCTGATAAAA
ATTATACAGAAGATCTTTCAAATTAACAGTCTCTTATATGTGGTCCTTCATTTGACATAGCTTCCATTATTCCGT
TCTTGGAGCCACTTTTCAGAAGACACTATTGCCGGCCTCAGTGTCCATGTTCTGTGTCTGTACACGCTTGAAAGAGT
ATGAACAGTGCATAGACATACTGTTAGAGAGATGCCCGGAGGCAGTCATTCCATATGCTAATCATGAAGTGAAG
AAGAGAACCGGACTCTGTGGTGGAAAAAAGTGTGCTGAAGTCTTGTGAGAGAATAAAATGTGGTGGAGAGAAGT
ATCAACTCTACCTGTCATCATTAAAAGAAACATTGTCAATTGTTGCTGTGGAAGTGAAGTGAAGGATTTTCATGA
ATGTTCTCCAGAAAGATGGTACTGCAACATTTTTCTTGCCATATCTTCTATTGCAGTCGAAAGAAACCATTTGA
CTTAAAGGTATCATTTGAAAAATACCATAATGGCATTGAGACTGAATTTCTAAAAATTGAATGCCAAAGTACAA
GTAGAGGAGTTTTTTATTTTATATATACACACACACACACACACACACACATATATGATACAA
ATGCTTTACAGGCTGCTTACCTTACCGTGTAGTGGTAACCTATTCACTTCTTAATTTATGACCTCAATCAATTTAAT
TGTCTAGAATGTAAAAAGTCTTTAAGACATAAGAATTCCTCAAAGAAGCCATACATTTTTTAAAGGTGGGGATTGA
CTTTTATTCCAAGGAACAACATCAGTTCACTGTTGTTGGAGACATGACAATCATTTTTCATCCCAAGAACACTTTA
AGGAAACATTTTACAAGTATGCTTGAAAGAATGTCACTAACTGGTCCAGAATTTTATCTTCTTGATTTTTCCAGA

1376/6881
FIGURE 1280B

TTTCTCTATGTTTTTGAGAAAGATGTTAATGTTTTGCCATGGTAAAAGATTTCAAACCTCATTTTTTTTTGTTCCT
TTTCTTGTTACTTTTAAGAAAACATGCTCTGTTTCTCTGAATCAAATGAAGTAGAAGTTTACAAAGCTAACTT
TCTTCTTGCTAGCTATTAACATGATTTGTCAAATGCATGTTTTTTTCAGCCAAAGCCTTGTTTCCATTTTTGTT
GATGTGTACTCTTGCTCTTTTAGCTAGAGTGTATGTGAAAATAAAGAAATACATCATTGTATTACAAAAAAAAA
AAAAAAAAAAAA

1377/6881
FIGURE 1281

MVQLYNLHPFGSQQVVPCKLEPDRFCGGGRDALFVAAGCKVEAFVAVAGQELCQPRCAFSTLGRVLRRLAYSEAGDY
LVAIEEKNKATFLRAYVNWRNKRTENSRCIRMIGHNVEGPFKAFRDQMYIIEMPLSEAPLCISCCPVKGDLLV
GCTNKLVLFSKYQIINEEFSLDDFERSLIIHIDNITPVEVSFCVGYVAVMSDLEVLIVKLES GPKN GERVHHHP
HKTNNRIRRTEEGISNEISQLESDDFVICQKPLELLGEKSEQSGLSVTLESTGLADEKRYSHFQHLLYRRFAPD
ISSYVLSDDIKLHSLQLLPIYQTGSLTSDGKNLSQEKELLSLFCFFSLPHVG YLYMVVKSVELMSVYQYPEKSQQ
AVLTPQFLHVITSNNLQCFTVRCSAAAAREEDPYMDTTLKACPPVSM DV CALRIQLFIGLKAICHFKNHIILLTK
AEPEAIPERRQSPKRLLSRKDTSVKIKIPPVAEAGWNLYIVNTISP VQLYKEMVDYSNTYKTVKTQSCIHLLSEA
HLLVRAALMDASQLEPGGEKAELLEAFKESCGHLGDCYSRLDSQHSHLTLPYYKMSGLSMAEVLARTDWTVEDGLQ
KYERGLIFYINHSLYENLDEELNEELA AKVVQMFYVAEPKQVPHILCSPSMKNINPLTAMSYLRKLDTS GFSSIL
VTLTKAAVALKMGDLD MHRNEMKSHSEMKLVCGF ILEPRLLIQQRKGQIVPT ELALHLKETQPGLLVASVLGLQK
NNKIGIEEADSFFKVLCAKDEDTIPQLLVDFWEAQLVACL PDVVLQELFFKLTSQYIWRLSKRQPPDTTPLRTSE
DLINACSHYGLIYPWVHVVISSDSLADKNYTEDLSKLQSLICGPSFDIASIIPFLEPLSEDTIAGLSVHVLCTR
LKEYEQCIDILLERCPEAVIPYANHELKEENRTLWWKKLLPELCQRIKCGGEKYQLYLSSLKETLSIVAVELELK
DFMNVLPEDGTATFFLPYLLYCSRKKPLT

1378/6881
FIGURE 1282

GGCACGAGGGCTTCTCCTGCGCCTCCTTTTCGCCCAGCACTAGCGCCTTAGGCCAGCTCGGGGGATGTGAGAGCC
GAAGCCCTTAGACTGCCAGGCACAGAGTCGGGTCGGGATTTGTTCAGCCAAGCCTCGGCTCCAGCTCCGCAATCTC
GGGACTCACCCGAGCGACCCAGGCCCGACGGCAAGTTCGGGCGGGACGGCGGCCGCCGCGCTCAGGCTCAGCT
TCGCTGCCCCGCCAGAAAGATGAATCCGGCCTCGGCGCCCCCTCCGCTCCCGCCGCTGGGCGAGCAAGTGATCCAC
GTCACGCAGGACCTAGACACAGACCTCGAAGCCCTCTTCAACTCTGTTCATGAATCCGAAGCCTAGCTCGTGCGG
AAGAAGATCCTGCGGAGTCTTTCTTTAAGGAGCCTGATTCGGGCTCGCACTCGCGCCAGTCCAGCACCGACTCG
TCGGGCGGCCACCCGGGGCCTCGACTGGCTGGGGGTGCCAGCATGTCCGCTCGCACTCGTCGCGCGCTCCCTG
CAGCTGGGCACCGGCGCGGGTGCTGCGGGTAGCCCCGCGCAGCAGCAGCGCACCTCCGCCAGCAGTCTACGAC
GTGACCGACGAGCTGCCACTGCCCCCGGGCTGGGAGATGACCTTCACGGCCACTGGCCAGAGGTACTTCCTCAAT
CACATAGAAAAAATCACCACATGGCAAGACCCTAGGAAGGCGATGAATCAGCCTCTGAATCATATGAACCTCCAC
CCTGCCGTCAGTTCCACACCAAGTGCCTCAGAGGTCCATGGCAGTATCCAGCCAAATCTCGTGATGAATCACCAA
CACCAGCAGCAGATGGCCCCCAGTACCCTGAGCCAGCAGAACACCCCACTCAGAACCCACCCGCGAGGGCTCATG
AGTATGCCCAATGCGCTGACCACTCAGCAGCAGCAGCAGCAGAACTGCGGCTTCAGAGAATCCAGATGGAGAGA
GAAAGGATTTCGAATGCGCCAAGAGGAGCTCATGAGGCAGGAAGCTGCCCTCTGTGACAGCTCCCCATGGAAGCT
GAGACTCTTGCCCCAGTTCAGGCTGCTGTCAACCCACCCACGATGACCCAGACATGAGATCCATCACTAATAAT
AGCTCAGATCCTTTCTCAATGGAGGGCCATATCATTGAGGGAGCAGAGCACTGACAGTGGCCTGGGGTTAGGG
TGCTACAGTGTCCCCACAACCTCCGGAGGACTTCCTCAGCAATGTGGATGAGATGGATACAGGAGAAAACGCAGGA
CAAAACACCCATGAACATCAATCCCCAACAGACCCGTTTCCCTGATTTCTTGGACTGTCTTCCAGGAACAAACGTT
GACTTAGGAACTTTGGAATCTGAAGACCTGATCCCCCTCTTCAATGATGTAGAGTCTGCTCTGAACAAAAGTGAG
CCCTTTCTAACCTGGCTGTAAATCACTACCATTGTAACCTGGATGTAGCCATGACCTTACATTTCTTGGGCCTCTT
GGAAAAAGTGATGGAGCAGAGCAAGTCTGCAGGTGCACCATTCCCGCCTCCATGACTCGTGCTCCCTCCTTTTT
ATGTTGCCAGTTTAATCATTGCCTGGTTTTGATTGAGAGTAACTTAAGTTAAACATAAAATAAATATTCTATTTTC
ATTTTCTGCAAGCCTGCGTTCTTGTGACAGATTATACAGAATTGTGTCTGCAGGATTGATTATGCAGAATACTTT
TCTCTTTCTTCTCTGCTGCCCCATGGCTAAGCTTTATGGGTGTTAATTGAAATTTATACACCAATTGATTTTAAA
CCATAAAAAGCTGACCACAGGCAGTTACTTCTGAGGGCATCTTGGTCCAGGAAATGTGCACAAAATTCGACCTGA
TTTACAGTTTCAAAAACGTATTGATGACAGTAGTACCAAATGCTTTAAAAACTATTTAACTTGAGCTTTAAAAA
TCATTGTATGGATAGTAAAATTCTACTGTATGGAATACAATGTAATTTTGAATCCAAAAAAAAAAAAAAAAAAAAA

1379/6881
FIGURE 1283

MNPASAPPPPLPPPGQQVIHVTQDLDTDLEALFNSVMNPKPSSWRKKILPESFFKEPDSGSHSRQSSTDSSGGHPG
PRLAGGAQHVRSHSSPASLQLGTGAGAAGSPAQQHAHLRQQSYDVTDELPLPPGWEMTFTATGQRYFLNHIEKIT
TWQDPRKAMNQPLNHMNLHPAVSSTPVPQRSMASQPNLVMNHQHQQQMAPSTLSQQNHPTQNPPAGLMSMPNAL
TTQQQQQQKLRLQRIQMERERIRMRQEELMRQEAALCRQLPMEAETLAPVQAAVNPPMTTPDMRSITNNSDPFL
NGGPYHSREQSTD SGLGLGCYSVPTTPEDFLSNVDEMDTGENAGQTPMNINPQQTRFPDFLDCLPGTNVDLGTE
SEDLIPLFNDVESALNKSEPFLLTWL

1380/6881
FIGURE 1284

CTTCTCTTTCACTCCGCGCTCACGGCGGCGGCCAAAGCGGCGGCGACGGCGGCGGCGAGAACGACCCGGCGGCCA
GTTCTCTTCTCTGCGCACCTGCCCCGCTCGGTCACTCAGTCGGCGGCGCGGCGCCCGGCTTGTGCTCAGACCTC
GCGCTTGGCGGCGCCAGGCCAGCGGCCGTAGCTAGCGTCTGGCCTGAGAACCTCGGCGCTCCGGCGGCGCGGGC
ACCACGAGCCGAGCCTCGCAGCGGCTCCAGAGGAGGCAGGCGAGTGAGCGAGTCCGAGGGGTGGCCGGGGCAGGT
GGTGGCGCCGCGAAGATGGTTCGCCAAGCAAAGGATCCGTATGGCCAACGAGAAGCACAGCAAGAACATCACCCAG
CGCGGCAACGTCGCCAAGACCTCGAGAAATGCCCCGAAGAGAAGGCGTCTGTAGGACCCCTGGTTATTGGCTCTC
TTCATTTTTGTGTCTGTGGTTCTGCAATTTTCCAGATTATTCAAAGTATCAGGATGGGCATGTGAAGTGAAGTGA
CCTTAAGATGTTTCCATTCTCCTGTGAATTTTAACTTGAAGTCAATTCCTGATGTTTGATACCCCTGGTTGAAAACA
ATTGAGTAAAGCATCCTGCCTCAGAATGACTTTCCTATCATGCTTCATGTGTCATTCCAAGGTTTCTTCATGAGT
CATTCCAAGTTTCTAGTCCATACACAGTGCCTTGCAAAAAACACCACATGAATAAAGCAATAAAATTTGATTG
TTAAGATACAGTAGTGGACCCCTACTTATTCAGTCAATTAAGAGTAAGTTTTTTTATGTGGTTATTAATAACAGTAT
GAACAATTAGTCTAACTCTGCATAGACAGGGTCTAGATTTTGTTAACCCAAATGTATAACTGCAGTTAGCTTAA
TTACAATTTGAAGTCTTGTTGGTTTTTATATAGCTAGGCACTTTATTACTCTTTTGAAGTGAAGCACACTCCCTT
ATAGGTTTATGTAAGTCTGCTGTAATAAGGTGCTTATAAATGGAACAACTACACAGCCTAGTTTTGCCACAACCT
TTAGCATCTAAAAAGTTTTTAAAGCTTCTAAATGTCTAATATAAAGGGAGATGCTTATAGCCACAACATCTATTT
TACCAATATTGTTTCCATTACACTACCTTGGAATTTGCATGAGTGAGTATAGTAACCCAAGATGCCATAAAAAA
AACTTGATCGTTTTCTGACTTAATTAGTTACTGTGGTTTCACTAAAAGCTACCGTGGTGGAGTGAAAGTCAGTCAG
GGAAGGTTTGTATGTTACATTTATTTACCAGAACTATTTTAAATATATCAAAGGGGTTTACTATGCCAAACAA
AATTCTAGGGAAAAATACTGCTAAAAATGGATGCCTCATCAGAACATGCTGTTGAGTCCAATGTGCCATAAGACA
TTTTAGCATGTTAAATAGCACTTTTTAATAGCAAAAAAAGGCACATCAACTGCGAAGTTATCCTTAGTTTTGCAAT
GCTTTTTCTAGATTAATGATTTTTCAATCATTAGGGTACTAGACACATCAGCCTAAAGTGGCATCTGGAATTGAA
TGGATTTACTGATAATGATCAGTCTTTAGTCTTCCCTTTGTTATATGACTTTTATAGGTTATGATTGATCAAATTT
ACGTTTTACTAATGGTAAGGGTGAGGGTCATAGGGCAGGTTTTGGGTTTTCTAGTACTGTTGAAAAGTGAAGTA
TTGGCTATTTGTATACCTTAGCCATAAAGTGGTGAACCAAAACCTGAGCAGTGTCTATGTATTAATGCGTTGGAAA
GAAAGCTGCTTGTGTTTGCCTTGTAAATTGCCTCAGGATATTTCTTTTAAATAAGCTGTTTTAAGAGGAACAGA
AGGGAAATCTGCTACCTAGTCTATACACAGCGTGAACCTCACAGGGGGCTTCTGATACCCTCAAACATGGAGAAC
AGTAAGGGAGCAGAGTGGTTAAGGACTTTTCAAGAACTTAACTATTCTGGAATAAGGAATGAATCAACTGACCTTG
GGCCAGCAGGTTTTTAACTAAATTGTTACTTGCCTTTCTCAGGAGTAAATCAGTCTCTGTACTTGTTCCTTTT
TTGAAACAAGTGTCTTGGTTAACTAATTCTGTTTTATGGTTGTGCTAAATTCATAGCAGGTGCCTTATTCTTTGC
TTTTAGTCAAACCATTCATATCAGAAATTTTCTTGGTTTACTATAGATATTTGGCTTTAAGTTGTTGTTTGTGT
TTTTTAATGTACAATGTTCTGATAAATTTGACTGTAAATTGCTATAGCTAGCAATCATTTTACATATGTAAAAA
ATTGCATTCCCTTTGTATTTTATGTTGTAATTCACCAATTAAGTGCAGTTTATATTGAGTTGGATTATGCATGTT
TAGGTAAACGAAAGCTGTGTCTTACTTGATTTATTCTTTAAAAATAAAGTTCCTGAATATTTGAAAAA
AAAAA

1381/6881
FIGURE 1285

MVAKQRIRMANEKHSHKNITQRGNVAKTSRNASPEEKASVGPWLLALFIFVVCGSAIFQIIQSIRMGM

1382/6881
FIGURE 1286

GCATGAGGAGACGTGTAGGGGCCGGGTTTCGGCCCTGGTGAACCTCTCACCCGAGCGGTTTCTCTTTCCGGGACAAC
ATGGCGCCGTCCACGCCGCTCTTGACAGXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXGGAATCTGGGAAGAATTGCAAAGTCTGTATCTTTAGTAAGGATGGGACCTTG
TTTGCTGGGGCAATGGAGAAAAAGTAAATATTATCAGTGTCACTAACAAGGGACTACTGCACCTCCTTCGACCTC
CTGAAGGCAGTTTGCCTTGAATTCTCACCCAAAAATACTGTCCTGGCAACGTGGCAGCCTTACACTACTTCTAAA
GATGGCACAGCTGGGATACCCAACCTACAACCTTTATGATGTGAAAACCTGGGACATGTTTGAAATCTTTCATCCAG
AAAAAATGCAAAATTGGTGTCCATCCTGGTCAGAAGATGAAACTCTTTGTGCCCCGAATGTTAACAATGAAGTT
CACTTCTTTGAAAACAACAATTTTAACACAATTGCAATAAATTGCATTTGCAAAAAATTAATGATTTTGTATTA
TCACCTGGACCCCAACCATAACAAGGTGGCTGTCTATGTTCCAGGAAGTAAAGGTGCACCTTCATTTGTTAGATTA
TATCAGTACCCCAACTTTGCTGGACCTCATGCAGCTTTAGCTAATAAAAAGTTTCTTTAAGGCAGATAAAGTTACA
ATGCTGTGGAATAAAAAAGCTACTGCTGTGTTGGTAATAGCTAGCACAGATGTTGACAAGACAGGAGCTTCCTAC
TATGGAGAACAACTCTACACTACATTGCAACAAATGGAGAAAGTGCTGTAGTGCAATTACCAAAAAATGGCCCC
ATTTATGATGTAGTTTGGAAATTCTAGTTCTACTGAGTTTTGTGCTGTATATGGTTTTATGCCTGCCAAAGCGACA
ATTTTCAACTTGAAATGTGATCCTGTATTTGACTTTGGAACCTGGTCCTCGTAATGCAGCCTACTATAGCCCTCAT
GGACATATATTAGTATTAGCTGGATTTGGAAATCTGAGGGGACAAATGGAAGTGTTGGGATGTGAAAACTACAAA
CTTATTTCTAAACCGGTGGCTTCTGATTCTACATATTTTGCTTGGTGCCCGGATGGTGAGCATATTTTAACAGCT
ACATGTGCTCCCAGGTTACGGGTTAATAATGGATACAAAATTTGGCATTATACTGGCTCTATCTTGACACAAGTAT
GATGTGCCATCAAAATGCAGAATTATGGCAGGTTTCTTGGCAGCCATTTTGGATGGAATATTTCCAGCAAAAACA
ATAACTTACCAAGCAGTTCCAAGTGAAGTACCCAATGAGGAACCTAAAGTTGCAACAGCTTATAGACCCCCAGCT
TTAAGAAATAAAACCAATCACCAATTCCAAATTGCATGAAGAGGAACCACCTCAGAATATGAAACCACAATCAGGA
AACGATAAGCCATTATCAAAAACAGCTCTTAAAAATCAAAGGAAGCATGAAGCTAAGAAAGCTGCAAAGCAGGAA
GCAAGAAGTGACAAGAGTCCAGATTTGGCACCTACTCCTGCCCCACAGAGCACACCACGAAACACTGTCTCTCAG
TCAATTTCTGGGGACCCTGAGATAGACAAAAAATCAAGAACCTAAAGAAGAACTGAAAGCAATCGAACAACCTG
AAAGAACAAGCAGCAACTGGAAAACAGCTAGAAAAAATCAG

1383/6881
FIGURE 1287

MQNWCPSWSEDETLCAARNVNNEVHFFENNNFNTIANKLHLQKINDFVLSPGPQPYKVAVYVPGSKGAPSFVRLYQ
YPNFAGPHAALANKSFFKADKVTMLWNKKATAVLVIASTDVDKTGASYIGEQLHYIATNGESAVVQLPKNGPIY
DVVWNSSSTEFCAVYGFMPAKATIFNLKCDPVDFDGTGPRNAAYYSPHGHILVLAGFGNLRGQMEVWDVKNYKLI
SKPVASDSTYFAWCPDGEHILTATCAPRLRVNNGYKIWHYTGSIHKEYDVPSNAELWQVSWQPFLLDGIFPAKTIT
YQAVPSEVPNEEPKVATAYRPPALRNKPIITNSKLHEEEPPQNMKPQSGNDKPLSKTALKNQKHEAKKAQKQEAR
SDKSPDLAPTPAPQSTPRNTVQSISGDPEIDKKIKNLKKKLKAIEQLKEQAATGKQLEKNQLEKIQKETALLQE
LEDLELGI

1384/6881
FIGURE 1288A

GGCCGTTGCTCCAGGGAGAACTGCAAATATCTTCATCCACCCCCACATTTAAAAACGCAGTTGGAGATAAATGGA
CGCAATAAAGTTGATTTCAGCAGAAGAACATGGCCATGTTGGCCCAGCAAATGCAACTAGCCAATGCCATGATGCCT
GGTGGCCCCATTACAACCCGTGCCAATGTTTTTCAGTTGCACCAAGCTTAGCCACCAATGCATCAGCAGCCGCTTT
AATCCCTATCTGGGACCTGTTTCTCCAAGCCTGGTCCCGGCAGAGATCTTGCCGACTGCACCAATGTTGGTTACA
GGGAATCCGGGTGTCCCTGTACCTGCAGCTGCTGCAGCTGCTGCACAGAAATTAATGCGAACAGACAGACTTGAG
GTATGTCGAGAGTACCAACGTGGCAATTGCAACCGAGGAGAAAAATGATTGTGGTTTGCTCATCCTGCTGACAGC
ACAATGATTGACACCAATGACAACACAGTCACTGTGTGTATGGATTACATCAAAGGGAGATGCTCTCGGGAAAAAG
TGCAAATACTTTTCATCCCCCTGCACATTTGCAAGCCAAGATCAAGGCTGCCCAATACCAGGTCAACCAGGCTGCA
GCTGCACAGGCTGCAGCCACCGCAGCTGCCATGACTCAGTGGCTGTCAAATCACTGAAGCGACCCCTCGAGGCA
ACCTTTGACCTGGGAATTCCTCAAGCTGTACTTCCCCCATTACCAAAGAGGCCTGCTCTTGAAAAAACCAACGGT
GCCACCGCAGTCTTTAACACTGGTATTTTCCAATACCAACAGGCTCTAGCCAACATGCAGTTACAACAGCATACA
GCATTTCTCCACCAGTTCCCATGGTGCACGGTGCTACGCCAGCCACTGTGTCCGCAGCAACAACATCTGCCACA
AGTGTTCCTTTCGCTGCAACAGCCACAGCCAACCAGATACCCATAATATCTGCCGAACATCTGACTAGCCACAAG
TATGTTACCCAGATGTAGAATTTTCATCACTAAACAATCATGCTAAAGAGGAAAGGACAGTGTGCTTGTTAGAG
TAAAGGACGAGGTCATTAGCCATATTGTATATATCGTCAAGCAACACACACAAAAGTTCCTCAGCCACAAGACAT
CCACATATTGCATGTTAACCAGAAGAAAAGACAACATTTTCCGGAAATCCACTGCACACTGTTGCCTATACACTT
TGTACATTTAATTGATATTTGTGCTGAGGTGATATTCCTGTCTAAAAGAACAACATTGTCTTTCTTTTCTAGCAC
AGAGTTATGCATTCAAAGATGCATACCTAGTTAGTTTCTATATATTTCATGCCATCTTGAAAAGACAGACTATGG
TGTAACCATGATTCTATTATGTATTGGTACGTCTGTAGACCAAGATATAATTTTTTAAAAATAAGTTTATTTCTT
TCAAGGTTTACAATAACAAAGGTGCACCTTGATTTTAAATTTGCCATTATAGATGAGAGCGTGCATGCACAGTC
ATTTTTGTTTTAAGAGTAATATTTTTAATGTAATAGATTGTAAGACGTGGTGAGGGAGGGATCTGCACAGAGATGAA
TGTGCCAAGCAAAACCACAACCTGTGTATATTTTAAAGCACATCATGGCTTAAAGTACCATGTTGTTAAGGATTCT
CATGAAGTGCCATAGACTGTACATCAAATTAGAGTATTATTTCTTCAGTGTTATTGTTTTTCAGAGCCACATTTTG
TTGCATATTTGCTAGTACTAATCAGTCAAAGGGCACCATTCTTTTTTTTTTTTTTTTGAACCAAAGCTGTCTCAG
AAATGGCCAATTTAACTTTACAGTAACAATAGACAGCACACAACAACTCTCTCAATACAGATAAACTCACACAT
ACTGGAGATATATATATAATAGATATATATAAAATTATTTTAAATGCATTGTAGTGTAATATTTATGCATACTATA
CTGTATAACATGTTATTCAAAGGGATTGCCATTTCTGAGACACAGTAACAAAAAATGAGGAAATTATTTTGCT
TCTATTTATAGCCTCTGTCAAAAGTCAAAAGACTATAAATGCTTTGCAAAAATGGTTTCACGTTTGCTTAAATGC
TTCATCACAGTCACATTTCAAATAGTGACTCTAAACAAAGAAGAAAGCAGCACTGTGCATCAGATGCATGATAAAC
CAAAATATGAAAATGGGAAATGTTTAATTAACCTAGTAATTGGGTGGGTAAAGTACATGGGTGAATTTTATATGT
GATTTTTGTTTTGTTTTGTTTTGTTTCAGATTAACTGCTTATAGCCTTAGAAAAGCCTTTTACAAAATTAAAAAAA
AATAGATGTGCATTTCAGTTTTTAAAGATGGAATCATCCAAAGGAATTCCTTTTTTTGAGGTTTGATGTTGCAGC
TAGTAAAGGATATTTTTGCTCTGTTTCAGCAGTTCTAAAAATTGCTGAAGTAGGGGCCAGGTCACTGGTAGTTATA
GTATGGAATGGGAGAAGTGAAAAGTTCAGTTATAGAAGTTTCCATACCTTCCAAGTTTACTGCAAGTTTTTATGCTT
GAGAGAGATGCTTTCTAATATAAGACTGATGTGTTGATTTTACTGATTGTACTGTACATCTATTAAAGCCTTAGA
TTATTACATTACGGGTTGGAACCCATACCAATGTAATTTCAATCGTGTTAAGAAAGTAATGGTGACTTCACATGT
TATTGTAGTTAGTTACATTATAGAATATTACTTATTTTTCTTGTTAAATGTAGTTTTTCATTTCTACATTTAT
TAGATTTTCATTTTCTATTAACAATTGAATACCATTTTCAGTTTATAGACTTGTTTTATTAGATTTTACCAATGAA
TTTTTCAAAAATACAAAAAAGTAGTTTTCTTCATAACATACTCAGTTTTGAATTACATGTAGTGTACATGA
ATATTCGTATTGTTAACTAAATGATTATATTTTACTGATTTAATATTACAGTGTAAGAATGTCAGTCATTGTTA
GTTCTTGTCTAGTTTTTCATTAAGAACAAGATCTTTTATATGGATATCTTATAAATATATAATCATTGCTAAG
TAAGAAGTTAAGTTGTTGCTATCGCAACAATCCTGGCAGACAATTGAGTAATATTTTGATGATTTATTTGTTTG
TAATTAGTTATTATAAGAAGATCTAGATCCTAGATATTAGAATAAAATTTATTTTCTACTGTATCCATTTCAAAT
GTTAAATATTGTTTAAATATTTTGAATCCCTGAGTATCAGGCCTTGTTATAAATAAGCTGCATAATCAATAAA
TAGAACAAGGGACTTTTTGTTGATAATCCAAATACTCAAAGTTTACGTAATGAAAATTATAGCGTGTGTGCAAC
TCTTGAGGGTTGATTATGCTGCAATTTAGCATGTTGGAACGTCTAGGGAGAAGGTTGACTTTTTGCACTTCTGTA
TATAGTCAAAAGAGAGAAACCTGTATAATAGTAAGATCTTATTTTGAATAAAAACGTCTATAATTACAAGGAGTT
TTGTTAAGGCTAATACAATGACAGACTGAGCAAAATGCTTGCAAAAGTGGCACAGAGTTAGCACTCCATACCCC

1385/6881
FIGURE 1288B

TTCAAACATGTTGCTTTGCTTTCTTGTGGACAGCTTGTAGTTTGCCAGGATTTTTTCAGCTGGAAAGATACGCCA
TCCTTTCAAACCCCTCATGACTGACAAAACTCCATGGGGCCAAATCTGCCTGAAGATCATTACCAAAAAATAGCAG
GTACTTCTACCATTAAGGTGAAATCATGGATCAGATATTCCTTACATTTTTTCAAACACTACTGCATGTTTAAACT
TCAACAAAAAAGAGAGAAAGAACTATACTAAGAACATATATTATTCAGATCAGTTTCTGCCAATTTTCAGTGTT
TATTGTTTCAAAAAAATCTTCAAACAAGTATTGACTTTCACAAAATTTAAATCATAACAGGCAAACCAAACA
GCACACTGTAGCTATAGTTGTTATGTGATTGTTTTTAATTGCTGTAGGATCCTGTTCTTTCAGCAGGTGAAAAA
TAAAACGCAGTTCAAATTTCTATGGTTTTAATTTTCAACTCAGAAGCACTCAAAAATGCAAAATGTGATAATGGGC
ACTTGTTTTAAAAGAATTAGTGTATCCAGCCTTCACTCCAGCTGGTTAAAAATGTTGCACTTATCAGCAACCCTAC
CACTTTCATCTGCTGAAAGGACAAATGTGCTTGGTTTTACTATTATGTAATCACAACCTACTTTCTGCTTGTAGT
TGCTTAAATTTATGTATTTTGTCTTGGGCTGCAATTTGTTTTATGCTTATTTTATTATTACTGCAGTAGTTGACT
TTGCTGTATGGAAAAATAAAGTGAAATTGCCCTAATAAACTTCTCTTTCTTAAGT

1386/6881
FIGURE 1289

ATGTGGAGAAAGCCAGGGGACCCACAGAAGGCTGCCTGTGGCCACGT CATAGCAAAGGAAC TTTATGGAGAGGAG
CAGGAAGTCAGAGAGCCAGCTGAATTCAAGAATCTGATAGGAGAGAAGATGTCAGTCCCTCTGGAAGAAGTTAGC
AAAGTTGTGGCCTTGAATGGGAAGGGACAGAAGAGAGGTT CAGGGTTCGAGGCTGAGGCAACAGGAAACTGCCTG
GAATGGAAC TTGCCAAGGGGGATAGGAGGTGCAGGCCGGGGCCTCTTGGGAGAAAGAGCTGCACCATCTTCCAAC
ACCTGTGGGAATGCTGTCTTGAAAACACTGCAGCAGCCAGTCATGAGCCAAGGAAGCAGACAAGAGCAACGAACA
CAGGCATTGTGCATACAGACCTACCCAGAGAAGCCAGTATCCATGGCTTTGGAGAGTTCAAATATTCAATTTTCC
GTTCAAAAAAAGGCCACGCCACCGGCTAAGAGTTCCGCCAGGGGCCAGCTCTCAGGAGGCCTCTTCGGTGCCGC
CAGCCTCCCGAAGTCATCCAAGGTAGCAGGCAAATCCGGCAGCAGCAA ACTAGCTCGGATTTCGGCTTCGGTTTTT
CTCCTGGCCGGCGCCACAGGCCCTCCTCCCGGGCGGGCTCCTCGGCCCTCCTTCTCAACCTCAGCCCCGGCGC
CGACCCCTTCGGGCACCTTCCCGCCCCGTCTCGTACTGTGCGCGTCACCGCCGCGGCTCCGGCCCTGGCCCCGATG
GCTCTGTGCAACGGAGACTCCAAGCCTTGGGCTCCGCGGCGGTTAGGCCGTTCTGGACGAACCCCTCGGAGCTG
CACTGTCTTCCCCCTCCCCAACGCCCCCTGCAGGCCCGCGTGAGGGCTGGTGGCCCCAGGGTCGCGCACTCCGTT
CTCCCTCCCGCTTCTTCTCAGAGAGGAAAGGGTGTGTGTCCAGGTCCCGCCTCCGTCCAGCTTGCTCCCTGTC
GAGCTTGCTGGTTTTCGGGGTAACCCGCTTCCCGCCTTTGGGGTCCCTCCCGGGACGCGAGCCGTGCCAGCTC
GCCCAGGCCTGGGCAGTCCGGAGTTCCGGAGTGCTGGAAAAGTTGCCGCTTGACGTACCGGGCGGGGAGAGCA
CGTTTGACCGCTGCTGCTCATCTCTCCTCCAAC TACTTTTCTTAGACCGTTCTTACTTTTCGTCCCGCTTTT
GAATTGGGCACCTTCGCTTTCACCTCTGTATTAAAATTTTCATTGGCCTGGAGTTCTTTCTGA

1387/6881
FIGURE 1290

AGGCATAGCAAAATGAATCTAAAAAGTTATATGGAGCACAGTTCACCCTGAAGTTGGCCTTACAGAAAATGGAAA
AGTAATACTGAAGAATTTTCCTTTATGATATAGCTGGATGCAGTGGAACCTTCACCGTGCAGAACAGAGAACTTGA
GTGTATTTCGAGAGATCAAAGAGAGAGTAGGCACGTCAAAAGTTTTGGTTTTACTCAGTGGTGGAGTAGACTCAAC
AGTTTGTACAGCTTTGCTAAATCGTGCTTTGAACCAAGAACAAGTCATTGCTGTGCACATTGATAATGGCTTTAT
GAGAAAACGAGAAAAGCCAGTCTGTTGAAGAGGCCCTCAAAAAGCTTGGAATTCAGGTCAAAGTGATAAATGCTGC
TCATTCTTTCTACAATGGAACAACAACCCTACCAATATCAGATGAAGATAGAACCCACGGAAAAGAATTAGCAA
AACGTTAAATATGACCACAAGTCCTGAAGAGAAAAGAAAAATCATTGGGGATACTTTTGTTAAGATTGCCAATGA
AGTAATTGGAGAAATGAACTTGAAACCAGAGGAGGTTTTCTTGCCCAAGGTACTTTACGGCCTGATCTAATTGA
AAGTGCATCCCTTGTTGCAAGTGGCAAAGCTGAACTCATCAAAACCCATCACAATGACACAGAGCTCATCAGAAA
GTTGAGAGAGGAGGGAAAAGTAATAGAACCTCTGAAAGATTTTCATAAAGATGAAGTGAGAATTTTGGGCAGAGA
ACTTGGACTTCCAGAAGAGTTAGTTTCCAGGCATCCATTTCCAGGTCTGGCCTGGCAATCAGAGTAATATGTGC
TGAAGAACCTTATATTTGTAAGGACTTTCCTGAAACCAACAATATTTGAAAATAGTAGCTGATTTTTCTGCAAG
TGTTAAAAGCCACATACCTATTACAGAGAGTCAAAGCCTGCACAACAGAAGAGGATCAGGAGAAGCTGATGCA
AATTACCAGTCTGCATTCACTGAATGCCTTCTTGCTGCCAATTA AAACTGTAGGTGTGCAGGGTGACTGTCTGTTT
CTACAGTTACGTGTGTGGAATCTCCAGTAAAGATGAACCTGACTGGGAATCACTTATTTTTCTGGCTAGGCTTAT
ACCTCGCATGTGTACACAACGTTAACAGAGTTGTTTATATATTTGGCCCAACAGTTAAAGAACCTCCTACAGATGT
TACTCCCACTTTCTTGACAACAGGGGTGCTCAGTACTTTACGCCAAGCTGATTTTGAGGCCCATACATTCTCAG
GGAGTCTGGGTATGCTGGGAAAATCAGCCAGATGCCGGTGATTTTGACACCATTACATTTTGATCGGGACCCACT
TCAAAAGCAGCCTTCATGCCAGAGATCTGTGGTTATTGCAACCTTTATTACTAGTGACTTCATGACTGGTATAACC
TGCAACACCTGGCAATGAGATCCCTGTAGAGGTGGTATTAAAGATGGTCACTGAGATTAAGAAGATTCTTGAT
TTCTCGAATTATGTATGACTTAACATCAAAGCCCCAGGAACCTACTGAGTGGGAGTAATAAACTTC

1388/6881
FIGURE 1291

GACCCTTTTCACAACATGGCGCCGAAAGCGAAGAAGGAAGCTCCTGCCCCCTCCTAAAGCTGAAGCCAAAGCGAAG
GCTTTAAAGGCCAAGAAGGCAGTGTTGAAAGGTGTCCACAGCCACAAAAAGAAGAAGATCCGCACGTCACCCACC
TTCCGGCGGCCGAAGACACTGCGACTCCGGAGACAGCCCAGATATCCTCGGAAGAGCGCTCCCAGGAGAAACAAG
CTTGACCACTATGCTATCATCAAGTTTCCGCTGACCACTGAGTCTGCCATGAAGAAGATAGAAGACAACAACACA
CTTGTGTTTCATTGTGGATGTTAAAGCCAACAAGCACCAGATTAAACAGGCTGTGAAGAAGCTCTATGACATTGAT
GTGGCCAAGGTCAACATCCTGATTCGGCCTGATGGAGAGAAGAAGGCATATGTTGACTGGCTCCTGATTACGAT
GCTTTGGATGTTGCCAACAAAATTGGGATCATCTAACTGAGTCCAGCTGCCTAATTCTGAATATATATATATAT
ATATCTTTTCACCAT

1389/6881
FIGURE 1292A

GATGAAGAGGAAGAAATCAAACAAGAAATTAACATGTTGAAGAAATATTCTCATCACCGGAATATTGCTACATAC
TATGGTGCCTTTTATCAAAAAGAACCCACCAGGCATGGATGACCAACTTTGGTTGGTGATGGAGTTTGTGGTGCT
GGCTCTGTACCGACCTGATCAAGAACACAAAAGGTAACACGTTGAAAGAGGAGTGGATTGCATACATCTGCAGG
GAAATCTTACGGGGGCTGAGTCACCTGCACCAGCATAAAGTGATTTCATCGAGATATTAAAGGGCAAAATGTCTTG
CTGACTGAAAATGCAGAAGTTAACTAGTGGACTTTGGAGTCAGTGCTCAGCTTGATCGAACAGTGGGCAGGAGG
AATACTTTCATTGGAACCTCCTACTGGATGGCACCAGAAGTTATTGCCTGTGATGAAAACCCAGATGCCACATAT
GATTTCAAGAGTGACTTGTGGTCTTTGGGTATCACCGCCATTGAAATGGCAGAAGGTGCTCCCCCTCTCTGTGAC
ATGCACCCCATGAGAGCTCTCTTCCTCATCCCCGGAACCCAGCGCCTCGGCTGAAGTCTAAGAAGTGGTCAAAA
AAATTCCAGTCATTTATTGAGAGCTGCTTGGTAAAGAATCACAGCCAGCGACCAGCAACAGAACAATTGATGAAG
CATCCATTTATACGAGACCAACCTAATGAGCGACAGGTCCGCATTCAACTCAAGGACCATATTGATAGAACAAAG
AAGAAGCGAGGAGAAAAAGATGAGACAGAGTATGAGTACAGTGGAAGTGAGGAAGAAGAGGAGGAGAATGACTCA
GGAGAGCCCGAGTCCATCCTGAATCTGCCAGGGGAGTCGACGCTGCGGAGGGACTTTCTGAGGCTGCAGCTGGCC
AACAAGGAGCGTTCTGAGGCCTACGGAGGCAGCAGCTGGAGCAGCAGCAGCGGGAGAATGAGGAGCACAAAGCGGC
AGCTGCTGGCCGAGCGTCAGAAGCGCATCGAGGAGCAGAAAAGAGCAGAGGCGGGCGGCTGGAGGAGCAACAAAGGC
GAGAGAAGGAGCTGCGGAAGCAGCAGGAGAGGGAGCAGCGCCGGCCTATGAGGAGCAGATGCGCCGGGAGGAGG
AGAGGAGGCGTGCGGAGCATGAACAGGAATACATCAGGCGACAGTTAGAGGAGGAGCAGAGACAGTTAGAGATCT
TGCAGCAGCAGCTACTGCATGAACAAGCTCTACTTCTGGAATATAAGCGCAAACAATTGGAAGAACAGAGACAAG
CAGAAAGACTGCAGAGGCAGCTAAAGCAAGAAAGAGACTACTTAGTTTCCCTTCAGCATCAGCGGCAGGAGCAGA
GGCCTGTGGAGAAGAAGCCACTGTACCATTACAAAGAAGGAATGAGTCCTAGTGAGAAGCCAGCATGGGCCAAGG
AGGTAGAAGAACGGTCAAGGCTCAACCGGCAAAGTTCCCTTGCCATGCCTCACAAGGTTGCCAACAGGATATCTG
ACCCCAACCTGCCCCCAAGGTGCGAGTCCTTCAGCATTAGTGGAGTTCAGCCTGCTCGAACACCCCCCATGCTCA
GACCAGTCGATCCCCAGATCCACATCTGGTAGCTGTAAAATCCCAGGGACCTGCCTTGACCGCCTCCAGTCAG
TGCACGAGCAGCCCACAAAGGGCCTCTCTGGGTTTCAGGAGGCTCTGAACGTGACCTCCCACGCGTGAGATGC
CACGCCAGAACTCAGATCCACCTCGGAAAATCCTCCTCTCCCCACTCGCATTGAAAAGTTTGACCGAAGCTCTT
GGTTACGACAGGAAGAAGACATTCCACCAAAGGTGCCTCAAAGAACAATTCTATATCCCCAGCATTAGCCAGAA
AGAATTCTCCTGGGAATGGTAGTGCTCTGGGACCCAGACTAGGATCTCAACCCATCAGAGCAAGCAACCTGATC
TCCGGAGAAGTGAAGCCATCTTGAGAGGCCCTTGAGAGGACCAGCAGTGGCAGTTTCTCCAGCTCCAGCACCC
CTAGCTCCCAGCCCAGCTCCCAAGGAGGCTCCCAGCCTGGATCACAAGCAGGATCCAGTGAACGCACCAGAGTTC
GAGCCAACAGTAAGTCAGAAGGATCACCTGTGCTCCCCCATGAGCCTGCGAAGGTGAAACCAGAAGAATCCAGGG
ACATTACCCGGCCCAGTCGACCAGCTAGCTACAAAAAAGCTATAGATGAGGATCTGACGGCATTAGCCAAAGAAC
TAAGAGAAGTCCGGATTGAAGAAACAACCGCCCAATGAAGAAGGTGACTGATTACTCCTCCTCCAGTGAGGAGT
CAGAAAGTAGCGAGGAAGAGGAGGAAGATGGAGAGAGCGAGACCCATGATGGGACAGTGGCTGTGACGCACATAC
CCAGACTGATACCAACAGGAGCTCCAGGCAGCAACGAGCAGTACAATGTGGGAATGGTGGGGACGCATGGGCTGG
AGACCTCTCATGCGGACAGTTTCAGCGGCAGTATTTCAAGAGAAGGAACCTTGATGATTAGAGAGACGTCTGGAG
AGAAGAAGCGATCTGGCCACAGTGACAGCAATGGCTTTGCTGGCCACATCAACCTCCCTGACCTGGTGCAGCAGA
GCCATTCTCCAGCTGGAACCCCGACTGAGGGACTGGGGCGCGTCTCAACCCATTCCCAGGAGATGGACTCTGGGA
CTGAATATGGCATGGGGAGCAGCACCAAAGCCTCCTTCACCCCCCTTTGTGGACCCAGAGTATACCAGACGTCTC
CCACTGATGAAGATGAAGAGGATGAGGAATCATCAGCCGCAGCTCTGTTTACTAGCGAACTTCTTAGGCAAGAAC
AGGCCAAACTCAATGAAGCAAGAAAGATTTGCGTGGTAAATGTAAACCCAACCAACATTGCGCCTCATAGCGACA
CACCAGAAATCAGAAAAATACAAGAAACGATTCAACTCAGAAATACTTTGTGCAGCTCTGTGGGGTGTAACCTTC
TGGTGGGGACTGAAAATGGCCTGATGCTTTTGGACCGAAGTGGGCAAGGCAAAGTCTATAATCTGATCAACCGGA
GGCGATTTTCAGCAGATGGATGTGCTAGAGGGACTGAATGTCCTTGTGACAATTTTCAGGAAAGAAGAATAAGCTAC
GAGTTTACTATCTTTCATGGTTAAGAAACAGAATACTACATAATGACCCAGAAGTAGAAAAGAAACAAGGCTGGA
TCACTGTTGGGGACTTGGAAGGCTGTATACATTATAAAGTTGTTAAATATGAAAGGATCAAATTTTTGGTGATTG
CCTTAAAGAATGCTGTGGAATATATGCTTGGGCTCCTAAACCGTATCATAAATTCATGGCATTAAAGTCTTTTG
CAGATCTCCAGCACAAAGCCTCTGCTAGTTGATCTCACGGTAGAAGAAGGTCAAAGATTAAAGGTTATTTTTGGTT
CACACACTGGTTTTCCATGTAATTGATGTTGATTTCAGGAACTCTTATGATATCTACATACCATCTCATATTACAGG
GCAATATCACTCCTCATGCTATTGTCTATCTTGCTTAAACAGATGGAATGGAAATGCTTGTGTTGCTATGAGGATG

1390/6881
FIGURE 1292B

AGGGGGTGTATGTAAACACCTATGGCCGGATAACTAAGGATGTGGTGCTCCAATGGGGAGAAATGCCCACGTCTG
TGGCCTACATTCATTCCAATCAGATAATGGGCTGGGGCGAGAAAGCTATTGAGATCCGGTCAGTGGAACAGGAC
ATTTGGATGGAGTATTTATGCATAAGCGAGCTCAAAGGTTAAAGTTTCTATGTGAAAGAAATGATAAGGTATTTT
TTGCATCCGTGCGATCTGGAGGAAGTAGCCAAGTGTTTTTCATGACCCTCAACAGAAATTCCATGATGAACTGGT
AACAGAAGAGCACTTGGCACTTATCTTCATGGCGTTATTTCTAATTTAAAAGAACATAACTCATGTGGACTTATG
CCAGTCTAGAGGCAGAATCAGAAGGCTTGGTTGAACATATCGCTTTCCCTTTTTCTCTCCCTCCGCCCCCTCCCA
GTACAGTCCATCTTTCAATGTTGCAGCCTGGTTGAGAAGGAGAGAAAAAGGTGGCAGGAATTTCCAGGAGATCCC
CAAGAATGCTGCCTTGTCTGTGGACAAAGATGGACCATGTGCCCTTCGGAATTAGGGATAGAAACAAATATTGTG
TGCTCTTAACGATTAAGCTGTGTTATGGTGGGTTTTTACGTTTTTTTACCTTTTTTCTTTACCCCTTTTACTCTGCAA
GAATGGGGAAAGAATGCATACTGCGAAAATGAGTCTTTTAAATTCGTCTGCCTACTAGTTTTAAGTATATGGTA
TGTTGTAAAATTTCCAATGATGAGAGACAGCACATAAATGTACCTTATCTCCTTAGGCTGAAGGCCATAACTAC
ATAGTGGAGTAATTTAAGAACTCTCTTGCCCTTACCAACCCAAAAAGGTTGCTTTTTGATAGCAACTGGCTAAATGA
ATTTTTAAAAAGAGAAGAAAAATACTAGTTTTCCCTCTTTTGGGAAATAGAFTTTTAAATGGCTAAACTACTAGC
CTTAAACTACTAGTCTAATAAAATCAACTACCACTTTTGTGAATCTGACAGGCCACATTTTTATATGGCCCTTT
ACAGAATGGAGTGTGTTGAACAGGATACTAACGCCATTGAGTTGAGCTGGCCTAGCGATGGAGGGACACTCTAAC
ACAACTTTCCCTCAGCTATTATGCAACAGATCAGGGAAAAAGATGGGATGACAGATGGGGTCAGACAGAAAGAGC
TTCTGGGAAACAAGCTTACATAGTCTTTTTTAAATGCACAAAGCCTCCCAGCTAAGAGGTCACTTGGTTTGGGC
TTCATTAGGACTGAGACTTTGTTGAGTTCTTTCTGGGACTTGGAGAGTGGATGATATTCAGGCTCTGAACATTCC
CAGCGCTCTCCCGAGGGTGCCACTTTCTCAAGATGAAACTGTGACTGAAAAATTAATAATAAATGTTTCTGAG
CTGCCTGTGTTCTCCCTGTGTGGGTGAGAGAAGGGACTAGACTCCTAAGCCTGCCTCAGATACAAGAGGCATCAT
TGGCTCCAATTTTAGAGAACTTGAAAGCAAGGCTTTGGACAAAATTTGAGACCCTAATCACTTTACCTTCTCC
AAATTACCCAACATACGGTAAACAACATTTGTGCAGAAGTATGTATGTATTTAGTTTCAGGTTGACTTGTGTCCTT
ATAAACTCTTACTCAAATGATTGAACTTT

1391/6881
FIGURE 1293

MPHKVANRISDPNLP PRSEFSISGVQPARTPPMLRPVDPQIPHLVAVKSQGPALTASQSVHEQPTKGLSGFQEA
LNVTS HRVEMPRQNSDPTSENPPLPTRIEKFDRSSWLRQEEDIPPKVPQRTTISIPALARKNSPGNGSALGPRLG
SQPIRASNPDLRRTEPILESPLQRTSSGSSSSSSSTPSSQFSSQGGSQPGSQAGSSERTVRANSKSEGSFVLPHE
PAKVKPEESRDITRPSRPASYKKAIDEDLTALAKELRELRIEETNRPMKKVTDYSSSEESSESEEEEEEDGESET
HDGTVAVSDIPRLIPTGAPGSNEQYNVGMVGTHGLETSHADSFSGSISREGTLMIRETSGEKKRSGHSDSNGFAG
HINLPDLVQQSHSPAGTPTEGLGRVSTHSQEMDSGTEYGMGSSTKASFTPFVDPRVYQTSPTDEDEDEESSAAA
LFTSELLRQEQAKLNEARKISVVNVNPTNIRPHSDTPEIRKYKKRFNSEILCAALWGVNLLVGTENGLMLLDRSG
QGKVYNLINRRRFQQMDVLEGLNVLVTISGKKNKLRVYYLSWLRNRLHNDPEVEKKQGWITVGDLEGCIHYKV
KYERIKFLVIALKNAVEIYAWAPKPYHKFMAFKSFADLQHKPLLVDLTVEEGQRLKVIFGSHTGFHVIDVDSGNS
YDIYIPSHIQGNITPHAIVILPKTDGMEMLVCYEDEGVYVNTYGRITKDVVLQWGEMPTSVAYIHSNQIMGWGEK
AIEIRSVETGHLDGVMHKRAQRLKFLCERNDKVFFASVRSGGSSQVFFMTLNRNSMMNW

1392/6881
FIGURE 1294

GGGGGCAAAAAAAGAAGCAAGTTCTGAAGTTCACTCTTGATTGCACCCACCCTGTAGAATCATGGATGCTGCCA
ATTTTGAGCAGTTTTTGCAAGAAAGGATCAAAGTGAACGGAAAAGCTGGGAACCTTGGTGGAGGGGTGGTGACCA
TCGAAAGGAGCAAGAGCAAGATCACCGTGACATCCGAGGTGCCTTTCTCCAAAAGGTATTTGAAATATCTCACCA
AAAAATATTTGAAGAAGAATAATCTACGTGACTGGTTGCGCGTAGTTGCTAACAGCAAAGAGAGTTACGAATTAC
GTTACTTCCAGATTAACCAGGACGAAGAAGAGGAGGAAGACGAGGATTAAATTTTCAATTTATCTGGAAAATTTGT
ATGAGTTCTTGAATAAACTTGGGAACCAAAATGGTGGTTTATCCTTGTATCTCTGCAGTGTGGATTGAACAGAA
AATTGGAAATCATAGTCAAAGGGCTTCCTTGGTTCGCCACTCATTATTTGTAACCTTGACTTCT

1393/6881
FIGURE 1295

ATGAAGAGAGTGTCAGCAGAGGTCGCCTCCAGAGGAGGTGCTGTGGAGACTGAGCGCATAGCACCCCTTAAAATCC
TGGGACCAGGGCTTCTCCACGGGCTTGCTGAAGAAGGGAGAAAAAGAACAGCAAGAAGCGATTGAACACATTGAT
GAAGTACAAAATGAAACAGACAGACTTAATGAACAAGCCAGTCCCCTTACAAAGAAACAGACAGATGATTTAGGT
GATAATGACGGTGCTGAAGATGAAGATATTCGGGACAGTGGGGGTCCCAAACCAGTGATGGTGTATATCCATGGT
GGCTCATATATGGAAGGTACTGGAAATTTATATGATGGAAGTGTCTTGGCAAGTTATGGCAATGTGATCGTCATC
ACAGTCAACTATCGACTTGGAGTACTCGCTCTACATCCGAGTTATGATTCAGGAGCCACTGGGCAGGAAAATGTG
AGGACACAGAGGAAGCTGACTGAAGCAGGTAGACGAGAAGAGGAAACGGGTTGTGCGACGGCGGGGGTCGCTGCC
CGTCTGTCCGTCGGCTTCTCCAGCGGTAAAAGGAGAGCTGATGGAAGTGTGAATCAAATCGAAGGTGAAGCCACC
CCAGTTAACCTCACAGAGCCTGCCAAGCTGGAAGTTAAGTTTTCTGGTCACATAATTATCTGTCAAACACTTAC
TACATGTCACGCACTAAGGTTGCCATGATGAGCCGGACAGAGCTGGCCTTGGTACTTATGGAGCTCATTCCCAGT
GTGGATACTGACACGTGA

1394/6881
FIGURE 1296

TATTTTGTGAGATGTGTTGAACCTCGATTAAGATTGCATTATGACATTCTTGAAGACCGAGTTCCATCAGGACTT
ATTGTTGACTACCACAATCTGTTGTCTCAATGTGAGGAGAGTTACAGGAAATTTTAAATCTGAGAAGCAGTTTG
TCAAATTGTAACCTCTGATTCCGAGCAGGAAAATATCTCCATGGTGGAAGGGTTAAAATTGTATTCCGAGATGGAA
CAGTTGAAACAAAAGCTGAAACTCATTGAGAATCCTTTGTTGAGGTATGTGTTTGGTTATCAGAAGAATTCTAAC
ATCCAAGCAAAGGGTGTCCGTTCCAGCGGTGAGAAGATCACTCATGTGGTCTCCTCCACCATGATGGCTGGTCTC
CTGCGGTCCCTGCTTACGGACAGGCTTTGCCAGGAGCCTGGTGAGGAAGAAAGAGAAATTCAGTTCCATAGTGAT
CCATTGTCTGCTATAAATGCCTGCTTCGAAGGTGACACTGTTATTGTTTGTCTGGCCATTATGTGGTACATGGC
ACTTTCTCCATTGCTGACTCCATTGAGTTGGAAGGATATGGCCTACCAGATGACATTGTGATAGAAAAGAGGGGC
AAAGGCGACACTTTTGTGGACTGCACTGGTGCTGATTTAAAATCTCAGGCATAAAAATTTGTTTCAGCATGATGCT
GTAGAGGGGAATCTTAATTGTTACCGTGGTAAGACTACGCTGGAAAACGTGTGTGCTGCAGTGTGAGACGACCGGA
GTCACAGTGCGGACATCAGCAGAGTTTCTAATGAAGAACTCGGATTTATATGGCGCCAAGGGTGTGGTATAGAA
ATCTACCCTGGGAGTCAGTGACCCCTGAGTGACAATGGGATCCATCACTGCAAGGAAGGGATCCTCATTAAGGAC
TTCTTAGATGAACATTATGACATTCCCAAGATATCCATGGTGAATAATATAATACATAATAATGAAGGTTATGGT
GTTGTCTTGGTGAAACCTACAATCTTCTCTGACCTGCAAGAAAATGCTGAAGATGGAAGTGAAGAAAATAAGCG
CTTAAAATTCAGACAAGTGGAGAGCCAGATGTGGCTGAAAGAGTGGATCTAGAAGAGCTGATTGAGTGTGCAACT
GGTAAAATGGAGCTTTGTGCAAGAACTGACCCCTCTGAGCAAGTCGAGGGAAATTTGTGAAATGTAAATGAACCTA
ATTGCTGCCTCCACACAGAAAGGCCAGATAAAGAAGAAAAGGTTGAGTGAAGTGGGGATCACGCAAGCTGATGAC
AACTTAATGTCACAGGAGATGTTTGTGGGATTTGTGGGAACCAAGTTCAGTGAAGTGGGAAAGGTAGTTTGGC
ACATTTCTTTTCTGACTACAGTGATGTAAAGTAGATAGCAAAATACTGGATTTTGCACATGCTGCCCTAAGAATCA
CTGCTGCCATTGTAGTTTGTCTGATTGTCTGTATTTTATATTGATTATTTGGGCTTGAGTGAAAGGTAGATTTA
TTTCCATTTGCAGGTGTTGCACATAAAACACTCCCTCTTTATAAGAAAAATCATAAATGCATATAAAATAGAAAA
TATTTGGAGATTGCTTATCTGAAAGTCTTGCTTTCTTATACACATGGTTCTCTCATATTAAGCCTGGTAGTAACT
TTTTAGTGTAATTACCTTTAGCACTTCAAAGACGAGGAAGTAAGGAAGGGAAATGCAAGACTAGTGCAATAAAATG
CAATAGGTGTCATATGTACAGCATTCTTCTTAGAGTTGCCTTTTATCCCAATTACAGTGAGTCTGATTTCCATC
CTGTATTTGCATAATACTTGTCTTAAATAAAAAGCTTTTATGATTGGGAATTTATCTGCCTAATCAGACTTATTA
TTGAGACGTCAATGGGACGCATTTTCTGTTGAGCTATGCAGTCGTCAAAACAGCGATAGACAGCATAGGAGGTT
TGAAGCAGAAATGAAATGTGTTATTCAGAGCCAATGTTGTACATAGAGCATTTCCTATTGCTGAATGGGAATG
ATTAAAAACAAGGTATTTTTCGGGCCAGGCGGTGGCTCACGCTTGTAAATCGCAGCACTTTGGGAGGCTGAGGCAG
GAGGATCACTTGAGCCCAGGAGTTCAAGACTAGCCTAGGCAACATAGTGAGACCCTGTCTCTACTAAAAATAAAT
TTAAAAAAATTAGCTGAGTGTGGTGGTGCATGCATGTAGTTCCAGCTACTCAGGAGGCTGAGGCTAGAGGATCC
TTGAGCCCAGGAGGTTGAGGCTGCAGTGAGGTGTGATTGCGCCACTGCATTCCAGCTTGGGCGACAGAGCGAGAC
CCAGTCTCAAAAAAAAAAAAAAGTATTTTCTCTTACCGTTACAGTATTCTGATTATATTACTGACACAGTCAAA
ATGATTAACTGTACAACCTGTATCTGCTGGGTGTTCTTGTATCATATTGTAAACAGCTTTAAAAATATTTATA
TTTTAAAACTGTATGTGACATTAATATGCCTAATGATTAAATTTATAGTGATGAAATAACAAAA

1395/6881
FIGURE 1297

GTAGCCATGCGGCCCATGAGTTTGTTCGCGCGGGTTTCGGTTACTGCGGTGGCAGCTCTGTCTGGCCGGCCCCCTT
GGCACTCGCCTCGGATTTGGGGGCTTCCTCACTCGTGGCTTTCCGAAGGCTGCTGCTCCTGTTTCGACACAGTGGA
GACCATGGGAAAAAGACTATTTGTCATCAGACCTTCTAGATTCTATGACAGGCGTTTTTTGAAGTTATTGAGATTC
TACATTGCATTGACTGGGATTCCAGTAGCAATTTTCATAACTCTGGTGAATGTATTCAATTGGTCAAGCTGAACCTA
GCAGAAATTCCAGAAGGCTATGTCCAGAACACTGGGAATATTATAAGCATCCCATATCAAGATGGATTGCCCGT
AATTTCTATGATAGTCCTGAAAAGATATATGAAAGAACAATGGCCGTCCTTCAGATTGAAGCTGAAAAGGCTGAA
TTACGGGTAAAGGAGCTGGAAGTGCGAAAATTGATGCATGTGAGAGGAGATGGACCCTGGTATTACTATGAGACA
ATTGACAAGGAACCTTATTGATCATTCTCCGAAAGCAACTCCTGACAATTAAGCCTTTTTTCTCCAAATACAAAG
TATATTCTCTTTATTGGAAAATAAATTAATAAATATATTCTGTATTTTGTCTCTCCGTGAAAAACAAAAGAGCCT
CTGACATTACTGTCTCTCAGTGTGGTTCAGATTGAGGCTTTTGTGTTGAGGAGTTTGGCTTCCAGTCCCCAAAGA
AGGTTTAAATGTACTAATAAAAACTGGAGAAATAGGAATTTGTGAACCCCTAAAATTGTAGCAACTTTGAAAGG
TTAGTGTTTTATTACCTGACAAATGGAAGTTATAGAAGTCTAATAATGTTAAGCACCAGTAATTATAGTATTTT
GTACAAATGCCTGTACTGTAGATGCTGTATTATTGAGGGGCAACTCAGGATTTTAAGTTCCATAAAGTATTGAA
CCAACCTCTAAATGTTAACTCCTTAATAAACAGATTCTCAGTAAACAAATTTTAAAGTTAAAAAAAAAAAAAAAAA

1396/6881
FIGURE 1298

MAAMSLRRVSVTAVAALSGRPLGTRLGFGGFLTRGFPKAAAPVRHSGDHGKRLFVIRPSRFYDRRFLKLLRFYI
ALTGIPVAIFITLVNVFIGQAELAEIPEGYVPEHWEYYKHPISRWIARNFYDSPEKIYERTMAVLQIEAEKAE LR
VKELEVRKLMHVRGDGPWYYYETIDKELIDHSPKATPDN

1397/6881
FIGURE 1299

GTTTTGCCAGTTATGCGAAAACATGGCTGCGGCCGGTTTGGCCCTTCTTTGTAGGAGAGTTTCATCCGCCCTGAA
ATCTTCCCGATCGTTAATAACTCCTCAGGTCCCTGCCTGCACAGGGTTTTTTCTTAGTTTGTTCCTAAGAGTAC
ACCAAATGTGACATCCTTTACCAATATAGATTACTTCATACCACATTGTCAAGGAAAGGACTAGAAGAATTTTT
TGATGACCCAAAAAACTGGGGGCAAGAAAAAGTAAATCTGGAGCAGCATGGACCTGTCAGCAACTAAGGAACAA
AAGTAATGAAGATTACACAAACTTTGGTATGTCTTACTGAAAGAAAGAAACATGCTTCTAACCTAGAGCAGGA
GGCCAAGCGGCAGAGATTGCCAATGCCAAGTCCAGAGCGGTTAGATAAGGTAGTAGATTCCATGGATGCATTAGA
TAAAGTTGTCCAGGAAAGAGAAGATGCCCTAAGGCTTCTTCAGACTGGTCAAGAAAGAGCTAGACCTGGTGCTTG
GAGAAGAGACATCTTTGGAAGAATCATCTGGCACAAGTTCAAGCAGTGGGTTATACCTTGGCACCTAAATAAAAG
ATACAATAGGAAACGATTCTTTGCCTTGCCTTATGTGGACCATTTTCTCAGACTGGAACGTGAGAAACGAGCCCCG
CATCAAAGCACGGAAGGAAAATTTAGAGAGAAAGAAAGCAAAAATTTCTTTAAAAAAGTTTCCACATCTTGCTGA
AGCCCCAAAAGTCAAGTCTTGCTAAGATGTCTGAACTATTAAATTTACCATTTTGTTTTTCTTGAATAGTCTGTG
TACAGGAGTAAATATGTTAAGTGGTTTATAAAGAAATTCTGTTTTAGTCAAGTGACTTTACTAATCAGTTGTTT
TAAGTGTGAATATGGCATGCTAATTAGCTAATTTGGTAGAAGCTAATTTGCTTCTAAAAATCAGGTATAAAGTTC
AGATGAGATTCCCACTTTATAAATCTGACATTTAAGCAGGCTTTAAATGTCACCTGCTACCTTAGAGTGTGAAG
GTGATGGTAACTGCCACAGCAAAGGCAATACCGTAGTTTTTGAATTTGAATAATAGTTTTACCTCTGTTGTTAAT
AGGCTATGAAGAGGATGTGGGTATTGCTGTTAATAAACGGAGGACTTTGATTCAAAATAATGAGAAATACATTTA
GTCCTTAAAGTAGTAATCACAGTGCACAACAGTCCAAAATATATTTCTGGAATGGCTAATTTTTATTTAATTTCTG
TAAGCCTAAGGTAAAAAGCATAGGCAGTAACTTTTACTAGTCAATAAAAAAGCAGTTCTACCAATCCACTGGTAAT
TAATACACTAAACAGAGTTGGAAAGCATTTTACTGAAAGCAAAAATATTTAGAGAAAATAGACATTTATACAAAAT
TATAAATGCTTGTAATAAGAATAAGTGCATTTCAAGGAAAGCACAACTTAATTTATAGAGCCAGTTAAAGCTT
TAAAAAATTTAAGTGGAAATTGAAATATGCAAAAATGTATAAACATTCTACAAAAGATGGTCATTCTTTTCTCTGA
GTATACTAAAGCTATGAAACGTAAGGTGACAAAAGGAAGGTAGAAGCTTGGGAACCTTTTCTCAAGGGCATTTTC
TTTCTACACACTGCTTCCCTCCTTCTTCATATTCTTGCTTGGAAATCCACATCCCAACACTTGTGGTGACAACAT
GACTGACTCCTAACATTGTGTTTCTTGATAACCCCTTTACATTGGAAGGGTCAAATAATCCTTCTGGAATCTTTA
GCCGCTCTGCACCAAAATCACAATTGTAGCCATTGGGGAATTCATAATGAACAGTTGGCATCTGTGCAGCCACTT
GTTTCATCATAAGTTGAATCTGACACTTGAAGTACCGAAGCTTGAAAATCCTGGATAACACAATTACACATATAAT
TGTGCCAAGACCTCGTAACCTGAGGCAACTTCTCTTTTCTTTTCCAGTTTGCTGGAGATCCTTCACGAACAGCTT
CTTTTGATGCAATCATATATGGAGGAACCAATTCAATATTCAATTTCTTGGAAGAGTTCTCTGCACTGCATAGTAA
TAAAGTCTCCAGCAAGAGGGGATTTCACAATGCCTTGTTGAAGGACATAGCCATCGTGGACTGGAATTGCAGTGG
TATGAGTGGCTCCACTGTCCAAAATCAGCCCAGTAGAACGACCATTAGCAAATGCTGTCAAACACTGCAGTTTTGC
AAAGGAAGAAGGCAGGGATGTTGTAGTGTTCAAACATTAACCTCTGTCAGTTTCTCTCTCTTTGCTCTAGTATTCC
ACGGTGCCTCTGACATGAGAACAGGATGGAGACTGGCTTCTGATTTGACATGCATTTTGTAGGTATGATCCAAAA
TAGCTTGGAACATATCCCAGTCTTCAACCATCCCATTTTTTAGAGGTGAAATGGCCTCCATATTCTCCCTCGGAA
CACGCAGAGCATTAGTATCTATGTAGTAGGTGGGACCGCCTTGTTTGCCTTTATCGCCATCTATTTCCATTAATG
TGCTTCCGTCATCTCTTTCTACCACCATACCAATAGCTGTAGGAAAATCCACCTTGGGGCAGTCCTACCAGCAT
AACCAGCTCTCACAGTATAGGATCCAATGTCAAAAACAAGGGCTCCAACCTCACCTCCCCGTACACGCCGCCGC
TCATGGCTGCTGCCGGCGCGACTCCTACCCTAAGGGCTAACTGGCGAAGTGACTGCAGTGGCCGCGACTGCGAGT
CTCGAGGAGCGATAGCCCCTGACTCCCTTAACCTCCACCGCCACCCACCTCAGGCAACAAAGCGG

1398/6881
FIGURE 1300

CCGCTTTGTTGCCTGAGGTGGGTGGCGGTGGAAGTTAAGGGAGTCAGGGGCTATCGCTCCTCGAGACTCGCAGTC
GCGGCCACTGCAGTCACTTCGCCAGTTAGCCCTTAGGGTAGGAGTCGCGCCGGCAGCAGCC**ATG**AGCGGCGGCGT
GTACGGGGGAGATGAAGTTGGAGCCCTTGTTTTTGACATTGGATCCTATACTGTGAGAGCTGGTTATGCTGGTGA
GGACTGCCCCAAGGTGGATTTTCTACAGCTATTGGTATGGTGGTAGAAAGAGATGACGGAAGCACATTAATGGA
AATAGATGGCGATAAAGGCAAACAAGGCGGTCCACCTACTACATAGATACTAATGCTCTGCGTGTTCCGAGGGA
GAATATGGAGGCCATTTACCTCTAAAAAATGGGATGGTTGAAGACTGGGATAGTTTCCAAGCTATTTGGATCA
TACCTACAAAATGCATGTCAAATCAGAAGCCAGTCTCCATCCTGTTCTCATGTCAGAGGCACCGTGGAATACTAG
AGCAAAGAGAGAGAACTGACAGAGTTAATGTTTGAACACTACAACATCCCTGCCTTCTTCTTTGCAAACTGC
AGTTTTGACAGCATTTGCTAATGGTCGTTCTACTGGGCTGATTTTGGACAGTGGAGCCACTCATACCACTGCAAT
TCCAGTCCACGATGGCTATGTCCTTCAACAAGGCATTGTGAAATCCCCCTCTTGCTGGAGACTTTATTACTATGCA
GTGCAGAGAACTCTTCCAAGAAATGAATATTGAATTGGTTCCCTCCATATATGATTGCATCAAAAGAAGCTGTTTCG
TGAAGGATCTCCAGCAAACCTGGAAAAGAAAAGAGAAGTTGCCTCAGGTTACGAGGTCTTGGCACAAATTATATGTG
TAATTGTGTTATCCAGGATTTTCAAGCTTCGGTACTTCAAGTGTGAGATTCAACTTATGATGAACAAGTGGCTGC
ACAGATGCCAACTGTTCAATTATGAATTCCCCAATGGCTACAATTGTGATTTTGGTGCAGAGCGGCTAAAGATTCC
AGAAGGATTATTTGACCCCTTCCAATGTAAAGGGGTATCAGGAAACACAATGTTAGGAGTCAGTCATGTTGTCAC
CACAAGTGTGGGATGTGTGATATTGACATCAGACCAGGTCTCTATGGCAGTGTAAATAGTGGCAGGAGGAAACAC
ACTAATACAGAGTTTTACTGACAGGTTGAATAGAGAGCTGTCTCAGAAAACCTCCTCCAAGTATGCGGTTGAAATT
GATTGCAAATAATACAACAGTGGAACGGAGGTTTAGCTCATGGATTGGCGGCTCCATTCTAGCCTCTTTGGGTAC
CTTTCAACAGATGTGGATTTCCAAGCAAGAATATGAAGAAGGAGGGAAGCAGTGTGTAGAAAGAAAATGCCCT**TG**
AGAAAGAGTTCCCAAGCTTCTACCTTCTTTTGTACCTTACGTTTCATAGCTTTAGTATACTCAGGAAAAGAAT
GACCATCTTTTGTAGAATGTTTATACATTTTTGCATATTTCAATTTCCACTTAAATTTTTTAAAGCTTTAACTGG
CTCTATAAATTAAGTTTGTGCTTTTCTTGAATGCACTTATTCTTATTACAAGCATTTTATAATTTGTATAAAT
GTCTATTTTCTCTAAATATTTTGTCTTTCAGTAAATGCTTTCCAACCTCTGTTTAGTGTATTAATTACCAGTGGAT
TGGTAGAACTGCTTTTTATTGACTAGTAAAGTTACTGCCTATGCTTTTTACCTTAGGCTTACAGAATTAAATAA
AAATTAGCCATTCCAGAAATAT

1399/6881
FIGURE 1301

MSGGVYGGDEVGALVFDIGSYTVRAGYAGEDCPKVDFTAI GMVVERDDGSTLMEIDGDKGKQGGPTYIDTNAL
RVPRENMEAISPLKNGMVEDWDSFQAILDHTYKMHVKSEASLHPVLMSEAPWNTRAKREKLTLMFEHYNIPAFF
LCKTAVLTAFANGRSTGLILDGATHHTAIPVHDGYVLQQGIVKSPLAGDFITMQCRELFQEMNIELVPPYMIAS
KEAVREGSPANWKRKEKLPQVTRSWHNYMCNCVIQDFQASVLQVSDSTYDEQVAAQMPTVHYEFPNGYNCDFGAE
RLKIPEGLFDP SNVKGLSGNTMLGVSHVVTTSVGMCDIDIRPGLYGSVIVAGGNTLIQSFTDRLNRELSQKTPPS
MRLKLIANNTTVERRFSSWIGGSILASLGTFOQMWISKQEYEEGGKQCVERKCP

1400/6881
FIGURE 1302A

AGAGTACGTGTTTACAGATAAACTGGTACACTGACAGAAAAATGAGATGCAGTTTCGGGAATGTTCAATTAATGG
CATGAAATACCAAGAAATTAATGGTAGACTTGTACCCGAAGGACCAACACCAGACTCTTCAGAAGGAACTTATC
TTATCTTAGTAGTTTATCCCATCTTAACAACCTATCCCATCTTACAACCAGTTCCCTCTTTCAGAACCAGTCCTGA
AAATGAAACTGAACTAATTAAGAACATGATCTCTTCTTTAAAGCAGTCAGTCTCTGTACACTGTACAGATTAG
CAATGTTCAAACCTGACTGCACTGGTGATGGTCCCTGGCAATCCAACCTGGCACCATCGCAGTTGGAGTACTATGC
ATCTTCACCAGATGAAAAGGCTCTAGTAGAAGCTGCTGCAAGGATTGGTATTGTGTTTATTGGCAATTCTGAAGA
AACTATGGAGGTTAAAACCTCTTGGAACCTGGAACGGTACAACTGCTTCATATTCTGGAATTTGATTTCAGATCG
TAGGAGAATGAGTGTAATTGTTTCAGGCACCTTCAGGTGAGAAGTTATTATTGCTAAAGGAGCTGAGTCATCAAT
TCTCCCTAAATGTATAGGTGGAGAAATAGAAAAACCAGAATTCATGTAGATGAATTTGCTTTGAAAGGGCTAAG
AACTCTGTGTATAGCATATAGAAAATTTACATCAAAAGAGTATGAGGAAATAGATAAACGCATATTTGAAGCCAG
GACTGCCTTGCAAGCAGCGGGAAGAGAAATTGGCAGCTGTTTTCCAGTTCATAGAGAAAGACCTGATATTACTTGG
AGCCACAGCAGTAGAAGACAGACTACAAGATAAAGTTTCGAGAACTATTGAAGCATTGAGAATGGCTGGTATCAA
AGTATGGGTACTTACTGGGGATAAACATGAAACAGCTGTAGTGTGAGTTTATCATGTGGCCATTTTCATAGAAC
CATGAACATCCTTGAACCTTATAAACAGAAATCAGACAGCGAGTGTGCTGAACAATTGAGGCAGCTTGCCAGAAG
AATTACAGAGGATCATGTGATTACAGCATGGGCTGGTAGTGGATGGGACCAGCCTATCTCTTGCACTCAGGGAGCA
TGAAAACTATTTATGGAAGTTTGCAGAAATTGTTTCAGCTGTATTATGCTGTCTGATGGCTCCACTGCAGAAAGC
AAAAGTAATAAGACTAATAAAAATATCACCTGAGAAACCTATAACATTGGCTGTTGGTGATGGTGCTAATGACGT
AAGCATGATACAAGAAGCCCATGTTGGCATAGGAATCATGGGTAAAGAAGGAAGACAGGCTGCAAGAAACAGTGA
CTATGCAATAGCCAGATTTAAGTTCCTCTCCAAATTGCTTTTTTGTTCATGGTCATTTTTATTATATTAGAATAGC
TACCCTTGACAGTATTTTTTTTATAAGAATGTGTGCTTTATCACACCCAGTTTTTATATCAGTTCTACTGTTT
GTTTTCTCAGCAACATTGTATGACAGCGTGTACCTGACTTTATACAATATTTGTTTTACTTCCCTACCTATTCT
GATATATAGTCTTTTGAACAGCATGTAGACCCTCATGTGTTACAAAATAAGCCACCCTTTATCGAGACATTAG
TAAAAACCGCCTCTTAAGTATTAACATTTCTTTATTGGACCATCCTGGGCTTCAGTCATGCCTTTATTTTCTT
TTTTGGATCCTATTTACTAATAGGGAAGATACATCTCTGCTTGAAATGGCCAGATGTTTGGAACTGGACATT
TGGCACTTTGGTCTTCACAGTCATGGTTATTACAGTCACAGTAAAGATGGCTCTGGAACTCATTTTTTGGACTTG
GATCAACCATCTCGTTACCTGGGGATCTATTATATTTTATTTTGTATTTTCTTGTGTTTATGGAGGGATTCTCTG
GCCATTTTTGGGCTCCAGAAATATGTATTTTGTGTTTATTACAGCTCCTGTCAAGTGGTTCTGCTTGGTTTGCCAT
AATCCTCATGGTTGTTACATGTCTATTTCTTGATATCATAAAGAAGGTCTTTGACCGACACCTCCACCCTACAAG
TACTGAAAAGGCACAGCTTACTGAAACAAATGCAGGTATCAAGTGCTTGGACTCCATGTGCTGTTTCCCGGAAGG
AGAAGCAGCGTGTGCATCTGTTGGAAGAATGCTGGAACGAGTTATAGGAAGATGTAGTCCAACCCACATCAGCAG
ATCATGGAGTGCATCGGATCCTTTCTATACCAACGACAGGAGCATCTTGACTCTCTCCACAATGGACTCATCTAC
TTGTTAAAGGGGCGAGTAGTACTTTGTGGGAGCCAGTTCACCTCCTTTCTAAAATTCAGTGTGATCACCCTGTTA
ATGGCCACACTAGCTCTGAAATTAATTTCCAAAATCTTTGTAGTAGTTTCATACCCACTCAGAGTTATAATGGCAA
ACAAACAGAAAGCATTAGTACAAGCCCCCTCCAACACCCTTAATTTGAATCTGAACATGTTAAAATTTGAGAATA
AAGAGACATTTTTTCATCTCTTTGTCTGGTTTGTCCCTTGTGCTTATGGGACTCCTAATGGCATTTCAGTCTGTTG
CTGAGGCCATTATATTTTAAATATAAATGTAGAAAAAGAGAGAAATCTTAGTAAAGAGTATTTTTTAGTATTAGC
TTGATTATTGACTCTTCTATTTAAATCTGCTTCTGTAAATTATGCTGAAAAGTTTGCCTTGAGAACTCTATTTTTT
TATTAGAGTTATATTTAAAGCTTTTCATGGGAAAAGTTAATGTGAATACTGAGGAATTTTGGTCCCTCAGTGACC
TGTGTTGTTAATTCATTAATGCATTCTGAGTTCACAGAGCAAATTAGGAGAATCAITTCACCAACCATTATTTACTG
CAGTATGGGGAGTAAATTTATACCAATTCCTCTAAGTGTACTGTAACACAGCCTGTAAAGTTAGCCATATAAATG
CAAGGGTATATCATATATACAAATCAGGAATCAGGTCCGTTACCCGAACCTCAAATTGATGTTTACTAATATTTT
TGTGACAGAGTATAAAGACCCTATAGTGGGTAAATTAGATACTATTAGCATATTATTAATTTAATGTCTTTATCA
TTGGATCTTTTGCATGCTTTAATCTGGTTAACATATTTAAATTTGCTTTTTTCTCTTTACCTGAAGGCTCTGTG
TATAGTATTTTCATGACATCGTTGTACAGTTTAACTATATCAATAAAAAGTTTGGACAGTATTTAAATATTGCAAA
TATGTTTAAATTATACAAATCAGAATAGTATGGGTAAATTAATGAATACAAAAAGAAGAGCCTCTTTCTGCAGCCG
ACTTAGACATGCTCTTCCCTTTCTATAAGCTAGATTTTAGAATAAAGGGTTTTCAGTTAATAATCTTATTTTCAGG
TTATGTCATCTAACTTATAGCAAACTACCACAATACAGTGAGTCTGCCAGTGTCCAGTACAAGGCATATTTCA
GGTGTGGCTGTGGAATGTAAAAATGCTCAACTGTATCAGGTAATGTTAGCAATAAATTAATGCTAAGAATGAT

1401/6881
FIGURE 1302B

TAATCGGGTACATGTTACTGTAATTAACCTCATTGCACTTCAAAACCTAACTTCCATCCTGAATTTATCAAGTAGT
TCAGTATTGTCATTTGTTTTGTTTTATTGAAAAGTAATGTTGCTTAAGATTTAGAAGTGATTATTAGCTTGAG
AACTATTACCCAGCTCTAAGCAAATAATGATTGTATACATATTAAGATAATGGTTAAATGCGGTTTTACCAAGTT
TTCCCTTGAAAATGTAATTCCTTTATGGAGATTTATTGTGTCAGCCCTAAGCTTCCTTCCATTTTCATGAATATAA
GGCTTCTAGAATTGGACTGGCAGGGGAAAGAATGGTAGAGACAGAAATTAAGACTTTATCCTTGTTTGCTTGTA
ACTATTATTTTCTTGCTAATGTAACATTTGTCTGTTCCAGTGATGTAAGGATATTAAGTTATTAAGCTAAATATT
AATTTTCAAAAATAGTCCTTCTTTAACTTAGATATTTTCATAGCTGGATTTAGGAAGATCTGTTATTCTGGAAGTA
CTAAAAGAATAATACAACGTACAATGTCTGCATTCACTAATTCATGTTCCAGAAGAGGAAATAATGAAGATATA
CTCAGTAGAGTACTAGGTGGGAGGATATGGAAATTTGCTCATAAAATCTCTTATAAAACGTGCATATAACAAAT
GACACCCAGTAGGCCTGCATTACATTTACATGACCGTGTTATTTGCCATCAAATAAACTGAGTACTGACACCAG
ACAAAGACTCCAAAGTCATAAAATAGCCTATGACCAACTGCAGCAAGACAGGAGGTCAGCTCGCCTATAATGGTG
CTTAAAGTGTGATTGATGTAATTTTCTGTACTCACCATTGGAAGTTAGTTAAGGAGAACTTTATTTTTTAAAAA
AAGTAAATGGCAACCACTAGTGTGCTCATCCTGAACTGTTACTCCAAATCCACTCCGTTTTTAAAGCAAAATTAT
CTTGATGTTTTAAGAAAAGAGTTTTCTATTTATTTAAGAAAAGTAACAATGCAGTCTGCAAGCTTTCAGTAGTTTT
CTAGTGCTATATTCATCCTGTAAAACCTTTACTACGTAACCAGTAATCACAAGGAAAGTGTCCTTTTGCATATT
TCTTTAAAATTCCTTTTGGAAAGTATGATGTTGATAATTAACCTTACCCTTATCTGCCAAAACAGAGCAAAAT
GCTAAATACGTTATTGCTAATCAGTGGTCTCAAATCGATTTGCCTCCCTTTGCCTCGTCTGAGGGCTGTAAGCCT
GAAGATAGTGGCAAGCACCAAGTCAGTTTCCAAAATTGCCCTCAGCTGCTTTAAGTGACTCAGCACCTGCCTC
AGCTTCAGCAGGCGTAGGCTCACCTGGGCGGAGCAAAAGTATGGGCCAGGGAGAACTACAGCTACGAAGACCTGC
TGTCGAGTTGAGAAAAGGGGAGAATTTATGGTCTGAATTTTCTAACTGTCTCTTTCTTGGGTCTAAAGCTCATA
ATACACAAAGGCTTCCAGACCTGAGCCACACCCAGGCCCTATCCTGAACAGGAGACTAAACAGAGGCCAAATCAAC
CCTAGGAAATACTTGCATTCTGCCCTACGGTTAGTACCAGGACTGAGGTCATTTCTACTGGAAAAGATTGTGAGA
TTGAACCTATCTGATCGCTTGAGACTCCTAATAGGCAGGAGTCAAGGCCACTAGAAAATTGACAGTTAAGAGCCA
AAAGTTTTTAAAATATGCTACTCTGAAAATCTCGTGAAGGCTGTAGGAAAAGGGAGAATCTTCCATGTTGGTGT
TTTTCTGTAAAGATCAGTTTGGGGTATGATATAAGCAGGTATTAATAAAAATAACACACCAAGAGTTACGTAA
AACATGTTTTATTAATTTTGGTCCCCACGTACAGACATTTTATTTCTATTTTGAAATGAGTTATCTATTTTCATA
AAAGTAAAACACTATTAAAGTGCTGTTTTATGTGAAATAACTTGAATGTTGTTCCCTATAAAAAATAGATCATAAC
TCATGATATGTTTGTAATCATGGTAATTTAGATTTTATGAGGAATGAGTATCTGGAAATATTGTAGCAATACTT
GGTTTAAAATTTTGGACCTGAGACACTGTGGCTGTCTAATGTAATCCTTTAAAATTTCTCTGCATTGTCAGTAAA
TG TAGTATATTATTGTACAGCTACTCATAATTTTTTAAAGTTTATGAAGTTATTTTATCAAATAAAAACTTTCC
TATAT

1402/6881
FIGURE 1303

MQFRECSINGMKYQEINGRLVPEGPTPDSSEGNLSYLSSLSHLNNLSHLTTSSSFRTSPENETELIKEHDLFFKA
VSLCHTVQISNVQTDCTGDGPWQSNLAPSOLEYYASSPDEKALVEAAARIGIVFIGNSEETMEVKTILGKLERYKL
LHILEFDSDRRRMSVIVQAPSGEKL LFAKGAESSILPKCIGGEIEKTRIHVDEFALKGLRTL CIAYRKFTSKEYE
EIDKRIFEARTALQQREEKLA AVFQFIEKDLILLGATAVEDRLQDKVRETIEALRMAGIKVWVLTGDKHETAVSV
SLSCGHFHRTMNILELINQKSDSECAEQLRQLARRITEDHVIQHGLVVDGTSLSLALREHEKLFMEVCRNC SAVL
CCRMAPLQKAKVIRLIKISPEKPITLAVGDGANDVSMIQEAHVIGIGIMGKEGRQAARNSDYAIARFKFLSKLLFV
HGHFYYIRIATLVQYFFYKNVCFITPQFLYQFYCLFSQQTLYDSVYLTLYNICFTSLPILIYSLLEQHVDPHVLQ
NKPTLYRDISKNRLLSIKTFLYWTILGF SHAFIFFFGSYLLIGKDTSL LGNGQMF GNWTFGTLVFTVMVITVTVK
MALETHFWTWINHLVTWGSIIIFYVFSLFYGGILWPFLGSQNMVFVFIQLLSSGSAWF AII LMVVTCLFLDIKK
VFDRHLHPTSTEKAQLTETNAGIKCLDSMCCFPEGEAACASVGRMLERVIGRCSPTHISRSWSASDPFYTNDRSI
LTLSTMDSSTC

1403/6881
FIGURE 1304

TTTAGCAGTCTGTGATGATCAGCAAAAAAGCACATAAAGTAAAAATTAGTTGACCATGCTAAATTCAATTCTGGA
ATTTTTTTTTTTATTTGGGCATTTCTAGAACTTTTTACATTTGAAAGTACATGATGAGTATTAGTAACGATGACTTA
TGTATAATCAGAATCTTTATGACAATTTAGTTTTTACAAGGTCAGAAGAGATGAGTTTGCTAAACCCAGCTGTGAT
ACCTCAGTTGGAAAGGGAATTCAAAGGTATGCTTTGTAGAACAGAAAAAGTATAGTTTTTTTTTTCATGAACCTTTAA
TCATTTTCTGTTTTTCCCTCTATGTGAGTCAGCTACAAAAGTGGTCTAATTTTTTACAACAGTAGAACTTCCTCCTT
TTCTACTGTAATCTTCCCCTGACTTTACTGCACAGGTATGAAATACTAGTGTATTGGATCTTCAGTAACCTTTT
TATTTCCCTAGATGATTGAAATATAGGTATTTACTCCATTTAAACCAGGTGATAAGATGATGTAAATACTCAGGGA
GGGTATTAACCTTGTTACTTTTGCTCGTTTGGGGTGTAAAGTGCCATGACTGAATAATCTTCAATTCATGATTCTA
GAGTAAGTTTAATTTGGAAAAAGGGGCTTCACACATGGTGGTGGTTGAACATTGATTCTTTTATACTTAAAAAGA
TGAAATGTTTTGTGGACTGATACATTTTATCTTACTGAATATGAATTGTTT**ATGT**ATCTCTACTGTCAAATAGC
CTTTTGTAAACTCAGGAAAGACAAAGGTTCAATTACACCACTTTTGTCAATAAGCAAACCAGGTATTTTTTTTTT
CTCCTGTTGTCTGGATATGGCAATAGATTTTTTAAATTGCTGTGAGAAACCCATATATGAAAAGAGAGGAGTTGAA
TTGTTGTGTGCCTTTTATGTCTTGAGATTTATATGTGGAAAAGACGACATCTACTTCAAACCTGTATTTTTTTTCGTT
TTTTTTTTTTTTTGGGGAAAGGGGGGAGAACGGGGTCTTGCTCTGTGCGCCAGGCTGGAGTGCAGTGGCGCGATCT
CAGCT**GA**CTGCAACCTCCACCTCCCGGGTTCAAGGGATTCTGCCTCAGCCTCCCGAGTAGCTGAGACCACAGGTG
CGTGCCACCACACCCGGCTAATTTTTTTGTATTTTTTAGTAGAGACGGGGTTTAGTAGAGACGGATCACTCCTGAC
CACGTGATCCGCCCACCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCACCCCGGCCTGTATTTT
CAGAGAGGAGAGCTTGGTGTTTTTGTGGTGCCAAGTGGTAAGATAATGTCTCTTTGAGGCTTCCTATGGACTGCC
TTTATTTTTAGTAAACTCAAGACACCAGTTAACCTCAACAGAGTTTTGGCCTTATTAGAATTTGTTGTGCATCTTA
TTGAAAGCCAGGTTTACATCACCTCACCCATTATTCTTTTTAGTTAAATAAATTTACCATGCCAAGTAACCAGA
ATGGAGCAAATTGGTTGATCTTTAAGGCAGTAGGTTTGACTAGCTAGCTATCATTATTGTCACATCTAATGCTAG
GCACCAGAAACCATTTGAGCCAGGAGTGTGAATGAATAATTCCAGAGACACTTTAGACATTTTTTAAATGTTTTAT
ATGAACATTTTACATTTGTGTGATTGCCTTAGATATTAAATTTTCTAGTGCTGATAAAAACAGCAACATTCATA
ACTTATTTTATATATTGTTCCAAAGAAAAGAATTTGTTTTAATGGTTTCAAATAACTGCACCTGAATTTGTTTA
TGTGCCTTAAGTTCTCTAGTGCTATTTCAACTTTTTTTTTCAATCTAAATGAAGCTTACCTTAGATAAGGTTTATA
TTTGTTCCTATAGAGTAAATAAACTTCCCTTCTTAAATTGTGTAATAAGCACCAACGTGTGGTTGCTTGGCAG
AATGAGAATGTAAAGGGAGATTGTTGGAIGTTTGGAGTTTCATTATATTTTTTGTTTTTATTTTTTGATACCTAG
GTGCTTTTTTAAATATTCAGACAAATATCTATCTTACATTGATTAAACCCGTGTAAATTCATTTGCAGTATCTAC
ATCGAATGTCAAAAAAGTATACTTATTTTTGTTCCATACTTATGTACAATTTTTTCCCTCTTCAGGCTTTTTTCAT
TTACCTTTTTTGAAAAAGCACTTACTCTCCCTTCCCTATCACCCCTCCCCAAGGTTTCTTTATTTAAATTTTTTA
TTGAGAGTTGTTGGAGCTCTAAGACAATACAAATTTAGAGTTGAACAAAAAGTATAATCTGCTTTACAACCTAGTAT
AGACCTAAGGTCATTTGCTTTCAATTAGAGGCTCCAGAGTCTTCATAGTGGAAGAATGCTTTGTATTTAATTGT
TCTTAGTTAAGTTGTAGCACGTGAATACTTACTTACATGTTTTGTTTAAATATACTTCTTGCATAGTTTAATTTT
TTAAAAGTTGTATCTAATAAAATGTCTTTTAACCATTATTACTTGACTATATGGTTGTATTAAATTTTTGTTTACG

1404/6881
FIGURE 1305

MYLYCQIAFLKLRKDKGSITPLLSISKPGIFFFSCCLDMAIDFLNCCENPVMKREELNCVCLLCLEIYMWKRRHL
LQTVFFSFFFFFFGEGGRTGSCSVAQAGVQWRDLS

1405/6881
FIGURE 1306

GTCTGGAATCAAGCGAACCATCAAAGAAACCGACCCTGATTACGAGGATGTATCTGTGGCCCTTCCAAATAAGCG
GCATAAAGCAATTGAGAATTCAGCTCGAGATGCTGCTGTGCAGAAGATTGAGACTATTATCAAAGAACAGTTTGC
TCTTGAAATGAAGAATAAGGAACATGAAATTGAAGTCATTGACCAGCGACTGATTGAAGCAAGAAGGATGATGGA
TAAACTGCGTGCCTGCATTGTAGCAAACACTACTATGCTTCTGCAGGTCTTCTAAAAGTTTCTGAGGGATCAAAGAC
ATGTGATACGATGGTTTTTAATCATCCTGCTATCAAGAAATTTTGGAAATCACCATCTAGGTCATCATCTCCTGC
CAATCAGAGAGCAGAAAACACCATCAGCCAATCATTGAGAAAGTGATTCTTTATCTCAGCACAAATGACTTCTTATC
TGACAAAGATAATAACAGCAATATGGATATAGAGGAAAGACTCTCAAACAACATGGAGCAGAGACCAAGCCGAAA
TACTGGAAGGGATACTTCTAGAATTACTGGCTCCCATAAAACAGAACAGCGGAATGCTGATCTCACAGATGAGAC
TTCACGACTTTTTGTAAAGAAAACAATAGTAGTGGGCAATGTGTCCAAGTATATACCTCCGGATAAGAGGGGAAGA
AAATGACCAGTCAACTCATAAGTGGATGGTATATGTCCGAGGGTCCCGTAGAGAACCCAGCATTAATCATTTTGT
CAAGAAGGTTTGGTTCTTCCTTCATCCTAGCTATAAACCAAATGACCTTGTGGAAGTTAGAGAGCCTCCTTTTCA
CCTGACCAGAAGAGGCTGGGGTGAGTTTCCCGTCAGAGTTCAAGTTTCATTTTAAGGACAGCCAGCTCAAACCACT
CAGCGTAAACACATCTGGAGGGGTGCAGACGATCCTGATGCCTGTGAATAAAGTGGTTTCAGTCATTTTCTACCAG
CAAGCCACCTGCCATTCTGCCTGTAGCTGCCCCAACTCCAGTTGTCCCCAGCTCTGCTCCAGCAGCTGTTGCAAA
AGTGAAGACTGAACCAGAAACACCTGGACCGAGTTGCCTCTCTCAGGAGGGTCAGACAGCAGTGAAAAACAGAAGA
AAGTTCTGAGCTGGGAAACTATGTTCATTAAGATAGACCATTTAGAACTATCCAGCAACTCCTAACTTAGTAAAG
AAGATTCCATTAATCACTGCAAAAAGTGAAGATGCCAGCTGCTTTTCTGCAAAGTCTGTGGAGCAGTACTATGGC
TGGAACATTGGAAAAAGGAGAGCCGCTGAGTGGCAAAGAGCAATGACAATGCGAAAAGTCTTACAAGAAATCCTG
GAGAAGAATCCGAGATTTACCCACCTGACTCCCCTCAAACCAAGCACATCGCTCACTGGTGCCGCTGTCAATGGC
TACACCCACCCGGACCCCTGAGAGCCTGAGGAATGACGGGGACTCCATCGAGGACGTGCTGACCCAGATCGACAGC
GAGCCCAGGTGCCCATCATCATTCTCCTCTGCTGACAACCTCTGCCGCAAACCTGGAGGACCTGCAACAGTTCCAG
CCCTGGTGACAGAGGAGACCCCGTCTCAAAAATTGATTGATCAATTCAGCATCTGAGGGCTGCAAGTACAGAAGG
AATCTATTCTCAGCAGGGCATAGGGCACGCACTGGCTTAACAGTTTAGTATATAAGGCTCAAATAGTCTATACCT
GAACTGCTATAAGCAAGGTCGATAGGGAAGTGGATAGATTGCTTCAGCAAAGTGAAGTGTGAGATCTCCAGGACA
GAGGGAGAAAGATCTGATCCAAATGAGAACAGATTGGTTATTGCAGGTATCACAGCCTAAAGAAATTATCTTTTT
GCAAAAGAAATATTAAATGATTTAGCAGTCTCCACGTGTGTTAATGTTTCAAACGTGTATCATAATGTGTATAAT
TGTGTAACAAAATTGTCTACAATAAATCTTTTGGTATTTGT

1406/6881
FIGURE 1307

MKNKEHEIEVIDQRLIEARRMMDKLRACIVANYYASAGLLKVSEGSKTCDTMVFNHPAIAKKFLESPPSRSSSPANQ
RAETPSANHSESDSLSQHNDFLSDKDNNNSNMDIEERLSNNMEQRP SRNTGRDTSRITGSHKTEQRNADLTDETSR
LFVKKTI VVG NVSKYIPPDKREENDQSTHKWMVYVRGSRREPSINHFVKKVWFFLHPSYKPNDLVEVREPPFHLT
RRGWGEFPVRVQVHFKDSQLKPLSVNTSGGVQTILMPVNKVVQSFSSTSKPPAILPVAAPTPVVPSSAPAAVAKVK
TEPETPGPSCLSQEGQTAVKTEESSELGNYVIKIDHLETIQQLLT

1407/6881
FIGURE 1308

ATGTCTAGAGCCCTTGATGTCCTGCAAATGAAGGAGGAGGATGTCCTTAAGTTCCTTGCAGCAGGAACCCACTTA
GGTGGTACCAACCTTGACTTCCAAATGGACAATACTGGCCAGAGGGCTGTGCTGAAGTTTGCTGCTGCCACTGGA
GCCACTCAAATTGTTGGCCGCTTCACTCCTGGAACCTTCACTAGCCAGACCCAGGCAGCCTTCAGGGAGCCACGG
CTTCTAGTGGTTACTGATCCCAGGGCTGACCACCAGCCTCTCACAGAGACATCTTATGTTAACCTACCTACCATT
GCTCTATGTCACACAGATTTTCCTCTGCGCTATGTGGACATTGCCATCACATGCAACAACAAGGGAGCTCCCTCA
GTGGGTCCGAGCTGGTGGATGCTGGCCCTGGAAGTTCTGCGCGTGTGTGGCACCATTTCCCTCGAACACCCATGG
GAGGTCATGCCTGATCTCTACTTCTACAGAGATCCTGAAGAGATTGGAAAAGAGGAGCAGGTTGCTGCTGAAAAG
ACTGTGACCAAGGAGGAATTTCAAGGCAAATGGACTGCTCCAGCTCCTGAGTTCACCGCTATTACAGCCTGAGGTT
GGAGACTGGTCTGATGGTGTACAGGTGCCCTCTGTGCCTATTATCAGGTCCCTACTGAAGACTGGAGTGCTCAG
CCTGCCACAGAAGACTGGTCTGCAGCTCCCACTGCTCAGGCCACTGAATGGGTAGAAACAACCACTGAATGGTCT
TAA

1408/6881
FIGURE 1309

MSRALDVLQMKEEDVLKFLAAGTHLGGTNLDFQMDNTGQRAVLKFAAATGATQIVGRFTPGETFTSQTQAAFREPR
LLVVTDPRADHQPLTETSYVNLPTIALCHTDFPLRYVDIAITCENNKGAPSVGPSWWMLALEVLRVCGTISLEHPW
EVMPDLYFYRDP EEIGKEEQVAAEKTVTKEEFQ GKWTAPAPEFTAIQPEVGDWSDGVQVPSVPIHQVPTEDWSAQ
PATEDWSAAPT AQATEWVETTTEWS

1409/6881
FIGURE 1310

TGCGTGCGGTGGCAGCTTCCTTGCGGAAGTGGTGACCGTGAGAGAAGAAGATGGCGGCCCTGTAGTGGCGCCGC
CTGGTGTGGTGGTTAGTCGGGGCTAACAAGCGCAGCGGCGCGGGGCCGGAGGCAGCGGTGGCGGGGGAGCCAGAG
GGGCGGAGGAGGAACCGCCGCCGCCCTACAAGCAGTTCTGGTGGCCGATAGCTTCGATCGCCGCTTCTTCCCCA
TCTCCAAGGACCAGCCTCGGGTCTCTTGCCCTGGCCAATGTGGCATTAAATTGACTACACTCTGGAATTCCTGA
CTGCCACAGGTGTACAGGAAACATTTGTCTTTTGTGCTGGAAAGCTGCTCAAATCAAAGAACATTTACTGAAGT
CAAAGTGGTGCCGCCCTACATCTCTCAATGTGGTTTGAATAATTACATCAGAGCTCTATCGATCACTGGGAGATG
TCCTCCGTGATGTTGATGCCAAGGCTTTGGTGCGCTCTGACTTTCTTCTGGTGTATGGGGATGTCTCTCAAACA
TCAATATCACCAGAGCCCTTGAGGAACACAGGTTGAGACGGAAGCTAGAAAAAATGTTTCTGTGATGACGATGA
TCTTCAAGGAGTCATCCCCCAGCCACCCAACTCGTTGCCACGAAGACAATGTGGTAGTGGCTGTGGATAGTACCA
CAAACAGGGTTCTCCATTTTCAGAAGACCCAGGGTCTCCGGCGTTTGCATTTCTCTGAGCCTGTTTCAGGGCA
GTAGTGATGGAGTGGAGGTTTCGATATGATTTACTGGATTGTCTATATCAGCATCTGTTCTCCTCAGGTGGCACAAAC
TCTTTACAGACAACTTTGACTACCAAACCTCGAGATGACTTTGTGCGAGGTCTCTTAGTGAATGAGGAGATCCTAG
GGAACCAGATCCACATGCACGTAACAGCTAAGGAATATGGTGCCCGTGTCTCCAACCTACACATGTACTCAGCTG
TCTGTGCTGACGTCATCCGCCGATGGGTCTACCCCTCTACCCCCAGAGGCGAACTTCACTGACAGCACCACCCAGA
GCTGCACTCATTCCCGGCACAACATCTACCGAGGGCCTGAGGTGAGCCTGGGCCATGGCAGCATCCTAGAGGAAA
ATGTGCTCCTGGGCTCTGGCACTGTCTATTGGCAGCAATTGCTTTATCACCAACAGTGTCTATTGGCCCCGGCTGCC
ACATTGGTGATAACGTGGTGCTGGACCAGACCTACCTGTGGCAGGGTGTTCGAGTGGCGGCTGGAGCACAGATCC
ATCAGTCTCTGCTTTGTGACAATGCTGAGGTCAAGGAACGAGTGACACTGAAACCACGCTCTGTCTCACTTCCC
AGGTGGTCTGGTGGGCCAAATATCACGCTGCCTGAGGGCTCGGTGATCTCTTTGCACCCTCCAGATGCAGAGGAAG
ATGAAGATGATGGCGAGTTTCACTGATGATTCTGGGGCTGACCAAGAAAAGGACAAAGTGAAGATGAAAGGTTACA
ATCCAGCAGAAGTAGGAGCTGCTGGCAAGGGCTACCTCTGGAAAGCTGCAGGCATGAACATGGAGGAAGAGGAGG
AACTGCAGCAGAATCTGTGGGGACTCAAGATCAACATGGAAGAAGAGAGTGAAAGTGAAAGTGAGCAAAGTATGG
ATTCTGAGGAGCCGGACAGCCGGGGAGGCTCCCCCTCAGATGGATGACATCAAAGTGTTCCAGAATGAAGTTTTAG
GAACACTACAGCGGGGCAAAGAGGAGAACATTTCTTGTGACAATCTCGTCTCTGGAAATCAACTCTCTCAAGTATG
CCTATAACGTAAGTCTAAAGGAGGTGATGCAGGTACTGAGCCACGTGGTCTCTGGAGTTCCCCCTGCAACAGATGG
ATTCCCCGCTTGACTCAAGCCGCTACTGTGCCCTGCTGCTTCTCTGCTAAAGGCCTGGAGCCCTGTTTTTAGGA
ACTACATAAAGCGCGCAGCCGACCATTGGAAGCGTTAGCAGCCATTGAGGACTTCTTCTTAGAGCATGAAGCTC
TTGGTATTTCCATGGCCAAGGTACTGATGGCTTTCTACCAGCTGGAGATCCTGGCTGAGGAAACAATTCTGAGCT
GGTTCAGCCAAAGAGATACAACCTGACAAGGGCCAGCAGTTGCGCAAGAATCAACAGCTGCAGAGGTTTCATCCAGT
GGCTAAAAGAGGCAGAAGAGGAGTCATCTGAAGATGACTGAAGTCACTGCCTGCTCCTTTGGGTGTGATTGAG
TGCCCTCCTGGCTCCTGGGCTGGGACAAGTGAGGAACTAGCTGCAGAGGGATGAGTGACCACCATCCAGGCTGAG
ACTGAAAGGAGCAGAGGCTGGAACCTACAGTATTCTTTCCCCTGCTAGCAACCATGTGCCTCCCATCCTGACTGTG
GAGTTGGGATGTGGAAGTGGGGCTGGAACAAAGCTTCTGCCTAGGGAGGAGCTAAGCAGGCCCGGCAGTTGGAGG
AAGGCCAGAGGAACAGCTTTGTGCTCCGGCTTTCCCTCAGGGAACAGCAGAGAGCAGTTGGCTCTTTCTGCTGCT
TGTATATGTTAATATTAAGAGAGTGGTGT

1410/6881
FIGURE 1311

MAAPVVAPPGVVVSRANKRSGAGPGGSGGGGARGAEEEEPPPPPLQAVLVADSFDRRFFPI SKDQPRVLLPLANVAL
IDYTLLEFLTATGVQETFFVCCWKAQIKEHLLKSKWCRPTSLNVVRIITSELYRSLGDVLRDVEDAKALVRSDFLL
VYGDVISNINITRALEEHRLRRKLEKNVSVMTMIFKESSPSHPTRCHEDNVVVAVDSTTNRVLHFQKTQGLRRFA
FPLSLFQGSSDGVEVRYDLLDCHISICSPQVAQLFTDNFDYQTRDDFVRGLLVNEEILGNQIHMHVTAKEYGARV
SNLHMYSAVCADVIRRWVYPLTPEANFTDSTTQSCTHSRHNIYRGPEVSLGHGSILEENVLLGSGTVIGSNCFIT
NSVIGPGCHIGDNVVDQTYLWQGVVVAAGAQIHQSLLCDNAEVKERVTLKPRSVLTSQVVVGPNTLPEGSVIS
LHPPDAEEDDDGEFSDDSGADQEKDKVKMKGYNPAEVGAAGKGYLWKAAGMNMEEEEELQQNLWGLKINMEEES
ESESEQSMDSEEPDSRGGSPQMDDIKVFQNEVLGTLQRGKEENISCDNLVLEINSLKYAYNVSLKEVMQVLSHV
LEFFLQQMDSPLDSSRYCALLLPLLKAWSFVFRNYIKRAADHLEALAAIEDFFLEHEALGISMAKVLMAFYQLEI
LAEETILSWFSQRDTTDKGQQLRKNQQQLQRFIQWLKEAEEESSEDD

1411/6881
FIGURE 1312

ATGGCGGCCCCTGTAGTGGCGCCGCCTGGTGTGGTGGTTAGTCGGGGCTAACAAGCGCAGCGGCGCGGGGCCGGGA
GGCAGCGGTGGCGGGGGAGCCAGAGGGGCGGAGGAGGAACCGCCGCCGCCCTACAAGCAGTTCTGGTGGCCGAT
AGCTTCGATCGCCGCTTCTTCCCCATCTCCAAGGACCAGCCTCGGGTCCTCTTGCCCCTGGCCAATGTGGCATT
ATTGACTACACTCTGGAATTCCTGACTGCCACAGGTGTACAGGAAACATTTGTCTTTTGTTGCTGGAAAGCTGCT
CAAATCAAAGAACATTTACTGTAAGGCCCTGCAACTTTTCTTTCCATGTTTCGCCATCTTTTTCCAGTTTTTCA
GGATGAATGTAACTAAGGGGAAATGTGAGAGGGGAAAAATGTGTCTACTTAGATGTCATTGTAAGTTCTAAGGGT
ATTTTCTACACTTATCAGGAGGTGAGCAGCTGAACTTTGTATCTGTCTGTCTTGGGTTTTCTGTGACAAAGATT
AAAGAATAAACTTGGGTTTTTCTGAATCTC

1412/6881
FIGURE 1313A

CAAGCGACACAAATGAACACGCCTTCTCAGCCCCGCCAGCACTTCTACCCTAGCCGGGCCCCAGCCCCGAGCAGT
GCAGCCTCCCGAGTGCAGAGTGCAGCCCCCTGCCCGCCCTGGCCCAGCTGCCCATGTCTACCCTGCTGGATCCCAA
GTAATGATGATCCCTTCCCAGATCTCCTACCCAGCCTCCCAGGGGGCCTACTACATCCCTGGACAGGGGCGTTCC
ACATACGTTGTCCCGACACAGCAGTACCCTGTGCAGCCAGGAGCCCCAGGCTTCTATCCAGGTGCAAGCCCTACA
GAATTTGGGACCTACGCTGGCGCCTACTATCCAGCCCAAGGGGTGCAGCAGTTTCCCACTGGCGTGGCCCCCACC
CCAGTTTTGATGAACCAGCCACCCAGATTGCTCCCAAGAGGGAGCGTAAGACGATCCGAATTCGAGATCCAAAC
CAAGGAGGAAAGGATATCACAGAGGAGATCATGTCTGGGGCCCCGACTGCCTCCACACCCACCCCTCCCCAGACG
GGAGGCGGTCTGGAGCCTCAAGCTAATGGGGAGACGCCCCAGGTTGCTGTCATTGTCCGGCCAGATGACCGGTCA
CAGGGAGCAATCATTGCTGACCGGCCAGGGCTGCCTGGCCCAGAGCATAGCCCTTCAGAATCCCAGCCTTCGTCTG
CCTTCTCCGACCCCATCACCATCCCCAGTCTTGGAACCGGGTCTGAGCCTAATCTCGCAGTCTCTCTATTCTCT
GGGGACACTATGACAACTATACAAATGTCTGTAGAAGAATCAACCCCATCTCCCGTGAACTGGGGAGCCATAT
CGCCTCTCTCCAGAACCCACTCCTCTCGCCGAACCCATACTGGAAAGTAGAAGTGACACTTAGCAAACCGGTTCCA
GAATCTGAGTTTTCTTCCAGTCTCTCCAGGCTCCACCCCTTTGGCATCTCACACAGTGGAATTCATGAGCCT
AATGGCATGGTCCCATCTGAAGATCTGGAACCAGAGGTGGAGTCAAGCCCAGAGCTTGCTCCTCCCCAGCTTGC
CCCTCCGAATCCCTGTGCCCATTTGCTCCAAGTGCCTCAACCTGAGGAAGTCTCAACGGAGCCCCCTCGCCACCA
GCTGTGGACTTAAGCCAGTCAGTGAGCCAGAGGAGCAGGCCAAGGAGGTGACAGCATCAATGGCGCCCCCACC
ATCCCTCTGCTACTCCAGCTACGGCTCCTTCAGCTACTTCCCCAGCTCAGGAGGAGGAAATGGAAGAAGAAGAA
GAAGAGGAAGAAGGAGAAGCAGGAGAAGCAGGAGAAGCTGAGAGTGAGAAAGGAGGAGAGGAACTGCTCCCCCA
GAGAGTACCCCTATTCCAGCCAACCTTGCTCAGAATTTGGAGGCAGCAGCAGCCACTCAAGTGGCAGTATCTGTG
CCAAAGAGGAGACGGAAAAATTAAGGAGCTAAATAAGAAGGAGGCTGTTGGAGACCTTCTGGATGCCTTCAAGGAG
GCGAACCCGGCAGTACCAGAGGTGGAATATCAGCCTCCTGCAGGCAGCAATCCAGGCCAGAGTCTGAGGGCAGT
GGTGTGCCCCCACGTCTGAGGAAGCAGATGAGACCTGGGACTCAAAGGAAGACAAAATTCACAATGCTGAGAAC
ATCCAGCCCCGGGGAACAGAAATATGAATATAAGTCAGATCAGTGAAGCCTCTAAACCTAGAGGAGAAAAACGT
TACGACCGTGAGTTCTGCTTGGTTTTTCAGTTTCATCTTTGCCAGTATGCAGAAGCCAGAGGGATTGCCACATATC
AGTGACGTGGTGCTGGACAAGGCCAATAAAACACCACTGCGGCCACTGGATCCCACTAGACTACAAGGCATAAAT
TGTGGCCAGACTTCACTCCATCCTTTGCCAACCTTGCCCGGACAACCTTAGCACCCGTGGGCCCCCAAGGGGT
GGGCCAGGTGGGGAGCTGCCCCGTGGGCCGGCTGGCCTGGGACCCCGCGCTCTCAGCAGGGACCCCGAAAAGAA
CCACGCAAGATCATTGCCACAGTGTTAATGACCGAAGATATAAACTGAACAAAGCAGAGAAAGCCTGGAAACCC
AGCAGCAAGCGGACGGCGGCTGATAAGGATCGAGGGGAAGAAGATGCTGATGGCAGCAAAACCCAGGACCTATTC
CGCAGGGTGCGCTCCATCCTGAATAAACTGACACCCAGATGTTCCAGCAGCTGATGAAGCAAGTGACGCAGCTG
GCCATCGACACCGAGGAACGCCTCAAAGGGGTCAATTGACCTCATTTTTGAGAAGGCCATTTTCAGAGCCCAACTTC
TCTGTGGCCTATGCCAACATGTGCCGTGCCTCATGGCGCTGAAAGTGCCCACTACGGAAGGCAACAGTGACT
GTGAACTTCCGAAAGCTGTTGTTGAATCGATGTGAGAAGGAGTTTGAGAAAAGACAAAGATGATGATGAGGTTTTT
GAGAAGAAGCAAAAAGAGATGGATGAAGCTGCTACGGCAGAGGAACGAGGACGCCTGAAGGAAGAGCTGGAAGAG
GCTCGGGACATAGCCCGGCGGCGCTCTTAGGGAATATCAAGTTTATTGGAGAGTTGTTCAAACCTGAAGATGTTA
ACAGAGGCAATAATGCATGACTGTGTGGTCAAACCTGCTTAAGAACCATGATGAAGAGTCCCTTGAGTGCCTTTGT
CGTCTGCTCACCACCATTGGCAAAAGACCTGGACTTTGAAAAAGCCAAGCCCCGAATGGATCAGTATTTCAACCAG
ATGGAAAAAATCATTAAGAAAAAGAGACGTATCCCGCATCCGCTTTATGCTGCAGGACGTGCTGGATCTGCGA
GGGAGCAATTGGGTGCCACGCCGAGGGGATCAGGGTCCCAAGACCATTGACCAGATCCATAAGGAGGCTGAGATG
GAAGAACATCGAGAGCACATCAAAGTGCAGCAGCTCATGGCCAAGGGCAGTGACAAGCGTCGGGGCGGTCTTCCA
GGCCCTCCCATCAGCCGTGGACTTCCCTTGTGGATGATGGTGGCTGGAACACAGTTCCCATCAGCAAAGGTAGC
CGCCCCATTGACACCTCACGACTACCAAGATACCAAGCCTGGCTCCATCGATTCTAACAACCAGCTCTTTGCA
CCTGGAGGGCGACTGAGCTGGGGCAAGGGCAGCAGCGGAGGCTCAGGAGCCAAGCCCTCAGACGCAGCATCAGAA
GCTGCTCGCCAGCTACTAGTACTTTGAATCGCTTCTCAGCCCTTCAACAAGCGGTACCCACAGAAAGCACAGAT
AATAGACGTGTGGTGCAGAGGAGTAGCTTGAGCCGAGAACGAGGCGAGAAAGCTGGAGACCGAGGAGACCGCCTA
GAGCGGAGTGAACGGGGAGGGGACCGTGGGGACCGGCTTGATCGTGC GCGGACACCTGCTACCAAGCGGAGCTTC
AGCAAGGAAGTGGAGGAGCGGAGTAGAGAACGGCCCTCCAGCCTGAGGGGCTGCGCAAGGCAGCTAGCCTCACG
GAGGATCGGGACCGTGGGCGGGATGCCGTGAAGCGAGAAGCTGCCCTACCCCAAGTGAGCCCCCTGAAGGCGGCT

1413/6881
FIGURE 1313B

CTCTCTGAGGAGGAGTTAGAGAAGAAATCCAAGGCTATCATTGAGGAATATCTCCATCTCAATGACATGAAAGTA
GGCAGTCCAGTGCGTGCAGGAGCTGGCCTCACCCCTCCTTGCTCTTCATCTTTGTACGGCATGGTGTGAGTCTAC
GCTGGAGCGCAGTGCCATTGCTCGTGAGCATATGGGGCAGCTGCTGCACCAGCTGCTCTGTGCTGGGCATCTGTC
TACTGCTCAGTACTACCAAGGGTTGTATGAAATCTTGGAATTGGCTGAGGACATGGAAATTGACATCCCCACGT
GTGGCTCTACCTAGCGGAACTGGTAACACCCATTCTGCAGGAAGGTGGGGTGCCCATGGGGGAGCTGTTGAGGGA
GATTACAAAGCCTCTGAGACCGTTGGGCAAAGCTGCTTCCCTGTTGCTGGAGATCCTGGGCCTCCTGTGCAAAAG
CATGGGTCCTAAAAAGGTGGGGACGCTGTGGCGAGAAGCCGGGCTTAGCTGGAAGGAATTTCTACCTGAAGGCCA
GGACATTGGTGCAATTCGTCGCTGAACAGAAGGTGGAGTATACCCTGGGAGAGGAGTCGGAAGCCCCCTGGCCAGAG
GGCACTCCCCCTCCGAGGAGCTGAACAGGCAGCTGGAGAAGCTGCTGAAGGAGGGCAGCAGTAACCAGCGGGTGT
CGACTGGATAGAGGCCAACCTGAGTGAGCAGCAGATAGTATCCAACACGTTAGTTGAGCCCTCATGACGGCTGT
CTGCTATTCTGCAATTATTTTTGAGACTCCCCTCCGAGTGACGTTGCAGTGCTGAAAGCGCGAGCGAAGCTGCT
GCAGAAATACCTGTGTGACGAGCAGAAGGAGCTACAGGCGCTCTACGCCCTCCAGGCCCTTGTAGTGACCTTAGA
ACAGCCTCCCAACCTGCTGCGGATGTTCTTTGACGCACTGTATGACGAGGACGTGGTGAAGGAGGATGCCTTCTA
CAGTTGGGAGAGTAGCAAGGACCCCGCTGAGCAGCAGGGCAAGGGTGTGGCCCTTAAATCTGTACAGCCTTCTT
CAAGTGGCTCCGTGAAGCAGAGGAGGAGTCTGACCACAACCTGAGGGCTGGTGGGGCCGGGGACCTGGAGCCCCAT
GGACACACAGATGGCCCGGCTAGCCGCCTGGACTGCAGGGGGGCGGCAGCAGCGGCGGTGGCAGTGGGTGCCTGT
AGTGTGATGTGTCTGAACTAATAAAGTGGCTGAAGAGGCAGGATGGCTTGGGGCTGCCTGGGCCCCCTCCAGGA
TGCCGCCAGGTGTCCCTCTCCTCCCCCTGGGGCACAGAGATATATTATATATAAAGTCTTGAAATTTGGTGTGTC
TTGGGGTGGGGAGGGGCACCAACGCCTGCCCCCTGGGGTCCTTTTTTTTATTTTCTGAAATCACTCTCGGGACTG
CCGTCTCTGCTGCTGGGGGCATATGCCCCAGCCCTGTACCACCCCTGCTGTTGCCTGGGCAGGGGGAAGGGGGG
GCACGGTGCCTGTAATTATTAAACAT

FIGURE 1314A

GCGCGGGCCACCGGAAGATGTCGCGGTGCGCAGTCCAGTCTGGGAGAGTGGGGAGCGGAAGCGGCGGGCGGGCGGT
 GGCGGGCGGCGCTGGGACCCGGTAGCGGCCGAGAAACAAGGGAGCTGGCGCCGCCAGCAGCCGCCGAGCTGGGTT
 GAGCCGCTGGGCGCGCCGCGCGCCGCGCGCTCTGGGAGGCTCGGCCCGGCCGCCGAGCAGGCCGCGCGCGGG
 CCGCCGGGCCCCGAGGCCAGAGCCATGGGCGAGACCAAGATCATCTACCACTTGGATGGGCAGGAGACGCCGTACC
 TTGTGAAGCTGCCCCCTGCCCCGCCGAGCGCGTACCTTGGCGGACTTTAAGGGCGTTTTTGACGCGACCCAGCTATA
 AGTTCTTCTTCAAGTCTATGGACGACGATTTTCGGAGTGGTGAAGGAGGAGATCTCGGATGACAATGCCAAGCTAC
 CATGCTTCAATGGCCGGGTGGTGTCTTGGCTGGTGTCTAGCTGAGGGCTCACACCCAGACCCAGCCCCCTTCTGTG
 CTGATAACCCATCGGAGCTGCCACCACCTATGGAGCGCACGGGAGGCATCGGGGACTCCCGACCCCCATCCTTCC
 ACCCTCATGCTGGTGGGGGCAGCCAGGAGAACCTGGACAATGACACAGAGACGGACTCTTTGGTGTCTGCCCAGC
 GAGAGCGGCCACGCCGGAGGGATGGCCAGAGCATGCAACCCGGCTAAATGGAAGTGCAGAGGGGGAACGGCGGC
 GAGAACCAGGGGGTTATGATAGCTCATCCACCCTTATGAGCAGTGAGCTGGAGACCACAGCTTCTTTGACTCAG
 ATGAGGATGACTCCACCAGCAGGTTTCAGCAGCTCCACAGAACAGAGCAGTGCCTCACGCCTGATGAGAAGACACA
 AGCGGCGGCGGCGGAAGCAGAAGGTTTCTCGGATTGAGCGGTCTCTCGTCTTCAGCAGCATCACGGACTCCACCA
 TGTCACTCAACATCATCACGGTCACTCTCAACATGGAAAAATATAACTTCTTGGGCATCTCCATTGTGGGCCAAA
 GCAACGAGCGTGGTGACGGCGGCATCTACATTGGCTCTATCATGAAGGGTGGGGCCGTGGCTGCTGATGGACGCA
 TCGAGCCAGGAGATATGTTGTTACAGGTAAACGAGATCAACTTTGAGAACATGAGTAATGACGATGCAGTCCGGG
 TACTGCGGGAGATTGTGCACAAACCGGGGCCCATCACCTGACTGTAGCCAAGTGCTGGGACCCAAGTCCACGTG
 GTTGCTTACATTGCCCAGGAGCGAGCCCATCCGGGCCATTGACCCTGCGGCCTGGGTCTCCACACTGCAGCCA
 TGACCGGCACCTTCCCTGCATACGGCATGAGCCCCCTCCCTGAGCACCATCACCTCCACCAGCTCCTCCATCACCA
 GTTCCATCCCTGACACAGAGCGCCTAGACGACTTCCACTTGTCCATCCACAGTGACATGGCTGCCATCGTAAAAG
 CCATGGCCTCCCTGAATCAGGGTTGGAGGTCCGTGACCGCATGTGGCTCAAGATTACCATCCCTAATGCTTTCA
 TCGGCTCAGATGTGGTGGACTGGCTGTACCACAATGTGGAAGGCTTCACGGACCGGAGGGAGGCCCGCAAGTATG
 CCAGCAACCTGCTGAAAGCTGGCTTCATCCGCCATACCGTCAACAAGATCACCTTCTCCGAGCAGTGCTACTACA
 TCTTCGGTGACCTCTGCGGCAACATGGCCAACCTGTCTCTCCACGATCACGATGGCTCCAGTGCGCCTCTGACC
 AGGACACACTGGCCCCCTTTGCCGCACCCGGGGGCCGCCCTTGGGCCATGGCTTTTCCCGTACCAGTACCCGCCAC
 CCCCACACCCATACAACCCGCACCCGGGCTTCCCGGAGCTGGGCTACAGCTACGGCGGGGGCAGCGCCAGCAGTC
 AGCACAGCGAAGGCAGTCGGAGCAGTGGCTCCAACCGTAGCGGCAGCGATCGGAGGAAGGAGAAAGGACCCGAAGG
 CCGGGGACTCCAAGTCCGGGGGCAGCGGCAGCGAATCGGACCACACCACACGCAGCAGCCTGCGGGGGCGCGCGGG
 AGCGGGCGCCCAGCGAGCGCTCAGGGCCGGCGGCCAGCGAGCACAGCCACCGCAGCCACCATTCCCTGGCCAGCA
 GCCTTCGCAGCCACCACACACACCCGAGCTACGGTCTCTCCGGAGTGCCCCCTCTCTACGGCCCCCCCCATGCTGA
 TGATGCCCCCGCCGCCCGCGGCCATGGGGCCCCCAGGAGCCCCCTCCGGGCGCGACCTGGCCTCAGTGCCCCCGG
 AACTGACCGCCAGCAGACAGTCTTTCGCGATGGCCATGGGAAACCCAGTGAGTTCTTTGTGGATGTGATGTGAG
 CAGGGCCCCCTCCCCCAGCTCCATTCCGCTCCCACCCAGCCGGCTGCGTTCTCTCTCCATCCGTCCGTCTTTTT
 TACTTTGTCTGGTACCTGAAAGGGAAATAAAAGGAACTAAATCCAGGTGCGCTAACTGCTCGCAGGGTGCTGCGA
 GGGTGGGGTGACCTACCGATTGGCTCTGCAGCCCCCTAACCTGCCTCTGGCCCCAGTTCTGTTTCTCTGCCCCAC
 TAATCCCTGCGCAGGACTTCCCAGGACCCCTTTTTGTCTCTTGGGACCAGACTTGTTGGTGCTACCCCTTACTCCCC
 TCTGCAACCCCCATTTTGGGAGTTGACCCAGCAATGACCTTGGTGGCAGCTCACTCCCTCATTCTCTCGTTTC
 CCCTTTAGCTCCCTTTTACCATTATTTAGCTACATCATCCCTCTATTAACCCACCCCATCAGGCACGTGTGCA
 AACCTCTTGACTTTTACCCACATTACTGAAACCAAATATATTTGCTTCATCTGCCCTACTAACCATCCCCCTG
 CCTGCTGCCTCAGTCCGTGCAACCTAAAGCTGTAGTCGCCTCCAATAGCCATCCATGCCATCCCTGCCTGTGCCTA
 GATCAGAGGCCCAGAGGGCCCCCTCAGTTGCCTGAGCAGCTGGTGGCTTCCAGGGAGCATCTCTGCTCTACCCCT
 GCCCCATGCCTGCCTGCGTGCTGGTTTCCTTACAGCCCTTAACCTACTAACCAGCAGGCTCATCTCACCTCCAG
 GCCTGAAACATTTCTTTTCTTTCTTTTTTCTCCCCAATTTTCCCTGGGCCTGGAGCAGCCAAGAATTTTCGGGC
 TGTTTGACTTTCTGTGAGCCCCCAGCGAGGGGAGGCCAGCCTCCGAGGAGACCAGGAACCTGCTTCAGCAGCC
 CCTCAGGGCTTCCCAAGGATGTCCAGCCCCACACCCACACGTAAACATAATGAGTCACTAGGCTTCTGGGGAGG
 GCCCAACTTCACCCATGCATGAGAGACTCTCTCTTTTCCAGAGAGAAATCGGATCGCACCACGTGTGGCAGCCTG
 CGGCGGGGGGAGGGGGGCCCTCTTAGCTCTCTTTATCTTTCTCTCTCACTCATGTATGCATACATGCACAGAGAT
 GCATACACAGGTGCCTATGCAAGTTCATTTAAGCCTCAGGGCTGGTCCCTGCCCAAAGGGCTGGACCCTCCTAAT

1415/6881
FIGURE 1314B

CCTCTCCTAGGTTGTGGGGCTGGTCCCCTGACACCCTTCTCCCCTTCCTGGTAGACCTTAAACCTCGCACACATG
TCCCAGCATTTTCTCACCTGGATAAAGCCCATAAGCTGGGTCTCAGGCTGGGCTCAGCAAAGGACTCGCCTTGC
AACCGACAGGCCATTCCCACCCCCACACACAACCTCCCCTGTTTTCACATTACCATGGCATCCCAGAGCAAGGA
CACAGGAGCCCACAGGCCAGTTGAGGTTGGGCAAGGAGACTTCCAGGACTTCCAGACAGAGTACCAGGTTTTATT
TTTCACCTTATTCTCTACTTTAAACAAATCATAACTTTCTCTTTAAGCCTCTGCTATAAATTCTCCTGGCTCTCC
TGGGCTTCCATATTTTGGGGGCTGGGGTGTCAAAAGTGAGATGAAGTTCTTAGCTCCAGGTTTTGGGGTAAACCA
AGGTAGGAACATTTTGGCATTATTTCAATTAAACAATACTTCCTTGGACGGGTGCGGTGGCTCACGTCTGTAATC
CCAGCACTTTGGGAGGCTGAGACAGGTGGATCACTTGAGGTCGGGAGTTTCGAGACCAGCCTGGCCAACATAGCAA
AACCTGTCTCTACTAAAAATACAAAAATTAGATGGGTGTTTTGGCACCTGCCTGTAATCTCAGCTACTCAGGAG
GCTGAGGCACAAGAATCGCTTGAATCCAGGAAGCAAGCGGAGGTTGCAGTGAGTTGAGATCGCACTCCAGCCTGG
GTGACAGAGTGAGATTCTGTCTCAAAAGCAAATAACAAAGAAAAACAATACTTCCTGGGGTTTTGGTGTGCAGA
GGGCTTTGTTGGAAGTGTGACTCAATCTTGCCTGCCTTCTGGGAGCTCTAGAATTGTTCCCAACCCAGTCCATGG
CTTCTAGCCACCACTACAGGGCTGTTTTCATGTACTTCTCTCTGACTCTGTCTTGTCCGACTCTCTTGAGAATT
TCTCAACGATTGCTCATGCCTGTCAGTATCAGTGCTTCCATCGTTCCATCTTTGATTCACTTCTCTTTCCCTTTCT
ATTTACTCCCCAAATGGAGTCATTATCCTGATGTCTCTCAATTGCTGCTGATATGCTGGTGATTCCCCAAATACAT
AGCTCCAACCCCCAACTTCCCCCAGACTTTAGATCTGTATTGGTATTACCTACTGGACATCTCTATGGACAGTTC
CGTATAGACTCAACTCATCTGCCCAACCAAGTATGTTCCCTCCTGAATTCCCTCTCCTGGTTACTTCATCACAATCT
ACATAGGCTCACCAGCTAGAAACATTTATGAGCTTACATTCCCTTCTTCCCATATCTTATCAGCATATCATATCCA
TTTCACTCCAACACTCTGTCTTGAATTTGGCCCTCCCTCTCCCCTCTCTACTTTAATTCATTGGAGCATGGGATT
TGGAGTTAGGTGGTTTTTGGGTTTGAATTCCAGCTCTACTATTTTGGTTGTGTGATAGAGTTATTTAACCTCTCT
GAGCCTCAGTTCCCTCGTATGTAAATGATGATAATAATACCTACCTCACAGGGTTGTTGTGAGGATTTAAATTA
GATATTGTACGAAAAGTGCCTAGCACAGTGCCTGGCACACAGTAGAGTAGGTGCTCAATAAATGGTAGCTATTAT
TATT

1416/6881
FIGURE 1315

CCGAGGCAGCGGGCAGACGAGCAGGGGGCGGGCGGACATCTTGGGATCCGGAGAGTGGCCGGGCCGGCAGAGCAG
GGGGCCGAGGACACCAGGTCTGTTCTCAGAGCGATGGGGCCGCGGAGACTGATCTGCCGCCATGATTGGAGGCTTA
TTCATCTATAATCACAAGGGGGAGGTGCTCATCTCCCGAGTCTACCGAGATGACATCGGGAGGAACGCGAGTGGAT
GCCTTTTCGGGTCAATGTTATCCATGCCCGGCAGCAGGTGCGCAGCCCCGTCACCAACATTGCTCGCACCAGCTTC
TTCCACGTTAAGCGGTCCAACATTTGGCTGGCAGCAGTCACCAAGCAGAATGTCAACGCTGCCATGGTCTTCGAA
TTCCTCTATAAGATGTGTGACGTGATGGCTGCCTACTTTGGCAAGATCAGCGAGGAAAACATCAAGAACAATTTT
GTGCTCATATATGAGCTGCTGGATGAGATTCTAGACTTTGGCTACCCACAGAATTCCGAGACAGGCGCGCTGAAA
ACCTTCATCACGCAGCAGGGCATCAAGAGTCAGATGTAGACAAAAGAAGAGCAGTCACAGATCACCAGCCAGGTA
ACTGGGCAGATTGGCTGGCGGCGAGAGGGTATCAAGTATCGTCGGAATGAGCTCTTCCTGGATGTGCTGGAGAGT
GTGAACCTGCTCATGTCCCCACAAGGGCAGGTGCTGAGTGCCCATGTGTCTGGGCCGGGTGGTGATGAAGAGCTAC
CTGAGTGGCATGCCTGAATGCAAGTTTGGGATGAATGACAAGATTGTTATTGAAAAGCAGGGCAAAGGCACAGCT
GATGAAACAAGCAAGAGCGGGAAGCAATCAATTGCCATTGATGACTGCACCTTCCACCAGTGTGTGCGACTCAGC
AAGTTTGA CTCTGAACGCAGCATCAGCTTTATCCCGCCAGATGGAGAGTTTGAGCTTATGAGGTATCGCACAACC
AAGGACATCATCCTTCCCTTCCGGGTGATCCCGCTAGTGCGAGAAGTGGGACGCACCAAACCTGGAGGTCAAGGTG
GTCATCAAGTCCAACCTTTAAACCTCACTGCTGGCTCAGAAGATCGAGGTGAGGATCCCAACCCCACTGAACACA
AGCGGGGTGCAGGTGATCTGCATGAAGGGGAAGGCCAAGTACAAGGCCAGCGAGAATGCCATCGTGTGGAAGATC
AAGCGCATGGCAGGCATGAAGGAATCGCAGATCAGCGCAGAGATTGAGCTTCTGCCTACCAACGACAAGAAGAAA
TGGGCTCGACCCCCCATTTCCATGAACTTTGAGGTGCCATTTCGCGCCCTCTGGCCTCAAGGTGCGCTACTTGAAG
GTGTTTGAACCGAAGCTGAACTACAGCGACCATGATGTTCATCAAATGGGTGCGCTACATTGGCCGCGAGTGGCATT
TATGAAACTCGCTGCTAGCTGCCACTAGGCAGCTAGCCCACCTCCCCAGCCACCCTCCTCCACAGGTCCAGGTGC
CGCTCCCCCCCCACCACACACTAGTGTCTCCTCCCTCCTGCTTTGCTGCCTTCCCTTTGCACCAGCCCGAGTCT
AGGTCTGGGCCAAGCACATTACAAGTGGGACCGGTGGAGCAGCCCCTGGGCTCCCTGGGCAGGGGAGTTCTGAGG
CTCCTGCTCTCCCATCCACCTGTCTGTCTGGCCTAATGCCAGGCTCTGAGTTCTGTGACCAAAGCCAGGTGGGT
TCCCTTTCCCTTCCCACCCCTGTGGCCACAGCTCTGGAGTGGGAGGGTTGGTTGGCCCTCACCTCAGAGCTCCCC
AAAGGCCAGTAATGGATCCCCGGCCTCAGTCCCTACTCTGCTTTGGGATAGTGTGAGCTTCATTTTGTACACGTG
TGACTTCGTCCAGTTACAAACCCAATAAACTCTGTAGAGTGG

1417/6881
FIGURE 1316

GGTGGGCCCACACAAGCGGCGCACCGTTAAGATGGCGGCTGGGCTGCGGAAACGCGGCCGGTCCGGTTCCGCGGC
CCAGGCAGAGGGACTCTGCAAGCAATGGCTGCAGCGCGCCTGGCAAGAGCGGCGCCTGCTGCTGCGGGAGCCGCG
CTACACGCTGCTGGTGGCCGCCTGCCTCTGCCTGGCGGAGGTGGGCATCACCTTCTGGGTCAATTCACAGGGTGGC
ATACACAGAGATTGACTGGAAGGCCTACATGGCCGAGGTAGAAGGCGTCATCAATGGTACCTATGACTATACCCA
ACTGCAGGGTGACACCGGACCACTTGTGTACCCAGCTGGTTTCGTGTACATCTTTATGGGGTTGTACTATGCCAC
CAGCCGAGGCACTGACATCCGCATGGCCAGAACATCTTTGCTGTGCTCTACCTGGCTACCTTGCTGCTTGTCTT
CTTGATCTATCACCAGACCTGCAAGGTACCTCCCTTCGTCTTTTCTTCATGTGCTGCGCCTCTTACCGTGTCCA
CTCCATCTTTGTGCTGCGGCTCTTCAATGACCCAGTGGCCATGGTGTGCTCTTCCTCAGTATCAACCTCCTGCT
GGCCCAGCGCTGGGGCTGGGGCTGCTGCTTTTTTCAGCCTGGCAGTCTCTGTGAAGATGAATGTGCTGCTCTTCGC
CCCTGGGTTACTGTTTCTTCTCCTCACACAGTTTGGCTTCCGTGGGGCCCTCCCCAAGCTGGGAATCTGTGCTGG
CCTTCAGGTGGTGTGCTGGGGCTGCCCTTCCTGCTGGAGAACCCAGCGGCTACCTGTCCCGCTCCTTTGACCTGG
CCGCCAGTTTCTGTTCCACTGGACAGTGAAGTGGCGCTTCCTCCCAGAGGCGCTCTTCCTGCATCGAGCCTTCCA
CCTGGCCCTGTTGACTGCCCACCTCACCTGCTCCTGCTGTTTGCCCTCTGCAGGTGGCACAGGACAGGGGAAAG
TATCTTGTCGCTGCTGAGGGATCCCTCCAAAAGGAAGGTTCCACCCAGCCCCTTACACCCAACCAGATCGTTTC
TACCCTCTTCACCTCCAACCTTCATTGGCATCTGCTTCAGCCGCTCCCTCCACTACCAGTTCTACGTCTGGTATTT
CCACACACTGCCCTACCTCCTGTGGGCCATGCCTGCACGGTGGCTCACACACCTGCTCAGGTTGTTGGTGCTGGG
GCTCATCGAGCTCTCCTGGAACACATACCCTTCCACATCCTGCAGCTCTGCTGCCCTGCACATATGCCATGCCGT
CATCCTGCTGCAGCTCTGGCTGGGCCCGCAGCCTTTCCCCAAGAGCACCCAACACAGCAAGAAAGCCCCACTTGAAG
TCCACCCCTTTCCCTCAGGACCTGAGTCTACCCTCAGGACCTGGGGTGGGTGGACTCTGCCCTTCCAAATAAAC
CTTGCTAAGTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

1418/6881

FIGURE 1317

MAAGLRKRGRSGSAAQAEGLCKQWLQRAWQERRLLLREPRYTLLVAACLCLAEVGITFWVIHRVAYTEIDWKAYM
AEVEGVINGTYDYTQLQGDTGPDVYPAGFVYIFMGLYYATSRGTDIRMAQNIFAVLYLATLLLVFLIYHQTCKVP
PFVFFFMCCASYRVHSIFVLRLFNDPVAMVLLFLSINLLLAQRWGWGCCFFSLAVSVKMNVLLFAPGLLFLLLTQ
FGFRGALPKLGICAGLQVVLGLPFLLNPSGYLSRSFDLGRQFLFHWTNVNWRFLPEALFLHRAFLALLTAHLTL
LLLFALCRWHRTGESILSLLRDPSKRKVPPQPLTPNQIVSTLFTSNFIGICFSRSLHYQFYVWYFHTLPYLLWAM
PARWLTHLLRLLVLGLIELSWNTYPSTSCSSAALHICHAVILLQLWLGPQPFPKSTQHSSKKAH

1419/6881
FIGURE 1318

[illegible]

1420/6881
FIGURE 1319

MASPGAGRAPPPELPERNCGYREVEYWDQRYQGAADSAPYDWFGDFSSFRALLEPELRPEDRILVLGCGNSALS YE
LFLGGFPNVTSDYSSVVVAAMQARYAHVPQLRWETMDVRKLDFPSASFDDVLEKGTLDALLAGERDPWTVSSEG
VHTVDQVLSEVSRVLVPGGRFISMTSAAPHFRTRHYAQAYYGWSLRHATYGSGFHFHLYLMHKGGKLSVAQLALG
AQILSPPRPPTSPCFLQSDHEDFLSAIQL

1421/6881
FIGURE 1320

GAGGCTGCGCGCCGCGAGGTTCCGGCTGCTGGCGGCGTTGCGGCCGCGAGGTTTGACTCCCGTGCGGTGCGGCCAG
CAGCCACAAAGCTCCCGCTGCCATTGCTCCTTGTA TCTCCCGCCGTCAC TGCCGCTGTCCAACCCCTCCCCGGGG
CTTGCGCGGCGGCTCCACACCCCTCGGCCCGTGTA CGCGCTCTGCACCTGCCTGCCCCGAAAACATGTTGCAGAC
ACCAGAGAGCAGGGGGCTCCCGGTCCCGCAGGCCGAGGGGGAGAAGGATGGCGGCCATGATGGTGAGACCCGGGC
CCCGACCGCCTCGCAGGAGCGCCCCAAGGAGGAGCTTGCGCGCGGGAGGGAGGAGGGGGCTGCGGAGCCCGCCCT
CACCCGAAAAGGCGCGAGGGCCTTGCGGCCAAAGCCTTGCGCAAGGCGCAGGGCCTACCGCCGGCTGAATCGGAC
GGTGGCGGAGTTGGTGAGTTCCCTCCTGGTGAAAGACAAGAAGAGTCCCATCACACGCTCGGAGATGGTGAA
ATACGTTATTGGAGACTTGAAGATTCTGTTCCCGGACATCATCGCAAGGGCCGCAGAGCATCTGCGGTATGTCTT
TGGTTTTGAGCTGAAACAGTTTGACCGCAAGCACCACACTTACATCCTGATCAACAACTAAAACCTCTGGAGGA
GGAGGAGGAGGAGGATCTGGGAGGAGATGGCCCCAGATTGGGTCTGTTAATGATGATCCTGGGCCTTATCTATAT
GAGAGGTAATAGCGCCAGGGAGGCCAGGTCTGGGAGATGCTGCGTCGGTTGGGGGTGCAACCCTCAAAGTATCA
TTTCCTCTTTGGGTATCCGAAGAGGCTTATTATGGAAGATTTTGTGCAGCAGCGATATCTCAGTTACAGGCGGGT
GCCTCACACCAATCCACCAGAATATGAATTCTCTTGGGGTCCCCGAAGCAACCTGGAAATCAGCAAGATGGAAGT
CCTGGGGTTTCGTGGCCAACTGCATAAGAAGGAACCGCAGCACTGGCCAGTGCAGTACCGTGAGGCCCTAGCAGA
CGAGGCCGACAGGGCCAGAGCCAAGGCCAGAGCTGAAGCCAGTATGAGGGCCAGGGCCAGTGCTAGGGCCGGCAT
CCACCTCTGGTGAGGGTTGGTGAAAAGTTGGCCAGTGGGTCCCCGTGAGGACGAACTACTGTCTGTAGTCATAAG
TAATATGGGTGGGGCGAGGGTCTTATTCTGTAGAAATCGTGTGACTTTAAGGATTTAGATTTTGTATCTTATGT
TTGTAAACATTTAATAATTACTGTTAAATGCTGTTTGTAATGAGATTGGTCTACTTTTTCTGTAGGATTTTA
TTGTAGAGTTTTGCTGGTTTTGTAAATGGATGGAAGAACTTTGTATTTATACTGTGATTTTGAACAGATTATGC
AACATTGGAAGGAAGGCTGTACTTTGATGGTTTGAAGGAACTCAGCAGTATGATGATCTGGTTCCAGGGGAAAAA
AATAGCTGGTTGGTGTCTAGCCCCCAACACTTTTGTCTGTTGTGTATAAAAGAAGAAAGACTGGCATGTACCTT
CATTTGCTTAGCTATTTGAGTATCTAGAGAAAAATTAAATGCAATGAGTTAGCAGTATACCCTGGCACACTTAA
TAAATTAAACATTTGTGGAGC

1422/6881
FIGURE 1321

MLQTPESRGLPVPQAEGEKDGGHGGETRAPTASQERPKEELGAGREEGAAEPALTRKGARALAAKALARRRAYRR
LNRTVAELVQFLLVKDKKKSPITRSEMVKYVIGDLKILFPDIIARAAEHLRYVFGFELKQFDRKHHTYILINKLK
PLEEEEEEDLGGDGPRLGLLMMILGLIYMRGNSAREAQVWEMLRRLGVQPSKYHFLFGYPKRLIMEDFVQQRYS
YRRVPHTNPPEYEFWSGPRSNLEISKMEVLGFVAKLHKKEPQHWFPVQYREALADEADRARAKARAEASMRARASA
RAGIHLW

1423/6881
FIGURE 1322

AGAGCTATGGCTCGAATTCCCAGAGTTCGAGGTGGTGGGACTCACCGCTCTGGCCAGGGTGCTTTTGGAAACATG
TGTCGTGGAGGCCGAAGGTTTGCACCAACCAAAACCTGGCGCCGTTGGCATCGTAGAGTGAACACAACCCAAAA
CGATATGCCATCTGTTCTGCCCTGGCTGCCTCAGCCCTACCAGCACTGGTCATGTCTAAAGGTCATCGTATTGAG
GAAGTTCCTGAACCTCCTTTGGTATTTGAAGATAAAGTTGAAGGCTACAAGAAGACCAAGGAAGCTGTTTTGCTC
CTTAAGAACTTAAAGCCTGGAATGATATCGAAAAGGCAGCAGCTACCAAGAAACCAGCCCCTGAAAAGAAGCCT
GCAGAAAAGAAACCTACTACAGAGGAAAAGAAGCCTGCTGCATAAACTCTTAAATTTGATTATTCCATAAAGGTC
AAATCATTTTGGACAGCTTCTTTTGAATAAAGACCTGATTATACAGGC

1424/6881
FIGURE 1323

ATTCCCAGAGTTCGAGGTGGTGGGACTCACCGCTCTGGCCAGGGTGCTTTTGGAAACATGTGTTCGTGGAGGCCGA
AGGTTTGCACCAACCAAAACCTGGCGCCGTTGGCATCGTAGAGTGAACACAACCCAAAAACGATATGCCATCTGT
TCTGCCCTGGCTGCCTCAGCCCTACCAGCACTGGTTCATGTCTAAAGGTCATCGTATTGAGGAAGTTCCTGAACCT
CCTTTGGTATTTGAAGATAAAGTTGAAGGCTACAAGAAGACCAAGGAAGCTGTTTTGCTCCTTAAGAACTTAAA
GCCTGGAATGATATCGAAAAGGTCTATGCCTCTCAGCGAATGAGAGCTGGCAAAGGCAAGAAGCCTGTGGTAGGT
AAGAAAGGAAAGAAGGCTGCTGTTGGTGTTAAGAAGCAGAAGAAGCCTCTGGTGGGAAAAAGGCAGCAGCTACC
AAGAAACCAGCCCCTGAAAAGAAGCCTGCAGAAAAGAAACCTACTACAGAGGAAAAGAAGCCTGCTGCATAAACT
CTTAAATTTGATTATTCATAAAGGTCAAATCATTTTGGACAGCTTCTTTGAATAAAGACCTGATTATACAGGC
AGTGAGGAA

1425/6881
FIGURE 1324

MCRGGRRFAPTKTWRRWHRRVNTTQKRYAICSALAASALPALVMSKGHRIEEVPELPLVFEDKVEGYKKTKEAVL
LLKKLKAWNDIEKVYASQRMRA GTGKKPVVGKKGKKA AVGVKKQKKPLVGKKAATKKPAPEKKPAEKKPTTEEK
KPAA

1426/6881
FIGURE 1325

ATGACTGGAGTGAAGCTGGTCCTGAACTCGAGGCTGTGGAAAGCGCTCATGGAAAAGGCCTGTGCAAAATTATTA
CCCTTCTGTGAAGTACTTAAACCTACTCAAGGTGCAAGCTTTACACACCAATGCCGGGCTTGATTAATGGTATC
AGAGGAGTTCGGTTCCCCCGAGTTTCTCCACCCTCTGAAAATGCGGCCGGAACCCTAATCCGCTGCGAGGCT
GCAGCATCTTTCGGTGCTGTCCCTCCACACCCGTGTTATCCCCACCATCCCCAGGCCGCTGTTCCGGCTGCACT
TGCTGTGTCAATTTACCCCTCCCGGTGCTCTGGGGGGCAGCGCCTCTCAGACATTCCCTCAAACCTGCTTCCG
CCCCCTCCTCCCAACTGCGGAGCTCCGCCAAGCGTCTCTTCTCGCGAGCCTCCAAGTCCCTCGGGGCTCTCGAA
TCTCCAGAGACTGTGAAAGCCTCGCAACTCCGCGATCCCCATCCACTCGGGAGCCCCCGCACTCGCGCTCCGGG
GCGCTCCCCACGACGTGTGAAAGCCGCTCTCCCCGCGCTCCGGAACCGTTAGCCGCACCCGCCGACGCCTC
CCAGGAACCAAACCGGACCGGGCCGCGGGGGGAGGGGGCGGTCAACCCGGGGGGGGTCACCCCAGCTACTGCACC
CCGACTTTGAAGATTCTGAATCAGCCCGTGAACCTCTAGCCGGCTGGGCCTGTTCGGACAGTGGCCGGACGCCCT
TCCGATCTCCCCCTGCCCCCGCAAAGCCCCCTCACCTGAGGCGGCCTCTCTCCTCCCTTGCAGCGGCCCGGC
GGCGCAGGCGCGCTCACGCACGCGCGCAGCGGGCCTGGGCGCCTGGGCGAAAGGCTGGGCCGAACCGCTCCGAAG
ACGGTGAACCGCTCCGCGCACACGCGGCTGGACTCTGCGCCGAGCTGCCAACCAGGCTGGAGCGCTGGCCCGGC
CCCCGCGGCTCGCTGCTCCGCCCGCCGCCATTGGCCCGCGGCCTAG

1427/6881
FIGURE 1326

MTGVKLVLSRLWKALMEKACAKLLPFCEVLKTYSRCKLYTPMPGLINGIRGVRFPPEFSPPSENAAGTLIRCEA
AASFGAVPSTPVLSPSPGRCGCTCLCHLPPPGALGGSASQTFPSNCFPPPPNCGAPPSVSSREPPSPLGALE
SPETVKASQLRDPSTREPPHSRSGAPPPRRVESRSPRAPEPLAAPARRLPGTKPDRAAGGGGGQPGGGHPSYCT
PTLKILNQPVNSSRLGLSDQWPDAPSDLPPAPAKPPHLRRPLSSPCSGPGGAGALTHARSGPGRLGERLGRTAPK
TVNRSAHQR LDSAPQLPTRLERWPGPPRLAAPFAAIGPRP

1428/6881
FIGURE 1327

AATTCGGTTGAAACCATCCCTCAGCTCCTAGAGGGAGATTGTTAGATCATGAAACTAATTACCATCCTTTTCCT
CTGCTCCAGGCTACTACTAAGTTTAAACCCAGGAATCACAGTCCGAGGAAATTGACTGCAATGACAAGGATTTATT
TAAAGCTGTGGATGCTGCTCTGAAGAAATATAACAGTCAAAACCAAAGTAACAACCAGTTTGTATTGTACCGCAT
AACTGAAGCCACTAAGACGGTTGGCTCTGACACGTTTTATTCCCTTCAAGTACGAAATCAAGGAGGGGGATTGTCC
TGTTCAAAGTGGCAAACCTGGCAGGACTGTGAGTACAAGGATGCTGCAAAGCAGCCACTGGAGAATGCACGGC
AACCGTGGGGAAGAGGAGCAGTACGAAATTCTCCGTGGCTACCCAGACCTGCCAGATTACTCCAGCCGAGGGCCC
TGTTGGTGACAGCCCAGTACGACTGCCTCGGCTGTGTGCATCCTATATCAACGCAGAGCCCAGACCTGGAGCCCAT
TCTGAGACACGGCATTTCAGTACTTTAACAACAACACTCAACATTCCCTCCTTTCATGCTTAATGAAGTAAAACG
GGCCCAAAGACAGGTGGTGGCTGGATTGAACTTTTGAATTACCTACTCAATTGTGCAAACGAATTGTTCCAAAGA
GAATTTTCTGTTCTTAACTCCAGACTGCAAGTCCCTTTGGAATGGTGATACCGGTGAATGTACAGATAATGCATA
CATCGATATTCAGCTACGAATTGCTTCCTTCTCACAGAACTGTGACATTTATCCAGGGAAGGATTTTGTACAACC
ACCTACCAAGATTTGCGTGGGCTGCCCCAGAGATATACCCACCAACAGCCCAGAGCTGGAGGAGACACTGACTCA
CACCATCACAAAGCTTAATGCAGAGAATAACGCAACTTCTATTTCAAGATTGACAATGTGAAAAAAGCAAGAGT
ACAGGTGGTGGCTGGCAAGAAATATTTTATTGACTTCGTGGCCAGGGAAACCACATGTTCCAAGGAAAGTAATGA
AGAGTTGACCGAAAGCTGTGAGACCAAAAACTTGGCCAAAGCCTAGATTGCAACGCTGAAGTTTATGTGGTACC
CTGGGAGAAAAAATTTACCCTACTGTCAACTGTCAACCACTGGGAATGATCTCACTGATGAAAAGGCCTCCAGG
TTTTTCACCTTTCCGATCATCACGAATAGGGGAAATAAAAGAAGAAACAACCTAGTCACCTAAGGTCCTGCGAGTA
CAAGGGTCGACCCCCAAAGGCAGGGGCAGAGCCAGCATCTGAGAGGGAGGTCTCTTGACCAATGGGCAGAATCTT
CACTCCAGGCACATAGCCCCAACCACTCTGCCAGCAACCTTGAGAGGAAGGACAAGAAGAAAGATGGGATAGAA
TTTAAATAGAGAAGAATGCCATTTTATCACTCTGCCTCTGGGTGAAATAAAGATCAGTCTTGATGTTT

1429/6881
FIGURE 1328

MKLITILFLCSRLLLSLTQESQSEEIDCNDKDLFKAVDAALKKYNSQNQSNNQFVLYRITEATKTVGSDFYFVK
YEIKEGDCPVQSGKTWQDCEYKDAKAATGECTATVGKRSSTKFSVATQTCQITPAEGPVVTAQYDCLGCVHPIS
TQSPDLEPILRHGIQYFNNNTQHSSLFMLEVKRAQRQVVAGLNFRTYSIVQTNCSKENFLFLTPDCKSLWNGD
TGECTDNAYIDIQLRIASFSONCDIYPGKDFVQPPTKICVGCPRDIPTNSPELEETLTHITITKLNAENNATFYFK
IDNVKKARVQVVAGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQPLGM
ISLMKRPPGFSFRRSSRIGEIKEETTSHLRSCYKGRPPKAGAEPASEREVS

1430/6881
FIGURE 1329

GGCGGGAAGTCTGAGGCGACTGTGGGGACATCAGTGATCGTAAGTCTCCTGGGCCCCGTTATTCTCAGATTAGGTGAC
GGAGCTAAGACTTCGAGACCATCTCGTCCTTTTTGTATCGCGGAAACCTGAGGAACGAGCCGGCGCGGTGACCT
GCACGAGAAGCCAGGCTAACTGGGTGAAGTACCATGCAAGCATTCTTAAAGGTACATCCATCAGTACTAAACCC
CCGCTGACCAAGGATCGAGGAGTAGCTGCCAGTGCGGGAAAGTAGCGGAGAGAACAAGAAAGCCAAACCCGTTCCC
TGGGTGAAAAATATCGCCCAAAATGTGTGGATGAAGTTGCTTTCCAGGAAGAAGTGGTTGCAGTGCTGAAAAAA
TCTTTAGAAGGAGCAGATCTTCCTAATCTCTTGTTTACGGACCACCTGGAAGTGGAAAAACATCCACTATTTTG
GCAGCAGCTAGAGAACTCTTTGGGCCTGAAGTTTCCGATTAAAGAGTTCTTGAGTTAAATGCATCTGATGAACGT
GGAATACAAGTAGTTTCGAGAGAAAGTAAAAATTTTGTCTCAATTAAGTGTGTCAGGAAGTCGCTCAGATGGGAAG
CCGTGTCCGCCTTTTAAGATTGTGATTCTGGATGAAGCAGATTCTATGACCTCAGCTGCTCAGGCAGCTTTAAGA
CGTACCATGGAGAAGGAGTCGAAAACCAACCCGATTCTGTCTTATCTGTAAGTATGTCAGTCGAATAATTGAACCC
CTGACCTCTAGATGTTCAAAATTCGCTTCAAGCCTCTGTCAGATAAAATTCAACAGCAGCGATTACTAGACATT
GCCAAGAAGGAAAATGTCAAAATTAGTGATGAGGGAATAGCTTATCTTGTTAAAGTGTGAGAAGGAGACTTAAGA
AAAGCCATTACATTTCTTCAAAGCGCTACTCGATTAAACAGGTGGAAAGGAGATCACAGAGAAAGTGATTACAGAC
ATTGCTGGGGTAATACCAGCTGAGAAAATTGATGGAGTATTTGCTGCCTGTCAGAGTGGCTCTTTTGACAAACTA
GAAGCTGTGGTCAAGGATTTAATAGATGAGGGTCATGCAGCAACTCAGCTCGTCAATCAACTCCATGATGTGGTT
GTAGAAAATAACTTATCTGATAAACAGAAGTCTATTATCACAGAAAACTTGCCGTAATTGACAAATGCCTAGCA
GATGGTGCTGATGAACATTTGCAACTCATCAGCCTTTGTGCAACTGTGATGCAGCAGTTATCTCAGAATTGTTAA
CGTGAATATATCTGGATGGGGGGTTTTGTAAATAATGAAGTTGTAATAAAAAATAAAATGACCAAAAGCACC

1431/6881
FIGURE 1330

CCTCCAACCACCTGCACGCCTGCCTGCCAGGGCCTCTCTGGGGCAGCC**ATGA**AGTCCCTCGTCCTGCTCCTTTGT
CTTGCTCAGCTCTGGGGCTGCCACTCAGCCCCACATGGCCCAGGGCTGATTTATAGACAACCGAACTGCGATGAT
CCAGAAACTGAGGAAGCAGCTCTGGTGGCTATAGACTACATCAATCAAAACCTTCCTTGGGGATACAAACACACC
TTGAACCAGATTGATGAAGTAAAGGTGTGGCCTCAGCAGCCCTCCGGAGAGCTGTTTGAGATTGAAATAGACACC
CTGGAAACCACCTGCCATGTGCTGGACCCACCCCTGTGGCAAGATGCAGCGTGAGGCAGCTGAAGGAGCATGCT
GTCGAAGGAGACTGTGATTTCCAGCTGTTGAACTAGATGGCAAGTTTTCCGTGGTATACGCAAAATGTGATTCC
AGTCCAGACTCAGCCGAGGACGTGCGCAAGGTGTGCCAAGACTGCCCCCTGCTGGCCCCGCTGAACGACACCAGG
GTGGTGCACGCCGCGAAAGCTGCCCTGGCCGCGCTTCAACGCTCAGAACAACGGCTCCAATTTTCAGCTGGAGGAA
ATTTCCCGGGCTCAGCTTGTGCCCCCTCCACCTTCTACCTATGTGGAGTTTACAGTGTCTGGCACTGACTGTGTT
GCTAAAGAGGCCACAGAGGCAGCCAAGTGTAACCTGCTGGCAGAAAAGCAATATGGCTTTTGTAAGGCAACACTC
AGTGAGAAGCTTGGTGGGGCAGAGGTTGCAGTGACCTGCACGGTGTTCCAAACACAGCCCGTGACCTCACAGCCC
CAACCAGAAGGTGCCAATGAAGCAGTCCCCACCCCGTGGTGGACCCAGATGCACCTCCGTCCCCCTCCACTTGGC
GCACCTGGACTCCCTCCAGCTGGCTCACCCCCAGACTCCCATGTGTTACTGGCAGCTCCTCCAGGACACCAGTTG
CACCGGGCGCACTACGACCTGCGCCACACCTTCATGGGTGTGGTCTCATTTGGGGTCACCCTCAGGAGAAAGTGTG
CACCCCCGGAAAACACGCACAGTGGTGCAGCCTAGTGTTGGTGCTGCTGCTGGGCCAGTGGTTTCTCCATGTCCG
GGGAGGATCAGACACTTCAAGGTCT**TAGG**CTAGACATGGCAGAGATGAGGAGGTTTGGCACAGAAAACATAGCCAC
CATTTTGTCCAAGCCTGGGCATGGGTGGGGGGCCTTGTCTGCTGGCCACGCAAGTGTACATGCGATCTACATTA
ATATCAAGTCTTGACTCCCTACTTCCCGTCATTCTCACAGGACAGAAGCAGAGTGGGTGGTGGTTATGTTTGAC
AGAAGGCATTAGGTTGACAACCTGTGATGATTTTGACGGTAAGCCACCATGATTGTGTTCTCTGCCTCTGGTTGA
CCTTACAAAAACCATTGGAAGTGTGACTTTGAAAGGTGCTCTTGCTAAGCTTATATGTGCCTGTTAATGAAAGTG
CCTGAAAGACCTTCCTTAATAAGAAGGTTCTAAGCTG

1432/6881
FIGURE 1331

MKSLVLLLCLAQLWGCHSAPHGPGLIYRQPNCDDETEEAALVAIDYINQNLPGYKHTLNQIDEVKVWPQQPSG
ELFEIEIDTLETTCHVLDPTPVARCSVRQLKEHAVEGDCDFQLLKLDGKFSVYAKCDSSPDSAEDVRKVCQDCP
LLAPLNDTRVVHAAKAALAFNAQNNGSNFQLEEISRAQLVPLPPSTYVEFTVSGTDCVAKEATEAAKCNLLAEK
QYGFCKATLSEKLGGAEVAVTCTVFQTQPVTSQPQPEGANEAVPTPVVDPDAPPSPPLGAPGLPPAGSPPDShVL
LAAPPQHQLHRAHYDLRHTFMGVVSLGSPSGEVSHPRKTRTVVQPSVGAAAGPVVPPCPGRIRHFKV

1433/6881
FIGURE 1332

TTTCTTTAAGAGGAAGACGCGGTCGTAGGTGCGAGGATTTCTGGTCCGCATGCTCCTGCTCCTGACTCACCGCTG
TTCGCTCTCGCCGCCGAGGAACAAGTCGGTCATGAAGCCGCGCAGCAGCCATGGCTTTTAAGGATACCGGAAAAG
CACCCGTGGAGCCGGAGGTGGCAATTCACCGAATTCGAATCACCTAACAAGCCGCAGCGTAAAATCCTTGAAAA
AGGTGGGTGCTGACTTGATCAGAGGCGCAAAGCAAAGAATCTCAAAGTGAAAGGAGGAGTTCGAATGCCTTCCA
AGACTTTGAGAATCACTACAAGAAAACTCCTTGTTGGTGAAGGTTCTAAGACGTGGGATCGTTTCCAGATGAGAA
TTCACAAGCGACTCTTTGACTTGACAGTCCTTCTGAGATTGTTAAGCAGATTACTTCCATCAGTACTGAGCCAG
GAGTTGAGGTGGAAGTCACCATTGCAGATGCTTAAGTCAACTATTTTAATAAATTGATTACCAGTTGTT

1434/6881
FIGURE 1333

GGAAAGACTATGTTTTAGGTGACCCGTGTGGCCTTTTTGTTGAGGCCTTTAGGATACAAGGCCCCACCTAAAGA
CGCGACCCCTCCCGTAGGAGGGGGGCAGGGCCCCGGGGCGGGAGCACAGCGGGGCCCCAGCCTCAGGCGGCGCGTC
ACTGAGCACAAAGGAGACAACAGCGAGGCGGCAGCGGGCGCTGATCTTCGCTCGCCAGCCACTCGCAATTGCGGT
TACAGACCTGCAGCTCCCCCTCCCCCAGCCGGCCCCGCCGCTTTCTGTCTCCTCTCTCCCTCCGTACTGGACGG
CCCCGGTCCATTTCCGGGCTCCGGATATTTGGTATCGATTGGGGCCGGGGACGCGGAGCAGGTGGCCGCGGCGGG
GCAGCTGGGCGGCCAGCTTGGTGCCTCGGGGACCGTCTCCCGCTGCTTTGGTCACCGACCCCTGCCGCCCCGACC
CGCTCCGTCTCTCCGGCCTGCGAGCCCTGCCGGCCGGACTTTGCGCCGCGTCCGGCGCTGCTGCTGCGCTCGGGGC
CCCCTCGGCGCCGGCGGTGACCGGGAAGCCCCGCTTAAAGGGGCAACCGGGACCCCTGGCCCCGTATGGCTGAAG
TCAGCATCGACCAGTCCAAGCTGCCTGGAGTCAAGGAAGTATGCCGAGATTTTGCTGTCTTGAGGACCCACACCC
TGGCTCACAGCCTGCAGGAACAAGAGATTGAGCATCATTGGCATCGAACGTTTCAGCGGAACCGTTTGGTCCAGC
ATGATCTCCAGGTGGCTAAGCAGCTCCAAGAGGAAGATCTGAAAGCGCAGGCCAGCTCCAGAAGCGCTACAAAG
ACCTTGAACAACAAGACTGTGAAATTGCTCAGGAAATTCAGGAGAAGCTGGCTATTGAGGCAGAGAGACGACGCA
TTCAGGAGAAGAAGGATGAGGACATAGCTCGCCTTTTGCAAGAAAAGGAGTTACAGGAAGAGAAAAAGAGAAAGA
AACACTTTCAGAGTTCCTTGCAACCCGTGCTTATGCAGATAGTTACTATTATGAAGATGGAGGAATGAAGCCAA
GAGTGATGAAAGAAGCTGTATCTACTCCATCACGAATGGCCCCACAGGGATCAGGAATGGTATGATGCTGAAATTG
CCAGAAAACCTGCAAGAAGAAGAACTTTTGGCTACCCAGGTGGACATGAGAGCCGCTCAAGTAGCTCAAGATGAAG
AAATCGCTCGACTTCTAATGGCTGAAGAAAAGAAAGCTTACAAAAAGCCAAGGAGCGGGAGAAATCATCTTTGG
ACAAAAGAAAGCAAGACCCCGAGTGGAAGCCAAAAACAGCTAAAGCAGCAAATTCCAAGTCAAAAGAGAGTGATG
AACCTCACCATTTCTAAGAATGAAAGGCCAGCACGGCCACCACCACCTATCATGACAGATGGTGAAGATGCGGATT
ACACTCATTTTACAAACCAGCAGAGTTCCACACGGCATTCTCAAAATCAGAGTCCTCTCATAAAGTTTTTCATT
ACAAACATTAATAAACCTAGGAATCTGCCTTGAAAAATGGACTCACTATAGCAAATATTACTGGGTGATACAGAATG
AATTCTACACTTACTTTTTTTCTCCTGTGTTTGCATTCTCTGGGATTTATCCTCAAGTGCAATTTCTGACCATAAGT
AATTTTAATTCATTTCAAATGTTTTGGTTATTTCATGATCACTTGGGCAGTATAAGAAAAATGTAGCTTCTGAATAT
TGGCCACCTCTATGCTGCATATACTTCTTGGGATATAGTATCTAAGACCTTTGTAAACTGCCATTTTGTAGGTA
TGGAGTTTGGTATCTAGGGAGTAGGCCTTATTTAGCAATTCAAATTTTATGGAGATGAATGATCAAAGTGAAACA
ATGTTTGGATGCAACGCAGAATAAAAGAATATAAGAAATAGCTTTTTTGTTCATTAATGTATGATATTTTGAAGG
ACAGAGCCTTTGCTTTTTTGTATTCTTTAAGAAAAGCACAACCATAAAGTATTTTAAAAAAGAAACACTTGGAGC
AATTGAAATATGTTATTCTGACTAGATGGACTGTAGAGGTTTTGCATTTCTCAGCCCTCCTGGGGAGATTGGCCT
AGATAGCATTTCTTAACACTTCCTCTGCTTTTGCCTCAGTAGCAAGGCTTTCCTAAGCTCCTGGGCAATGGAACA
TTTATTAGTATTTATTGACAAAAATTTAGTTCTCTGAAATTTTAACTCATATATGAAAAACTTTGTATTCCAT
CTCTTCTTTTTTCAATTTACTTGTAGAGCCAAGGAAATGGAATTGAAAGATGATTGCATAAGTAATGATGCCATCCT
TCTCTCTGGCTGTAGACTGAGGCTTTTCTCTTGCTTCAAGTCAGAGCAGTATTTGTTGATAACCTCTCAATAATG
TTTGGTTTACATGCCAGTAATTAAATTAATTCAACATGAAGTTGAATTTGATGAAGTGCTCATCTATCCAAGTAT
TTGGTTTTTGTGTTTTGTTTTGTTTTGTTTTGAGTTGGAGTCTCGCCCTGTCACACAGGCTGGAGTGCAGTGGTG
CAATCTTGGCTCACTGCAACCTCCGCCACCTGGGCTGGAGCAATTCCTCTGCTCAGCCTCCCAAGTAGCTGGAA
TTACAGGCATGTGTCACCACACCCGGCTAATTTTTGTATTTTAGTAAAGAGCGGGTTTCACCATGTTGGCCAGG
CTGGTCTCGAACCCCTGACCTCAAGTGATCCACCTGC

1435/6881
FIGURE 1334

MAEVSIDQSKLPGVKEVCRDFAVLEDHTLAHSLQEQEIEHHLASNVQRNRLVQHDLQVAKQLOEEDLKAQAQLQK
RYKDLEQQDCEIAQEIQEKLAIEAERRRIQEKKDEDIARLLQEKELQEEKRKKHFPEFPATRAYADSYYYEDGG
MKPRVMKEAVSTPSRMAHRDQEWYDAEIARKLQEEELLATQVDMRAAQVAQDEEIARLLMAEEKKAYKKAKEREK
SSLDKRKQDPEWKPKTAKAANSKSKESDEPHHSKNERPARPPPIMTDGEDADYTHFTNQSSSTRHFSKSESSHK
GFHYKH

1436/6881
FIGURE 1335A

CGTTGATATCAAAGACAGTTGAAGGAAATGAATTTTGAACCTTCACGGTGTGCCACCCTACAGTACTGCCCTGAC
CCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTCTCTTGGAAAGAAAGTTATTACCGATCCACCATGTCC
CAGAGCACACAGACAAATGAATTCCTCAGTCCAGAGGTTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATA
TGTTTCAGTTTCAGCCATTGACTTGAACCTTTGTGGATGAACCATCAGAAGATGGTGCGACAAACAAGATTGAGATT
AGCATGGACTGTATCCGCATGCAGGACTCGGACCTGAGTGACCCCATGTGGCCACAGTACACGAACCTGGGGCTC
CTGAACAGCATGGACCAGCAGATTGAGAACGGCTCCTCGTCCACCAGTCCCTATAACACAGACCACGCGCAGAAC
AGCGTCACGGCGCCCTCGCCCTACGCACAGCCAGCTCCACCTTCGATGCTCTCTCTCCATCACCCGCCATCCCC
TCCAACACCGACTACCCAGGCCCGCACAGTTTCGACGTGTCTTCCAGCAGTGCAGCACCGCCAAGTCGGCCACC
TGGACGTATTTCCACTGAACTGAAGAACTCTACTGCCAAATTGCAAAGACATGCCCCATCCAGATCAAGGTGATG
ACCCACCTCCTCAGGGAGCTGTTATCCGCGCCATGCCTGTCTACAAAAAGCTGAGCACGTCACGGAGGTGGTG
AAGCGGTGCCCCAACCATGAGCTGAGCCGTGAATTCAACGAGGGACAGATTGCCCTCCTAGTCATTTGATTGGA
GTAGAGGGGAACAGCCATGCCCAGTATGTAGAAGATCCCATCACAGGAAGACAGAGTGTGCTGGTACCTTATGAG
CCACCCAGGTTGGCACTGAATTCAGCAGAGTCTTGTACAATTTTATGTGTAAACAGCAGTTGTGTTGGAGGGATG
AACCGCCGTCCAATTTTAATCATTGTTACTCTGGAAACCAGAGATGGGCAAGTCTTGGGCCGACGCTGCTTTGAG
GCCCGGATCTGTGCTTGCACAGGAAGAGACAGGAAGGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGGAC
AGTACAAAGAACGGTGATGGTACGAAGCGCCCGTTTCGTGAGAACACACATGGTATCCAGATGACATCCATCAAG
AAACGAAGATCCCCAGATGATGAACTGTTATACTTACCAGTGAGGGGCGGTGAGACTTATGAAATGCTGTTGAAG
ATCAAAGAGTCCCTGGAACCTCATGCAGTACCTTCTCAGCACACAATTGAAACGTACAGGCAACAGCAACAGCAG
CAGCACCAGCACTTACTTTCAGAAAACAGACCTCAATACAGTCTCCATCTTCATATGGTAACAGCTCCCCACCTCTG
AACAAAATGAACAGCATGAACAAGCTGCCTTCTGTGAGCCAGCTTATCAACCTCAGCAGCGCAACGCCCTCACT
CCTACAACCATTCCTGATGGCATGGGAGCCAACATTCCCATGATGGGCACCCACATGCCAATGGCTGGAGACATG
AATGGACTCAGCCCCACCCAGGCACTCCCTCCCCCACTCTCCATGCCATCCACCTCCAGTGACACCCCCACCT
CCGTATCCCACAGATTGCAGCATTGTGAGTTTCTTAGCGAGGTTGGGCTGTTTCATCATGTCTGGACTATTTACG
ACCCAGGGGCTGACCACCATCTATCAGATTGAGCATTACTCCATGGATGATCTGGCAAGTCTGAAAATCCCTGAG
CAATTTGACATGCGATCTGGAAGGGCATCCTGGACCACCGGCAGCTCCACGAATTCCTCTCCCTTCTCATCTC
CTGCGGACCCCAAGCAGTGCCCTCTACAGTCAGTGTGGGCTCCAGTGAGACCCGGGGTGAGCGTGTATTGATGCT
GTGCGATTACCCCTCCGCCAGACCATCTCTTTCCACCCGAGATGAGTGGAATGACTTCAACTTTGACATGGAT
GCTCGCCGCAATAAGCAACAGCGCATCAAAGAGGAGGGGGAGTGAGCCTCACCATGTGAGCTCTTCCTATCCCTC
TCCTAACTGCCAGCYCCCTAAAAGCACTCCTGCTTAATCTTCAAAGCCTTCTCCCTAGCTCCTCCCTTCTCTT
GTCTGATTTCTTAGGGGAAGGAGAAGTAAGAGGCTACCTCTTACCTAACATCTGACCTGGCATCTAATTCTGATT
CTGGCTTTAAGCCTTCAAACCTATAGCTTGCAGAACTGTAGCTGCCATGGCTAGGTAGAGTGAAGTGAAGCAAAAAAGAG
TTGGGTGTCTCCTTAAGCTGCAGAGATTTCTCATTGACTTTTATAAAGCATGTTACCCCTTATAGTCTAAGACTA
TATATATAAATGTATAAATATACAGTATAGATTTTTGGGTGGGGGGCATTGAGTATTGTTTAAATGTAATTTAA
ATGAAAGAAAATTGAGTTGCACTTATTGACCATTTTTTAATTTACTTGTTTGGATGGCTGTCTATACTCCTTC
CCTTAAGGGGTATCATGTATGGTGATAGGTATCTAGAGCTTAATGCTACATGTGAGTGACGATGATGTACAGATT
CTTTCAGTTCTTTGGATTCTAAATACATGCCACATCAAACCTTTGAGTAGATCCATTTCCATTGCTTATTATGTA
GGTAAGACTGTAGATATGTATTCTTTTCTCAGTGTTGGTATATTTTATATTACTGACATTTCTTCTAGTGATGAT
GGTTCACGTTGGGGTGATTTAATCCAGTTATAAGAAGAAGTTCATGTCCAAACGTCCTCTTTAGTTTTTGGTTGG
GAATGAGGAAAATTCTTAAAAGGCCCATAGCAGCCAGTTCAAAAACACCCGACGTCATGATTTTGAGCATATCAG
TAACCCCTTAAATTTAATACCAGATACCTTATCTTACAATATTGATTGGGAAAACATTTGCTGCCATTACAGAG
GTATTAAAACCTAAATTTCACTACTAGATTGACTAACTCAAATACACATTTGCTACTGTTGTAAGAATTCTGATTG
ATTTGATTGGGATGAATGCCATCTATCTAGTTCTAACAGTGAAGTTTTACTGTCTATTAATATTCAAGGGTAAATA
GGAATCATTTCAGAAATGTTGAGTCTGTACTAAACAGTAAGATATCTCAATGAACCATAAATTCAACTTTGTAAAA
ATCTTTTGAAGCATAGATAATATTGTTTGGTAAATGTTTCTTTTGGTTGGTAAATGTTTCTTTTAAAGACCTCC
TATTCTATAAACTCTGCATGTAGAGGCTTGTTTACCTTTCTCTCTCTAAGGTTTACAATAGGAGTGGTGATTTG
AAAAATATAAAATTATGAGATTGGTTTTCTGTGGCATAAATTGCATCACTGTATCATTTTTCTTTTTTAAACGGT
AAGAGTTTCAGTTTGTGGAAAGTAAGTGTGAGAACCAGTTTCCCGTCCATCTCCCTTAGGGACTACCCATAGA
CATGAAAGGTCCCCACAGAGCAAGAGATAAGTCTTTCATGGCTGCTGTGCTTAAACCACTTAAACGAAGAGTTC

1437/6881
FIGURE 1335B

CCTTGAAACTTTGGGAAAACATGTTAATGACAATATTCCAGATCTTTCAGAAATATAACACATTTTTTTTGCATGC
ATGCAAATGAGCTCTGAAATCTTCCCATGCATTCTGGTCAAGGGCTGTCATTGCACATAAGCTTCCATTTTAATT
TTAAAGTGCAAAAGGGCCAGCGTGGCTCTAAAAGGTAATGTGTGGATTGCCTCTGAAAAGTGTGTATATATTTTG
TGTGAAATTGCATACTTTGTATTTTGATTATTTTTTTTTTCTTCTTGGGATAGTGGGATTTCCAGAACCACACTT
GAAACCTTTTTTTATCGTTTTTGTATTTTCATGAAAATACCATTTAGTAAGAATACCACATCAAATAAGAAATAA
TGCTACAATTTTAAGAGGGGAGGGAAGGGAAAAGTTTTTTTTTATTATTTTTTTTAAAATTTTGTATGTTAAAGAGA
ATGAGTCCTTGATTTCAAAGTTTTGTGTACTTAAATGGTAATAAGCACTGTAACTTCTGCAACAAGCATGCAG
CTTTGCAAACCCATTAAGGGGAAGAATGAAAGCTGTTCCCTTGGTCCTAGTAAGAAGACAAACTGCTTCCCTTACT
TTGCTGAGGGTTTGAATAAACCTAGGACTTCCGAGCTATGTCAGTACTATTCAGGTAACACTAGGGCCTTGGA
TTCCTGTACTGTGTCTCATGGATTTGGCACTAGCCAAAGCGAGGCACCCTTACTGGCTTACCTCCTCATGGCAGC
CTACTCTCCTTGAGTGTATGAGTAGCCAGGGTAAGGGGTAAAAGGATAGTAAGCATAGAAACCACTAGAAAAGTGG
GCTTAATGGAGTTCTTGTGGCCTCAGCTCAATGCAGTTAGCTGAAGAATTGAAAAGTTTTTGTGTGGAGACGTTT
ATAAACAGAAATGGAAAGCAGAGTTTTTCATTAAATCCTTTTACCTTTTTTTTTTCTTGGTAATCCCTAAAATAA
CAGTATGTGGGATATTGAATGTTAAAGGGATATTTTTTTCTATTATTTTATAATTGTACAAAATTAAGCAAAT
GTTAAAAGTTTTATATGCTTTATTAATGTTTTCAAAGGTATTATACATGTGATACATTTTTTTAAGCTTCAGTTG
CTTGTCTTCTGGTACTTTCTGTTATGGGCTTTTGGGGAGCCAGAAGCCAATCTACAATCTCTTTTGTGTGCCAG
GACATGCAATAAAATTTAAAAATAAATAAAAACTAATTAAGAAATAAA

1438/6881
FIGURE 1336

MNFETSRCATLQYCPDPYIQRFVETPAHFWSWKESYYRSTMSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLN
FVDEPSEDGATNKIEISMDCIRMQSDLSDPMPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYA
QPSSTFDALSPSPAIPSN TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVI
RAMPVYKKAEHVTEVVKRCPNHEL SREFNEGQIAPPSHLIRVEGN SHAQYVEDPITGRQSVLVPYEPQVGTFT
TVLYNFM CNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTK
RPFQNT HGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIET YRQQQQQHQHLLQKQ
TSIQSPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQAL
PPPLSMPSTSQCTPPPPYPTDCSIVSFLARLGSSCLDYFTTQGLTTIYQIEHYSMDDLASLKIPEQFRHAIWKG
ILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVIDAVRFTLRQTISFP PRDEW NDFNFDMDARRNKQQRI
KEEGE

1439/6881
FIGURE 1337

CATTTTGCGAAGTTTAACCAACCCGGGTACCGCCGTTCTTGTCACCACCAACTGGTTTTGTAAACAGTTGCGAGAAC
CTTCTCCTTCTTTTTCTTTTCAACCTTGGATTTAGCGGCTGAGTACTTCCTCTTGTACATGGCCTTCTGGAATC
CATGGCAGATCGGGAATACCTGCCAATTCCTCTGACAAGGACAGGGTTGCGGCTGCAATGGGGCTTCCCCTTGTT
GGGCTTTTTAGCTTTGAGGTTACCCTTTTTACCTTGCCACCAGCATCAACCTTCTTGGCTTCGGGTTTCTTCTC
TTTAG

1440/6881
FIGURE 1338

ATGCCTGCTGCCACGTGGCTGGTCCTCCTCCTGCTGTGGCTGAGCCTTGGGGTGAAGACAGCTTCTCAGATG
ACCAAGATGGTGTCTGAGATGGTGTCTGAGGATGGAGAACCCACCAAGCCCCGCTAGGAGCCACCTAGACTGGATG
CAGAGCATGGAAATAAGCCTCGGTGTGGAGAGGGCCTGTCTCAGGGCCTGGCAGATGTAGGCGATTCTTACCAC
GTCTCCTTCGCTACCCCGAAAGGCACAATCATAGGCCTTTCTCGTCTTTTAAGGGTTTTTACTTCCATGGGGAAC
TATGTGTTGGATGAGAAAAGTATCCGGGGAAGGGACAGAGGTTTCAAGAAAGCTCTGCGAGTCTTGGACGCTGGTC
TGCCTTCTTGGCTCACCCCTGGAAGGTGGACGCTGGCCCCACACATCCCCTCTTAAAGACGCAGGCCGATAGCCAG
CAGATCCTGGGGCTTGTGGCCCCAAAGCAGACACTGCGATGACAACGGACGACACAGAAGTGCCCGCTATGACT
CTAGCACCGGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAGACCTCTTCTAGGGCCTCAACCCAGCC
GGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAAGAGAATTTCCCCTGCAAGAGAGACCAGGAGTTTACAAAA
ACATCTCCCAACTTCATGGTGTCTGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCT
GGAATGACCACAGTTCAGACCATCACAGGCAGTGATCCAGGGAAGCCATCTTTGACACCTTTGCACCGATGAC
AGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCACAGAAGCTAAGGGCCTG
TCCTCAGAGAGCAGCGCCTCTTCCGACAGCCCCCATCCAGTCATACCCCGTCACGGGCCTCAGAGAGCAGCGCC
TCTTCCGACGGCCCCCATCCAGTCATCACCCCGTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCAT
CCAGTCATCACCCCGTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCCGTCA
CGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCCGTCACGGGCCTCAGAGAGCAGC
GCCTCTTCCGACGGCCCCCATCCAGTCATCACCCCGTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCC
CATCCAGTCATCACCCCGTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCCG
TCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCCGTCACGGGCCTCAGAGAGC
AGCGCCTCTTCCGACGGCCTCCATCCAGTCATCACCCCGTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGC
CCCCATCCAGTCATCACCCCGTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACC
CCCTCATGGTCCCCGGGATCTGACGTCACTCTCCTCGCTGAAGCCCTGGTGACTGTACAAAACATCGAGGTTATT
AATTGCAGCATCACAGAAATAGAAACAACGACTTCCAGCATCCCTGGGGCCTCAGACACAGATCTCATCCCCACG
GAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACCAGCTCTGCCTGACTCCACTGAAGCAAAACACACATCACT
GAGGTCACAGCCTCTGCCGAGACCCTGTCCACAGCCGGCACACAGAGTCAGCTGCACCTGATGCCACGGTTGGG
ACCCCACTCCCCA¹TAACAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCCTCAGTGGAGCTCTG
GTCACAGTTAGCAGGAATCCCCTTGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTCAAAGTCTCA
GGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGACAGTGGGCAAAACAACCTTCTTTGCTGGGAGCTCTGCTTCC
TCCTACAGCCCCCTCGGAAGCCGCCCTCAAGAACTTACCCCTTCAAGACACCGACCATGGACATCGCAACCAAG
GGGCCCTTCCCCACCAGCAGGGACCCTCTTCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAAC
AGCACCTTAGCCAAGATCACAACTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCCACGACTGCCCGG
ACGAGGCCGACCACAGACGTGAGTGCAGGTGAAAATGGAGGTTTCCTCCTCCTGCGGCTGAGTGTGGCTTCCCCG
GAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGGAGAGGCTAACGGACATCAGCTGCAGCCAG
GCATGTCCCGTATGCCAAAAGAGGGTGTGCCCCTAGCCTGGGCCCCACCGACAGACTGCAGCTGCGTTACTGT
GCTGAGAGGTACCCAGAAGGTTCCCATGAAGGGCAGCATGTCCAAGCCCCTGACCCAGATGTGGCAACAGGACC
CTCGCTCACATCCACCGGAGTTTTGTTACATTGTACGTGCTCGAGGACAAGCAGCCGGTAGTATTACCTCTGTC
ATCACAGAAGCTGGCGTGGAGCCCTCCACATGA

1441/6881
FIGURE 1339

MTTDDTEVPAMTLAPGHAALETQTLAETSSRASTPAGPIPEAETRGAKRISPARETRSFTKTSPNFMVLIATSV
ETSAASGSPEGAGMTTVQTITGSDPREAIFDTLCTDDISEEAKTLTMDILTTLAHTSTEAKGLSSESSASSDGPHP
VITPSRASESSASSDGLHPVITPSRASESSASSDGLHPVITPSRASESSASSDGPHPVITPSWSPGSDVTLLAEA
LVTVTNIEVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTNTKPHITEVTASAETLSTAGTT
ESAAPDATIGTPLPTNSTIEREVTAPGATTLSGALATGNPLEETSALSVETPSYVKVSGAAPVSI EAGSAVGKTT
SFAGSSASSYSPLAALKNFTPSETLTDDIATKGPFPTSRAPLPSVPPTTTNSS

1442/6881
FIGURE 1340A

ACGCCACCCCTCTTCCTGTCACCAGCCTTTCTCAGTATCCACAGGTCACGCCACCCCTCTTGCTGTCAGCAGTG
CTACCTCAGCTTCCACAGTATCCTCGGACTCCCTCTGAAGATGGAAACACCAGGAATGACAACACCGTCACTGA
AGACAGACGGTGGGAGACGCACAGCCACATCACCACCCCCACAACCTCCCAGACCATCATTTCCACCATTCCCCA
GCACTGCCATGCACACCCGCTCCACAGCTGCCCCATCCCCATCCTGCCTGAGAGAGGAGTTTCCCTCTTCCCT
ATGGGGCAGGCGCCGGGGACCTGGAGTTCGTACAGGAGGACCGTGGACTTCACCTCCCCACTCTTCAAGCCGGCGA
CTGGCTTCCCCCTTGGCTCCTCTCTCCGTGATTCCCTCTACTTCACAGACAATGGCCAGATCATCTTCCCAGAGT
CAGACTACCAGATTTTCTCCTACCCCAACCCACTCCCAACAGGCTTCACAGGCCGGGACCCTGTGGCCCTGGTGG
CTCCGTTCTGGGACGATGCTGACTTCTCCACTGGTCGGGGGACCACATTTTATCAGGAATACGAGACGTTCTATG
GTGAACACAGCCTGCTAGTCCAGCAGGCCGAGTCTTGGATTAGAAAGATGACAAACAACGGGGGCTACAAGGCCA
GGTGGGCCCTAAAGGTCACGTGGGTCAATGCCACGCCTATCCTGCCAGTGGACCCTCGGGAGCAACACCTACC
AAGCCATCCTCTCCACGGACGGGAGCAGGTCTATGCCCTGTTTCTCTACCAGAGCGGTGGGATGCAGTGGGACG
TGGCCAGCGCTCAGGCAACCCGGTGCTCATGGGCTTCTCTAGTGGAGATGGCTATTTGAAAACAGCCCACTGA
TGTCCAGCCAGTGTGGGAGAGGTATCGCCCTGATAGATTCTGAATTCCAACCTCAGGCCTCCAAGGGCTGCAGT
TCTACAGGCTACACCGGGAAGAAAGGCCCAACTACCGTCTCGAGTGCCTGCAGTGGCTGAAGAGCCAGCCTCGGT
GGCCAGCTGGGGCTGGAACCAGGTCTCCTGCCCTTGTTCTTGGCAGCAGGGACGACGGGACTTACGATTCCAAC
CCGTACAGCATAGGTCTGTGGGGCTCGGCAGTAGGCAGCTGTGCAGCTTACCTCTTGGCGAGGAGGCGTGTGCT
GCAGCTACGGGCCCTGGGGAGAGTTTCTGTGAAGGCTGGCACGTGCAGCGTCTTGGCAGTTGGCCAGGAACCTGG
AGCCACAGAGCTGGTGTCTGCCGTGGAATGACAAGCCCTACCTCTGTGCCCTGTACCAGCAGAGGCGGCCCCACG
TGGGCTGTGCTACATACAGGCCCCACAGCCCGCCTGGATGTTTCGGGGACCCCCACATCACCACCTTGGATGGTG
TCAGTTACACCTTCAATGGGCTGGGGGACTTCTCTGTGGTTCGGGGCCCAAGACGGGAACCTCCTCCTCTCTGCTTC
AGGGCCGCACCGCCAGACTGGCTCAGCCCAGGCCACCAACTTCATCGCCTTTCGGGCTCAGTACCGCTCCAGCA
GCCTGGGCCCCGTACGGTCCAATGGCTCCTTGAGCCTCACGACGCAATCCGTGTCTCTGCTGGATAACCAGACTG
TGACATTTACGCTGACCATGAAGACGGCGGAGGCCAGGAGACGTTCAACGCCACCGGAGTCTCCTGAGCCGCA
ACGGCTCTGAGGTCTCGGCCAGCTTCGACGGCTGGGCCACCGTCTCGGTGATCGCGCTCTCCAACATCCTCCACG
CCTCCGCCAGCCTCCCGCCCGAGTACCAGAACCGCACGGAGGGGCTCCTGGGGGTCTGGAATAACAATCCAGAGG
ACGACTTCAGGATGCCCAATGGCTCCACCATTCCCCAGGGAGCCCTGAGGAGATGCTTTTCCACTTTGGAATGA
CCTGGCAGATCAACGGGACAGGCCTCCTTGGCAAGAGGAATGACCAGCTGCCTTCCAACCTTACCCCTGTTTTCT
ACTCACAACCTGCAAAAAACAGCTCCTGGGCTGAACATTTGATCTCCAACCTGTGACGGAGATAGCTCATGCATCT
ATGACACCCCTGGCCCTGCGCAACGCAAGCATCGGACTTCACACGAGGGAAGTCAGTAAAACTACGAGCAGGCGA
ACGCCACCCCTCAATCAGTACCCGCCCTCCATCAATGGTGGTTCGTGTGATTGAAGCCTACAAGGGGCAGACCACGC
TGATTAGTACACCAGCAATGCTGAGGATGCCAACTTCACGCTCAGAGACAGCTGCACCGACTTGGAGCTCTTTG
AGAATGGGACGTTGCTGTGGACACCCAAGTCGCTGGAGCCATTCACTCTGGAGATTCTAGCAAGAAGTGCCAAGA
TTGGCTTGGCATCTGCACTCCAGCCCAGGACTGTGGTCTGCCATTGCAATGCAGAGAGCCAGTGTGTGTACAATC
AGACCAGCAGGGTGGGCAACTCCTCCCTGGAGGTGGCTGGCTGCAAGTGTGACGGGGGCACCTTCGGCCGCTACT
GCGAGGGCTCCGAGGATGCCTGTGAGGAGCCGTGCTTCCCGAGTGTCCACTGCGTTCTTGGGAAGGGCTGCGAGG
CCTGCCCTCCAAACCTGACTGGGGATGGGCGGCAGTGTGCGGCTCTGGGGAGCTCTTTCTGTGTGAGAACCAGT
CCTGCCCTGTGAATTACTGCTACAATCAAGGCCACTGCTACATCTCCAGACTCTGGGCTGTGAGCCCATGTGCA
CCTGCCCCCAGCCTTCACTGACAGCCGTGCTTCTGGCTGGGAACAACCTCAGTCCAACCTGTCAACCTAGAAC
TTCCCTTAAGAGTCATCCAGCTCTTGCTCAGTGAAGAGGAAAAATGCCTCCATGGCAGAAGTCAACGCCTCGGTGG
CATAAGACTGGGGACCCCTGGACATGCGGGCCTTTCTCCGCAACAGCCAAGTGAACGAATCGATTCTGCAGCAC
CGGCCTCGGGAAGCCCCATCCAACACTGGATGGTTCATCTCGGAGTTCCAGTACCGCCCTCGGGGCCCGGTTCATTG
ACTTCTGAACAACAGCTGCTGGCCGCGGTGGTGGAGGCGTTCTTATACCACGTTCCACGGAGGAGTGAGGAGC
CCAGGAACGACGTGGTCTTCCAGCCCATCTCGGGGAAGACGTGCGCGATGTGACAGCCCTGAACGTGAGCACGC
TGAAGGCTTACTTCAGATGCGATGGCTACAAGGGCTACGACCTGGTCTACAGCCCCCAGAGCGGCTTCACTGCG
TGTCCCGTGCAGTAGGGGCTACTGTGACCATGGAGGCCAGTGCCAGCACCTGCCAGTGGGCCCCGCTGCAGCT
GTGTGTCTTCTCCATCTACACGGCCTGGGGCGAGCACTGTGAGCACCTGAGCATGAAACTCGACGCGTTCTTCG
GCATCTTCTTTGGGGCCCTGGGCGGCCTCTTGCTGCTGGGGGTTCGGGACGTTCTGTGGTCTGCGCTTCTGGGGTT
GCTCCGGGGCCAGGTTCTCCTATTTCTGAACTCAGCTGAGGCCTTGCCTTGAAGGGGCAGCTGTGGCCTAGGCT

1443/6881
FIGURE 1340B

ACCTCAAGACTCACCTCATCCTTACCGCACATTTAAGGCGCCATTGCTTTTGGGAGACTGGAAAAGGGAAGGTGA
CTGAAGGCTGTCAGGATTCTT

1444/6881
FIGURE 1341

AGTTCTGTGGAGCAGCGGTGGCCGGCTAGGATGGGCTGTCTCTGGGGTCTGGCTCTGCCCCTTTTCTTCTTCTGC
TGGGAGGTTGGGGTCTCTGGGAGCTCTGCAGGCCCCAGCACCCGCAGAGCAGACACTGCGATGACAACGGACGAC
ACAGAAGTGCCCGCTATGACTCTAGCACCGGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAGACCTCT
TCTAGGGCCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAAGAGAATTTCCCCTGCAAGA
GAGACCAGGAGTTTCAAAAAACATCTCCCAACTTCATGGTGCTGATCGCCACCTCCGTGGAGACATCAGCCGCC
AGTGGCAGCCCCGAGGGAGCTGGAATGACCACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTT
GACACCCTTTGCACCGATGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACC
TCCACAGAAGCTAAGGGCCTGTCTCAGAGAGCAGTGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCCGTCA
CGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCCGTCACGGGCCTCAGAGAGCAGC
GCCTCTTCCGACGGCCCCCATCCAGTCATCACCCCGTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCC
CATCCAGTCATCACCCCGTCATGGTCCCCGGGATCTGATGTCACTCTCTCGCTGAAGCCCCCTGGTGACTGTCA
AAACATCGAGGTTATTAATTGCAGCATCACAGAAATAGAAACAACAACCTTCCAGCATCCCTGGGGCCTCAGACAT
AGATCTCATCCCCACGGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACCAGCTCTGCCTGACTCCACTGAAGC
AAAACCACACATCACTGAGGTACAGCCTCTGCCGAGACCCTGTCTCAGCCCTCTCTGTTGAGACACCAAGTTA
CGTCAAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGAGCAGTGGGCAAACAACCTTCTTTGCTGG
GAGCTCTGCTTCTCTACAGCCCCCTCGGAAGCCGCCCTCAAGAACTTCAACCCCTTCCAGAGACACCGACCATGGA
CATCGCAACCAAGGGGGCCCTTCCCCACCAGCAGGGACCCTCTTCTTCTGTCCCTCCGACTACAACCAACAGCAG
CCGAGGGACGAACAGCACCTTAGCCAAGATCACAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCC
CACGACTGCCCGGACGAGGCCGACCACAGACGTGAGTGCAGGTGAAAATGGAGGTTTCTCTCTCTGCGGCTGAG
TGTGGCTTCCCCGGAAGACCTCACTGACCCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCACCGGGAACCTCCA
CGCCCACGCGCCTCACTTCCAGGTCTCCTTACTGCGTGTGAGGAGAGGCTAACGGACATCAGCTGCAGCCAGGCA
TGTCCCGTATGCCAAAAGAGGGTGCTGCCCCTAGCCTGGGCCCCCACCAGACAGACTGCAGCTGCGTTACTGTGCT
GAGAGGTACCCAGAAGGTTCCCATGAAGGGCAGCATGTCCAAGCCCCTAACCCAGATGTGGCAACAGGACCCTC
GCTCACATCCACCGGAGTGATGTATGGGGAGGGGCTTACCTGTTCCCAGAGGTGTCCTTGACTCACCTTGGC
ACATGTTCTGTGTTTCTAGTAAAGAGAGACCTGATCACCCATCTGTGTGCTTCCATCCTGCATTAAAAATCACTCA
GTGTGGCCAG

1445/6881
FIGURE 1342

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTLAETSSRASTPAGPI
PEAETRGAKRISPARETRSFTKTSPNFMVLIATSVETSAASGSPEGAGMTTVQTITGSDPEEAIFDTLCTDDSSSE
EAKTLTMDILTTLAHTSTEAKGLSSESSASSDGPHPVITPSRASESSASSDGPHPVITPSRASESSASSDGPHPV
TPSRASESSASSDGPHPVITPSWSPGSDVTLAEALVTVTNIEVINCSITEIETTTSSIPGASDIDLIPTEGVKA
SSTSDPPALPDSTEAKPHITEVTASAETLSTAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLSGALVTVSR
NPLEETSALSVETPSYVKVSGAAPVSI EAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETPTMDIATKGPFPT
SRDPLPSVPPTTTNSSRGTNSTLAKITTSAKTTMKPPTATPTTARTRPTTDVSAGENGGFLLLRLSVASPEDLTD
PRVAERLMQQLHRELHAHAPHFQVSLLRVRRG

1446/6881
FIGURE 1343

GGGCCGCACTGGACCAGGGATGAGAGTGGGTGCCCGGGACTCGCCTATACTGCCTGGGGGTGCAGCCCGCACTCC
TCACTATAGTCAAATCGACTATGCGTGCTTTCCAGGGGCCCCGGGAGAGGACTCCATGGGGAGGGATGCTTACCTT
GTGGGCTTTTGAATATAAGCCCTTTTCATCTTCTCCGCTGGTCCCTACCACGTTGGCAAGGCAGGTATTGTGACCC
TGTTTTCTCAGGTGAGGACATGGAGGCTGGGAGGGGTCTAGAGACTGGCCTGGCTAGTAGGAGGCTGAGTCAGGA
TTTGAACCAGCAGATCATCTGACCCAGAGCCGGTCTGTGGGCGGCACAGCGGGAGCTGCAACCGAGGCTCTTGAC
TCCTGCCTCGTCATTCCTGAGGTCCACAGGACAACCAGCTGGGGACCTGGAGCCCCATCCTGACGTCCTGGGGA
GAGGTGCTAGGCCCCCTTTTGGGTCTATGAGCTACTTTTGGGCCAGTGGAGCCGGGTAAAGACCATCTCAAACCT
GTGCCAGGGGAGGTCAGACTCCAAGAGCGCCACCTTTGGGCTTCCAGCTGTGTGGGCTGCACCAAGAAGGCTCAG
AGAATTAGGGGGTTCGTATTTGATCCTTTTCCTTCCAAGACTGGGATTACCAGATAAAACACAGGGCATCCAGTT
ACATTTGAATTTGAGTAACAATTTTTTTTTTAAGTGTAAGTACGTAGCCAATATTGCATGAGAAATACTCATGCT
AAAAAGTTATTCGTCATTTATCTGAAGTGCAGGTTCAAATTTAACCAGTAGTACCCTGTATTTTTATTGCTAAATC
TAGAAACCTCTCCAAGAGACTCCTTGGCCCACTCACAGGGAGAGCCCGATCTCCCTCTAGACAGGGGAGGCCCC
CTTTCTCAGGCCAGAAAAGATCTTGTAGTAACTACTCAAGAGGCTGAGGCAGGAGGATCGCTTGAGCCCAGGAA
TTCAAGACCTGCCTGGGCAACAGAGCAAGACCCTGTCTCTAGGGGAAGATATCCTACCGTAGCCTCCCTCGGGGAC
TCCCATTCTCCACCTCAGGGCCAGTCAAGGGAACAGGCCTCTGCTCTGGGCAGAAGTGCCGGCAGCCGCTCTC
TGAAAAGCTAGGTGTTGCCTCAGGGGCTCCCGGTGTCTGTGGAAAATGCCTGGCCACGGTTTCCATGGTTCCCA
GGCTCCAACCTGCAGTTCTCGGCCCTCATTCAGGAGGGGCTCGGCAGGGTGGGGGTGCCGTCTTTCCCTTGC
CGGAGCCCCAAGGACTCTGCCGGCTCCCTCGCTTTGGCAGCAGCACTGCCACCCTGTCTCTGGAGGTTCCCCCG
CCTCAATCCACCCAGCTACCCCGAAAGGCACAATCATAGGCCTTTCTCGTCTTTTAAGGGTTTTTACTTCCATG
GGGAATATGTGTTGGATGAGAAAAGTACCCGGGGAAGGCGACAGAGGTTCAAGAAAGCTCTGCGAGTCTTGACG
CTGGTCTGCCTTCTTGGCTCACCTTGAAGGTGGACGCTGGCCCCACACATCCCCTCTTAAAGACGCAGGCCGAT
AGCCAGCAGATCCTGGGGCTTGCTGGCCCCAAGTGAGTTGTGAGGTTTTCAGAGGACGCCAGTCATGGCAACCCC
AGCTCCATGGCTGCCACACAGGCCTGGGCTTCCCAGGACTGCCCTCTTCTTGTTCGCTTATGTAGATGAAAAATG
AGGTAACGGCACTCCCCTGCCCCACCCTCCTCCCAGAAGTGCCAGGGTGTAATGCAATAGCTTGTGTGAAGTC
CACTGGAACCCAGGCTCACCAAGTCAGTCTTAACCAACACAGGCCCCAGCACCCGCAGAGCAGACACTGCGATGA
CAACGGACGACACAGAAGTGCCCGCTATGACTCTAGCACCGGGCCACGCCGCTCTGGAACTCAAACGCTGAGCG
CTGAGACCTCTTCTAGGGCCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAAGAGAATTT
CCCCTGCAAGAGAGACCAGGAGTTTCAAAAAACATCTCCCAACTTCATGGTGCTGATCGCCACCTCCGTGGAGA
CATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACCACAGTTAGACCATCACAGGCAGTGATCCCGAGG
AAGCCATCTTTGACACCTTTGCACCGATGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACAT
TGGCTCACACCTCCACAGAAGCTAAGGGCCTGTCTCAGAGAGCAGTGCCCTCTTCCGACGGCCCCCATCCAGTCA
TCACCCCGTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATACCCCGTCACGGGCCT
CAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATACCCCGTCACGGGCCTCAGAGAGCAGCGCCTCTT
CCGACGGCCCCCATCCAGTCATACCCCGTCACGGGCCTCAGAGAGCAGTGCCCTCTTCCGACGGCCCCCATCCAG
TCATACCCCGTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATACCCCGTCATGGT
CCCCGGGATCTGATGTACTCTCCTCGCTGAAGCCCCTGGTGACTGTACAAACATCGAGGTTATTAATTGCAGC
ATCACAGAAATAGAAACAACAACCTTCCAGCATCCCTGGGGCCTCAGACATAGATCTCATCCCCACGGAAGGGGTG
AAGGCCTCGTCCACCTCCGATCCACCAGCTCTGCCTGACTCCACTGAAGCAAAACACACATCACTGAGGTCA
GCCTCTGCCGAGACCCTGTCCACAGCCGGCACACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTC
CCCACTAACAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCTCAGTGAGGCTCTGGTCAAGTT
AGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTCAAAGTCTCAGGAGCAGCT
CCGGTCTCCATAGAGGCTGGGTGAGCAGTGGGCAAAACAACCTTCCCTTTGCTGGGAGCTCTGCTTCTCTACAGC
CCCTCGGAAGCCGCCCTCAAGAACTTACCCCTTCCAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTC
CCCACAGCAGGGACCTCTTCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTA
GCCAAGATCACAACCTCAGCGAAGACCACGATGAAGCCCCATCTCTACTAAAAATACAAAATTAGCTGGGTGTG
GTGGCATGCACCTGTAGTCCCAGCTACTCGGGAGGTTGAGGCAGGAGAATCACTTGACCAGGGAGGTGGAGGTT
CGAGTGAGCCGAGATTGCGCCACTGCACTCCAGCCTGGGCAACAGAGCAAG

1447/6881
FIGURE 1344

CTTTTGAGCAGGAGTCCGGGCCCTCGTGTACCGCTCTGAAGTCAAGGAGAGGCTGGGAGGCGGCAGAATGCAGC
CAGAGGAGGGCACAGGCTGGCTGCTGGAGCTGCTGTCCGAGGTGCAGCTGCAACAGTACTTCCTGCGGCTCCGAG
ATGACCTCAACGTCACCCGCCTGTCCACTTTGAGTACGTCAAGAATGAGGACCTGGAGAAGATCGGCATGGGTC
GGCCTGGCCAGCGGCGGCTGTGGGAGGCTGTGAAGAGGAGGAAGGCCTTGTGCAAACGCAAGTCGTGGATGAGTA
AGGTGTTTCACTGGAAAGCGACTGGAGGCTGAGTTCCACCTCATCACTCTCAGAGCACCTTCCGGAAGACCTCGC
CCGCCCCTGGGGGCCAGCAGGGGAGGGGCCCTGCAGAGCCTCACCTGCCTCATTGGGGAGAAGGACCTGCGCC
TCCTGGAGAAGCTGGGTGATGGTTCCTTTGGCGTGGTGCAGGGGCGAGTGGGACGCGCCCTCAGGGAAGACGG
TGAGTGTGGCTGTGAAGTGCCTGAAGCCCGATGTCCTGAGCCAGCCAGAAGCCATGGACGACTTCATCCGGGAGG
TCAATGCCATGCACTCGCTCGACCACCGAAACCTCATCCGCCTCTACGGGGTGGTGCTCACGCCGCCCATGAAGA
TGGCATCAGTTTCCCAAATTGCCTCGAGGGAGAGGCCTGAGAACTGCAGGACTCCTAGAGGTCCCCAGACAGCA
GGCCAGGAAGGTGACAGAGCTGGCACCTCTGGGATCGTTGTTGGACCGGCTACGTAAGCACCAGGGCCACTTCCT
CCTGGGGACTCTGAGCCGCTACGCTGTGCAGGTGGCTGAGGGCATGGGCTACCTGGAGTCCAAGCGCTTTATTCA
CCGTGACCTGGCTGCCC GCAATCTGCTGTTGGCTACCCGCGACCTGGTCAAGATCGGGGACTTTGGGCTGATGCG
AGCACTACCTCAGAATGACGACCATTACGTCATGCAGGAACATCGCAAGGTGCCCTTCGCCTGGTGTGCCCCCGA
GAGCCTGAAGACACGCACCTTCTCCCATGCCAGCGAC

1448/6881
FIGURE 1345

TGTCTTCAGTGAAATGATACCGGTCCCCACTGCCAGCTCACCTCCCGGGGCTGCAGGAGGCACCGGAGATAATG
GCTGTAGAGGGTCTTGTAACCTGAACATTGCTTGCAAACATAAGGAATTCTAGTTACTGGGAGGAAGCACAGGGC
AGAGGCCAGAAGAGGCCCTCAGATTTGAGGCACCCTAGCCCAGACGGATAAGGATCCACCAGCTCTGGGGGCGTG
AGACCCAAGCTGGCAAGAATCTGCAATCTGGAGCCAAGGCTGTGGGTGCCTCAGTGGAGGCCGAGTCAGACCGAC
GTGGCCAGCTTTGACCCTCATGGCCTCCTTTCTTCTGTCCCTTGACCTTCGGCTCCTCCCTGTCCACCCTGGCCT
CCGAGTCTCCTCCACTTTTCCTTCCGTCTCAGCCCTCAGCTCTAGGCGCCCCCTCCAGAGACCCAGCTGTCTTCCC
AGGCCCCCTTCCCAGCAAGGACTAGCTTCATCTGAACCACACACACTCACGGTTCAACCTCAGACTAAAATTAT
CCTCTCCCCCTGGGCAGGATGAAGGGCAGCCGACTCCCTGGTGAGGGTGGAGACAGACAGCACCAAATGGTCAGGC
CAGAGAAGGGGCCAGGGCTAAAAATGGACAAGGAGGTGTCTGTGGAGGGCCCCCTGCGGCTCCATCGATCGGGGTT
AGGGCTGGAGTCTGCGGGGTGGCGGGTGACAGGAAGGGAGGGTGGGGCAGGACTGGGAGGAGACTCCGACCTTGGC
TGGGCGGTGCCCTCCCTCTCCACACAGCTGGGTGTGGGGCCGCTCAGCCACAGGCTGCATGCCTGTGCGTCTCTT
TCTGGCACCCCTCCTTGAGGCCAGCATCAGGCTTTGGGTTCATGTTTGGGGGTGTGCCCTGGACGGAGTGTGGGCC
TCCAGCCAGGCTGCCCCACTGACAGTTTGGCAAAACCAGGACCTATCTGGAAGCCGAAGCCGGGGATCACCAGGT
GGACCCAGCGGGGTGGGACTGAGTGACTGACCCCTGGGGTGTTGGATTCCATCTGGCCCCCGGCTGCCTTCAAACA
GGTGTTTCAGTGGAAGCGACTGGAGGCTGAGTTCCACCTCATCACTCTCAGAGCACCTTCCGGAAGACCTCGCC
CGCCCCCTGGGGGCCAGCAGGGGAGGGGCCCTGCAGAGCCTCACCTGCCTCATTGGGGAGAAGGACCTGCGCCT
CCTGGAGAAGCTGGGTGATGGTTCCCTTTGGCGTGGTGCAGAGGGCGAGTGGGACGCGCCCTCAGGGAAGACGGT
GAGCTCTCTGTGTCCTGCCAGCGCAGCAGAGGCATGGGACCCGGGGCTGGTAGTGGCTCTTCTGCCCCCAACCAG
GGTGTGGATGGGACTGGGGATGCGTCACAGTGTGGCTCATCCCAGAGTCCGTGCTCAGGATTTTTGGGGTTTTAT
TTATTTATTTATTTTGGAGATGGAGTCTCGCTCTGTGCGCCAGGCTGGAGTGCAGTAGGCACGATCTCGGCTTCC
TGCAACCTCCACTTTCCGGGTTCAGCAATCCTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCATGCAC
CACCACACTCAGTTAATTTTTGTATTTTTAGTAGAGACGGGGTTTACCATGTTGGCCAGGCTGGTCTCGAACTC
CTGACCTCAGATGATCTGCCCACTTTAGCCTCCCAAAGTGCTTGGATTACAGGTGTGAGCCACCACGTCCAGCCC
ATGCTCAGGTTTAACTAAGCACATTTATTATTTCAACTATAAAAATAATTTATTATAAAAGTTTGGAAGTATTT
G

1449/6881
FIGURE 1346

MRVRAGVCGVAGAGREGGAGLGGDSDLGWAVPSLSTQLGVGPI SHRLHACRSLSGTLLEASIRLWVHVWGCALDG
VWASSQAAPLTVWQNQDLSGSRSRGSPGGPSGVGLSD

1450/6881
FIGURE 1347

CATCCTCCCAGAGAAGGGGCCCCGAATCGCCGAAGGGCACTGCTTCGCCGATTTAAAAAACAAAGCAAAAAGCCCC
GCATCTGCATCAGGAAGGCGCCTCTGCCTACTCTGGGAGAGAGAAGGGCACCCCTCCCCCTTGCTACGTAGTCGT
CTGCGGAGGCACAAACCGTGGAACGGGAGCCGCCACCACCACCGCTCAAACCTCTCGGCCTGGCTGGGGTA
CAGGGAGCGGCTGCGAGCGAATGGGATAAGCGAGCCTCCAGTTCCCGTCTTCCAGAGCAAGTGGCTTCAGTGAT
ATCCAAGCGCCCTTCCAGCACCCATTCCCTGCCTCGCCAGCAGGCACCGGGGCCCCACTTGCGCTTTGCGGATTT
CAGCTGAATGGGAGGCGACACAATGAGACAAGAGCAAACCGTTTCTCAGCGTTCTTGCCCAGGGCCTTCCCGTCT
CGCGGCCCGGCCTCCCTCACCCGGAAGTGCTGGTCCCGGTACTGGCTCAGCTCCACGTAGGAGTCGCTGCGCAGC
GCCTTCAGGAGGCCACCCGACATAGTGACAGAGAAGCGGACCACAATGCGGCGACTCCCGGCACGAGGCTGCGTCC
GCGATGGCGGAAGCGGAAACGCGCGGAGGCGAGCATCTCATTGGACCCAATCCGAGGGCGGCAGTGTGTCGTCATCA
AGCTGCGCGGGGGCATAGACGTCCGGGTGCGGCGCCGCGGGGCGGAAGACGAGGGCGGCAGGTCGGGTTCCGGG
CGCTTGAGAGAAGATGGTGCTGCGGCGGCTGCTGGCCGCCCTGCTGCACAGCCCGCAGCTGGTGGAACGTCTGTCA
GAGTCGCGGCCTATCCGACGTGCGGCGCAGCTCACGGCCTTCGCACTGCTGCAGGCCCAGCTGCGGGGCCAGGAC
GCGGCCCCGCCGCTGACAGGACCTCGCGGCTGGGCCCCGTGGGCTCCCTGTGCCGCCGCGCTGAGCGATTTAGAGAC
GCCTTCACCCAGGAGCTACGCCGCGGCCTCCGAGGCGCCTCGGGGCCACCACCAGGTAGCCAGAGGGGCCCTGGC
GCAAAACATTTAATCCTGGGCTGTGCGGGGCCGAGGCTGCTTGCTTTTCCCTTCCGGGCTCTACAGTGGCATCAATG
TGGAGGGGTCAATCCGGGCACTGCGCGCGGCTTCGAATCCCGACTGGGATTGTTGGCCTGCAGACATCCCACGCA
TAAGAGCCTAGGCCAGACCGCCCCGCTCCGTTGAAGTCTTGTGATTGGACAAGACACAGTGTGGAGAAAGACCCCT
AAGCCTAACAGAGATGAAGGTAGGCTGGGTCCAGACACGGCACCTACGGAGAGCCACGGACCGAAGCCAGAGAGC
CTTTCCTCTGCAAGTGGGACTGAACTCTTGACAGATGCTGCTCAATCTGACTGGTATAGCAGGACAGTTAATTC
CAGGGACGATATGGATGAAAAGACAACCTACAGCTGCCAAATTCCTTTGATTAAATGTGTGAGCTGGTTGATAG
GCATGAGTGTGATACTTCTCAGGCAAGATGTGTTAAGAATACCGGGGACTGTAGGCCATGTTAATAATAAACAC
GTATTTTATGAAATGA

1451/6881
FIGURE 1348

CCGGCTGCTGCGGACCTCCTCGGACCCGGACCCAGCCCCAGCCCGGCCCCAGCCAGCCCCGACGGCGCCATGCGG
GGTCCGAGCGGGCTCTGTGGCTGCTCCTGGCTCTGCGCACCGTGCTCGGTGGCATGGAGGTGCGGTGGTGCGCC
ACCTCGGACCCAGAGCAGCACAAGTGCGGCAACATGAGCGAGGCCTTCCGGGAAGCGGGCATCCAGCCCTCCCTC
CTCTGCGTCCGGGGCACCTCCGCCGACCACTGCGTCCAGCTCATCGCGGCCAGGAGGCTGACGCCATCACTCTG
GATGGAGGAGCCATCTATGAGGCGGGAAGGAGCACGGCCTGAAGCCGGTGGTGGGCGAAGTGTACGATCAAGAG
GTCGGTACCTCCTATTACGCCGTGGCTGTGGTCAGGAGGAGCTCCCATGTGACCATTGACACCCTGAAAGGCGTG
AAGTCCTGCCACACGGGCATCAATCGCACAGTGGGCTGGAACGTGCCCGTGGGCTACCTGGTGGAGAGCGGCCGC
CTCTCGGTGATGGGCTGCGATGTACTCAAAGCTGTCAGCGACTATTTTGGGGGCAGCTGCGTCCCGGGGGCAGGA
GAGACCAGTTACTCTGAGTCCCTCTGTGCGCTCTGCAGGGGTGACAGCTCTGGGGAAGGGGTGTGTGACAAGAGC
CCCCTGGAGAGATACTACGACTACAGCGGGGCCTTCCGGTGCCTGGCGGAAGGGGCAGGGGACGTGGCTTTTGTG
AAGCACAGCACGGTACTGGAGAACACGGATGAAAGTCCATCACGAAGGCAAAACATGGACCAGATCTGAGGAGGAA
GAAGGCGAGTGCCCTGCACACGAGGAAGCACGTAGGACGATGCGCTCTAGTGCTGGGCAAGCCTGGAAATGGGCT
CCCGTTACAGGCCCCAGGACGAGTCTGACAAAGGAGAATTTGGAAAACGGGCAAAGAGTAGGGATATGTTGGGT
TAAGAATCAGCTCTTTCAAACCTTGGGGTTTTTTTTTGGGATGGGGGTCTCACCATGTTGCCAGGCTGGTCTCAA
CCCCAGCCTCAACTGATCCTCGCATCTCAGCCTCCTGAGTAGCTGGGATGACAGGCGTGACCTGGCAGCTTTT
TCAAAGTGTTGATGGTAATCTGAGGCAATCTAAGGGAGTCATTTTTTAAGTGACTTTATACAGAAAGATTGGTAA
GAGCCAAGGGGTAGAAGTGGCATAAATGTCTAAAGCAGGGAAGTGACAGGACTTTCATTGTTCTTGGCTGAGGAG
AAGCGGGAGTGGCTGATGGAAGCACCTAAATGATGCCTTTGTCTGTGGGAAGGCAAATGATGCCCCAGAGCTCTA
ACCAAAGGTTTTTGCAGCCGCCGAAAAACAGGAAAGTTGGGAAGCGGGGGTAGGACTACACTGAATCATTAACAGT
GCTGTAAACTACCATGTGGCCATTAACAATGACCTTTAGGGAGTTTTCTTAAACGATCACTCTGGTGCGGGTGT
TGTTTTTTGTTTTAAATAGCTTTGCAGTGAAAGCTTTTCATGACCATACAAATTATCTTTTTTCTTCCTATTTCT
TGTAGAGGTTTTTTTCTCCTTGTCTTAAGGTCATAAAAATATTGTTATGTGGGAAAAAAAAAAAAAAAAAAAAA
A

1452/6881
FIGURE 1349

MRGPSGALWLLLALRTVLGGMEVRWCATSDPEQHKCGNMSEAFREAGIQPSLLCVRGTSADHCVQLIAAQEADAI
TLDGGAIYEAGKEHGLKPVVGEVYDQEVGTSYYAVAVVRRSSHVTIDTLKGVKSCHTGINRTVGWNVPVGYLVES
GRLSVMGCDVLKAVSDYFGGSCVPGAGETSYSESLCRLCRGDSSGEGVCDKSPLERYDYSGAFRCLAEGAGDVA
FVKHSTVLENTDESPSRRQTWTRSEEEEGECPAHEEARRTMRSSAGQAWKWAPVHRPQDESDKGEFGKRAKSRDM
LG

1453/6881

FIGURE 1350

GGGCGCCGCGGGGCGGAAGACGAGGGCGGCGAGGTCGGGTTCGCGGCGCTTGGAGAAGATCGTGCTGCGGCGGGCT
GCTGGCCGCCCTGCTGCACAGCCCGCAGCTGGTGGAACGTCTGTCAGAGTCGCGGCCTATCCGACGTGCGGCGCA
GCTCACGGCCTTCGCACTGCTGCAGGCCCAGCTGCGGGGCCAGGACGCGGCCCCGCGCCTGCAGGACCTCGCGGC
TGGGCCCCGTGGGCTCCCTGTGCCGCCGCGCTGAGCGATTTAGAGACGCCTTCACCCAGGAGCTACGCCGCGGCCT
CCGAGGCCGCTCGGGGCCACCACCAGGTAGCCAGAGGGGCCCTGGCGCAAACATTTTAATCCTGGGCTGTGCGGGG
CCGAGGCCGCTTGCTTTTCCTTCGCGGCTCTACAGTGGCATCAATGTGGAGGGGTCATTCCGGGCACTGCGCGCG
GCTTCGAATCCCGACTGGGATTGTTGGCCTGCAGACATCCACGCATAAGAGCCTAGGCCAGACCGCCCCGCTCCG
TTGAAGTCTTGATGATTGGACAAGACACAGTGTGGAGACAGCCCTAAGCCTAACAGAGATGAAGGTAGGCTGGGTC
CAGACACGGCACCTACGGAGAGCCACGGACCGAAGCCAGAGAGCCTTTCCTCTGCAAGTGGGACTGAAACTCTTG
ACAGATGCTGCTCAATCTGACTGGTATAGCAGGACAGTTAATTCCAGGGACGATATGGATGAAAAGACAACCCTA
CAGCTGCCAAATTCCTTTGATTAAATGTGTGAGCTGGTTGATAGGCATGAGTGTGATACTTCTCAGGCAAGATGT
GTTAAGAATACCGGGGACTGTAGGCCTATGGTAATAATAAACACGTATTTTATGAAATGA

1454/6881
FIGURE 1351

MVLRRLAALLHSPQLVERLSESRPIRRAAQLTAFALLQAQLRGQDAARRLQDLAAGPVGSLCRRRAERFRDAFTQ
ELRRGLRGRSGPPFGSQRGPGANI

1455/6881
FIGURE 1352

ATGCCTGTCTTCATCTTGAAAGAAAAGCTCCAGGTCCTTCTCCAGCCACCCAGCCCCAAGATGGTGATGCTGCT
GCTGCTGCTTTCCGCACTGGCTGGCCTCTTCGGTGCGGCAGAGGGACAAGCATTTCATCTTGGGAAGTGCCCCAA
TCCTCCGGTGCAGGAGAATTTTGACGTGAATAAGTATCTCGGAAGATGGTACGAAATTGAGAAGATCCCAACAAC
CTTTGAGAATGGACGCTGCATCCAGGCCAACTACTCACTAATGGAACCGGAAAGATCAAAGTGTTAAACCAGGA
GTTGAGAGCTGATGGAAGTGTGAATCAAATCGAAGGTGAAGCCACCCAGTTAACCTCACAGAGCCTGCCAAGCT
GGAAGTTAAGTTTTCTGGTTTATGCCATCGGCACCGTACTGGATCCTGGCCACCGACTATGAGAAGTATGCCCT
CGTGTATTCCTGTACCTGCATCATCCAACCTTTTTCAGGTGGATTTTGCTTGGATCTTGGCAAGAAACCCTAATCT
CCCTCCAGAAACAGTGGACTCTCTAAAAAATATCCTGACTTCTAATAACATTGATGTCAAGAAAATGACGGTCAC
AGACCAGGTGAACTGCCCCAAGCTCTCGTAAACCAGGTTCTACAGGGAGGCTGCACCCACTCCATGTTACTTCTGC
TTCGCTTTCCCTACCCCAACCCCCCCCCATAAAGACAAACCAATCAACCACGACAAAGGAAGTTGACCTAAACAT
GTAACCATGCCCTACCCTGTTACCTTGCTAGCTGCAAAATAAACTTGTTGCTGACCTGC

1456/6881
FIGURE 1353

MVMLLLLLLSALAGLFGAEGQAFHLGKCPNPPVQENFDVNKYLGRWYEIEKIPTTFENGRCIQANYSLMENGKIK
VLNQELRADGTIVNQIEGEATPVNLTEPAKLEVKFSWFMPSPAPYWILATDYENYALVYSCTCIIQLFHVDFAWILA
RNPNLPPETVDSLKNILTSNNIDVKKMTVTDQVNCPKLS

1457/6881
FIGURE 1354

GC GCGAGTGGGAGGTGGCAGGCCTGCGACTCCGGCCTTGTCCGCGCCCGCTCTCGGCGCGACGTCTCCAGCCATG

AACCGGTTTTGGTACCCGGTTGGTGGGAGCCACGGCGACTTCTTCGCCGCCGCCGAAGGCCCGCAGCAATGAAAC
CTCGACAAAATAGATATGTCTTTGGATGATATCATCAAGTTGAATCGAAAGGAAGGGAAGAAGCAGAATTTTCCA
AGACTAAATAGAAGACTCCTCCAGCAAAGTGGTGCCAGCAATTCAGGATGAGAGTGCGATGGGGAATCCAACAG
AATTCTGGTTTTGGTAAGACTAGTCTGAATCATAGAGGAAGAGTAATGCCTGGAAAGAGACGTCCTAATGGAGTT
ATCACTGGCCTTGCAGCTAGGAAAACGACTGGAATTCGAAAAGGAATTAGTCCTATGAATCGTCCACCTCTAAGT
GACAAGAATATAGAACAATATTTTCCAGTGTTAAAAAGGAAGGCAAACCTTCTGAGACAAAATGAAGGGCAGAGG
AAACCAGTAGCAGTTCTCAAGAGACCTAGCCAGCTAAGCAGAAAAAATAACATTCCAGCTAATTTTACCAGGAGT
GGAAATAAATTAAATCATCAGAAAGATACTCGTCAGGCAACTTTTCTTTTCAGAAGAGGCCTGAAGGTGCAGGCC
CAGTTGAATACAGAACAACCTGCTAGACGATGTAGTAGCAAAGAGAACTCGTCAATGGCGGACTTCCACCACAAAT
GGAGGGATTTTGA CTGTATCTATTGACAATCCTGGAGCAGTGCAATGCCCAGTAACTCAGAAACCACGATTAAC
CGTACTGCTGTACCTTCATTTTTTAACAAAGCGGGAGCAAAGTGACGTCAAGAAAGTTCCTAAAGGTGTTCCCTG
CAGTTTGACATAAACAGTGTCGGAAAAACAGACAGGGATGACGTTGAATGAGCGGTTTGGGATCCTGAAGGAACAA
AGAGCCACTCTCACATACAACAAAGGGGGAAGCCGCTTTGTACCGTGGGATTAGGTCCCATGTCAAAGGAACCTTT
TGAGTGATGACTCTGAGAAGTTGAATTGCTTGAAGAGTTCATCACGGAAATTCAAGAACTTTACTTCAAATAT
TCACAAGGCTAAATAACTCTTATTTTTATTTTTGAAGTTTTTTTTTTTTTAAAAAAGCTATAAAATAATG
CCCTGAAAGAATAATAGGGATTATACCTGTCTGTTCTTAAAGATTTTCATGGTTGGCTCAGACAGAACAATCATCT
GTTTGACTTCTTTGGTTTCTCATGCAGCAGAAGGAAGACAGAAGGATAGAAATTGATTATTTTTATGATAGCGGT
ATTCAGGATCTCATCACCTTTGCCCCGTGTTTTAGACTTTGTTCATGGTAAATCCTGGTCTTCATAAACATGAGTAG
GTCCCTTGCGTTGCTGTCACTTGCCCTTTAATAGTGTGATGTAGTCAGTGCCGTTGCCTTTTCTTCATTAGAGAC
ACAGAACAATGTATTAGAATTTCCAGCTGTGGGTTTGAAGACTTAGGGGGACATCCAGAACGTGCTTCCTCTTTC
AGACGGTGTAAGTCCCCTGGAATTACACAGCTTTTAGTGCTGAGCTTTTAACAGGAAATGTGGCCCTAGGTATTA
GTCTTAGTTTTAAATGTTGGTGTTTAGAGACTGTAAATGCATATTCACAAAGTTATCTGATAGGGCCTTGGAGGA
GAAGGTCCAGTTTTTAAAAATGACAGTTTGTGTTTAATAAATGAAGGCATGAGAGGAAGTAAGTAGCAAGTTGA
GGACAGGTAGTTGAGATGAACACTTCAAACCCCTGGTTATAGATGTACTGTTTGATGTAGCATAGTCTTGAGT
CTAGCGTCCACAAAGAATTATTCAAATGATATTTAGAAGAATTATACTATTACATTGAATGGAGTCCCTTGGAT
ATTTTGATAGTAAATTAATAGCCATAAAGTCCTAGACTTCTTATTTGAAGTTAAATTTCTTATTTGAAAAGTT
GAAATTTATGAGCTTTGAAGATTGCTAAATTAATAATTTATAGCTCCAAAAACAAAAATATACTTGTATATGTC
ACAGAGAAAAAAATGCAAATTTATAATAGAGTTACATTAACCTTGTTGTTTACCTTTCAGTATTCTTATAT
GGTATAAATTAAAGTTCAGGCATTTATGGGGAGAAAAGGCCCTCCCCACCGACCCGCCACCTGCCACCTCTGACG
GAGTGGGAGAAGTTAGTCTGTGCTAAGATAGTACTGAGTCCCAGATGTTGTATACTGTAAATTACAGTATAATG
CCAAATGCAGCAAATCTTCCAGCTGTACGTTACAAGTTTGGTTCATTTTGAAGCTTGACATTTTAGTTTGCCATT
ATGTTAAAAACATCTAAATAGGTGTTAGTTTCTCAGGAGTAGATTGTTAGTGTGACTTTTCCCTGTAAAGCAGAC
ATCGTTCTTGCCCTGCCCTGCATTGTATACTAGATTTTCATTGTTGTCTCTCATGCTTCTTGAGTTGCTTCATGGT
TTATGCTCGCCATGGAAAGCTATCAGTAACAGTTTCATGCTTATACCAAAGAATTAAATCTGATCTTTAATATCT
GATATTTTCTGTTACTCGTACTGATAAGGGATTATTGGAAGTCAGTCACAGAATTTGGAAATAAATTCTAGTCT
CTCCTTAGCTATTTGATGCTTTTCATATAGGCCAAGAACTCATTGCAAACATTTTGGCAAGGATGAATGCCTGT
ATTTGGTCTAGGAACAGTACATTTTAGTCTGATTTAGAATTACTGGTAGCTTATTTTAAAGCAAGGAAAAGCAGC
TGAGCTCAAGTTTGCTGTCTTTAGAATGGTTTGTGAAAATATGGTATAAAGGTGTTTTTCATTTTCTGTTCTTAC
CTATTATTGTATAGAGCTATTCATGCCATTTTTTGGGAAAACTTTTAAAAATTGCCCAAATACTGACATTGAGTG
CATTAATAACAAATTATCTTTGATACATTAACTTTTATCTTCATGCATCTGTAATTTAATTTAAGTATAAT
GTTTTGCCCTTTGGTACAATAAATAAATCTTGGTGGTCACATATTGTATATAAACAACAAATATGCTTTGT
TGAAGGAAAATTTCTTTATTGGAATGTGGTTGTAATCCTGTTCAGTTCTTAAGTTTCGGTTTTTTTTTAAAAAC
AGGATGCAACTTAACTTTTCTTTGCATCAAGGTATATGCAAAACATTGGTGCCGTGCATACCAAATGAAAGTT
TGTATTTAACGAGGAGGTGCTTTTACACTGTACTTTTTGGTGTTTTTTGGAAAAGTTACATTTAGATCTATTCTGA
AGCTGTTTCATTTTTTAACAAATAAAATGTTACAGGTTTCACATGATTTATTCTCAGCTCTAAAAAAAAAAAAAAAA
AAA

1458/6881
FIGURE 1355

MNRFGTRLVGATATSSPPPKARSNENLDKIDMSLDDI IKLNRKEGKKQNFPRLNRRLLQSGAQQFRMRVRWGIQ
QNSGFGKTSLNHRGRVMPGKRRPNGVITGLAARKTTGIRKGISPMNRPPISDKNIEQYFPVLKRKANLLRQNEGQ
RKPVAVLKRPSQLSRKNNIPANFTRSGNKLNHQKDTRQATFLFRRGLKVQAQLNTEQLLDDVVAKRTRQWRTSTT
NGGILTVSIDNPGAVQCPVTQKPRLTRTAVPSFLTKREQSDVKKVPKGVPLQFDINSVGKQTGMTLNERFGILKE
QRATLTYNKGGSRFVTVG

1459/6881
FIGURE 1356

AATCAAGAGGTTCCAATCTTCGTGTTCACTTTAAGAACACTCGTGGAAGTCTCAGGCCACCAAGGGTATGCATA
TACGAAAAGCCACGAAGTATCTGAAAGATGTCACTTTACAGAAACAGCGTGTACCATTCCGACGTTACAATGATG
GAGTTGGCAGGTGTGCGCAGGCCAAGCAGTGGGGCTGGACACAAGGTCGGTGGCCCAGAAAGAGTGCTGAATTCT
CTGGTCATTGAGCATATCCAAGTGAACAAAGCACCTGAGATGTGCCGCCGGACCTACAGAGCTCATGGTCGGATT
AACCATAACATGAGCTCTCCCTGCCACATTGAGATGATCCTTATGGAAAAGGAACAGATTGTTTCCTAAACCAGAA
GAGGAGGTTGCCCAGAAGAAAAAGATATCCCAGAAGAACTGAAGAAACAAAACTTACGGCACGGGAGTAAATT
CAGCATTAAAATAAATGTAATTAAAAGG

1460/6881
FIGURE 1357

MSLYRNSAYHSDVTMVELASVRRPSSGAGHKVGGPKRVLNSLVIEYIQVNKAPKMLRRTYRAHGRINSYMSSPWH
IEMILTEKEQIVPKPEKEVAQKKKISQKKLKKQKL MARK

1461/6881
FIGURE 1358

TGTAGATTAGCTGTGAATATCTTGACTCCTTTAAGGTAATAAGGCTTTTGTTTGTTTTATCTTTCACAGCTAGA
AAATTATGGCATGCCGTTTAGCAGAACTGAAGATGGGAAGATTATCAGCGTGCATTTGGTGGACAGAGCCTCAA
GTTTGGAAGGGCAGGCAGGCCCATCGGTGCTGCTGTGTGGCTGATCGGACCGGCCACTCAATATTGCACACCTC
ATATGGGAGGTCTCTGAGATATGATACCAGCTGTTTTGTGGAGTATTTTGCCTTGGATCTCCTGATAGAGAACAG
GGAGTGCCGTGGTGTTCATTGCACTGTGCATAGAGGACGGGTCCATCCATCACATAAGAGCAAAGAACACTGTTGT
TGCCACAGGGTAGG

1462/6881
FIGURE 1359

TTTCCGTGCTACCTGCAGAGGGATCCATACGGCGTTGTTCTGGATTCCCGTCATAACTTAAAGGGAACTTTTCAC
AATGTCCGGAGCCCTTGATGTCCTGCAGATGAAGGAGGAGGATGTCCTTAAGTTCCTTGCAGCAGGAACCCACTT
AGGTAGCACCAATCTTGACTTCCAGATGGAACAGTACATCTATAAAAGGAAAAGTGATGGCGTCTATATCATAAA
TCTGAAGAGGACCTGGGAGAAGCTTCTGCTGGCAGCTTGTGCTGTTGTTGCCATTGAAAACCCTGCTCATGTCAG
TGTTAAATCCTCCAGGAATACTGGCCAGAGGGCTGTGCTGAAGTTTGCTGCTGCCACTGGAGCCACTCCAATTGC
TGGCCGCTTCACTCCTGGAACCTTCACTAACGAGATCCAGGCAGCCTTCTGGGAGCCACGGCTTCTTGTGGTTAC
TGATCCCAGGGCTGACCACCAGCCTCTCACAGAGGCATCTTAAGTTAACCTACCTACCATTGCTCTGTGTAACAC
AGATTCTCCTCTGTGCTGTGTGGACATTGCCATCCCATGCAACAGCAAGGGAGCTCACTCAGTGGGTTTGATGTG
GTGGATGCTGGCTTGGGAAGTTCTGCGCATGCATGGCACCATTTCCCGTGAACACCCATGGGAGGTCATGCCTGA
TCTCTACTTCTACAGAGATCCTGGAGAGATTGAAAAAGAAGAGTAGGCTGCTGCTGAAAAGGCAGTGACCGAGGA
GGAATTTCAGGGTGAATGGACTGCTCCAGCTCCTGAGTTCAGTCTACTCAGCCTGAGGTTGCAGACTGGTCTGA
AGGTGTGCAGGTGCCCTCTGTGCCATATTCAGCAGTTCCTACTGAAGACTGGAGCGCTCAGCCTGCCATAGAAGA
CTGGTCTGCAGCTCCCACTGCTCAGGCCACTGAATGTGTAGGAGCAACCACTGAATGGTCTTAAGCTGTTCTTGC
ATAGGCTCTTAAGCAACATGGAAAAATGGTTAATGGAAAATAAACATCAGTTTCT

1463/6881
FIGURE 1360

GGGAAACTTTCAACAATGTCCGGAGCCCTTGATGTCCTGCAGATGAAGGAGGAGGATGTCCTTAAGTTCCTTGCGAG
CAGGAACCCACTTAGGTAGCACCAATCTTGACTTCCAGATGGAACAGTACATCTATAAAAGGAAAAGTGATGGCG
TCTATATCATAAATCTGAAGAGGACCTGGGAGAAGCTTCTGCTGGCAGCTTGTGCTGTTGTTGCCATTGAAAACC
CTGCTCATGTCAGTGTTAAATCCTCCAGGAATACTGGCCAGAGGGCTGTGCTGAAGTTTGCTGCTGCCACTGGAG
CCACTCCAATTGCTGGCCGCTTCACTCCTGGAACCTTCACTAACGAGATCCAGGCATCTTAAGTTAACCTACCTA
CCATTGCTCTGTGTAACACAGATTCTCCTCTGTGCTGTGTGGACATTGCCATCCCATGCAACAGCAAGGGAGCTC
ACTCAGTGGGTTTGATGTGGTGGATGCTGGCTTGGGAAGTTCTGCGCATGCATGGCACCATTTCCTCGTGAACACC
CATGGGAGGTCATGCCTGATCTCTACTTCTACAGAGATCCTGGAGAGATTGAAAAGAAGAGTAGGCTGCTGCTG
A

1464/6881
FIGURE 1361

ATCTGCAGTGGAGCCGCCACCAAAATGCAGATTTTCGTGAAAACCCTTACGGGGAAGACCATCACCCCTCGAGGTT
GAACCCCTCGGATACGATAGAAAATGTAAAGGCCAAGATCCAGGGTAAGGAAGGAATTCCTCCTGATCAGCAGAGA
CTGATCTTTGCTGGCAAGCAGCTGGAAGATGGACGTACTTTGTCTGACTACAATATTCAAAGGAGTCTACTCTT
CATCTTGTGTTGAGACTTCTGGTGGTGCTAAGAAAAGGAAGAAGAAGTCTTACACCACTCCCAAGAAGAATAAGC
ACAAGAGAAAAGAAGGTTAAGCTGGCTGTCCTGAAATACTATAAGGTGGATGAGAATGGCAAAATTAGTCGCCTTC
GTCGAGAGTGCCCTTCTGATGAATGTGGTGCTGGGGTGTTTATGGCAAGCCACTTTGACAGACATTATTGTGGCA
AATGTTGTCTGACTTACTGCTTCAACAAACCAGAAGACAAGTAACTGTATGAGTTAATAAAAGACATGAACTAAA
AAAAA

1465/6881
FIGURE 1362

MQIFVKTLTGKTTITLEVEPSDTIENVKAKIQGKEGIPPDQQRLLIFAGKQLEDGRTLSDYNIQKESTLHLVLRLLV
VLRKGRSLTPLPRRISTRERRLSWLS

1466/6881
FIGURE 1363

CCCGCCCGCTAATGTTTTGGCCGCTTCAAGATGGCGGTGCAGGAGTCGGCGGCTCAGTTGTCCATGACCCTGAAG
GTCCAGGAGTACCCGACCCTCAAGGTGCCCTACGAGACGCTGAACAAACGCTTTCGCGCCGCTCAGAAGAACATT
GACCGGGAGACCAGCCACGTCACCATGGTGGTGGCCGAGCTGGAGAAGACGTTGAGCGGCTGCCCCGCCGTGGAC
TCCGTGGTCAGCCTGCTGGACGGCGTGGTGGAGAAGCTCAGCGTCCTCAAGAGGAAGGCGGTGGAATCCATCCAG
GCCGAGGACGAGAGCGCCAAGCTGTGCAAGCGCCGGATCGAGCACCTCAAAGAGCATAGCAGCGACCAGCCCGCG
GCGGCCAGCGTGTGGAAGAGGAAGCGCATGGATCGCATGATGGTGGAGCACCTGCTGCGTTGCGGCTACTACAAC
ACGGCTGTCAAGCTGGCGCGCCAGAGCGGCATCGAGGACCTAGTGAATATTGAGATGTTCTGACGGCCAAAGAG
GTGGAGGAGTCCCTGGAGAGGCGTGAGACGGCCACCTGCCTGGCCTGGTGCCATGACAACAAGTCCCGGCTCCGG
AAGATGAAGAGCTGCCTGGAGTTTCAAGCTCAGAATCCAGGAGTTCATTGAACTCATCCGGCAGAATAAGAGACTG
GACGCTGTGAGACATGCAAGAAAGCACTTCAGCCAAGCAGAAGGGAGCCAGCTGGACGAGGTGCGCCAGGCCATG
GGCATGCTGGCCTTCCCGCCCGACACGCACATCTCCCGTACAAGGACCTTCTGGACCCTGCACGGTGGCGGATG
CTGATCCAGCAGTTCGGGTACGACAACCTACCGACTACACCAGCTGGGAAACAATTCTGTGTTTACCCTCACCCCTG
CAGGCTGGCCTCTCAGCCATCAAGACACCACAGTGCTACAAGGAGGACGGCAGCTCCAAGAGCCCTGACTGCCCT
GTGTGCAGCCGCTCCCTGAACAAGCTGGCGCAGCCCTGCCCATGGCCCACTGTGCCAACTCCCGCCTGGTCTGC
AAGATTTCTGGCGACGTGATGAACGAGAACAATCCGCCCATGATGCTGCCCAACGGCTACGTCTACGGCTACAAT
TCTCTGCTTTCTATCCGTCAAGATGATAAAGTCGTGTGCCCCGAGAACCAGAAAGTCTTCCACTTCTCACAAGCC
GAGAAGGTGTACATCATGTAGGCCCCACGTGCTGAAGCGCACGCTCGGGGACGGGCTGCAGTGGGCGGGGAGGC
CACGCCTTCCTCCTGTCCACGCTCCAGCCTGCCGCGGCGTTTTCTGTTTCTTGCGACCAAAGATCCGTGAGCAAC
GATAAATACTCTTAGGAAGAGAGAAAATAAGGTTTTATAAGTTTGTACTTGAAAACATTTGGATTGGTAGGATTT
TGTAACACGTCAACCATTTGATGCTTCTGAAAAGTACTTTCAACTTGCGAAGGAACTCTTCTTTAAAGACTGAC
CTAAACACCGAGGGAACTTAAGAACGTTTAAAATATAGGAGTCCGTGATTTCCCTGTGTTTTAGTTTCTTTCC
TTCTGTGAACGATGAGACTTGGAGAACGGGCTGGTCCTTCACCACTTCTGTTGGCCCTGGCCTGGCCGGGGAAG
GTGGCAGCGGCACCGGACTGACCTGCAGTGACCCGCGATGCCGCGCCACGAGGGACACTTATGGCTTCATTGAG
AGCTGCTGCCAAAACGCTGGCGCCGCCACCGTCGGGGGCTGGCTTCGAGGACGCCCGCCTGCCTCGCGGGTCTGT
GTCCGCGGGACTGTGTTTCGTACGTGCATAGTTTCGATATCACATCGCGGGGCTGTGTTTCGTAGCTGCGTCGTTTC
GATATCACACCCTCTGTGTGCCGCCTTACTTCCTGCTTCGAGAATGTATAACGTGGAAATCCACGGGACCAAATT
TCTGCAGAGGCCTTGCCGGATGGTTCCATAACTGTAGAGTCTAATTGCTATCCATTACAGAAATTAATCGTTTCA
TTGAAAGAAGTACTGATGACTTTTTCAAACAAATGAACCACCGTAGCTGACAGAGAACCGTATCGTAGAGGTTTG
TAGTTAGTGCTTATTTTTGCATGTTGATGTTGACTAGCTAATAAACTGTAAATGTAAACCATGCGAATAAAATGG
TTTTCTATTTCTC

1467/6881
FIGURE 1364

CCCCAGGTCCGGACAGGCCGAGATGACGCCGAGCCCCCTGTTGCTGCTCCTGCTGCCGCCGCTGCTGCTGGGGGC
CTTCCCGCCGCGCCGCCGCCGAGGCCCCCAAGATGGCGGACAAGGTGGTCCACGGCAGGTGGCCCGGCT
GGGCGCACTGTGCGGCTGCAGTGCCAGTGAGGGGGACCCGCCCGCTGACCATGTGGACCAAGGATGGCCG
CACCATCCACAGCGGCTGGAGCCGCTTCCGCGTGCTGCCGAGGGGCTGAAGGTGAAGCAGGTGGAGCGGGAGGA
TGCCGGCGTGACGTGTGCAAGGCCACCAACGGCTTCGGCAGCCTGAGCGTCAACTACACCCTCGTCGTGCTGGA
TGACATTAGCCCAGGGAAGGAGAGCCTGGGGCCCGACAGCTCCTCTGGGGGTCAAGAGGACCCCGCCAGCCAGCA
GTGGGCACGACCGCGCTTCACACAGCCCTCCAAGATGAGGCGCCGGGTGATCGCACGGCCCGTGGGTAGCTCCGT
GCGGCTCAAGTGCGTGCCAGCGGGCACCTCGGCCCGACATCACGTGGATGAAGGACGACCAGGCCTTGACGCG
CCCAGAGGCCGCTGAGCCAGGAAGAAGTGGACACTGAGCCTGAAGAACCTGCGGCCCGAGGACAGCGGCCAA
ATACACCTGCCGCGTGTCGAACCGCGGGGCGCCATCAACGCCACCTACAAGGTGGATGTGATCCAGCGGACCCG
TTCCAAGCCCGTGCTCACAGGCACGCACCCCGTGAACACGACGGTGGACTTCGGGGGGACACGTCCTTCCAGTG
CAAGGTGCGCAGCGACGTGAAGCCGGTGATCCAGTGGCTGAAGCGCGTGAGTACGCGCCGAGGGCCGCCACAAC
TCCACCATCGATGTGGGCGGCCAGAAAGTTTGTGGTGCTGCCACGGGTGACGTGTGGTCGCGGCCCGACGGCTCC
TACCTCAATAAGCTGCTCATCACCCGTGCCCGCCAGGACGATGCGGGCATGTACATCTGCCTTGCGCCAAACACC
ATGGGCTACAGCTTCCGCAGCGCCTTCCTCACCGTGCTGCCAGACCCAAAACCGCCAGGGCCACCTGTGGCCCTCC
TCGTCTCGGCCACTAGCCTGCCGTGGCCCGTGGTCATCGGCATCCCAGCCGGCGCTGTCTTCATCCTGGGCACC
CTGCTCCTGTGGCTTTGCCAGGCCCAGAAGAAGCCGTGCACCCCGCGCCTGCCCTCCCTGCCTGGGCACCCG
CCGCCGGGGACGGCCCGCGACCGCAGCGGAGACAAGGACCTTCCCTCGTTGGCCGCCCTCAGCGCTGGCCCTGGT
GTGGGGCTGTGTGAGGAGCATGGGTCTCCGGCAGCCCCCAGCACTTACTGGGGCCAGGCCAGTTGCTGGCCCT
AAGTTGTACCCCAAACCTCTACACAGACATCCACACACACACACACACTCTCACACACACTCACACGTGGAG
GGCAAGGTCCACCAGCACATCCACTATCAGTGCTAGACGGCACCCGTATCTGCAGTGGGCACGGGGGGGCGGCCA
GACAGGCAGACTGGGAGGATGGAGGACGGAGCTGCAGACGAAGGCAGGGGACCCATGGCGAGGAGGAATGGCCAG
CACCCAGGCAGTCTGTGTGTGAGGCATAGCCCTGGACACACACACACAGACACACACTGCCTGGATGCATG
TATGCACACACATGCGCGCACACGTGCTCCCTGAAGGCACACGTACGCACACACGCACATGCACAGATATGCCG
CTGGGCACACAGATAAGCTGCCCAAATGCACGCACACGCACAGAGACATGCCAGAACATAAAGGACATGCTGCC
TGAACATACACACGCACACCCATGCGCAGATGTGCTGCCTGGACACACACACACACACGGATATGCTGTCTGGAC
GCACACACGTGCAGATATGGTATCCGGACACACACGTGCACAGATATGCTGCCTGGACACACAGATAATGCTGCC
TTGACACACACATGCACGGATATTGCCTGGACACACACACACACACGTGTGCACAGATATGCTGTCTGGACACGC
ACACACATGCAGATATGCTGCCTGGACACACACTTCCAGACACACGTGCACAGGCGCAGATATGCTGCCTGGACA
CACGCAGATATGCTGTCTAGTCACACACACACGCAGACATGCTGTCCGGACACACACACGCATGCACAGATATGC
TGTCCGGACACACACACGCACGCAGATATGCTGCCTGGACACACACAGATAATGCTGCCTCAACACTCACACA
CGTGCAGATATTGCCTGGACACACACATGTGCACAGATATGCTGTCTGGACATGCACACACGTGCAGATATGCTG
TCCGGATACACACGCACGCACACATGCAGATATGCTGCCTGGGCACACACTTCCGGACACACATGCACACACAGG
TGCAGATATGCTGCCTGGACACACGCAGACTGACGTGCTTTTGGGAGGGTGTGCCGTGAAGCCTGCAGTACGTGT
GCCGTGAGGCTCATAGTTGATGAGGGACTTTCCCTGCTCCACCGTCACTCCCCCAACTCTGCCCGCCTCTGTCCC
CGCCTCAGTCCCCGCCTCCATCCCCGCTCTGTCCCCTGGCCTTGGCGGCTATTTTTTGCCACCTGCCTTGGGTGC
CCAGGAGTCCCCTACTGCTGTGGGCTGGGGTTGGGGGCACAGCAGCCCCAAGCCTGAGAGGCTGGAGCCCATGGC
TAGTGGCTCATCCCCACTGCATTCTCCCCCTGACACAGAGAAGGGGCTTGGTATTTATATTTAAGAAATGAAGA
TAATATTAATAATGATGGAAGGAAGACTGGGTTGCAGGGACTGTGGTCTCTCCTGGGGCCCCGGGACCCGCTGGT
CTTTCAGCCATGCTGATGACCACACCCCGTCCAGGCCAGACACCACCCCCACCCACTGTGCTGGTGGCCCCAG
ATCTCTGTAATTTTATGTAGAGTTTGTAGCTGAAGCCCCGTATATTTAATTTATTTTGTAAACATGAAAGTGCAT
CCTTCCCTCC

1468/6881
FIGURE 1365

CCAAAGATGTTGACCAGGAAGATCAAGCTGTGGGACATCAACGCCCACATCACCTGCCGCCTGTGCAGCGGGTAC
CTCATCGACGCCACCACGGTGACCGAGTGTCTGCACACCTTCTGCAGGAGCTGCCTGGTGAAGTACCTGGAGGAG
AACAAACACCTGCCCCACCTGCAGGATTGTGATCCACCAGAGCCACCCCTGCAGTACATCGGTCATGACAGAACC
ATGCAAGATATTGTTTACAAATTGGTACCAGGCCTCCAAGAAGCGGAAATGAGAAAGCAGAGGGAGTTCTATCAC
AAATTGGGCATGGAGGTGCCGGGAGACATCAAGGGGGAGACCTGCTCTGCAAAACAGCACTTAGATTCCCATCGG
AATGGTGAAACCAAAGCAGACGACAGTTCAAACAAAGAGGCCGCGGAGGAGAAGCCGGAGGAGGACAACGACTAC
CACCGCAGCGACGAGCAGGTGAGCATCTGCCTGGAGTGTAACAGCAGCAAACCTGCGCGGGCTGAAGCGGAAGTGG
ATCCGCTGCTCAGCCCAGGCGACCGTCTTGCACTCTGAAGAAGTTCATCGCCAAAAAACTCAACCTTTCATCCTTT
AACGAGCTGGACATTTTATGCAACGAGGAGATCCTGGGCAAGGACCACACACTCAAGTTCGTGGTTGTCACTAGG
TGGAGATTCAAGAAGGCGCCGCTCCTGCTGCACTACAGACCCAAGATGGACTTGCTGTGAATGGTGCCACACAGC
GCCACAGACTGGGCCCTCGCACCCCTGGGTGCTCCCGGCCGCGCCTTAAGAACATTGCCTCTGGGTGTCATG
TGGACCAGACTTCTGAATAGAGAATATTTATAACTTTTGTATGAGAGAG

1469/6881
FIGURE 1366

GGGCTTGTGCGGCATCCTGCTCCGTCTGCAGGTTGTGCTTCCGGTGCGGAGGTCATGGACAAAATGGTGCCACCG
GTGCAGGICTCTCCGCTCATCAAGCTCGGCCGCTACTCCGCCCTGTTCCCTCGGTGTGGCCTACGGAGCCACGCGC
TACAATTACCTAAAACCTCGGGCAGAAGAGGAGAGGAGGATAGCAGCAGAAGAGAAGAAGAAGCAGGATGAACTG
AAACGGATTGCCAGAGAATTGGCAGAAGATGACAGCATATTAAAGTGAGTGACCCTGCGACCCACTCTTTGGACC
AGCAGCGGATGAATAAAGCTTCCTGTGTTGTGTGAT

1470/6881
FIGURE 1367

MVPPVQVSPLIKLGRYSALFLGVAYGATRYNYLKPRAEERRIAAEEKKKQDELKRIARELAEDDSILK

1471/6881
FIGURE 1368

GGAGTGGCAGCCGGAGTCTGAACTGTCCTGGGGGACCAAGCAGGAGCTTAAGATGGGCAAGACCTGGGGCCCTGG
GCAGACGCATCAAAGCAGGCAGAAGCAGGCATGGCCAGCAGGAAGACCAAGAAGAAGGAAGGGGGTGCCCTCCGG
GCCCAGAGAGCCTCATCCAATGTCTTCTCCAACTTGAGCAGACTCAGATCCAGGAGTTCAAGGAGGCATTCACA
CTCATGGATCAGAACCGAGATGGCTTCATTGACAAGGAGGACCTGAAGGACACCTATGCCTCCCTGGGCAAGACC
AACGTCAAGGACGACGAGCTGGACGCCATGCTCAAAGAGGCCTCGGGGGCCATCAACTTCACCATGTTTCTGAAC
CTGTTTGGGGAGAAGCTGAGCGGTACCGACGCCGAGGAGACCATTCCTAACGCCTTCAAGATGCTGGACCCGGAC
GGGAAAGGGAAAATCAACAAGGAGTACATCAAGCGTCTGCTGATGTCCCAGGCTGACAAGATGACGGCGGAAGAG
GTGGACCAGATGTTCCAGTTCGCCTCCATCGATGTGGCGGGCAACCTGGACTACAAGGCGCTCAGCTACGTGATC
ACCCACGGGGAGGAGAAGGAGGAGTGAGACCCAGCCGGGTCAATAAACCTGGACGCTTGGA

1472/6881
FIGURE 1369

MASRKTKKKKEGGALRAQRASSNVFSNFEQTQIQEFKEAFTLMDQNRDGFIDKEDLKDTYASLGKTNVKDDDEL
DAMLKEASGPINFTMFLNLFGEKLSGTDAEETILNAFKMLDPDGKGKINKEYIKRLLMSQADKMTAAEVDQMFQFASI
DVAGNLDYKALSYVITHGEEKEE

1473/6881
FIGURE 1370

CAGTAGTCCTTGGGGCGGAACTGGCCCCCGTGGCCCGGGCCGGCTCGGCCCCACCTCCGCCCGCAGGCGGTCCC
GGCCCCACGCGGGAAGGTCCTTAAGCCCGGGCGGCCGGCGGGACCGGCGGAGACCCGTGGAGGCCGCCGACG**ATGG**
CGGGGCCGACGGAGGCCGAGACGGGGTTGGCCGAGCCCCGGGCCCTGTGCGCGCAGCGGGGCCACCGCACCTACG
CGCGCCGCTGGGTGTTCCGTGCTCGCGATCAGCCTGCTCAACTGCTCCAACGCCACGATCAACTGGCTGTCACTGG
TCTACCTCGTGGTATCCACCCCATTTGGCGTGGCGGCCATCTGGATCCTGGACTCCGTGCGGCTCCGTGCGGCGC
TCGGTGTCTATAACCATCCCTGCTGGCGTCGTCTGCCTGCTGTCCACCATCTGCCTGTGGGAGAGTGTGCCCCCA
CCCCGCCCTCTGCCGGGGCTGCCAGCTCCACCTCAGAGAAGTTCCTGGATGGGCTCAAGCCGCAGCTCATGTGGA
ACAAGGCCTATGTCATCCTGGCTGTGTGCTTGGGGGGAATGATCGGGATCTCTGCCAGCTTCTCAGCCCTCCTGG
AGCAGATCCTCTGTGCAAGCGGCCACTCCAGTGGGTTTTCCGGCCTCTGTGGCGCTCTCTTCATCACGTTTGGGA
TCCTGGGGGCACTGGCTCTCGGCCCTATGTGGACCGGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGT
GCCTGTTCTCTCTGGCCTGCGTGCCCTTTGCCCTGGTGTCCAGCTGCAGGGACAGACCCCTGGCCCTGGCTGCCA
CCTGCTCGCTGCTCGGGCTGTTTGGCTTCTCGGTGGGCCCCGTGGCCATGGAGTTGGCGGTCGAGTGTTCTTCC
CCGTGGGGGAGGGGGCTGCCACAGGCATGATCTTTGTGCTGGGGCAGGCCGAGGGAATACTCATCATGCTGGCAA
TGACGGCACTGACTGTGCGACGCTCGGAGCTGTCCTTGTCCACCTGCCAGCAGGGGGAGGATCCACTTGACTGGA
CAGTGTCTCTGCTGCTGATGGCCGGCCTGTGCACCTTCTTCAGCTGCATCCTGGCGGTCTTCTTCCACACCCCAT
ACCGGCGCCTGCAGGCCGAGTCTGGGGAGCCCCCTCCACCCGTAACGCCGTGGGCGGCGCAGACTCAGGGCCGG
GTGTGGACCGAGGGGGAGCAGGAAGGGCTGGGGTCTTGGGGCCAGCACGGCGACTCCGGAGTGACGGCGAGGG
GGGCCTCGCTAGAGGACCCCAGAGGGCCCGGGAGCCCCACCCAGCCTGCCACCGAGCGACTCCCCGTGCGCAAG
GCCAGCAGCCACCGACGCGCCCTCCCGCCCCGGCAGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTTATTGACC
CGGCTGGGTCTCACTCCTCCTTCTCCTCCCCGTGGGTGATCAG**TAG**CTGAGCGCCTTGTAAGTCCAGGTTGCCCG
CCACATCGATGGAGGCGAACTGGAACATCTGGTCCACCTGCGGGCGGGGGCGAAAGGGCTCCTTGCGGGCTCCGG
GAGCGAATTACAAGCGCGCACCTGCAAAAAAAAAAAAAAAAAAAAA

1474/6881

FIGURE 1371

MAGPTEAETGLAEPRALCAQRGHRITYARRWVFLLAISLLNCSNATINWLSLVYLVVSTPFGVAAIWILDSVGLRA
ALGVYTIPAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKPQLMWNKAYVILAVCLGGMIGISASFSA
LEQILCASGHSSGFSGLCGALFITFGILGALALGPYVDRTHKFTEATKIGLCLFSLACVPFALVSQIQGQTLALA
ATCSLLGLFGFSVGPVAMELAVECSFPVGEAATGMIFVLGQAEGLIMLAMTALTVRRELSLSTCQQGEDPLD
WTVSILLMAGLCTFFSCILAVFFHTPYRRLQAESGEPPSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTA
RGASLEDPRGPGSPHPACHRATPRAQGAATDAPSRPGRLAGRVQASRFIDPAGSHSSFSSPWVIT

1475/6881
FIGURE 1372

GGCACGAGGGGTTCCGTTTCCGGAGTGAGGGGCACGCCAGGGTGTCTGAAGCTGAGACCCCGGGCTCGCAGTCGC
CCCATGAATTTTCGAGTTCCGCAACTGACGCTACTGGGCGGGGCTTCATGGCCAGGGCCTCGCTCAGGCCTAAGTT
TCCCCACCTGTGCTCAATGCACAGGTGCGGTGCCGCCTCCAGGGCCGGCCGAGAAGAGAGGGCCGACCCGCACGG
GGACTGCATCTCCCAGAGCGCCCCGCGAGCGGCCGAGCGGGGACTCCATGCCCTAGAGTGCCCCGCGGGCGGC
CGGGCGGCGGGACTCCATGTCTTAGAGTGCCCCGCGGGCGGCCGGGCGGGGACTCCATGTCTTAGAGTGCCCC
GCGGGCGGCCGGGCGGGGACTCCATGTCTTAGAGTGCCCCGCGGGCGGCCGGGCGGGGCGGCCGCCGAACCGAC
AGGTCCGGGACTGGGCGCTGCGGCCTCGTCCGCGCGCCGGGGCGGGGGCTAGCTCGACAGCTTCCCGGCGGCTG
CGCG**ATG**GACAGCCCCGAGGTGACCTTCACTCTCGCCTATCTGGTGTTCGCCGTGTGCTTCGTGTTACGCCCAA
CGAGTTCCACGCGGGCGGGGCTCACGGTGCAGAACCTGCTGTGGGCTGGCTGGGCAGCGAGGACGCCGCCTTCGT
GCCCTTCCACTTGCGCCGCACGGCCGCCACGCTGTTGTGCCACTCGCTGCTGCCGCTCGGCTACTACGTGGGCAT
GTGCCTTGCGGCTTCAGAAAAGCGGCTCCACGCCCTCAGCCAGGCCCCTGAGGCCTGGCGGCTCTTCTGTGCT
GGCCGTGACCTTCCCTCCATCGCCTGCATCCTGATCTACTACTGGTCCCCTGACCGGTGGGCTGCCACCCACT
GGCGCGCACCTTGGCCCTCTACGCCCTCCACAGTCTGGCTGGCAGGCTGTTGCCTCCTCTGTCAACACTGAGTT
CCGGCGGATTGACAAGTTTGCCACCGGTGCACCAGGTGCCCCGTGTGATTGTGACAGACAGTGGGTGATGAAGGT
AACCACCTACCGAGTGACGTGGCCAGCAGCAGGACGTGCACCTGACTGTGACGGAGTCTCGGCAGCATGAGCT
CTCGCCAGACTCGAACTTGCCCGTGCAGCTCCTCACCATCCGTGTGGCCAGCACCAACCTGCTGTGACGGCCTT
TGACATCTGGAGCTGGAGGCCTGCAT**TAG**GCTGCATGCAGACACGTGCCAGCGTGAAGCTGGTGAAGACCTGCCAG
GAGGCAGCCACAGGCGAGTGCCAGCAGTGTTACTGCCGCCCATGTGGTGCCTCACCTGCATGGGCAAGTGGTTC
GCCAGCCGCCAGGACCCCCCTGCGCCCTGACACCTGGCTGGCCAGCCGCGTGCCTGCCCCAECTGCCGCGCACGC
TTCTGCATCCTGGATGTGTGCACCGTGCCTGAGTGGGCTGGGGCCTTGAGGTGACTCTGTGTCTCCCCGCAAAG
CCACAGGGCAGGGAAGGGGGTGGCTGGGCCTCCTGGCTGGCAAAGGGCTCTACTTAAAGCACATGATGTAGAGCA
ACTCGCCTCTGCCCTGGGTCTGCAGAAGGCTGAGGACTTTTGGTTAAAAGCAATCCTCATGAAAACACCCACCC
TGCTTGGCAGCCAGGGTACAAGTCTGGGCACCTCCTCTTTGCCCTCCCTCCTGCCCCCTTCTGCTGGTGGGGC
AGATCCTGCACACACAGACACAGCGTCTGCCCCGAGCCATTCCCTGGAGACCCTGGGTCTACCCCAGGTGGTCG
TCATCTGGGCCATTTGCCCTTACTTCTCTGGAGCATACCACCCCTCAGTTACGTGCCAGACCTGGACCGCATTC
CTGCCCTGTCTTGGAGCTGGCCCCCTGGCTGCCTGGAGGACCTGGGTAGGTCTGAGGGTGGGATGGAGAAGAGG
GCACTGCTGTGGTGTGGGAGCAGTCTGGGGCTTCTGGTGGCTGTGACCAGTTGAGGGGCTGTTCTGGGTGGG
GTGGCAATGGGAGGACAGGTGAGAGCGCCCTCATTTGTGGGGCTGCCCTCCGGGTTTCTCATCCTGTCTTGGT
GCCTTTTTCTGCCCAACAAGTCCAGGGAAGGCCGAGGTCTCAGACTCCTGGGTAGGGGTGGGGGTTTGAGTTGAG
GACCAAAGTGCCATAGCGACATCCAGAACACAAGCCCACCAGGGGTCCAGCCAGGCTACCCACTCCCCTAGGGT
CTCCCAGGCTCAGAAGGGGATGCACGCCCCCTGTGGTCAAGCCTCTGGTGGGCGTCTTGCCCAGTTCTGTATGGT
TCAAGGGGAGGGGGGATGTTGGCCAGGCCCCAGGGCACAGCCCTGACACAGGTGTGGCTACTGGAGGGGCCTTCA
TACCTGCGGCCCCAAAGCCCCTGGGCTTGGCTGTTTGAGGCAGAGGTGATGGACTCCGGGGGCTGACACTTGGG
ATTTGGGAGGCTTCTAGAGCGCTCAGCAGGTGAAGGCAGCAGGGGCCATGGCCGGGAGCCAGGCTAGCTTTGA
ACTGAGTTTCAAGGGCTGCCAAAGAGGGGCAGTGGGTTGGGGTTGTTTTACTACAAAATAAGTTACTTAGTTTT
ATAAAGACAAACCGATTGTAGCCAAATGACACCATATTTAATAAAATTTAGTCTGAAGTGAAAAAAAAAAAAAA
AAAAAA

1476/6881
FIGURE 1373

MDSPEVTFTLAYLVFAVCFVFTPNEFHAAGLTVQNLLSGWLGSEDA AFVPFHLRRTAATLLCHSLLPLGYYVGMC
LAASEKRLHALSQAPEAWRLFLLLAVTLPSIACILIIYYWSRDRWACHPLARTLALYALPQSGWQAVASSVNTEFR
RIDKFATGAPGARVIVTDTWVMKVTTYRVHVAQQQDVHLTVTESRQHELSPDSNLPVQLLTIRVASTNPAVQAFD
IWSWRPA

1477/6881
FIGURE 1374

GGCGGCGGTAGCAGCCAGGCTTGGCCCCGGCGTGGAGCAGACGCGGACCCCTCCTTCCTGGCGGCGGCGGCGCG
GGCTCAGAGCCCGGCAACGGGCGGGCGGGCAGAAATGAGTCTGCAGGTCTTAAACGACAAAAATGTCAGCAATGAA
AAAAATACAGAAAATTGCGACTTCCTGTTTTCGCCACCAGAAAGTTACCGGAAGATCGTCTGTTCTTCGTGTGTCA
CAGAAAAGAAAATGTGCCACCCAAGAACCTGGCCAAAGCTATGAAGGTGACTTTTCAGACACCTCTGCGGGATCCA
CAGACGCACAGGATTCTAAGTCCTAGCATGGCCAGCAAACCTTGAGGCTCCTTTCACTCAGGATGACACCCCTTGGA
CTGGAAAACCTCACACCCGGTCTGGACACAGAAAGAGAACCAACAGCTCATCAAGGAAGTGGATGCCAAAACCTACT
CATGGAATTCTACAGAAACAGTGGAGGCTGACACCGACCTCCTGGGGGATGCAAGCCCAGCCTTTGGGAGTGGC
AGCTCCAGCGAGTCTGGCCCAGGTGCCCTGGCTGACCTGGACTGCTCAAGCTCTTCCAGAGCCCAGGAAGTTCT
GAGAACCAAATGGTGTCTCCAGGAAAAGTGTCTGGCAGCCCTGAGCAAGCCGTGGAGGAAAACCTTAGTTCTCTAT
TCCTTAGACAGAAGAGTGACACCCGCCTCTGAGACCCTAGAAGACCCTTGCAAGGACAGAGTCCCAGCACAAAGCG
GAGACTCCGCACGGAGCCGAGGAAGAATGCAAAGCGGAGACTCCGCACGGAGCCGAGGAGGAATGCCGGCACGGT
GGGTCTGTGCTCCCGCAGCAGTGGCCACTTCGCCTCCTGGTGCAATCCCTAAGGAAGCCTGCGGAGGAGCACCC
CTGCAGGGTCTGCCTGGCGAAGCCCTGGGCTGCCCTGCGGGTGTGGGCACCCCCGTGCCAGCAGATGGCACTCAG
ACCCTTACCTGTGCACACACCTCTGCTCCTGAGAGCACAGCCCCAACCAACCACCTGGTGGCTGGCAGGGCCATG
ACCCTGAGTCCTCAGGAAGAAGTGGCTGCAGGCCAAATGGCCAGCTCCTCGAGGAGCGGACCTGTAAAACCTAGAA
TTTGATGTATCTGATGGCGCCACCAGCAAAAGGGCACCCCCACCAAGGAGACTGGGAGAGAGGTCCGGCCTCAAG
CCTCCCTTGAGGAAAGCAGCAGTGAAGGAGCAAAAGGGCCCCGAGGAGGTGGAGGAGGACGACGGTAGGAGCGGA
GCAGGAGAGGACCCCCCATGCCAGCTTCTCGGGGCTCTTACCACCTCGACTGGGACAAAATGGATGACCCAAAC
TTCATCCCGTTTCGAGGTGACACCAAGTCTGGTTGCAGTGAAGGCCAGCCCCCAGAAAGCCCTGAGACCAGGCTG
GGCCAGCCAGCGGTGAACAGTTGCATGCTGGGCCTGCCACGGAGGAGCCAGGTCCCTGTCTGAGCCAGCAGCTG
CATTAGCCTCAGCGGAGGACACGCCTGTGGTGCAGTTGGCAGCCGAGACCCCAACAGCAGAGAGCAAGGAGAGA
GCCTTGAACCTCTGCCAGCACCTCGCTTCCACAAGCTGTCCAGGCAGTGAAGCAGTGGCCACCCATCAGCAGGGG
CAGCCTGCCTTGAGCTGAAAGAGGAGAGCTTCAGAGACCCCGCTGAGGTTCTAGGCACGGGCGCGGAGGTGGAT
TACCTGGAGCAGTTTGAACTTCCTCGTTTAAGGAGTCGGCCTTGAGGAAGCAGTCCTTATACCTCAAGTTCGAC
CCCCCTCCTGAGGGACAGTCTTGGTAGACCAGTGGCCGTGGCCACCGAGACCAGCAGCATGCACGGTGCAAATGAG
ACTCCCTCAGGACGTCCGCGGGAAGCCAAGCTTGTGGAGTTCGATTTCTTGGGAGCACTGGACATTCTGTGCCA
GGCCACCCCCAGGTGTTCCCGCGCCTGGGGGCCACCCCTGTCCACCGGACCTATAGTGGACCTGCTCCAGTAC
AGCCAGAAGGACCTGGATGCAGTGGTAAAGGCGACACAGGAGGAGAACCAGGAGCTGAGGAGCAGGTGTGAGGAG
CTCCACGGGAAGAACCTGGAACTGGGGAAGATCATGGACAGGTTTGAAGAGGTTGTGTACCAGGCCATGGAGGAA
GTTTCAAGCAGAAGGAACTTTCCAAAGCTGAAATCCAGAAAGTTCTAAAAGAAAAAGACCAACTTACCACAGAT
CTGAACTCCATGGAGAAGTCCTTCTCCGACCTCTTCAAGCGTTTTGAGAAACAGAAAGAGGTGATCGAGGGCTAC
CGCAAGAACGAAGAGTCACTGAAGAAGTGCCTGGAGGATTACCTGGCAAGGATCACCCAGGAGGGCCAGAGGTAC
CAAGCCCTGAAGGCCACGCGGAGGAGAAGCTGCAGCTGGCAAACGAGGAGATCGCCAGGTCCGGAGCAAGGCC
CAGGCGGAAGCGTTGGCCCTCCAGGCCAGCCTGAGGAAGGAGCAGATGCGCATCCAGTCGCTGGAGAAGACAGTG
GAGCAGAAGACTAAAGAGAACGAGGAGCTGACCAGGATCTGCGACGACCTCATCTCCAAGATGGAGAAGATCTGA

CCTCCACGGAGCCGCTGTCCCCGCCCCCTGCTCCCGTCTGTCTGTCTGATTCTCTTAGGTGTATGTTCT
TTTTTCTGTCTTGTCTTCACTTTTTTTTAAACTAGATTGCTTTGAAAACATGACTCAATAAAAGTTTCCTTTC
AATTTAAAAAAA

1478/6881
FIGURE 1375

MSLQVLNDKNVSNEKNTENCDFLFSPPEVTGRSSVLRVSQKENVPPKNLAKAMKVTFQTPLRDPQTHRILSPSMA
SKLEAPFTQDDTLGLENSHPVWTQKENQQLIKEVDAKTTHGILQKPVEADTDLLGDASPAFGSGSSSESGPGALA
DLDCSSSSQSPGSSSENQMVSPGKVSQSPEQAVEENLSSYSLDRRVTPASETLEDPCRTESQHKAETPHGAEEEECK
AETPHGAEEEECRHGGVCAPAAVATSPPGAIPKEACGGAPLQGLPGEALGCPAGVGTPVPADGTQTLTCAHTSAPE
STAPTNLHVAGRAMTILSPQEEVAAGQMASSSRSGPVKLEFDVSDGATSKRAPPPRRLGERSGLKPPLRKA AVRQQ
KAPQEEVEEDDGRSGAGEDPPMPASRGSYHLDWDMDDPNFIPFGGDTKSGCSEAQPPEPETRLGQPAAEQLHAG
PATEEPGPCLSQQLHSASAEDTPVVQLAAETPTAESKERALNSASTSLPTSCPGSEPVPVTHQQGQPALELKEESF
RDPAEVLGTGAEVDYLEQFGTSSFKESALRKQSLYLKFDPLLRDSPGRVPVATETSSMHGANETPSGRPREAKL
VEFDLGLALDIPVPGPPPVGVPAPGGPPLSTGPIVDLLQYSQKDLDAVVKATQEEENRELRSRCEELHGKNLELGKI
MDRFEEVVYQAMEEVQKQKELSKAEIQKVLKEKDQLTTDLNSMEKSFSDLFKRFKQKEVIEGYRKNEESLKKCV
EDYLARITQEGQRYQALKAHAEKQLLANEEIAQVRSKAQAEALALQASLRKEQMRIQSLEKTVEQKTKENEELT
RICDDLISKMEKI

1479/6881
FIGURE 1376A

TGGTCTTGAACTCCTGACCTTGTGATCCGCTCGCCTCAGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACC
GTGCCTGTCTAGAACCACTGGTAACCTCTTAACCTGAGACAAGATTTCGCCATGTTGCCAGGCTGGTCTCGAACT
TCTGAGCTCAAGCGATCTACCTGCCTCGTCTCCCAAAGTGTTGGAATTGCAGGTGTGAGCCACTGCACCCGGCC
CTTGCTCATGTTTGAATGATAATTTACCTGGGCATAAAATCTGGACACTTGTGGTGGCAGCAGCTGTCTGCTT
TTCTGTGGAGACTGCGGGTTGCAGACACCAGCAGCCCCCTATTGCTGCACGTCAGGTGTCTCCACCTCAGTACT
GTGGACATCTCGGGCCGCATAGCCCTGTTGCGCGGGCATCCTGTGCGTTGCAGGAGATGCAGCAGCATCCATGAC
CGCAACCCATCAGAGTGTTCTAAGAACGGAAGCATCTGGGCTGGATGGAATTTAGCATCAAGCAGAGTCCCTTT
CTGTTTCAGAGTGTTGTAAAGTGCATAAAGATGAAGCAGGCACCAGAAATCCTCGGCAGTGCCAACGGGAAGACTC
CGAGCTGCGAGGTGAACCGCGAGTGTTCTGTGTTTCTCAGCAAAGCCCAGCTCTCCAGTAGCCTGCAGGAGGGGG
TCATGCAGAAGTTTAAACGGCCACGACGCCCTGCCCTTTATTCCAGCCGACAAGCTGAAAGATCTTACTTCCCGGG
TGTTTAATGGAGAACCCGGCGCACACGATGCCAAACTGCGTTTTGAGTCCCAGGAAATGAAAGGGATTGGGACAC
CCCCTAACACTACCCCTATCAAAAATGGCTCTCCAGAAATTAAGCTGAAAATCACCAAAACATACATGAATGGGA
AGCCTCTCTTTGAATCTTCCATTTGTGGTGACAGTGCTGCTGATGTGTCTCAGTCAGAAGAAAATGGACAAAAAC
CAGAAAACAAGGCGAGAAGGAACAGGAAGAGGAGCATAAAAATATGACTCCTTGCTGGAGCAGGGCCTTGTCGAAG
CAGCTCTTGTTGTCTAAGATCTCAAGTCCTTCAGATAAAAAAGATTCCAGCTAAGAAAGAGTCTTGTCAAAACACTG
GAAGAGACAAAGACCACCTGTTGAAATACAACGTTGGTGATTTGGTGTGGTCCAAAGTGTCGGGTTACCCTTGGT
GGCCTTGCGATGGTTTCTGCAGATCCACTCCTTCACAGCTATACCAAACCTTAAAGGTCAGAAAAAGAGTGACGCC
AGTATCACGTACAGTTCTTTGGTGACGCCCCAGAAAGAGCTTGGATATTTGAGAAGAGCCTCGTAGCTTTTGAAG
GAGAAGGACAGTTTGAAAAATTATGCCAGGAAAGTGCCAAGCAGGCACCCACGAAAGCTGAGAAAAATTAAGCTAT
TGAAACCAATTTAGGGAAATTGAGGGCCAGTGGGAAATGGGCATTGTTCAAGCAGAAGAAGCTGCAAGCATGT
CAGTGGAGGAGCGGAAAGCCAAGTTCACCTTTCTCTATGTGGGGACCAGCTTCATCTCAACCTCAAGTAGCCA
AGGAGGCTGGCATTGCTGCAGAGTCTTTGGGAGAAATGGCAGAATCCTCAGGAGTCAGTGAAGAAGCTGCTGAAA
ACCCCAAGTCTGTGAGAGAAGAGTGCAATCCCATGAAGAGAAGGCGGAGGGCCAACTGTGTAGCTCTGCAGAGA
CCCTGGAGAGTCACCCGACATAGGGAAGAGTACTCTCAAAGACGGCAGAGGCTGACCCCAAGAGAGGAGTAG
GGTCTCCTCCTGGGAGGAAGAAGACCACAGTCTCCATGCCACGAAGCAGGAAGGGAGATGCAGCATCCAGTTTTT
TGGTCTTCTGTCAAAAACACAGGGATGAGGTGGTAGCTGAGCACCCAGATGCTTCAGGTGAGGAGATTGAAGAGC
TGCTCAGGTACAGTGGAGTCTGCTGAGTGAGAAGCAGAGAGCACGCTACAACACCAAGTTTGCCCTGGTGGCCC
CTGTCCAGGCTGAAGAAGACTCTGGTAATGTAAATGGGAAAAAAGAAACCACACAAAGAGGATACAGGACCCTA
CAGAAGATGCTGAAGCTGAGGACACACCCAGGAAAAGACTCAGGACGGACAAGCACAGTCTTCGGAAGAGAGACA
CAATCACTGACAAAACGGCCAGAACAAGCTCTTACAAGGCCATGGAGGCAGCCTCCTCGCTCAAGAGCCAGGCAG
CAACGAAAAATCTGTCTGATGCATGTAAACCACTGAAGAAGCGAAATCGGGCTTCCACGGCAGCATCTTCAGCTC
TTGGGTTTAGCAAAAGTTCATCTCCTTCTGCATCCTTAACTGAGAATGAGGTCTCGGACAGCCCGGGAGACGAGC
CCTCGGAGTCCCCATACGAAAGTGACAGACGAAACACAACTGAAGTATCTGTCTCATCAAAAAGTCTGAGCGAG
GAGTGAAGTCCAAAAAGGAGTATGTGTGCCAGCTGTGTGAGAAAGCCGGGCAGCCTCCTGCTCTGTGAAGGACCCT
GCTGCGGAGCTTTCCACCTCGCCTGCCTTGGGCTTTCCCGGAGGCCAGAAGGGAGGTTACCTGCAGCGAGTGTG
CCTCAGGGATTCACTCATGTTTTCGTGTGTAAAGAGAGCAAGACAGATGTTAAGCGCTGTGTGGTAACTCAGTGTG
GAAAATTTTACCATGAGGCTTGTGTGAAAAAATACCCTCTGACTGTATTTGAGAGCCGAGGTTTCCGCTGCCCCC
TCCACAGCTGTGTGAGCTGCCATGCTTCCAACCCCTTCAAACCAAGGCCGTCAAAGGTAAAATGATGCGGTGTG
TCCGCTGCCCCGTTGCCTATCACAGCGGGGATGCTTGTCTGGCAGCAGGATGCTCAGTGATCGCCTCCAACAGCA
TCATCTGCACTGCCACTTCACTGCTCGGAAGGGGAAGCGACACCACGCCACGTCAACGTGAGCTGGTGTCTCG
TGTGCTCCAAAGGGGGGAGCCTTCTGTGCTGTGAGTCTGCCCAGCGGCCTTCCACCCTGACTGCCTGAACATCG
AGATGCCTGACGGCAGCTGGTTCTGCAATGACTGCAGGGCTGGGAAGAAGCTGCACTTCCAGGATATCATTGGG
TGAACTTGGGAACTACAGATGGTGGCCGGCAGAAGTTTGCCATCCCAAAAATGTTCCCCCAATATTCAGAAAA
TGAAGCACGAGATTGGAGAATTCCTGTGTTTTTCTTTGGGTCTAAAGATTATTACTGGACGCATCAGGCGCGAG
TGTTCCCGTACATGGAGGGGGACCGGGCAGCCGCTACCAGGGGGTCAGAGGGATCGGAAGAGTCTTCAAAAACG
CACTGCAAGAAGCTGAAGCTCGTTTTCTGTAAATTAAGCTTCAGAGGGAAGCCCGAGAAACACAGGAGAGCGAGC
GCAAGCCCCCACCATACAAGCACATCAAGGTGAATAAGCCTTACGGGAAAGTCCAGATCTACACAGCGGATATTT
CAGAAATCCCTAAGTGCAACTGCAAGCCACAGATGAGAATCCTTGTGGCTTTGATTCCGAGTGTCTGAACAGGA

1480/6881
FIGURE 1376B

TGCTGATGTTTGAGTGCCACCCGCGAGGTGTGTCCCGCGGGCGAGTTCTGCCAGAACCAGTGCTTCACCAAGCGCC
AGTACCCAGAGACCAAGATCATCAAGACAGATGGCAAAGGGTGGGGCCTGGTCGCCAAGAGGGACATCAGAAAGG
GAGAATTTGTTAACGAGTACGTTGGGGAGCTGATCGACGAGGAGGAGTGCATGGCGAGAATCAAGCACGCACACG
AGAACGACATCACCCACTTCTACATGCTCACTATAGACAAGGACCGTATAATAGACGCTGGCCCCAAAGGAACT
ACTCTCGATTTATGAATCACAGCTGCCAGCCCCAACTGTGAGACCCTCAAGTGGACAGTGAATGGGGACACTCGTG
TGGGCCTGTTTGCCGTCTGTGACATTCTGTCAGGGACGGAGCTGACTTTTAACTACAACCTCGATTGTCTGGGCA
ATGAAAAAACGGTCTGCCGGTGTGGAGCCTCCAATTGCAGTGGATTCTCTGGGGATAGACCAAAGACCTCGACGA
CCCTTTCATCAGAGGAAAAGGGCAAAAAGACCAAGAAGAAAACGAGGCGGCGCAGAGCAAAAGGGGAAGGGAAGA
GGCAGTCAGAGGACGAGTGCTTCCGCTGCGGTGATGGCGGGCAGCTGGTGCTGTGTGACCGCAAGTTCTGCACCA
AGGCCTACCACCTGTCTGCTGGGCCTTGGCAAGCGGCCCTTCGGGAAGTGGGAATGTCTTGGCATCATTGTG
ACGTGTGTGGCAAACCTTCGACTTCATTTTGCCACCTCTGCCCAATTCTGTTCTGTAAGGAGCACCAGGACGGGA
CAGCCTTCAGCTGCACCCCGGACGGGGCGGTCTACTGCTGTGAGCATGACTTAGGGGCGGCATCGGTGAGAAGCA
CCAAGACTGAGAAGCCCCCCCCAGAGCCAGGGAAGCCGAAGGGGAAGAGGCGGCGGGGAGGGGCTGGCGGAGAG
TCACAGAGGGCAAATAGCGCCAGGCGGCCGCTTGGCCGGATCCAGGGGCGGTGCAGGGCGGCCGGCCCTGCCTGC
GGGAGAGGGCGAGCATGAAGTGGCCCCGAGGACCCAGCTCGAGCCGCCAGGACACAGACGTACAGGCCTCCTCGG
GAGGGAGCGCCTCCCCACCCTGAGCCATCCTCAGCAGCGTCCGCTGCGTCTGCACTGATGACCGTCTGAGCCCA
GCTCAGCGTTCTTGGACAAACAGCCTCACTCCTCAGCGTTACCGCCACACTTGAATTTCTCCGAATGTCAAGGTT
CCCTCCCACTCTATTTTTTTTAGGTTAAAGTTAATTGGCATATGGAATGTTTTAATCTCCTCTGAAATGTGTAGCG
TAGGCTTTTCCCAAGGGTCGCTAGAACTCGTCTTCGCGTTGCCCCCTTCTGGCTCTCAGCGCCGTCGCCACTC
GGGAGAGGCTGGGTGAGGCCCGTGTGAGGACTGACCCTGGATTCTCGAAACTGCCATTGTGATCATTACTCTGC
TCTTTGGAAATGGCTGTATCATTTTTTTGTACTAATGTGAATTGTTCTCAGAAACGCTTCTTTTCCATCCTAGT
GAGAAGCTGGCCCTGCAGGTGGTGGCAGCAATGGTGTGTGAAGATTTCTCCCGTAGTTTTTTCTCCTCATGGAT
TTGAATGAAATGCCAATAACACGTCCACTTTCAACGTGTAGTTTACGCGGAGCACTTTCGAGGCCTGGCCGGGT
GGGCCTACTTCTACCTGGGCCTATCTTCTGAACCTCGTAGGTTCTTATCAACATTTGGGGGATAACTTTGTATA
TTTTTTTCAATTTGGCTTTTCTTTACCAGTTTCTGATTTTTTATTCTCAATATATTTTTGTAAACCTATTTACAA
ATCACCACCGACTGAAGTGTGTGTTTACTGATGCGGCCCTGAGCTCCATGGCGAAAGGAGTGACTTTGCAGGGCG
TGAGACCGCAGTCTGCTTAGAGCACAGGAAGTGACAACCTAGGGAGCCCCGTAGGGCGCTGCAGGCCCCGGGGAC
CCCAGCACGTGGGTCTAAAGAGAGACGGAGTCTAGCTCTCCTGCCACCCAGAGTGGCTTCCATCTCAGCACTCTG
TGGGTCTGGTGATGGAAGATGCAGTCTCTGCTGATCATATGTGCCCTCTGCCAGGGCACCTACTGAGAGGTGCGG
TCCTGGGGGTGGAGGCCTGCCTGGCAGGTGTGCGTGCCTCGTACGTGTGTTATGGGCACCTGGTCTAGGCCAGGTA
TGACACCCACTCTCCTGTGAGATTTACATTTAGTTTTTAAAAGGTCCAGTTCTACAGAGTGAGACCTATCTATCT
GAGTACTACATATGTTTTAAGACTTGGTCTTTTTTTTGGAGGATCCTTGACCCTGGGAAGTCTGGAGCACCTGA
GAAGGGGGCACCATGTGTGCCCTTTGCCACGTGTCCTGAGGGGCTGCTTGTCTGGGAGGGAGGGAGAGAACATTC
AGCAGCAGGTGCTTTTTTATGGCCTTTTCTTAAATAACCTAAGGGGGACACATCCATCTTGACAGAGAAGTTTAC
AGAACTCCCCCTTGAAAACCTGCTGCTGAGGCTCCTGTTAAATTTTCTGTGGCATCTTTTATGCCTTGGTAAAACT
GCAGTGTCTTTGGACCTGAGAGTGGCTACTCCGTGGTTTTTGTGACCTGTAAGCGTGGGGTTTCAGGGGTGTGTGGC
CCTGCAGGGTCCCACGCCTCCCTGAGCACTGACTGGAAGTTTCACTGGCTGGTGGCTGTCCCTTCTCCCATCAGG
GTCCCAGCAAAGTTAACTACACAGAGGACCCAGGGGAACGAGCTGTGTAGCCACTGACTTGCTCGCGCGGGCCG
TGGCCTCTGAGGGGCACTCGCCGGTTAAGACAGGGTGGGAGTAGTGCTTTCCAGTTCAGACTCTAACTTCTCCCA
AAGTGTCTTAAGAAAATACTGGATCGGCTCATAGATTTATGCTCCTTATGATGCCCTAACTTGAAGGTTGTCT
AGGGACAGGCCGGGCAGTGTCCCCACACACCTTAGAGTGAAGGCCCCAGGGCCCCGCTGTCACTTGCCCCAA
AGATCCCTTCCGGCAGGTAAGGGACTACCAATGCTTACGTCAAAACAGCAGAATCGGCTTTGCAGTGCACCTTGG
GGAGCAGATATTAACCTATTTTTGTGTTGGACAGTAGTGAAATCTGTGATTTTTAATCGCTTTGATAATACTTC
CAAATTTTATGATTTTTCTGAAGGAAATAATGCAAACATTTTAAATATGTTTCTCCCCCTTTCCAAAACCTGTTA
AATAATGAGCAAGTAACACTAATTTGAATGTCTCTACAATACCCGTTGATAACTCAGTGGAGCCAGGCTTTGG
GGTAGCGGCCCTGAGCTTGCAGGGTTTCTCGCCACTGGGGCTGACCACGCCCCCAGCTGTGACCGTGGGTGTGGC
TGGCTCTCGGCCCTGCCAGCTTTGTTCTGAGGACGTGGTGACTTCTGAACATCAGCTTCAATCCTCCATCATT
AATGTGAAGCAAAACACAAAACCGCCCCAATCCTCAGGATTCCTTGGCATCCGAAACCAGCATCTGCACCTAA

1481/6881
FIGURE 1376C

ACCCATACCCACCCGCTGTGCGCCACAGGGGGATGTGTCCGAATGGGCAGCTTAAAATGTGGTCACCTGTGGGGG
AAACTCTTCAGGCACCTGAAGTGAGAACCCAGCTGTCCGTCCTCAGGCCGGCCTTTCTTCCGGCGACACCCGTCC
ATGGCTGGCTGGGTCCCTTCGCAGTGTGTTGTCTGTCTTGACATCTAAACCCCGGCGTGTGCAGTGCCCATCTTC
CAGGACTACCTTATTTTCCAGAATTAAACCTGTTTTATAATTCAAGTTAATGCAAATGACTGTCAGTTGCCAAAT
ATCTTGATCCTGTGAGTGTAGTTGATGACTGTTTGTTAGTCAGTAGAGTAAAATGCTGTGTCCACGGGGTGTAC
AGCCTCACCATAACCCTGTTGAGGTGTGAAATGCCCCGTCAGAAATTAAATACAAACTTAAATGTGCCTATTGGTG
TCTAAACTTCATACAATGTAAGGTCAGATTCCTTTTAGGAATACTGGGTGCTGTCACCAGGTTTGATAGTTAGAC
TTAAAACTTGAAATTCACTTTTTGGGGGGAGGGATATACTGAAATAGAGAGTTGAGACTTGCCAGTTGGGGGAA
AATAGCATTTAAATGGAAAGCTGTGTTTGAAAATTGTGTATGAGTATTTTGTATTAAAAACATTTTAAAGGC
TTTTTCTTAA

1482/6881
FIGURE 1377

MEFSIKQSPLSVQSVVKCIKMKQAPEILGSANGKTPSCEVNRECSVFLSKAQLSSSLQEGVMQKFNHGDALPFI
ADKLDLTSRVFNGEPEGHAHDAKLRFESQEMKGIGTPPNTTPIKNGSPEIKLKITKTYMNGKPLFESSICGDSAAD
VSQSEENGQKPENKARRNRKRSIKYDSLLEQGLVEAALVSKISSPSDKKIPAKKESCPNTGRDKDHLLKYNVGD
VWSKVSQYPWWPCMVSAADPLLSYTKLKGQKKSARQYHVQFFGDAPERAWIFEKSLVAFEGEGQFEKLCQESAKQ
APTKAEKIKLLKPI SGKLRAQWEMGIVQAEAAASMSVEERKAKFTFLYVGDQLHLNPPQVAKEAGIAAESLGEMAE
SSGVSEEAENPKSVREECIPMKRRRRRAKLCSSAETLESHPDIGKSTPQKTAEADPRRGVGSPPGRKKTIVSMR
SRKGDAAASQFLVFCQKHRDEVVAEHPDASGEEIEELLRSQWLLSEKQARARYNTKFALVAPVQAEEDSGNVNGKK
RNHTKRIQDPTEDAEADTPRKRLRTDKHSLRKRDTITDKTARTSSYKAMEAASSLKSAATKNLSDACKPLKKR
NRSTAASSALGFSKSSSPSASLTENEVSDSPGDEPSESPYESADETQTEVSVSSKKSERGVTAKEYVCQLCEK
PGSLLLCEGPPCCGAFHLACLGLSRRPEGRFTCSECASGIHSCFVCKESKTDVKRCVVTQCGKFYHEACVKKYPLT
VFESRGFRCPHSCVSCHASNPSPRPSPKGMRCVRCVPVAYHSGDACLAAGCSVIASNSI ICTAHFTARKGKRH
HAHVNVSWCFVCSKGGSLCCESCFAAFHPDCLNIEMPDGSWFCNDCRAGKKLHFQDI IWVKLGNRRWWPAEVCH
PKNVPPNIQKMKHEIGEFFVFFFGSKDYWTHQARVFPYMEGDRGSRYQGVRGIGRVFKNALQEAEARFREIKLQ
REARETQESERKPPPYKHIKVNKPYGKVQIYTADISEIPKCNCKPTDENPCGFDSECLNRMLMFECHPQVCPAGE
FCQNQCFTKRQYPETKIIKTDGKGWGLVAKRDIRKGEFVNEYVGELIDEEECMARIKHAHENDITHFYMLTIDKD
RIIDAGPKGNYSRFMNHSCQPNCE TLKWTVNGDTRVGLFAVCDIPAGTELTFNYNLDCLGNEKTVCRCGASNC SG
FLGDRPKTSTTLSSEEKGKKTKKKTRRRRAKGEGRQSEDECFRCGDDGQLVLCDRKFCTKAYHLSCLGLGKRPF
GKWECPWHHCDVCGKPSTSFCHLCPNSFCKEHQDGTAFSCTPDGRSYCCEHDLGAASVRSTKTEKPPPEPGKPKG
KRRRRRGWRRVTEGK

1483/6881
FIGURE 1378A

TGGTCTTGAACCTCTGACCTTGTGATCCGCTCGCCTCAGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACC
GTGCCTGTCTAGAACCACTGGTAACCTTAACTGAGACAAGATTTGCGCATGTTGCCAGGCTGGTCTCGAACT
TCTGAGCTCAAGCGATCTACCTGCCTCGTCCTCCCAAAGTGTTGGAATTGCAGGTGTGAGCCACTGCACCCGGCC
CTTGCCCTCATGTTTGAATGATAATTTACCTGGGCATAAAATTCTGGACACTTGTGGTGGCAGAGCTGTCTGCTT
TTCTGTGGAGACTGCGGGTTGCAGACACCAGCAGCCCCCTATTGCTGCACGTCAGGTGTCTCCACCTCAGTACT
GTGGACATCTCGGGCCGCATAGCCCTGTTGCGCGGGCATCCTGTGCGTTGCAGGAGATGCAGCAGCATCCATGAC
CGCAACCCATCAGAGTGTTCTAAGAACGGAAGCATCTGGGCTGGATGAATTTAGCATCAAGCAGAGTCCCCCTTT
CTGTTTCAAGTGTTGTAAAGTGATAAAGATGAAGCAGGCACCAGAAATCCTCGGCAGTGCCAACGGGAAGACTC
CGAGCTGCGAGGTGAACCGCGAGTGTTCTGTGTTCCCTCAGCAAAGCCCAGCTCTCCAGTAGCCTGCAGGAGGGGG
TCATGCAGAAGTTTAAACGGCCACGACGCCCTGCCCTTTATTCCAGCCGACAAGCTGAAAAGATCTTACTTCCCGGG
TGTTTTAATGGAGAACCCGGCGCACACGATGCCAAACTGCGTTTTGAGTCCCAGGAAATGAAAGGGATTGGGACAC
CCCCTAACACTACCCCTATCAAAAATGGCTCTCCAGAAATTAAGCTGAAAATCACCAAAACATACATGAATGGGA
AGCCTCTCTTTGAATCTTCCATTTGTGGTGACAGTGCTGCTGATGTGTCTCAGTCAGAAAGAAATGGACAAAAAC
CAGAAAACAAGGCGAGAAGGAACAGGAAGAGGAGCATAAAATATGACTCCTTGCTGGAGCAGGGCCTTGTCGAAG
CAGCTCTTGTGTCTAAGATCTCAAGTCCTTCAGATAAAAAGATTCCAGCTAAGAAAGAGTCTTGTCCAAACACTG
GAAGAGACAAAGACCACCTGTTGAAATACAACGTTGGTGATTTGGTGTGGTCCAAAGTGTCGGGTTACCCCTTGGT
GGCCTTGTCATGGTTTTCTGCAGATCCACTCCTTCACAGCTATACCAAATTAAGGTCAGAAAAGAGTGCACGCC
AGTATCACGTACAGTTCTTTGGTGACGCCCCAGAAAGAGCTTGGATATTTGAGAAGAGCCTCGTAGCTTTTGAAG
GAGAAGGACAGTTTGAAAAATTATGCCAGGAAAGTGCCAAGCAGGCACCCACGAAAGCTGAGAAAATTAAGCTAT
TGAAACCAATTTTCAAGGAAATTGAGGGCCCAGTGGGAAATGGGCATTGTTCAAGCAGAAGAAGCTGCAAGCATGT
CAGTGGAGGAGCGGAAAGCCAAGTTCACCTTTCTCTATGTGGGGGACCAGCTTCATCTCAACCCTCAAGTAGCCA
AGGAGGCTGGCATTGCTGCAGAGTCTTTGGGAGAAATGGCAGAATCCTCAGGAGTCAGTGAAGAAGCTGCTGAAA
ACCCCAAGTCTGTGAGAGAAGAGTGCAATCCCATGAAGAGAAGGCGGAGGGCCAACTGTGTAGCTCTGCAGAGA
CCCTGGAGAGTCACCCCGACATAGGGAAGAGTACTCCTCAAAAGACGGCAGAGGCTGACCCCGAAGAGGAGTAG
GGTCTCCTCCTGGGAGGAAGAAGACCACAGTCTCCATGCCACGAAGCAGGAAGGGAGATGCAGCATCCAGTTTTT
TGGTCTTCTGTCAAAAACACAGGGATGAGGTGGTAGCTGAGCACCCAGATGCTTCAGGTGAGGAGATTGAAGAGC
TGCTCAGGTACAGTGGAGTCTGCTGAGTGAGAAGCAGAGAGCACGCTACAACACCAAGTTTGCCCTGGTGGCCC
CTGTCCAGGCTGAAGAAGACTCTGGTAATGTAAATGGGAAAAAAGAAACCACACAAAGAGGATACAGGACCCTA
CAGAAGATGCTGAAGCTGAGGACACACCCAGGAAAAGACTCAGGACGGACAAGCACAGTCTTCGGAAGAGAGACA
CAATCACTGACAAAACGGCCAGAACAAGCTCTTACAAGGCCATGGAGGCAGCCTCCTCGCTCAAGAGCCAGGCAG
CAACGAAAAATCTGTCTGATGCATGTAAACCACTGAAGAAGCGAAATCGGGCTTCCACGGCAGCATCTTCAGCTC
TTGGGTTTAGCAAAAGTTTCATCTCCTTCTGCATCCTTAAGTGAAGTGAAGTCTCGGACAGCCCGGGAGACGAGC
CCTCGGAGTCCCCATACGAAAAGTGACAGACGAAACACAACTGAAGTATCTGTCTCATCAAAAAGTCTGAGCGAG
GAGTGACTGCCAAAAGAGGATATGTGTGCCAGCTGTGTGAGAAGCCGGGCAGCCTCCTGCTCTGTGAAGGACCCT
GCTGCGGAGCTTTCCACCTCGCCTGCCTTGGGCTTTCCCGGAGGCCAGAAGGGAGGTTACCTGCAGCGAGTGTG
CCTCAGGTGTGCGCCGGCACAGTCTGGGGTCTGTGAGGATGATGAGAGGACACCTGCACAGCCGTGGCCCTTCTCT
GCCTACTCACCGGGCCCAAGGAGTCTCCTATCTCACGTGAGAACACTTCTGGGTGAGGAAGACACCTGGAGAGT
CTCCAGGCCATGGCAGCCCCACAGCAGCACCTCACTTATGGGAGTGCTGTCTGCCTGCCAGAAATGATAAGTG
ACTGCTCCACCACTGGCCAGCTGCTCTCAAGGAGGAAAGGCCTCTTTTCATAGGAGCCCTTCTTTCAAGCTTCT
TGCCAGTTAGACTGGGCCTCCCCAGCCAGGCTGCCTAGTAAGATTCTCCTGTATTTTCAAGGTGAAGCTGGAGCTCA
GATCGCAGCAAGGTAATCCTTGATGGCTGGATCTTTTTGCTGGAGAATGCTTGGACTAGTGAGCAAGGTTGGAAA
CAGGGCCAGGTGCTTTAGCAGCGTGGCTGCCTCTGAAGAGGAGTTGCTTGAATTTAGTGGCTCAGAACTGCAATT
TAATCTTGTCTTTGCACCTCTCTCTCCACCCCTTCTTTAACTTTTTGTTAGGGATTCACTCATGTTTCGTGTG
TAAAGAGAGCAAGACAGATGTTAAGCGCTGTGTGGTAACTCAGTGTGAAAATTTTACCATGAGGCTTGTGTGAA
AAAATACCCTCTGACTGTATTTGAGAGCCGAGGTTTCCGCTGCCCCCTCCACAGCTGTGTGAGCTGCCATGCTTC
CAACCCTTCAAACCCAAGGCCGTCAAAGGTAATAATGATGCGGTGTGTCCGCTGCCCCGTTGCCTATCACAGCGG
GGATGCTTGTCTGGCAGCAGGATGCTCAGTGATCGCCTCCAACAGCATCATCTGCACTGCCACTTCACTGCTCG
GAAGGGGAAGCGACACCACGCCACGTCAACGTGAGCTGGTGTCTCGTGTGCTCCAAAGGGGGGAGCCTTCTGTG

1484/6881
FIGURE 1378B

CTGTGAGTCCTGCCAGCGGCCCTTCCACCCTGACTGCCTGAACATCGAGATGCCTGACGGCAGCTGGTTCTGCAA
TGA CTGCAGGGCTGGGAAGAAGCTGCACTTCCAGGATATCATTGGGTGAACTTGGGAACACAGATGGTGGCC
GGCAGAAGTTTGCCATCCCAAAATGTTCCCCAAATATTAGAAAATGAAGCACGAGATTGGAGAATTCCCTGT
GTTTTCTTTGGGTCTAAAGATTATTACTGGACGCATCAGGCGGAGTGTTCCTGTACATGGAGGGGGACCGGGG
CAGCCGCTACCAGGGGGTCAGAGGGATCGGAAGAGTCTTCAAAAACGCACTGCAAGAAGCTGAAGCTCGTTTTCG
TGAAATTAAGCTTCAGAGGGAAGCCCGAGAAACACAGGAGAGCGAGCGCAAGCCCCACCATAACAAGCACATCAA
GGTGAATAAGCCTTACGGGAAAGTCCAGATCTACACAGCGGATATTTAGAAAATCCCTAAGTGCAACTGCAAGCC
CACAGATGAGAATCCTTGTGGCTTTGATTCCGAGTGTCTGAACAGGATGCTGATGTTTGAGTGCCACCCGCAGGT
GTGTCCCGCGGGCGAGTTCCTGCCAGAACAGTGTTCACCAAGCGCCAGTACCCAGAGACCAAGATCATCAAGAC
AGATGGCAAAGGGTGGGGCCTGGTCCGCAAGAGGGACATCAGAAAGGGAGAATTTGTTAACGAGTACGTTGGGGA
GCTGATCGACGAGGAGGAGTGCATGGCGAGAATCAAGCACGCACACGAGAACGACATCACCCACTTCTACATGCT
CACTATAGACAAGGACCGTATAATAGACGCTGGCCCCAAAGGAACTACTCTCGATTTATGAATCACAGCTGCCA
GCCCCAAGTGTGAGACCCCTCAAGTGGACAGTGAATGGGGACACTCGTGTGGGCCTGTTTGCCGTCTGTGACATTCC
TGCAGGGACGGAGCTGACTTTTAACTACAACCTCGATTGTCTGGGCAATGAAAAACGGTCTGCCGGTGTGGAGC
CTCCAATTGCAGTGGATTCTCTCGGGGATAGACCAAAGACCTCGACGACCCTTTCATCAGAGGAAAAGGGCAAAAA
GACCAAGAAGAAAACGAGGCGGCGCAGAGCAAAAAGGGGAAGGGAAGAGGCAGTCAGAGGACGAGTGTCTCCGCTG
CGGTGATGGCGGGCAGCTGGTGTGTGTGACCGCAAGTCTGCACCAAGGCCTACCACCTGTCTGCTGGGCCT
TGGCAAGCGGCCCTTCGGGAAGTGGGAATGTCTTGGCATCATTGTGACGTGTGTGGCAAACTTCGACTTCATT
TTGCCACCTCTGCCCAATTTCGTTCTGTAAAGGAGCACCAGGACGGGACAGCCTTCAGCTGCACCCCGGACGGGCG
GTCTTACTGCTGTGAGCATGACTTAGGGGCGGCATCGGTGAGAAGCACCAGACTGAGAAGCCCCCCCCAGAGCC
AGGGAAGCCGAAGGGGAAGAGGCGGCGGCGGAGGGGCTGGCGGAGAGTCAAGAGGGGCAATAGCGCCAGGCGGC
CGCTTGGCCGATCCAGGGGCGGTGCAGGGCGGCGGCCCTGCCTGCGGGAGAGGGCGAGCATGAACTGGCCCGG
AGGACCCAGCTCGAGCCGCCAGGACACAGACGTACAGGCCTCCTCGGGAGGGAGCGCCTCCCCACCACTGAGCCA
TCCTCAGCAGCGTCCGCTGCGTCTGCACTGATGACCGTCTGAGCCAGCTCAGCGTTCCTGGACAAACAGCCTCA
CTCCTCAGCGTTACCGCCACACTTGAATTTCTCCGAATGTCAAGGTTCCCTCCCACTCTATTTTTTTAGGTTAA
GTTAATTGGCATATGGAATGTTTTAATCTCCTCTGAAATGTGTAGCGTAGGCTTTTCCCAAGGGTCGCTAGAAAC
TCGTCTTCGCGTTGCCCCCTTTCTGGCTCTCAGCGCGTGCCTACTCGGGAGAGGCTGGGTGAGGCCCGTGTGAG
GACTGACCCTGGATTCTCGAACTGCCATTGTGATCATTACTCTGCTCTTTGGAATGGCTGTATCATTTTTTT
GTACTAATGTGAATTGTTCTCAGAAACGCTTCTTTTCCATCTAGTGAGAAGCTGGCCCTGCAGGTGGTGGCAG
CAATGGTGTGTGAAGATTTCTCCCGTAGTTTTTTCTCCTCATGGATTTGAATGAAATGCCAATAACACGTCCAC
TTTCAACGTGTAGTTTACGCGGAGCACTTCGAGGCCTGGCCGGGTTGGGCCTACTTCTCACCTGGGCCTATCTT
CTGAACTCGCTAGGTTCTTATCAACATTTGGGGGATAACTTTGTATATTTTTTTTCAATTTGGCTTTTCTTTACCAG
TTTCTGATTTTTTATTCTCAATATATTTTTGCTAAACCTATTTACAAATCACCACCGACTGAAGTGTGTGTTTAC
TGATGCGGCCCTGAGCTCCATGGCGAAAGGAGTGACTTTGCAGGGCGTGAGACCGCAGTCTGCTTAGAGCACAGG
AAGTGACAACCTAGGGAGCCCCGTAGGGCGCTGCAGGCCCGGGGACCCAGCACGTGGGTCTAAAGAGAGACGG
AGTCTAGCTCTCCTGCCACCCAGAGTGGCTTCCATCTCAGCACTCTGTGGGTCTGGTGATGGAAGATGCAGTCTC
TGCTGATCACATGTGCCCTCTGCCAGGGCACCTACTGAGAGGTGCGGTCTTGGGGTGGAGGCCTGCCTGGCAGG
TGTGCGTGCCTCGTACGTGTGTTATGGGCACTGGTCTAGGCCAGGTATGACACCCACTCTCCTGTGAGATTTAC
TTTAGTTTTTAAAGGTCCAGTTCTACAGAGTGAGACCTATCTATCTGAGTACTACATATGTTTTAAGACTTGGT
TCTTTTTTTGAGGGATCCTTGACCCTGGGAAGTCTGGAGCACCTGAGAAGGGGGCACCATGTGTGCCTTTGCC
ACGTGTCTGAGGGGCTGCTTGTCTGGGAGGGAGGGAGAGAACATTACAGCAGCAGGTGCTTTTTTATGGCCTTTT
CTTAAATAACCTAAGGGGGACACATCCATCTTGAGAGAAGTTTACAGAACTCCCTTGAAAACCTGCTGCTGAG
GCTCCTGTTAAATTTTCTGTGGCATCTTTTATGCCCTTGGTAAAAACTGCAGTGTCTTTGGACCTGAGAGTGGCTA
CTCCGTGGTTTTGTGACCTGTAAGCGTGGGGTTCAGGGGTGTGTGGCCCTGCAGGGTCCCACGCCTCCCTGAGCA
CTGACTGGAAGTTTCACTGGCTGGTGGCTGTCCCTTCTCCCATCAGGGTCCCAGCAAAGTTAACTACACAGAGG
ACCCAGGGGAAACGAGCTGTGTAGCCACTGACTTGTCTCGCGCGGCCGTGGCCTCTGAGGGGCACTCGCCGGTTAA
GACAGGGTGGGAGTAGTGCTTTCCAGTTCAGACTCTAACTTCTCCCAAAGTGTCTAAGAAAATACTGGATCGGC
TCATAGATTTATGCTCCTTATGATGCCCTAACTTGAAGGTTGTTCTAGGGACAGGCCGGGCAGTGTCCCCACAC

1485/6881
FIGURE 1378C

ACACCTTAGAGTCGAAGGCCCCAGGGCCCCGCTGTCACTTGCCCCAAAAGATCCCTTCCGGCAGGTAAGGGACTAC
CAATGCTTACGTCAAAACAGCAGAATCGGCTTTGCAGTGCACCTTTGGGGAGCAGATATTAACCTTATTTTTGTGTT
GGACAGTAGTGAAATCTTGTGATTTTTAATCGCTTTGATAATACTTCCAAATTTTATGATTTTTCTGAAGGAAAT
AATGCAAAACATTTTTAAATATGTTTCTCCCCCTTTCCAAAACTGTAAACTAATGAGCAAGTAACACTAACTTTG
AATGTCTCTACAATACCCGTTGATAACTCAGTGGAGCCAGGCTTTGGGGTAGCGGCCCTGAGCTTGCAGGGTTTC
TCGCCACTGGGGCTGACCACGCCCCCAGCTGTGACCGTGGGTGTGGCTGGCTCTCGGCCCTGCCAGCTTTGTTC
TGAGGACGTGGTGACTTCCTGAACATCAGCTTCAATCCTCCATCATTAATGTGAAGCAAAACACAAAAACCGCCC
CAATCCCTCAGGATTCCCTTGGCATCCGAAACCAGCATCTGCACCTAAACCCATACCCACCCGTGTGCGCCACAG
GGGGATGTGTCCGAATGGGCAGCTTAAATGTGGTCACCTGTGGGGGAAACTCTTCAGGCACCTGAAGTGAGAAC
CCAGCTGTCCGTCCCTCAGGCCGGCCTTTCTTCCGGCGACACCCGTCCATGGCTGGCTGGGTCCCCTTCGCAGTGT
TTGTCTGTCTTGACATCTAAACCCGGCGTGTGCAGTGCCCATCTTCAGGACTACCTTATTTTCCAGAATTAAA
CCTGTTTTTATAATTCAAGTTAATGCAAATGACTGTCAGTTGCCAAATATCTTGATCCTGTGAGTGTAGTTGATGA
CTGTTTGTTAGTCAGTAGAGTAAATGCTGTGTCCACGGGGTGTACAGCCTCACCATAACCTGTTGAGGTGTGA
AATGCCCCGTCAGAAATTAAATACAACTTAAATGTGCCTATTGGTGTCTAACTTCATACAATGTAAGGTCAGA
TTCCTTTTAGGAATACTGGGTGCTGTACACAGGTTTGATAGTTAGACTTAAAACTTGAAATTCACTTTTTGGGG
GGAGGGATATACTGAAATAGAGAGTTGAGACTTGCCAGTTGGGGGAAAATAGCATTTAAATGGAAAGCTGTGTT
TGAAAATTGTGTATGAGTATTTTTGTATTAAAAACATTTTAAAGGCTTTTTTCTTAA

1486/6881
FIGURE 1379

MEFSIKQSPLSVQSVVKCIKMKQAPEILGSANGKTPSCEVNRECSVFLSKAQLSSSLQEGVMQKFNGHDALPFIP
ADKLDLTSRVFNGEPGAHDAKLRFESQEMKGIGTPPNTTPIKNGSPEIKLKITKTYMNGKPLFESSICGDSAAD
VSQSEENGQKPENKARRNRKRSIKYDSLLEQGLVEAALVSKISSPSDKKIPAKKESCPNTGRDKDHLLKYNVGD
VWSKVSGYPWWPCMVSAADPLLHSYTKLKGQKKSARQYHVQFFGDAPERAWIFEKSLVAFEGEGQFEKLCQESAKQ
APTKAEKIKLLKPI SGKLRAQWEMGIVQAEAAASMSVEERKAKFTFLYVGDQLHLNPQVAKEAGIAAESLGEMAE
SSGVSEEAENPKSVREECIPMKRRRRRAKLCSSAETLESHPDIGKSTPQKTAEADPRRGVGSPPGRKKT TVSMR
SRKGDAAASQFLVFCQKHRDEVVAEHPDASGEEIEELLRSQWSLLSEKQRARYNTKFALVAPVQAEEDSGNVNGKK
RNHTKRIQDPTEDAEAEDTPRKRLRTDKHSLRKRDTITDKTARTSSYKAMEAASSLKSAATKNLSDACKPLKKR
NRASTAASSALGFSKSSSPSASLTENEVSDSPGDEPSESPYESADETQTEVSVSSKKSERGV TAKKEYVCQLCEK
PGSILLCEGPCCGAFHLACLGLSRRPEGRFTCSECASGVARHSLGSVRMMRGHLHSRGPSCLLTGPKESPISRQN
TSWVRKTPGESPRPWQPHSSTSLMGVSVCLPRMISDCSTTGQLLSRRKGLFS

1487/6881
FIGURE 1380A

TGGTCTTGAACCTCCTGACCTTGTGATCCGCTCGCCTCAGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACC
GTGCCTGTCTTAGAACCCTGGTAACCTCTTAACCTGAGACAAGATTTGCGCATGTTGCCAGGCTGGTCTCGAACC
TCTGAGCTCAAGCGATCTACCTGCCTCGTCTCCCAAAGTGTTGGAATTGCAGGTGTGAGCCACTGCACCCGGCC
CTTGCCCTCATGTTTGAATGATAATTTACCTGGGCATAAAATTTCTGGACACTTGTGGTGGCAGCAGCTGTCTGCTT
TTCTGTGGAGACTGCGGGTTGCAGACACCAGCAGCCCCCTATTGCTGCACGTCAGGTGTCTCCACCTCAGTACT
GTGGACATCTCGGGCCGCATAGCCCTGTTGCGCGGGCATCCTGTGCGTTGCAGGAGATGCAGCAGCATCCATGAC
CGCAACCCATCAGAGTGTTCTAAGAACGGAAGCATCTGGGCTGGATGGAATTTAGCATCAAGCAGAGTCCCTTTT
CTGTTTCAAGAGTGTTGTAAAGTGCATAAAGATGAAGCAGGCACCAGAAATCCTCGGCAGTGCCAACGGGAAGACTC
CGAGCTGCGAGGTGAACCGCGAGTGTTCTGTGTTCTCAGCAAAGCCCAGCTCTCCAGTAGCCTGCAGGAGGGGG
TCATGCAGAAGTTTAAACGGCCACGACGCCCTGCCCTTTATTCCAGCCGACAAGCTGAAAGATCTTACTTCCCGGG
TGTTTAAATGGAGAACCCGGCGCACACGATGCCAAACTGCGTTTTGAGTCCCAGGAAATGAAAGGGATTGGGACAC
CCCCTAACACTACCCCTATCAAAAATGGCTCTCCAGAAATTAAGCTGAAAATCACCAAAACATACATGAATGGGA
AGCCTCTCTTTGAATCTTCCATTTGTGGTGACAGTGCTGCTGATGTGTCTCAGTCAGAAGAAAATGGACAAAAAC
CAGAAAACAAGGCGAGAAGGAACAGGAAGAGGAGCATAAAATATGACTCCTTGCTGGAGCAGGGCCTTGTCTGAAG
CAGCTCTTGTGTCTAAGATCTCAAGTCCTTCAAGATAAAAAGATTCCAGCTAAGAAAGAGTCTTGTCCAAAACACTG
GAAGAGACAAAGACCACCTGTTGAAATACAACGTTGGTGATTTGGTGTGGTCCAAAGTGTCGGGTTACCCCTTGGT
GGCCTTGCATGGTTTCTGCAGATCCACTCCTTACAGCTATACCAAACCTTAAAGGTCAGAAAAGAGTGACACGCC
AGTATCACGTACAGTTCTTTGGTGACGCCCCAGAAAGAGCTTGGATATTTGAGAAGAGCCTCGTAGCTTTTGAAG
GAGAAGGACAGTTTGA AAAAATTATGCCAGGAAAGTGCCAAGCAGGCACCCACGAAAGCTGAGAAAATTAAGCTAT
TGAAACCAATTTTCAAGGAAATTGAGGGCCAGTGGGAAATGGGCATTGTTCAAGCAGAAGAAGCTGCAAGCATGT
CAGTGGAGGAGCGGAAAGCCAAGTTACCTTTCTCTATGTGGGGGACCAGCTTCATCTCAACCCTCAAGTAGCCA
AGGAGGCTGGCATTGCTGCAGAGTCTTTGGGAGAAATGGCAGAATCCTCAGGAGTCAGTGAAGAAGCTGCTGAAA
ACCCCAAGTCTGTGAGAGAAGAGTGCATTCCCATGAAGAGAAGGCGGAGGGCCAAACTGTGTAGCTCTGCAGAGA
CCCTGGAGAGTCACCCCGACATAGGGAAGAGTACTCTCAAAAGACGGCAGAGGCTGACCCCGAAGAGGAGTAG
GGTCTCCTCCTGGGAGGAAGAAGACCACAGTCTCCATGCCACGAAGCAGGAAGGGAGATGCAGCATCCAGTTTTT
TGGTCTTCTGTCAAAAACACAGGGATGAGGTGGTAGCTGAGCACCCAGATGCTTCAGGTGAGGAGATTGAAGAGC
TGCTCAGGTACAGTGAGTCTGTGAGTGAAGCAGAGAGCACGCTACAACACCAAGTTTGGCCTGGTGGCCC
CTGTCCAGGCTGAAGAAGACTCTGGTAATGTAAATGGGAAAAAAGAAACCACACAAAGAGGATACAGGACCCTA
CAGAAGATGCTGAAGCTGAGGACACACCAGGAAAAGACTCAGGACGGACAAGCACAGTCTTCGGAAGAGAGACA
CAATCACTGACAAAACGGCCAGAACAAGCTCTTACAAGGCCATGGAGGCAGCCTCCTCGCTCAAGAGCCAGGCAG
CAACGAAAAATCTGTCTGATGCATGTAAACCACTGAAGAAGCGAAATCGGGCTTCCACGGCAGCATCTTCAGCTC
TTGGGTTTTAGCAAAAGTTTCTATCTCCTTCTGCATCCTTAACCTGAGAATGAGCTTTTGTGGGAGCCACACCAGTCA
AGTTGGATTTGAACCCAGCTGCTCTGTACTGCACTTAGAATGATGTAATATTCCAGGATGCTGCTGCAGGTGGCG
TATCATCGTACACACTCAGTGACATTTCTATCACAATCATTTTATGGAAGATGTGTGATAATCTGTTTTTACTGG
TATTAATAAACACATACAATGAAGAAAACAGATAACAAATTTTAAAGACCAAGGTCTCGGACAGCCCGGGAGACGA
GCCCTCGGAGTCCCCATACGAAAAGTGACAGACGAAACACAACTGAAGTATCTGTCTCATCCAAAAGTCTGAGCG
AGGAGTGACTGCCAAAAGGAGTATGTGTGCCAGCTGTGTGAGAAGCCGGGCAGCCTCCTGCTCTGTGAAGGACC
CTGCTGCGGAGCTTTCCACCTCGCCTGCCTTGGGCTTTCCCGGAGGCCAGAAGGGAGGTTACCTGCAGCGAGTG
TGCTCAGGGATTCACTCATGTTTTCGTGTGTAAAGAGAGCAAGACAGATGTTAAGCGCTGTGTGGTAACCTCAGTG
TGGAAAATTTTACCATGAGGCTTGTGTGAAAAAATACCCTCTGACTGTATTTGAGAGCCGAGGTTTCCGCTGCCC
CCTCCACAGCTGTGTGAGCTGCCATGCTTCCAACCCTTCAAACCCAAGGCCGTCAAAAGGTAAAATGATGCGGTG
TGTCCGCTGCCCCGTTGCCTATCACAGCGGGGATGCTTGTCTGGCAGCAGGATGCTCAGTGATCGCCTCCAACAG
CATCATCTGCACTGCCCACTTCACTGCTCGGAAGGGGAAGCGACACCACGCCCACGTCAACGTGAGCTGGTGCTT
CGTGTGCTCCAAAGGGGGGAGCCTTCTGTGCTGTGAGTCCTGCCAGCGGCCTTCCACCCTGACTGCCTGAACAT
CGAGATGCCTGACGGCAGCTGGTTCTGCAATGACTGCAGGGCTGGGAAGAAGCTGCACTTCCAGGATATCATTTG
GGTGAAACTTGGGAACACAGATGGTGGCCGGCAGAAGTTTGCCATCCCAAAAATGTTCCCCCAAATATTTCAGAA
AATGAAGCACGAGATTGGAGAATTCCTGTGTTTTTCTTTGGGTCTAAAGATTATTACTGGACGCATCAGGCGCG
AGTGTTCCTGATGAGGGGGGACCGGGGCAGCCGCTACCAGGGGTGAGAGGGATCGGAAGAGTCTTCAAAAA

1488/6881
FIGURE 1380B

CGCACTGCAAGAAGCTGAAGCTCGTTTTTCGTGAAATTAAGCTTCAGAGGGAAGCCCCGAGAAACACAGGAGAGCGA
GCGCAAGCCCCCACCATAACAAGCACATCAAGGTGAATAAGCCTTACGGGAAAGTCCAGATCTACACAGCGGATAT
TTCAGAAATCCCTAAGTGAAGTCAAGCCCACAGATGAGAATCCTTGTGGCTTTGATTTCGGAGTGTCTGAACAG
GATGCTGATGTTTGTAGTGCCACCCGCAGGTGTGTCCCGCGGGCGAGTTCTGCCAGAACCAGTGCTTCACCAAGCG
CCAGTACCCAGAGACCAAGATCATCAAGACAGATGGCAAAGGGTGGGGCCTGGTCGCCAAGAGGGACATCAGAAA
GGGAGAATTTGTTAACGAGTACGTTGGGGAGCTGATCGACGAGGAGGAGTGCATGGCGAGAATCAAGCAC'GCACA
CGAGAACGACATCACCCACTTCTACATGCTCACTATAGACAAGGACCGTATAATAGACGCTGGCCCCAAAGGAAA
CTACTCTCGATTTATGAATCACAGCTGCCAGCCCAACTGTGAGACCCCTCAAGTGGACAGTGAATGGGGACACTCG
TGTGGGCCTGTTTGCCGCTCTGTGACATTCTGCAGGGACGGAGCTGACTTTTAACTACAACCTCGATTGTCTGGG
CAATGAAAAAACGGTCTGCCGGTGTGGAGCCTCCAATTGCAGTGGATTCTCGGGGATAGACCAAAGACCTCGAC
GACCCTTTTCATCAGAGGAAAAGGGCAAAAAGACCAAGAAAGAAAACGAGGCGGCGCAGAGCAAAAAGGGGAAGGGAA
GAGGCAGTCAGAGGACGAGTGTCTCCGCTGCGGTGATGGCGGGCAGCTGGTGTCTGTGTGACCGCAAGTTCTGCAC
CAAGGCCTACCACCTGTCCTGCCTGGGCCTTGGCAAGCGGCCCTTCGGGAAGTGGGAATGTCTTGGCATCATTG
TGACGTGTGTGGCAAACCTTCGACTTCATTTTGCCACCTCTGCCCAATTCGTTCTGTAAAGGAGCACCAGGACGG
GACAGCCTTCAGCTGCACCCCGGACGGGCGGTCTACTGCTGTGAGCATGACTTAGGGGCGGCATCGGTCTAGAAG
CACCAAGACTGAGAAGCCCCCCCCAGAGCCAGGGAAGCCGAAGGGGAAGAGGCGGCGGCGGAGGGGGCTGGCGGAG
AGTCACAGAGGGCAAATAGCGCCAGGCGGCCGCTTGGCCGGATCCAGGGGCGGTGCAGGGCGGCCGCGCCCTGCCT
GCGGGAGAGGGCGAGCATGAACTGGCCCGGAGGACCCAGCTCGAGCCGCCAGGACACAGACGTACAGGCCTCCTC
GGGAGGGAGCGCCTCCCCACCACTGAGCCATCCTCAGCAGCGTCCGCTGCGTCTGCACTGATGACCGTCTGAGCC
CAGCTCAGCGTTCTTGGACAAACAGCCTCACTCCTCAGCGTTACCGCCACACTTGAATTTCTCCGAATGTCAAGG
TTCCCTCCCCTCTATTTTTTTTAGCTTAAAGTTAATTGGCATATGGAATGTTTTAATCTCCTCTGAAATGTGTAG
CGTAGGCTTTTCCCAAGGGTGCCTAGAACTCGTCTTCGCGTTGCCCCCTTTCTGGCTCTCAGCGCCGTGCGCCAC
TCGGGAGAGGGCTGGGTGAGGCCCGTGTGAGGACTGACCTGGATTCTCGAAACTGCCATTGTGATCATTACTCT
GCTCTTTGGAAATGGCTGTATCATTTTTTTGTACTAATGTGAATTGTTCTCAGAAACGCTTCTTTTCCATCCTA
GTGAGAAGCTGGCCCTGCAGGTGGTGGCAGCAATGGTGTGTGAAGATTCTCCCGTAGTTTTTTCTCCTCATGG
ATTTGAATGAAATGCCAATAACACGTCCACTTTCAACGTGTAGTTTACGCGGAGCACTTTTCGAGGCCTGGCCGGG
TTGGGCCTACTTCTCACCTGGGCCTATCTTCTGAACTCGCTAGGTTCTTATCAACATTTGGGGGATAACTTTGTA
TATTTTTTTTCATTTGGCTTTTCTTTTACCAGTTTCTGATTTTTTATTCTCAATATATTTTTTGCTAAACCTATTTTAC
AAATCACCACCGACTGAAGTGTGTGTTTACTGATGCGGCCCTGAGCTCCATGGCGAAAGGAGTGAATTTGCAGGG
CGTGAGACCGCAGTCTGCTTAGAGCACAGGAAGTGACAACCTTAGGGAGCCCCGTAGGGCGCTGCAGGCCCCGGGG
ACCCACGACGCTGGGTCTAAAGAGAGACGGAGTCTAGCTCTCCTGCCACCCAGAGTGGCTTCCATCTCAGCACTC
TGTGGGTCTGGTGTGGAAGATGCAGTCTCTGCTGATCATATGTGCCCTCTGCCAGGGCACCTACTGAGAGGTGC
GGTCTTGGGGGTGGAGGCCTGCCTGGCAGGTGTGCGTGCCCTCGTACGTGTGTTATGGGCAGTGGTCTAGGCCAGG
TATGACACCCACTCTCCTGTGAGATTTCACTTTAGTTTTTAAAAGGTCCAGTTCTACAGAGTGAACCTATCTAT
CTGAGTACTACATATGTTTTAAGACTTGGTTCTTTTTTTGAGGGATCCTTGACCCTGGGAAGTCTGGAGCACCCCT
GAGAAGGGGGCACCATGTGTGCCTTTGCCACGTGTCTTGAGGGGCTGCTTGTCTGGGAGGGAGGGAGAGAACAT
TCAGCAGCAGGTGCTTTTTTATGGCCTTTTCTTAAATAACCTAAGGGGGACACATCCATCTTGACAGAGAAGTTT
ACAGAACTCCCCCTTGAAAACCTGCTGCTGAGGCTCCTGTTAAATTTTCTGTGGCATCTTTTATGCCTTGGTAAAAA
CTGCAGTGTCTTTGGACCTGAGAGTGGCTACTCCGTGGTTTTTGTGACCTGTAAGCGTGGGGTTTCAGGGGTGTGTG
GCCCTGCAGGGTCCACAGCCTCCCTGAGCACTGACTGGAAGTTTCACTGGCTGGTGGCTGTCCCTTCTCCCATCA
GGGTCCCCAGCAAAGTTAACTACACAGAGGACCCAGGGGAAACGAGCTGTGTAGCCACTGACTTGCTCGCGCGGC
CGTGGCCTCTGAGGGGCACTCGCCGGTTAAGACAGGGTGGGAGTAGTGCTTTCCAGTTCAGACTCTAACTTCTCC
CAAAGTGTCTTAAGAAAATACTGGATCGGCTCATAGATTTATGCTCCTTATGATGCCCTAACTTGGAAGGTGTT
CTAGGGACAGGCCGGGCAGTGTCCCCACACACACCTTAGAGTCAAGGCCCCAGGGCCCCGCTGTCACTTGCCCA
AAAGATCCCTTCCGGCAGGTAAGGGACTACCAATGCTTACGTCAAAACAGCAGAATCGGCTTTGCAGTGAATTT
GGGAGCAGATATTAACCTATTTTTGTGTTGGACAGTAGTGAAATCTTGTGATTTTTAATCGCTTTGATAATACT
TCCAAATTTTATGATTTTTCTGAAGGAAATAATGCAAACATTTTAAATATGTTTCTCCCCCTTTCCAAAACTGT
TAACTAATGAGCAAGTAACACTAATTTGAATGTCTCTACAATACCCGTTGATAACTCAGTGGAGCCAGGCTTT

1489/6881
FIGURE 1380C

GGGGTAGCGGCCCTGAGCTTGCAGGGTTTCTCGCCACTGGGGCTGACCACGCCCCCAGCTGTGACCGTGGGTGTG
GCTGGCTCTCGGCCCTGCCCAGCTTTGTTCTGAGGACGTGGTGACTTCCTGAACATCAGCTTCAATCCTCCATCA
TTAATGTGAAGCAAAACACAAAAACCGCCCCAATCCCTCAGGATTCCCTGGCATCCGAAACCAGCATCTGCACCT
AAACCCATACCCACCCGTGTGCGCCACAGGGGGATGTGTCCGAATGGGCAGCTTAAAATGTGGTCACCTGTGGG
GGAAACTCTTCAGGCACCTGAAGTGAGAACCCAGCTGTCCGTCCCTCAGGCCGGCCTTTCTTCCGGCGACACCCGT
CCATGGCTGGCTGGGTCCCTTCGCAGTGTTTGTCTGTCTTGACATCTAAACCCGGCGTGTGCAGTGCCCATCT
TCCAGGACTACCTTATTTTCCAGAATTAAACCTGTTTTATAATTCAAGTTAATGCAAATGACTGTCAGTTGCCAA
ATATCTTGATCCTGTGAGTGTAGTTGATGACTGTTTGTAGTCAGTAGAGTAAATGCTGTGTCCACGGGGTGTG
ACAGCCTCACCATAACCCTGTTGAGGTGTGAAATGCCCCGTCAGAAATTAAATACAACTTAAATGTGCCTATTGG
TGTCTAAACTTCATACAATGTAAGGTCAGATTCCTTTTAGGAATACTGGGTGCTGTCACCAGGTTTGATAGTTAG
ACTTAAAAACTTGAAATTCACTTTTTGGGGGGAGGGATATACTGAAATAGAGAGTTGAGACTTGCCAGTTGGGGG
AAAATAGCATTTAAAATGGAAAGCTGTGTTTGAAAAATTGTGTATGAGTATTTTGTATTAAAAACATTTTAAAG
GCTTTTTTCTTAA

1490/6881
FIGURE 1381

MEFSIKQSPLSVQSVVKCIKMKQAPEILGSANGKTPSCEVNRECSVFLSKAQLSSSLQEGVMQKFNGHDALPFIP
ADKLDLTSRVFNGEPGAHDAKLRFSQEMKGIGTPPNTTPIKNGSPEIKLKITKTYMNGKPLFESSICGDSAAD
VSQSEENGQKPENKARRNRKRSIKYDSLLEQGLVEAALVSKISSPSDKKIPAKKESCPNTGRDKDHLKYNVGD
VWSKVSGYPWWPCMVADPLLHSYTKLKGQKKSARQYHVQFFGDAPERAWIFEKSLVAFEGEGQFEKLCQESAKQ
APTKAEKIKLLKPI SGKLRAQWEMGIVQAEAAASMSVEERKAKFTFLYVGDQLHLNPQVAKEAGIAAESLGEMAE
SSGVSEEAENPKSVREECIPMKRRRRRAKLCSSAETLESHDPDIGKSTPQKTAEADPRRGVGSPPGRKKTTVSMR
SRKGAASQFLVFCQKHRDEVVAEHPDASGEEIEELLRSQWSLLSEKQRARYNTKFALVAPVQAEEDSGNVNGKK
RNHTKRIQDPTEDAEAEDTPRKRLRTDKHSLRKRDTITDKTARTSSYKAMEAASSLKSQAATKNLSDACKPLKKR
NRSTAASSALGFSKSSSPSASLTENELLWEPTPVKLDLNPAALYCT

1491/6881
FIGURE 1382

TAGCGAGGGACGCGTAGGTGTCTTCATAAGATGCCGGGGCAGCGGCGCGCTTTCCCCCAAG**ATG**GCGTCCATG
CGGGAGAGCGACACGGCCTGTGGCTGCACAACAAGCTGGGGGCCACGGACGAGCTGTGGGCGCCGCCAGCATC
GCGTCCCTGCTCACGGCCGCGGTTCATCGACAACATCCGTCTCTGCTTCCATGGCCTCTCGTCGGCAGTGAAGCTC
AAGTTGCTACTCGGGACGCTGCACCTCCCGCGCCGCACGGTGGACGAGATGAAGGGCGCCCTAATGGAGATCATC
CAGCTCGCCAGCCTCGACTCGGACCCCTGGGTGCTCATGGTCGCCGACATCTTGAAGTCCTTTCCGGACACAGGC
TCGCTTAACCTGGAGCTGGAGGAGCAGAATCCCAACGTTAGGATATTTTGGGAGAACTTAGAGAAAAGGTGGGT
GAGTGTGAAGCGTCTGCCATGCTGCCACTGGAGTGCCAGTACTTGAACAAAAACGCCCTGACGACCCCTCGCGGGA
CCCCTCACTCCCCCGGTGAAGCATTTCAGTTAAAGCGGAAACCCAAGAGCGCCACGCTGCGGGCGGAGCTGCTG
CAGAAGTCCACGGAGACCGCCACGAGTTGAAGCGGAGCGCCGGGGTGCCCTTCCACGCCAAGGGCCGGGGGCTG
CTGCGGAAGATGGACACCACACCCCACTCAAAGGCATCCCGAAGCAGGCGCCCTTCAGAAGCCCCACGGCGCCC
AGCGTCTTCAGCCCCACAGGGAACCGGACCCCCATCCCGCCTTCCAGGACGCTGCTGCGGAAGGAACGAGGTGTG
AAGCTGCTGGACATCTCTGAGCTGGATATGGTTGGCGCTGGCCGAGAGGCGAAGCGGAGAAGGAAGACTCTCGAT
GCGGAGGTGGTGGAGAAGCCGGCCAAGGAGGAAACGGTGGTGGAGAACGCCACCCCGGACTACGCAGCCGGCCTG
GTGTCCACGCAGAACTTGGGTCCCTGAACAATGAGCCTGCGCTGCCCTCCACGAGCTACCTTCCCTCCACGCCC
AGCGTGGTTCCCGCCTCCTCCTACATCCCCAGCTCCGAGACGCCCCCAGCCCCATCTTCCCGGAAGCCAGCCGC
CCACCAGAGGAGCCAGCGCCCCGAGCCCCACGTTGCCAGCGCAGTTCAAGCAGCGGGCGCCCATGTACAACAGC
GGCCTGAGCCCTGCCACACCCACGCTGCGGCGCCACCTCGCCTCTGACACCCACCACACCTCCGGCTGTGCCC
CCTACCACTCAGACACCCCCGGTTGCCATGGTGGCCCCGAGACCCAGGCCCTGCTCAGCAGCAGCCTAAGAAG
AACCTGTCCCTCACGAGAGAGCAGATGTTGCTGCCAGGAGATGTTCAAGACGGCCAACAAAGTCACGCGGCCC
GAGAAGGCCCTCATCTGGGCTTCATGGCCGGCTCCCGAGAGAACCCGTGCCAGGAGCAGGGGGACGTGATCCAG
ATCAAGCTGAGCGAGCACACGAGGACCTGCCAAGGCGGACGGCCAGGGTAGCACAACCATGCTGGTGGACACA
GTGTTTGAGATGAACTATGCCACGGGCCAGTGGACGCGCTTCAAGAAGTACAAGCCCATGACCAATGTGTCC**TAG**

AACCACCTGCCTCACAGCTGGCCGTCACTTGTGGGGGTCCACGGGACGATGGCTTTGCCAGCTTAAAGTAACCGG
ATGGCGGACACCTGGCCCCCGAGGTCCCCCGGCCGCCGCCCTGCTGCTGACCCAGCCTGTTTTAAGTTCTGGATG
CATTTCTCTGGGGTATTTGGGGCTTATTTTTAAATTTTAATATGGGTTCCTTTTTTGTGTGATTTAAAGACACTT
TTTGACTCAACGTTACATTTTTGAATGTAGTAAGTAAATTAACCAAAAAAGTTACAACCTTCTAATTTTAGTGA
CAGCTCTGCCTGTTTGTAGACTCTTACTTTTTAAATCTTTTCTATTTTCCCTCGCTGGGGCAGTGCCCTCCTA
CCCCCAGGGTTGAGGGGACCAAGGTGGCACGGTGGTACTGGGGGTGCGGCAGGGACACCCGACCACACCAGAGCG
TGGGAGACGGTGGGCCTTGTCCTGCTGCTGCTGGGAGTTTTGTATTTCATCTTTTGTATAGTTGTGGAC
ATTTAAGACAGTCTTTGGGTACCTATTTTCATTGTAAACTATCTGAACCATTAAAGTCGAGCTTTTCTAAAGAA
AAAAAAAAAAAA

1492/6881
FIGURE 1383

MASMRESDTGLWLHNKLGATDELWAPPSIASLLTAAVIDNIRLCFHGLSSAVKLKLLLGTLLHLPRRTVDEMKGAL
MEIIQLASLDSDPWVLMVADILKSFPDTGSLNLELEEQNPNVQDILGELREKVGECEASAMLPLECQYLNKNALT
TLAGPLTPPVKHFQLKRKPKSATLRAELLQKSTETAQQLKRSAGVPPHAKGRGLLRKMDTTTPLKGIPKQAPFRS
PTAPSVFSPTGNRTPIPPSRTLLRKERGKLLDISELDMVGAGREAKRRRKTLD AEVVEKPAKEETVVENATPDY
AAGLVSTQKLGSNNPALPSTSYLPSTPSVVPASSYIPSETPPAPSSREASRPPEEPSAPSPTLPAQFKQRAP
MYNSGLSPATPTPAAPTSP LPTTPPAVAPTQTTPPVAMVAPQTQAPAQQQPKKNLSLTREQMFAAQEMFKTANK
VTRPEKALILGFMAGSRENPCQEQGDVIQIKLSEHTEDLPKADGQGSTTMLVDTVFEMNYATGQWTRFKKYPMT
NVS

1493/6881
FIGURE 1384A

TCCCAGCCTGAAACCAACACATTTTCTAATAAGTTATTTAGACAGAATAGCACTCTGCATGACTTTAATTCTTGG
GACAAAACGGTAGTTTGTACCCTAAGACACAGTTTCTGGCCCACTGTGATGGGGGTGGGTGGCCGGGTGGGTGGA
GCGTTTTTGTCTGTTGGAAACCTGGAGGGAACCTGATTGGATGTCATTTCTGCCATGGAGCACGCCTCCCAGCC
CTGGCCTGCAGGGTGGGCAGGGTGGGGGGCAAGGGAGTCCGCAGCCTCCGGGAGGAGGGGCAGGGCGCTGCCTTG
GGCTGGGTGGGAAGAGGGGTGGCCGCCTCGGCTTCCGCTGGCCATGCTCCTGGTCTCTCCTTCTGAGGTCACAG
GCAGGGGCTGCCCTGGACGGGGGGCGGGGGGGTGGCCTGGAAGGGGAGACAGAGGTGGAGGGTGGCACAGGCTG
CACATTCAGCTTAGAAGTGGACCTGGCTTTGGTGGCAGGAGAAGAATAAACACTTGCCAGACCCCTTTGTGTGG
GGGAATTGGGGAGGGGTCGTGGCAGGCAGGGTGGGCCACGGAAGTGGGTCCCAGGCATCAAGGCCACGTGCAGGG
CCATGGAGGGATGCTTCTCACGAGGCGCTTCAGAAGCGAGCGAAGGGACAGAGAAGCCCTGCGTCCAAGGGCCTT
TTGTCTCTGTTAGCAATTGAGGTGTGCAGAGCACTGTACAGACCCCACTCCCCTGTACATTCTCCTTGGAGGTGC
CCGGTCCCCGCTTGGGGATGGGAGTTTTGTAGACTGTACAGAAATCGGCACCCTATTTTCTTGCAGCTCAGATTT
TGTTAATCTGGAATATACAGACAGACGTAAAGTGTTTTAGCAAAATGGAAACAAACAGTTGTGCCTTTTTCTCT
TTTGGTTTTGGTTTGGGTTTGGCCTGGGGCTGGTCCCAGTTGGTGCGGGGCATGCTGGGGGCAGGAGGGGCAGGGC
GGGCCAGGTGGAGTCAGGTCTTGGGGGTGTCTATGTGCGGGTGTGCGCAGCGTCCCTTGGTCTGTGCCTTTGGAG
CCTCGGGCTCCTGGGGTGCAGGGTGTCTGGGGGTGGCTGTTGGAGCCCACCGACGCCAGGGCAGGGCCTGGAGGC
CCAGGGACTGCCAGTGTCTCCTTGATATTGATCCTAGCAGATCCCCCTCCTGGGGGTTCTGAGAGTCTTGGGCAG
TGTGGCCTTCTCTCATTTCTGGTGGCATCTGCGCCCGTGAGTGACCTCTTCTTGGCTGCACTGCCCTGTGGGTGG
TGAGACGCTTGGCCTTTTTTGTGCTGCCAGGACTTGGTAGAGATGGCAGGAAGGGTGTGCGGGGTGGTTGTGTG
CAGAACCCTGCCGCCCTGAGGTGAGCAGAGGCACTGGTGTGCTGCCAGGCTGGGGCGGAGCTGCCCGGAACCCCT
TGCCAGGCCAATGTGTAGCTTGGTGGCGCCCTTGAAGGCCACTGGGGGTAGGTGTGTCTCCCCCGGGGCTGGA
GGCCGGGTGCCTGGTGGGTGGGCCTGACCTGGCCACCTCATCCCTCCAGCCTGGGATCTCACTGCTCTGCACCT
GTGCACTGACGTGAATTTTATACGTTTGTAGAACTCTGATGTAACCTTCTTCTACCTCTGAAGCGCCCTCCTGGG
CCTGCTGTACGTGGCTGGTGGCGCTTCCCCGAGTGCTGGCCCCCTGCCGCTCCCATGGGCACCCACCACTC
AAACTCTGCGTGETGAGGCCCGGGGAAAGCCAGGCCGGGGCCCTAGCACTGCTCAGGGGCTGGGGCTCCTGGGAT
TTCTGTGTGTTTGAAGCCTCTGTTTTTGGAGTGGGGGGCGTGGAAGCGGGAGGGGCTGACAGTGCCTGGGGCC
AGAGCTGGGCGAAGGAGGACATCCTCACTGGACGAGCACTGCAGGCCCTGACGAGAGGCTCCGGGCAGCTGAGGGC
TGAAGCGCCTCGGGATGCCCCACACTGCCCAGAGCCACGGGTCTTGCTGTGCTGGGGGTGGGGTGGCCCCAGGCA
GCTGCCACTGCCCAGGTGTGAGTCGCTGCAGACCTGGTCCCTGAGGGTGGGAGGCCTGCTTGTGCTGAAGCTGCC
ATGTGGTCTGGCCCCCAGAAGGGCTCCTGAGCGTAGGGAGTTGAGCCCCGAGCCGTGGCGGCATCTCCTCCTCC
TTCCTCCGCCCCATGCCAGCCTTGCTTCCGGCTGGTGGCATGCCTTGGGGCCGGGCAGCAGGTGAGAAGCTGCC
CCCGGAGGGAGGGGGCCAAGGGCTGGGTGAGTCTGGCCTGAGGGGTGGATGGCTGGCCCTGGGGGAAGGCTGGGC
TGGGAGGGCCTGTGGACAGCAGGCCTGAGGCCACGAGGTCTGGGGCCACCCCTCTCCTGCTCTGGGTGTCTTTC
TCAGAGAAGATGGCAGAAGGCTGCAGGCCCTAGAGGGGACGACGGGCTGGGGACGCCCTGAGCTTCTTGGCTGTG
TGGCAGGTGCTGGGGAAGCTCTCTGGGCCATAGGGACCTGGCTCCCCCTGAGAGGCCCGCCTGCCCTGGGACAC
CCAGGGCTGTGCTGGTGGCCTGAGGCTGGGAACCTGGGTTCTTGGGCTCTGCTGGCGCCTGGGCTTTGTGGGGGC
CGAAGGTGGTTGCCCGCCGGGCAGGGGGCTGTGTGGGCCCTCGTGGGGCCACCTTCTGTGAGTGCCCGAGGGA
CGGTGGGACAGTTGCCCTGCGCCAAGGGAGCCCACTGCCATCCCCCGTGGGCTGGCGCTGCAGTCGCGCACCCCT
GTGTTGCCCTGCTGACTTGCCTTATGTCTGTTTGAAGCTGCTTCTGTTTGGCCACAGGCCTGTGTTCTTGGGCTGA
TGGCCACAGAGCTGACACTTGGGGTTTGAAGTCCAGACTTGACAGACCTGGGATCCGCTTACTCCTCCGCGCCAC
GGCTGCTGTGCTTCCAGAGGTGGCGTGATGCCTCCCGGGGCCACGGTGGGGTGAAGGATGGCGAGCCGGACATAC
CATTGTTGGATGTATTTTTTTTTTAAACAGCAATAATTAGCCATTTTAAAGGAGGGATGTACCTGTGTGTGTGCAT
GTGCACGTGTTTGAAGCTGTGTGTGTGCAAGTGGGTCTTGGATATGTGTAGTGTGAGCATGTGTGCATGT
GTGAGCCTGTGCACGTGCATGTTGTAGGTGCATAAGCATGTACACGCGTGAGCATGCATGTGCGTGTACACGTGT
ATAGGTGTACATGTGCATGAGTTGTGTACATGCGTGAGCACGTGTATAGATGTACGTGTGTGTGCGCATGTGTGC
GTGTACATGTGTTTGTGTCTTGGGTATGCATAAGCATGCACGTGTGTATGAATGTGCGTGTGTATGCATGAGCAC
GTATGCATGTGTGATGCGCATGTTCTTGTGTACTTCTCTGAGGGGGCACATATGTATGAGTGTATGAGTGCATAC
ATATGCATATGGTGTACGTGTGTGTACTTTGTGTGTGGGCATGTATGCGTATGAGTACTTGTGTGTGGCTGGTGT
ATGGGTGAGCATGCACATGTGTATGGATGCATATGTGAGCTGTACATGTAGAGTGTACATGTGTGTTGCATGAGC

1494/6881
FIGURE 1384B

ATGCATGCGTGCGAGTGCCTGTGTGTGTACTTGCATATATGTGGCTGTGCAGGTACCCGGCGGTGGTGGGCTGGC
AGTGCCCGGGGAAGCAGGTCCTGCTCACGGCTTCCCTGCTGGGCCCCAGGCCCCGGGCTGAGCCTCCCTGGCCCC
TCTTGCCCCCTCAGTGGAGCAGGGCCTGGGTGGAGGGCCTGGGCAGCTCCAGGGCAGGTCCGGGGAGGCCAGGCTT
GGGAGCACAGGGGGTGGGGTTCACCTGCTGCTGTTTGTTCGAACTGTACTGTGAGCCACGGCGGGGGCAG
ATTGTTCTGAGGCCCCAGATGTGCCAAAACAGCCCCAGGGTGGGGGCGAGCGAGTTCTGAGGAGAGGGGCTGCG
GGGGCCGGGGTGGGTGTGTGCCCCCTCCCTGAATGGCCCCAATGCTGCTGTTTTTCAATAAAACCAGAGTTGA
AGGC

1495/6881
FIGURE 1385

MSMHACECLCVYLHICGACGTRRWWAGSARGSRSCSRLPCWAFGPGLSLPGPSCPSVEQGLGGGPQQLQGRSGEA
RLGEHRGWGSPAAVCSRNCTVSPRRGQIVLRPQMCQNSPQGGGERVLRRGAAGAGGGCVPLP

1496/6881
FIGURE 1386

GAGGAGCTCTCCTGGGCGGCTGAAGAAGGAGCTTCTTCTCCGGAGTGCGAAGGCGGTGGCGCCTGCGGACCTAAC
TAGCTCCAGGTTAGGCCGAGCTTTGCGGGAAGCAGCGGACTTGAAAATACTGGAAATCTGTCCGGATCCAAATT
ATTTTGCAAGCCAGATGAGTAACCAGAGGGCATGAAAGGTTGAGAACATTTGACTTCCCTGCAAACCTTGGTATA
GATCACTTCTTTTCTGTAGGAAAGGAAAGGCACCAAAGAGCACAATGAGTACAAGAAAGCGTCGTGGTGGAGCA
ATAAATTCTAGACAAGCTCAGAAGCGAACTCGGGAAGCAACCTCCACCCCGAGATCTCCTTGGAAGCAGAACCC
ATAGAACTCGTGAAACTGCTGGAGATGAAATTGTGGACCTCACTTGTGAATCTTTAGAGCCTGTGGTGGTTGAT
CTGACTCACAATGACTCTGTTGTGATTGTTGACGAAAGAAGACCAAGGAGGAATGCTAGGAGGCTGCCCCAG
GACCATGCTGACAGCTGTGTGGTGAGCAGTGACGATGAGGAGTTGTCCAGGGACAGAGACGTATATGTGACTACC
CATACTCCCAGAAACGCCAGGGATGAGGGCGCTACAGGCCTCAGGCCCTCAGGTACTGTGAGTTGTCCCATCTGC
ATGGACGGATACTCAGAGATCGTGCAGAATGGACGTCTCATCGTTTCCACAGAATGCGGCCATGTCTTCTGTAGC
CAGTGCCTCCGTGATTCCCTGAAGAATGCTAATACTTGCCCAACTTGTAGGAAAAAGATCAACCACAAACGGTAC
CACCCCATTATATATGAAGTATTGAGAGCCCCCAGGAGAGACGGATGGACAGACAGACAGCCAGGTTCTCCAG
TGGTATCTGCCTCCATTTTCTGAGATCAAAAAGACTGTTTCGAAACCAACATCTGATATGTAAACTGCTCTTTT
GTTTCCAACCCCTTCCTTTTGTTATCTCCAGTTTGATGCTATGGCGCTGGACCCAGGGCCCTCCCAGGCCATCTC
TGTTCTCTGGGGTGGTCCAGTTCTAGAGTGGGAGAAAGGGAGTCAGGCGCATTGGGAATCGTGGTTCCAGTCTG
GTTGCAGAATCTGCACATTTGCCAAGAAATTTTCCCTGTTTGGAAAGTTTGCCCCAGCTTTCCCGGGCACACCAC
CTTTTGTCCCAAGTGCTGCGCGGTGACCAATCTGCCTGCCACACATTGACCAAGCCAGACCCGGTTACCCAGC
TCGAGGATCCCAGGTTGAAGAGTGGCCCCCTTGAGGCCCTGGAAAGACCAATCACTGGACTTCTTCCCTTGAGAGT
CAGAGGTCACCCGTGATTCTGCCTGCACCTTATCATTGATCTGCAGTGATTTCTGCAAATCAAGAGAAACTCTGC
AGGGCACTCCCCCTGTTTCCCTAAGAACGAAAAAGTGCAATAAAGGCCATTTCGTTACCTACTTTTTCAGCAGCCCACA
AGATGTAGCACTATTAGTGTCCCCCTCAGAGGCTTAATGTTGCCTGTGGAGCAGTGCCCATCCCAGCCCGTTTCT
GCCACCAGTTGTTCTCAGGAACCTTACCCATGCTCCAGCGTCCTTCACCTGGCACAGGACATGCAAGATAAATA
GGGCAGGCACGTGTTTGGGTGTCCTCTCTTTTCTGATAAAATCCATCCCGTGTGTGGCACACGCCCTCCAGTCCT
CAGTTCCCCTGCTAACGTCTGCCCCGTGTAGATACTGAGAGGTGGTGGCAGTAATTGTGGCCTTATCAGCCG
CTCAGTTCCAGGCTTTTGCCCAGGTCAGTGTGCCCCATGTTTCGAGAACCTGGCCACCTGTCTTGGCTTTCTC
ATCCTTCCCAACCCAGTGCCGTTTATTTGAGAAGCTTCTTGCCCACTGGGCTTGGATGCTTCGGGCTTCTGACTG
CTCCATAGGTTTTGACTGGTGAACAGGGGCCAGATGACAACCTCTCCTTCGCTCCACAGGTACGCGGGAGCCT
CAGGTTCTCTCAGGGGCAGCAAAGTGGCCCAAGCTGCCCTGACAGCACAGGGCCTGGGGGTGGCTAACGAGAGA
GGCCTTACAGTGCCGGCATGCCCTCTTCCACTGTCGTCTTCTCAGAGGGCCTCACGCCAAACAAACGGCCT
TTTCGTGTGAAACATCTTCAGGGCGGGAAGGGGCCACTTCTGGCTTTGTTAGCAATAACTGACCTTCAGTTTAC
CCTTCTGAAGGAGCAGGGACTCAGCACAGAATTCAGTTTAGACGGGGCTGAAGGAGTGTCCTCCTCTATGTGAA
AAGAAAATTGTTTTATTCTTCATTCTGACTTTTTAACTGTTTGGCTCACTTCCAGTTAGTTTGAATGAAAATAAT
AATTTTCTACTTGGAGTTGAAGAGGGCAGAATCCGAGCTCTCATCATTGTGATGTGTAGCATGTCTGCCCTCTG
ACTGGACATCATTGCCATTAACTTTCTTCTGGGCATCACGGCAGTGTACGATGCCAGACTTGGAGCAAGGCAA
CCTTGGAGTCAGTCCACTCATAAAATATGGTAACACCCATTTTAAAAATTTAAGTTTTGTCCTTAAAGACAACCTC
AGTGGTTAATTATAAAAAGTTGTGTTACTTCGTCCTAAATTAATTTGATAGAAAGATTTAAAAATGTGTTTTGTTT
CTACTATTGAGAACTGCGAACTAGGGAAAGGTTGGTATGAAAAAATGTCTTTCTTTTTTCAATGTACATAGTT
CAACTCTTTCTTTGTTACATTTAACTATATCCATGGATATCAGTCTGCTTTGGACTCCTCTGCTAGTGTTACAG
ATGGAAATAAAACCATTAATTTGAACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

1497/6881
FIGURE 1387

MSTRKRRGGAINSRQAQKRTREATSTPEISLEAEPIELVETAGDEIVDLTCEPLEPVVVDLTHNDSVVIVDERRR
PRRNARRLPQDHADSCVVSSDDEELSRDRDVYVTHTPRNARDEGATGLRPSGTVSCPICMDGYSEIVQNGRLIV
STECGHVFCSQLRDSLKNANTCPTCRKKINHKRYHPYI

1498/6881
FIGURE 1388A

CGGCGCGCTCGCCGGCCGAGGTGGGATCCCGAGGCCTCTCCAGTCCGCCGAGGGCGCACACCACCGGCCCGTCTCGC
CCGCCGCGCCGGGAGGTGGAGCACGAGCGCACGTGTTAGGAACCTAGAAAGATTGTACAATGAATGGTGATTCT
CGTGCTGCGGTGGTGACCTCACCACCCCGACCACAGCCCTCACAAGGAGAGGTACTTCGACCGAGTAGATGAG
AACAAACCAGAGTACTTGAGGGAGAGGAACATGGCACCAGACCTTCGCCAGGACTTCAACATGATGGAGCAAAAG
AAGAGGGTGTCCATGATTCTGCAAAGCCCTGCTTTCTGTGAAGAATTGGAATCAATGATACAGGAGCAATTTAAG
AAGGGGAAGAACCCACAGGCCTATTGGCATTACAGCAGATTGCAGATTTTATGACCACGAATGTACCAAATGTC
TACCCAGCAGCTCCGCAAGGAGGGATGGCTGCCTTAAACATGAGTCTTGGTATGGTGACTCCTGTGAACGATCTT
AGAGGATCTGATTCTATTGCGTATGACAAAGGAGAGAAAGTTATTACGGTGTAAATTGGCAGCGTTTTATAGACTA
GCAGATCTCTTTGGGTGGTCTCAGCTTATCTACAATCATATCACAACCAGAGTGAACCTCCGAGCAGGAACACTTC
CTCATTGTCCCTTTTGGGCTTCTTTACAGTGAAGTGACTGCATCCAGTTTGGTTAAGATCAATCTACAAGGAGAT
ATAGTAGATCGTGGAAGCACTAATCTGGGAGTGAATCAGGCCGGCTTCACCTTACACTCTGCAATTTATGCTGCA
CGCCCGGACGTGAAGTGCGTGCATTCACACCCAGCAGGGGCTGCGGTCTCTGCAATGAAATGTGGCCTC
TTGCCAATCTCCCCGGAGGCGCTTTCCCTTGGAGAAGTGGCTTATCATGACTACCATGGCATTCTGGTTGATGAA
GAGGAAAAAGTTTTGATTAGAAAAATCTGGGGCCTAAAAGCAAGGTTCTTATTCTCCGGAACCATGGGCTCGTG
TCAGTTGGAGAGAGCGTTGAGGAGGCCTTCTATTACATCCATAACCTTGTGGTTGCCTGTGAGATCCAGGTTTGA
ACTCTGGCCAGTGCAGGAGGACCAGACAACCTTAGTCTGCTGAATCCTGAGAAGTACAAAGCCAAGTCCCGTTCC
CCAGGGTCTCCGGTAGGGGAAGGCACTGGATCGCCTCCCAAGTGGCAGATTGGTGAGCAGGAATTTGAAGCCCTC
ATGCGGATGCTCGATAATCTGGGCTACAGAAGTGGCTACCTTATCGATACCCTGCTCTGAGAGAGAAGTCTAAA
AAATACAGCGATGTGGAGGTTCTGCTAGTGTACAGGTTACTCCTTTGCTAGTGACGGTGATTCTGGGCACTTGC
TCCCCACTCAGACACAGTTTTTCAGAAGCAGCAGCGGGAGAAGACAAGATGGCTGAACTCTGGCCGGGCGACGAA
GCTTCCGAGGAAGGGCAGAATGGAAGCAGTCCCAAGTCAAGACTAAGTGGACTAAAGAGGATGGACATAGAAGT
TCCACCTCTGCTGTCCCTAACCTGTTTGTTCATTGAACACTAACCCAAAAGAGGTCCAGGAGATGAGGAACAAG
ATCCGAGAGCAGAATTTACAGGACATTAAGACGGCTGGCCCTCAGTCCAGGTTTTGTGTGGTGTAGTGATGGAC
AGGAGCCTCGTCCAGGGAGAGCTGGTGACGGCCTCCAAGGCCATCATTGAAAAGGAGTACCAGCCCCACGTCATT
GTGAGCACCACGGGCCCCAACCCCTTACCACACTCACAGACCGTGAGCTGGAGGAGTACCGCAGGGAGGTGGAG
AGGAAGCAGAAGGGCTGTGAAGAGAATCTGGACGAGGCTAGAGAACAGAAAGAAAAGAGTCTCCAGACCAGCCT
GCGGTCCCCCACCCGCTCCACGACTCCCATCAAGCTGGAGGAAGGAGACGGATGCGCTAGAGAGTACCTGTTA
CCCTAACTTGTGCCGGAGCCGACTACTGGAGATGACAGTGATGCTGCCACCTTTAAGCCAACCTCTCCCCGATCT
GTCCCTGATGAACCTTCAGAAGCACTCGGCTTCCCAATGTTAGAGAAGGAGGAGGAAGCCCATAGACCCCCAAG
CCCCACTGAGGCCCTTACTGAGGCCAGCCCGAGCCAGCCCCAGCCCCGCGTGGCTGAAGAGGCTGCCCC
CTCAGCTGTGAGGAGGGGGCCGCCGCGGACCCTGGCAGCGATGGGTCTCCAGGCAAGTCCCCGTCCAAAAAGAA
GAAGAAGTTCCGTACCCCGTCTTTCTGAAGAAGAGCAAGAAGAAGAGTGACTCCTGAAAGCCCTGCGCTAACAC
TGTCTGTCCGGAGCGACCCTGGCTCTGCCAGCGTCCCCGGCCACGTCTGTGCTCTGTCTTGTGTAATGGAATG
CAAAAAAGCCAAGCCCTCCGCCTAGAGGTCCCTCACGTGACCAGCCCCGTGTAGCCCCGGGCTGACCCAGTGTG
TGCTCAGCAGCCCCACCCACCCCTGCCCTTGTCTCTCAGAGCCTCAGCTTCTGGGGGAGACATGCTCTCCCCA
CAGGGGGGAGGCACTAAGTCATGGTCTTGGCTGGAAGGTACTGAAGGCTTCTGCAGCTTTGGCTGCACGTCACCC
TCCTGAGCCTCACCTTTCTTGCCGTCCCTCCTGTTGTGAAATCACCACATTCTGTCTCTGCTTGGCTTCCCTCC
ACCCTAAAGTCTCAGGTGACGGACTCAGACTCCTGGCTTCATGTGGCATTCTCTCTGCTCAGTGATCTCACTTAA
ATCTATATACAAAGCCTTGGTCCCGTGAACACTCGTGTGCCACCAGCGGCCCTTGAAGAGGCAGGTCTGGGCC
AGATGCTGGGCAGGAACCCAGCGGCAGATGGGCCTGTGTGCACCCAACGTGATGCTATGCATGTCTGACCGAC
GATCCCTCGACCAGAATCAGATTCAGGAGCTCAGTTTCTTTTCACTTGGGTCTCTGGATTCTGTCTATAGGGAA
GGTATATCAGGAGGGGAAGAGAGCCTTTCTAGAATTTTCTTTGAGCAGGTTTACAATTTAGCTTACATTTTTCGAC
TGTGAACGTGAATAGGCTGCTTTTGTCTTTCTTTCCAGACCCACAGTAGAGCACTTTTCACTTATTTGGGG
GAGGCTTACGGGACTGTTCTCACCTTAACTCAGCCAGAAAGATGCCCTAGTTGTGATCAAAGGTAACTCGAGGT
GGAGGCTAGCCCTGGGGCCCCCTCGACATCACCGTCATTGATGGAGCCTGAACCGTGTGCTCCTCGGCAGATGCTG
TTGTTGTTACTTCCCTCCAAGAGGCTGGAAAAGGGCTCAGAGCTGCTGAGCAGGAACCGGAGGGGTGACCCATTT
AGGAGGTGCCGGTACCAGCCTGACTAGGTACAGGCAAGCTTGTGTGGGCCCAACAGGCCCTTGGTAGAGCTGGTG
CCAGATGTGGGCTCAGATCCTGGGCATGATGGGCCGAGCCACCTCGGATCCCACTGATTGGCCAGCCGAGCGAGA

1499/6881

FIGURE 1388B

ACCAGGCTGCTGCATGGCACTGACCGCCGCTTCCAGCTTCCTCTGAGCCGCAGGGCCTGCTACGCGGGCAAGCGT
GCTGCCCTCTCTTCTGTGTCGTTTTGTTGCCAAGGCAGAATGAAAAGTCCTTAACCGTGGACTCTTCCTTTATCCC
CTCCTTTACCCACATATGCAATGACTTTTAATTTTCACTTTTGTAGTTTAATCCTTTGTATTACAACATGAAAT
ATAGTTGCATATATGGACACCGACTTGGGAGGACAGGTCCTGAATGTCCTTCTCCAGTGTAACATGTTTTACTC
ACAAATAAAATTCTTTCAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

1500/6881
FIGURE 1389

MNGDSRAAVVTSPPPTTAPHKERYFDRVDENNPEYLREERNMAPDLRQDFNMMEQKKRVSMILQSPAFCEELESMI
QEQFKKGKNPTGLLALQQIADFMTTNVNVYPAAPQGGMAALNMSLGMVTPVNDLRGSDSIAYDKGEKLLRCKLA
AFYRLADLFGWSQLIYNHITTRVNSEQEHFLIVPFGLLYSEVTASSLVKINLQGDIVDRGSTNLGVNQAGFTLHS
AIYAARPDVKCVVHIHTPAGAAVSAMKCGLLPISPEALSLGEVAYHDYHGILVDEEEKVLIQKNLGP KSKVLILR
NHGLVSVGESVEEAFYYIHNLVVACEIQVRTLASAGGPDNLVLLNPEKYKAKSRSPGSPVGEGTGSPPKWQIGEQ
EFEALMRMLDNLGYRTGYRYPALREKSKKYSDEVPASVTGYSFASDGDSGTCSPLRHSFQKQQREKTRWLNS
GRGDEASEEGQNGSSPKSKTKWTKEDGHRTSTSAVPNLFVPLNTNPKEVQEMRNKIREQNLQDIKTAGPQSQVLC
GVVMDRSLVQGELVTASKAIIKEYQPHVIVSTTGPNPFTTLTDRELEEYRREVERKQKGCEENLDEAREQKEKS
PPDQFAVPHPPPSTPIKLEEGDGCAREYLLP

1501/6881
FIGURE 1390A

CGGCGCGCTCGCCGGCCGAGGTGGGATCCCGAGGCCCTCTCCAGTCCGCCGAGGGCGCACACCACCGGCCCGTCTCGC
CCGCCGCGCCGGGAGGTGGAGCACGAGCGCACGTGTTAGGAACCTAGAAAGATTGTACAATGAATGGTGATTCT
CGTGCTGCGGTGGTGACCTCACCACCCCGACCACAGCCCCTCACAAGGAGAGGTACTTCGACCGAGTAGATGAG
AACAAACCAGAGTACTTTGAGGGAGAGGAACATGGCACCAGACCTTCGCCAGGACTTCAACATGATGGAGCAAAAG
AAGAGGGTGTCCATGATTCTGCAAAGCCCTGCTTTCTGTGAAGAATTGGAATCAATGATACAGGAGCAATTTAAG
AAGGGGAAGAACCCACAGGCCTATTGGCATTACAGCAGATTGCAGATTTTATGACCACGAATGTACCAAATGTC
TACCCAGCAGCTCCGCAAGGAGGGATGGCTGCCTTAAACATGAGTCTTGGTATGGTGACTCCTGTGAACGATCTT
AGAGGATCTGATTCTATTGCGTATGACAAAGGAGAGAAGTTATTACGGTGTAAATTGGCAGCGTTTTATAGACTA
GCAGATCTCTTTGGGTGGTCTCAGCTTATCTACAATCATATCACAACCAGAGTGAACCTCCGAGCAGGAACACTTC
CTCATTGTCCCTTTTGGGCTTCTTTACAGTGAAGTGACTGCATCCAGTTTGGTTAAGATCAATCTACAAGGAGAT
ATAGTAGATCGTGGAAGCACTAATCTGGGAGTGAATCAGGCCGGCTTCACCTTACACTCTGCAATTTATGCTGCA
CGCCCGGACGTGAAGTGCGTCGTGCACATTACACCCCAGCAGGGGCTGCGGTCTCTGCAATGAAATGTGGCCTC
TTGCCAATCTCCCCGGAGGCGCTTTCCCTTGGAGAAGTGGCTTATCATGACTACCATGGCATTCTGGTTGATGAA
GAGGAAAAAGTTTTGATTGAGAAAAATCTGGGGCCTAAAAGCAAGGTTCTTATTCTCCGGAACCATGGGCTCGTG
TCAGTTGGAGAGAGCGTTGAGGAGGCCTTCTATTACATCCATAACCTTGTGGTTGCCTGTGAGATCCAGGTTCGA
ACTCTGGCCAGTGCAGGAGGACCAGACAACCTTAGTCCTGCTGAATCCTGAGAAGTACAAAGCCAAGTCCCCTTCC
CCAGGGTCTCCGGTAGGGGAAGGCACTGGATCGCCTCCCAAGTGGCAGATTGGTGAGCAGGAATTTGAAGCCCTC
ATGCGGATGCTCGATAATCTGGGCTACAGAAGTGGCTACCTTATCGATAACCTGCTCTGAGAGAGAAGTCTAAA
AAATACAGCGATGTGGAGGTTCCCTGCTAGTGTACAGGTTACTCCTTTGCTAGTGACGGTGATTTCGGGCACCTTGC
TCCCCACTCAGACACAGTTTTTCAAGCAGCAGCGGAGAGAAGACAAGATGGCTGAACCTCTGGCCGGGGCGACGAA
GCTTCCGAGGAAGGGCAGAATGGAAGCAGTCCCAAGTCGAAGACTAAGGTGTGGACGAACATTACACACGATCAC
GTGAAACCTTGTGTCAGTCTCTCTCGTCCGGTGTCTGCGTGCCAAGCTGTATTACCAACTGCTTGTGGACTAAA
GAGGATGGACATAGAATTCACCTCTGCTGTCCCTAACCTGTTTTGTTCCATTGAACACTAACCCAAAAGAGGTC
CAGGAGATGAGGAACAAGATCCGAGAGCAGAATTTACAGGACATTAAGACGGCTGGCCCTCAGTCCCAGGTTTTG
TGTGGTGTAGTGATGGACAGGAGCCTCGTCCAGGGAGAGCTGGTGACGGCCTCCAAGGCCATCATTGAAAAGGAG
TACCAGCCCCACGTCATTGTGAGCACCACGGGCCCCAACCCCTTACCACACTCACAGACCGTGAGCTGGAGGAG
TACCGCAGGGAGGTGGAGAGGAAGCAGAAGGGCTGTGAAGAGAATCTGGACGAGGCTAGAGAACAGAAAGAAAAG
AGTCTCCAGACCAGCCTGCGGTCCCCACCCGCTCCAGCACTCCCATCAAGCTGGAGGAAGACCTTGTGCCG
GAGCCGACTACTGGAGATGACAGTGATGCTGCCACCTTTAAGCCAACCTCTCCCCGATCTGTCCCCTGATGAACCT
TCAGAAGCACFCGGCTTCCCAATGTTAGAGAAGGAGGAGGAAGCCCATAGACCCCCAAGCCCCACTGAGGCCCCCT
ACTGAGGCCAGCCCCGAGCCAGCCCCAGACCCAGCCCCGGTGGCTGAAGAGGCTGCCCCCTCAGCTGTGCGAGGAG
GGGGCCGCCGCGGACCCCTGGCAGCGATGGGTCTCCAGGCAAGTCCCCGTCCAAAAGAAGAAGAAGTTCCGTACC
CCGTCTTTCTGAAGAAGAGCAAGAAGAAGAGTGACTCCTGAAAGCCCTGCGCTAACACTGTCTGTCCGGAGCG
ACCCTGGCTCTGCCAGCGTCCCCGGCCACGTCTGTGCTCTGTCTTGTGTAATGGAATGCAAAAAAGCCAAGCCC
TCCGCCTAGAGGTCCCCTACGTGACCAGCCCCGTGTAGCCCCGGGCTGACCCAGTGTGTGCTCAGCAGCCCCAC
CCCACCCTGCCCCCTTGTCTCTCAGAGCCTCAGCTTCTGGGGGAGACATGCTCTCCCCACAGGGGGGAGGCACTA
AGTCATGGTCTCTGGCTGGAAGGTACTGAAGGCTTCTGCAGCTTTGGCTGCACGTACCCCTCCTGAGCCTCACCTT
TCCTGCCGTCCCTCCTGTTGTGAAATCACCACATTCTGTCTCTGCTTGGCTTCCCCTCCACCCTAAAGTCTCAGG
TGACGGACTCAGACTCCTGGCTTCATGTGGCATTCTCTCTGCTCAGTGATCTCACTTAAATCTATATACAAAGCC
TTGGTCCCGTGAAAACACTCGTGTGCCACCCAGCGGCCCTGAAGAGGCAGGTCTGGGCCAGATGCTGGGCAGGAA
ACCCAGCGGCAGATGGGCCTGTGTGCACCCAACGTGATGCTATGCATGTCTGACCGACGATCCCTCGACCAGAA
TCAGATTGAGGAGCTCAGTTTCTTTTTCACTTGGGTCTCTGGATTCTGTGTCATAGGGAAGGTATATCAGGAGGGG
AAGAGGCCTTTCTAGAAATTTCTTTGAGCAGGTTTACAATTTAGCTTACATTTTTCGACTGTGAACGTGAATAGG
CTGCTTTTTGCTTTCTTTTCCAGACCCACAGTAGAGCACTTTTCACTTATTTGGGGGAGGCTTCAGGGGACT
GTTCTCACCTTAACCTCAGCCAGAAAGATGCCCTAGTTGTGATCAAAGGTAACCTCGAGGTGGAGGGTAGCCCTGGG
GCCCTCGACATCACCGTCATTGATGGAGCCTGAACCGTGTGCTCCTCGGCAGATGCTGTTGTTGTTACTTCCCT
CCAAGAGGCTGGAAAAGGGCTCAGAGCTGCTGAGCAGGAACCGGAGGGTGACCCATTTTCAAGAGGTGCCGGTACC
AGCCTGACTAGGTACAGGCAAGCTTGTGTGGGCCCAACAGGCCCTTGGTAGAGCTGGTGCCAGATGTGGGCTCAG

1502/6881
FIGURE 1390B

ATCCTGGGCATGATGGGCCGAGCCACCTCGGATCCCACTGATTGGCCAGCCGAGCGAGAACCAGGCTGCTGCATG
GCACTGACCGCCGCTTCCAGCTTCCTCTGAGCCGCAGGGCCTGCTACGCGGGCAAGCGTGCTGCCTCTCTTCTGT
GTCGTTTTGTTGCCAAGGCAGAATGAAAAGTCCTTAACCGTGGACTCTTCCTTTATCCCCCTCCTTTACCCACAT
ATGCAATGACTTTTAATTTTCACTTTTGTAGTTTAATCCTTTGTATTACAACATGAAATATAGTTGCATATATGG
ACACCGACTTGGGAGGACAGGTCCTGAATGTCCTTTCTCCAGTGTAAACATGTTTTACTCACAAATAAAATTCTTT
CAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

1503/6881
FIGURE 1391

MNGDSRAAVVTSPPPPTTAPHKERYFDRVDENNPEYLREERNMAPDLRQDFNMMEQKKRVSMILQSPAFC EELESMI
QE QFKKGKNPTGLLALQQIADFMTTNVFNVPAAAPQGGMAALNMSLGMVTPVNDLRGSDSIAYDKGEKLLRCKLA
AFYRLADLFGWSQLIYNHITTRVNSEQEHFLIVPFGLLYSEVTASSLVKINLQGDIVDRGSTNLGVNQAGFTLHS
AIYAARPDVKCVVHIHTPAGAAVSAMKCGLLPISPEALS LGEVAYHDYHGILVDEEEKVLIQKNLGP KSKVLILR
NHGLVSVGESVEEAFYYIHNLVVACEIQVRTLASAGGPDNLVLLNPEKYKAKSRSPGSPVGEGTGSPPKWQIGEQ
EFEALMRMLDNLGYRTGYRYPALREKSKKYSDEV PASVTGYSFASDGDSGTCSPLRHSFQKQ QREKTRWLNS
GRGDEASEEGQNGSSPKSKTKVWTNITHDHVKPLLQSLSSGVCVPSCITNCLWTKEDGHRITSTS AVPNL FVPLNT
NPKEVQEMRNKIREQNLQDIKTAGPQSQVLCGVVMDRSLVQGELV TASKAII EKEYQPHVIVSTTGPNPFTTLD
RELEEYRREVERKQKGCEENLDEAREQKEKSPPDQFAVPHPPPSTPIKLEEDLVPEPTTGDDSDAATFKPTLPDL
SPDEPSEALGFPMLEKEEEAHRPPSPTEAPTEASPEFAPDPAPVAEEAAPSAVEEGAAADPGSDGSPGKSPSKKK
KKFRTPSFLKKS KKKSDS

1504/6881
FIGURE 1392

GCACGTGTCTTAGGGTAGCGCGCGCCTGTCTCTCTTCGGGTCTCGGGCCCTTGGGCGCAGCGGGGCGCGCGCCAT
GGCGAAGGCGAAGAAGGTCGGGGCGCGAAGGAAGGCCTCCGGGGCGCCGGCGGGAGCGCGAGGGGGCCCCGGCGAA
GGCCAACCTCCAATCCGTTTCGAGGTGAAAGTTAACAGGCAGAAAGTTCCAGATCCTGGGCCGGAAGACGCGCCACGA
CGTGGGACTGCCCCGGGGTGTCTCGCGCACGGGCCCTCAGGAAGCGTACACAGACTTTACTAAAAGAGTACAAAGA
AAGGGATAAAATCCAATGTATTTCAGAGATAAACGCTTCGGAGAATACAACAGCAACATGAGCCCCGAGGAGAAGAT
GATGAAGAGGTTTGCTCTGGAACAGCAGCGACATCATGAGAAAAAAGCATCTACAATCTAAATGAAGATGAAGA
ATTGACTCATTATGGCCAGTCTTTGGCAGACATCGAGAAGCATAATGACATTGTGGACAGTGACAGCGATGCTGA
GGATCGAGGAACGTTGTCTGCTGAGCTGACTGCTGCCCCACTTTGGAGGAGGCGGTGGGCTCCTTCACAAGAAGAC
TCAACAGGAAGGCGAGGAGCGGGAGAAACCGAAGTCCCGGAAAGAGCTGATTGAAGAGCTCATTGCCAAGTCAAA
ACAAGAGAAGAGGGAGAGACAAGCTCAACGAGAAGATGCCCTCGAGCTCACGGAGAAGCTAGACCAAGACTGGAA
AGAAATTCAGACTCTCCTGTCCCAAAAACTCCCAAGTCAGAGAACAGAGACAAAAAGGAAAAACCCAAGCCCGA
TGCATATGACATGATGGTTTCGCGAGCTTGGCTTTGAAATGAAGGCGCAGCCCTCTAACAGGATGAAGACGGAGGC
AGAATTGGCAAAGGAAGAGCAGGAGCACCTCAGGAAGCTGGAGGCTGAGAGACTTCGAAGAATGCTTGGAAGGA
TGAGGATGAAAATGTTAAGAAACCAAAACATATGTTCAGCAGATGATCTGAATGATGGCTTCGTGCTAGATAAAGA
TGACAGGCGTTTGTCTTTCCTACAAAGATGGAAGATGAATGTTCAGGAAGATGTCCAGGAAGAGCAAAGCAAGGA
AGCCAGTGACCCTGAGAGCAACGAGGAAGAAGGTGACAGTTTCAGGCGGGGAGGACACAGAGGAGAGCGACAGCCC
AGATAGCCACTTGGACCTGGAATCCAACGTGGAGAGTGAGGAAGAAAACGAGAAGCCAGCAAAAGAGCAGAGGCA
GACTCCTGGGAAAGGGTTGATAAGCGGCAAGGAAAGAGCTGGAAAAGCTACCAGAGACGAGCTGCCCTACACGTT
CGCAGCCCCCTGAATCCTATGAGGAACCTGAGATCTCTGTTGTTAGGAAGATCGATGGAAGAGCAGCTTTTGGTGGT
GGAGAGAATTCAGAAGTGCAACCACCCGAGTCTCGCAGAAGGAAACAAAGCAAAATTAGAAAACTGTTTGGCTT
TCTTTTGGAAATACGTTGGCGATTGGCTACAGATGACCCACCAGACCTCACAGTCATTGATAAGTTGGTTGTGCA
CTTATATCATCTTTGCCAGATGTTTCTGAATCTGCAAGTGACGCTATCAAATTTGTTCTCCGAGATGCGATGCA
TGAGATGGAAGAAATGATTGAGACCAAGGCCGGGCGGCATTGCCAGGGTTGGATGTGCTCATTTATTTGAAAT
CACTGGGCTGCTATTTCCAACCTCCGACTTCTGGCACCCAGTGGTGACCCCTGCCCTCGTGTGCCTCAGTCAGCT
GCTCACCAAGTGCCCCATCCTGTCCCTCCAGGACGTGGTGAAGGGCCTGTTCTGTGCTGCCTGTTCTTGAGTA
TGTGGCTTTGTCCCAGAGGTTTATACCTGAGCTTATTAATTTTCTTCTTGGGATTCTTTACATAGCAACTCCAAA
CAAAGCAAGCCAAGGTTCCACTCTGGTGCACCCTTTCAGAGCGCTTGGGAAGAACTCGGAAGCTGCTCGTGGTGTG
TGCTAGAGAGGATGTGGCCACGTGGCAGCAGAGCAGCCTCTCCCTCCGCTGGGCGAGTAGACTGAGGGCCCCAAC
TTCGACAGAGGCCAATCATATCCGACTGTCTGCCTGGCTGTGGGCTGCCCCCTGCTGAAGCGCTGCGTGTCTCAT
GTACGGGTCCCTGCCATCCTTCCACGCCATCATGGGGCCTCTCCAAGCCCTCCTCACGGATCACCTGGCGGACTG
CAGCCACCCGCGAGGAGCTCCAGGAGCTGTGTGAGAGCACACTGACCGAAATGGAAAGCCAGAAGCAGCTCTGCCG
GCCGCTGACCTGTGAGAAGAGCAAGCCTGTCCACTGAAGCTTTTTCACACCCCGGCTGGTCAAAGTCTCGAGTT
TGGAAGAAAACAAGGCAGTAGTAAGGAGGAACAGGAAAGGAAGAGGCTGATCCACAAACACAAGCGTGAATTTAA
AGGGGCCGTTTCGAGAAATCCGCAAGGACAATCAGTTTCTGGCGAGGATGCAACTCTCAGAAATCATGGAACGGGA
TGCGGAAAGAAAGCGGAAAGTAAAGCAGCTTTTTTAACAGCCTGGCTACACAGGAAGGCGAATGGAAGGCTCTGAA
GAGGAAAAAGTTCAAAAAATTAATTACATTTTATAAATAAGGCAAGGAAGTGGACATTACCTCACATCTGCAATT
CCAACCTCTGGGAGGCCAAGGCAGGAAGATTGCTTCAGCCAGGAGTTCGAGACCAGCCTGGGCAACACAGGAA
GACCCCGTCTCTACCAAAAAACATAAAAATTAGCCAAGTGTGGTGGCACGCACCTGTAGTCCCACTACTCGGG
AGGCTGAAGCAGGAGGACTGCTTGAGCTGAGTCCAAGGTTACAGTGAGCCGTGATTGAGCCACTGCACTCCAGCC
TCGGCCACAGTGCAAGACTGTGTCGCTTAAAAAAAATTTTTTTTTTTGAGACGGAGTTTTGCTCTTGTGCCCCA
GGCTGGAGTGCAATGGCACAACCTCCACCTCCTGGGTTCAAGCGATTCTCTGCCTCAGCCTCCCGAGTAGCTGG
GATTACAGACATGTGCCACCACGCCCAGCTAATTTTGTATTTTGTAGTAGAGACGGGGTTTTCTCATGTTGGTTCAG
GCTGGTCTCGAATTCCCGACCTCAGGTAATCCACCTGCCTTGGCCCCCAATTATAGGTGTGAGCCACAGCACCC
AGCCAAAAAGTAATTTTTTTTAGAGTAATAATGCTATAATGTTGGTGTGATTCCAACCTCCAGCTCCCCCACC
CGCTGCCTGCGGTTTTGTTTCTGTAAAACGTCACCTGATGAAATAGAATGAATCCTGAAATGCACCTCTGGGAT
CGGGAATGGTCTGTGTGTTATCAGCTGCGACTGGTTCACTGCGTCTGGACAAGCCTCATGGGGACTGGGGATTCT
GGCCAGTGTAATTTCTGTCAACCACGGACGTTTGCCTTCATGTGTAGAATTTACTGTTGTTATGCAAAATTATAT
TTCAATTATAAATG

1505/6881
FIGURE 1393

MAKAKKVGARRKASGAPAGARGGPAKANSNPFEVKVNRQKFQILGRKTRHDVGLPGVSRARALRKRTQTLLKEYK
ERDKSNVFRDKRFGEYNSNMSPEEKMMKRFALEQQRHHEKKS IYNLNEDEELTHYGQSLADIEKHNDIVDSDDA
EDRGTLTSAELTAAHFGGGGGLLHKKTQQEGEEREKPKSRKELIEELIAKSKQEKRRERQAQREDALELTEKLDQDW
KEIQTLTSHKTPKSENDRDKKEKPKPDAYDMMVRELGFEMKAQPSNRMKTEAELAKEEQEHLRKLEAERLRRLGK
DEDENVKKPKHMSADDLNDGFVLDKDDRRLLSYKDGKMNVEEDVQEEQSKEASDPESNEEEGDSSGGEDTEESDS
PDSHLDLESNVESEENEKPAKEQRQTPGKGLISGKERAGKATRDELPTFAAPESYEELRSLLLGRSMEEQLLV
VERIQKCNHPSLAEGNKAKLEKLFGLLEYVGDLATDDPPDLTVIDKLVVHLYHLCQMFPEASDAIKFVLRDAM
HEMEEMIETKGRAALPGLDVLIYLIKITGLLFPTSDFWHPVVT PALVCLSQLLTKCPILSLQDVVKGLFVCCLFLE
YVALSQRFIPELINFLLGILYIATPNKASQGSLVHPPFALGKNSELLVVSAREDVATWQSSLSLRWASRLRAP
TSTEANHIRLSCLAVGLALLKRCVLMYGS LPSFHAIMGPLQALLTDHLADCSHPQELQELCQSTLTEMESQKQLC
RPLTCEKSKPVPLKLF TPRLVKVLEFGRKQGSSKEEQERKR LIHKHKREFKGAVREIRKDNQFLARMQLSEIMER
DAERKRKVKQLFNSLATQEGEWKALKRKKFKK

1506/6881
FIGURE 1394A

CCCTCCGGCTCGGCGAAGCAGGGAAGGGGAGAGAAGCAGGAGTCTGGGAGACTGCACAGGCCAGAAAGTCTGCGGA
GCGGGCCGCGCCCCCTGGCCCGCCGGGCTCCAAGTCCCGCGTCGCCGCCCTGGCGGGGACGGTGCAGCAGGCGGC
GGGATGCGGCGGGGCGGCAGCCTGAGCGCCCCGGATGCCCCGCGGGCGGGCGGCCTGCAAGAGCGACGCGCGGCT
GCTGCTGGGGCGGGACGCGCTGCGGCCGGCGCCCGCCCTGCTGGCCCCCGCGTGCTGCTGGGCGCCGCGCTCGG
CCTCGGCCCTCGGCCTTTGGCTTGGCTGCCGCGGGGCCGCCAGCGCACGCGACACCAGAAAAGACGACACTCAAAA
TCTGCTCAAGAATTTGGAGTCTAATGCGCAGACCCCTCGGAACTGGCTCCCCATCAAGGAGGAGGAAGAGAGA
AGTGCAGATGTGGAAGACAAGGAAGCTGTTGATGAATGTGAGCCGCCTTCCAACAGCAATATCACAGCATTCGC
CCTGAAGGCCAAAGTCATCTACCCCATCAATCAGAAGTTCCGGCCTCTGGCCGATGGCTCCTCCAACCCGTCTCT
GCATGAAAACTTAAAGCAGGCTGTTTTGCCACACCAGCCGGTAGAGGCCCTCTCCTTCCAGCAGTCTGGGGAGCCT
GAGCCAGGGTGAGAAGGACGACTGCAGTCTCTCATCCAGCGTCCACTCGGCCACCAGCGATGACAGGTTTTCTCAG
CCGCACCTTCCTCCGGGTGAACGCCTTCCCTGAAGTGCTGGCCTGCGAGAGTGTAGACGTTGACCTGTGTATCTA
CAGCCTTCACTTAAAGACCTGCTGCATTTGGACACGGCACTGAGGCAGGAAAAGCATATGATGTTTATTTCAGAT
TTTTAAATGTGCCTCCTTGACCTTCTTCTAAAAAGAAGTCAGATGATGAATTATACCAGAAGATCCTTTCAA
ACAAGAAAAAGATTTGGAGGAACTAGAAAAGGGACTTCAGGTCAAACGTCAAACACAGAAATGTCGGGGGCTGG
TGACTCTGAGTACATCACCTGGCTGATGTGAAAAGAAGGAGAGAGAATACTCTGAACAGCTAATCGATAATAT
GGAAGCTTTCTGAAAACAGATGGCAAATATCCAGCACTTTCTTGTGGACCAGTTTAAGTGTTCCAGCTCCAAAGC
CCGACAGCTGATGATGACTCTGACGGAAGAATGATTGCAGCCGAAGGGCTATTGTGCGATTCTCAGGAGCTGCA
GGCTCTGGACGCCCTGGAGAGGACGATGGGGCGGGCGACATGGCAAAAGTGATTGAGTTTCTGAAGCTGCAAGT
CCAGGAGGAGACCAGGTGCCGGCTGGCTGCCATCTCCACGGCCTGGAGCTGCTGGCTGGTGAGGGGAAGCTGTC
CGGGCGGCAGAAGGAGGAGCTGCTCACGCAGCAGCACAAAGGCCTTCTGGCAGGAGGCAGAGCGCTTCAGCCGGGA
GTTTGTCCAGCGAGGCAAAGACCTGGTCACGGCGTCTCTGGCTCACCAGGTGGAGGGAACGGCAAACCTCACGCT
GGCCCAAGAGGAGGAACAGAGAAGCTTCCTGGCTGAGGCCAGCCGACTGCTGACCCGAAAAGTTTCTCGAGGC
TTTTCATGAGGTCTTGAGAGGCAGAGGCTGATGCAGTGTGACCTGGAGGAAGAGGAGAATGTCAGAGCCACCGA
GGCTGTGGTTGCACTCTGCCAGGAGCTGTACTTCAGCACCGTGGACACTTTCCAGAAGTTCGTGGATGCCCTGTT
CCTTCAGACGCTCCCTGGCATGACTGGCCTCCCCCGGAAGAGTGTGACTACTTGAGGCAGGAAGTCCAGGAGAA
CGCTGCCTGGCAGCTGGGGAAGTCAAATCGCTTCCGGAGGCAGCAGTGGAACTCTTCCAGGAGCTCCTAGAGCA
AGACCAGCAGGTGTGGATGGAGGAGTGTGCGCTGTCCAGCGTGTGTCAGACACACCTGCGGGAGGACCACGAGGG
CACCATCCGCGGCGTCTTGGGCCGACTGGGCGGCCTCACTGAAGAGTCCACGCGGTGTGCTGTCAGGGGCATGA
CCTGCTGTTGCGCTCAGCCCTCCGGAGGCTGGCACTCCGCGGCAACGCCCTGGCCACCCTGACGCAGATGCGGCT
ATCGGGGAAGAAGCACCTCCTGCAGGAGCTGCGGGAACAGCGTGCAGTGGAGCAGGGGTCTCCAGTGCCTGGA
CGAGCATCAGTGGCAGCTGCTCAGGGCCCTGGAGGCGCTGTGCTGGAGGAGGCCAGCCGGCTAGAGGAGGAAGC
ACAGCAGACACGGCTGCAGCTCCAGCAGCGGCTCCTGGCCGAGGCCAGGAGGTGGGGCAGCTTCTGCAGCAGCA
CATGGAGTGCGCCATTGGGCAGGCGCTGCTGGTGCATGCACGGAATGCAGCCACCAAGAGCCGGGCCAAGGACAG
GGATGACTTCAAGAGGACACTGATGGAGGCGGCAGTGGAGAGCGTCTACGTGACCAGCGCTGGTGTGAGCCGCT
GGTGCAGGCGTATTACCAGCAAATCGGAAGGATCATGGAGGACCACGAGGAGAGAAAACTGCAGCACCTGAAGAC
CCTGCAGGGTGAGAGGATGGAATAATTACAACTGCGGAAAAAGCAAGAACTCAGCAACCCTTCGTGCGGCAGCAG
GACGGCAGGTGGCGCTCATGAGACCTCCAGGCGGTCCACCAGAGGATGCTGTCCAGCAGAAGAGGTTCTGGC
CCAGTTCCAGTGCACCAGCAGATGCGTCTGCACGCCAGCAGCAGCAGGAGGAGTGCAGCTTCTGGAAGC
CCAGCTGGAGACCCAGCTACAGGAAGCTGAACAGAAGTTCATCTCCGAGCTGGCAGCCTTGGCCCGAGTGGCCCT
TGCTGAAAGCAAACCTGTTGCTGCTAAGCGTGGGCTGCTAGAGAAGCCCTAAGGACTAAAAGGAAGAAGCCCT
GCCCCAGGAAAAGAGGGGACCTGGGGGTGCCCAACAATGAGGACCTTGCCCTCCGGGGACCAGACCTCAGGCTCACT
CAGCAGCAAAAGGCTGAGTCAGCAAGAAAGTGAAGCTGGGGACAGTGGGAACCTCAAAGAAGATGCTAAAGAGAAG
AAGCAACTTGTAGTTTAAGACCAGTCGGTGGGACAAGACCTGAAGCCCTGGGTCTGGGTGTGAATTCCACCTTCC
CTCCTGCAGTGTGAGAGGCAGCGAGGACGGAGAGGACAGCGGCATCTCTAGGCTCTTCTGAGAGGGACAGAGAA
AGAATAGAAATGTGCCCTAAAAGCATAAATGAGTATCACCTGAGAAAATTAGGCATTCCCGTCTTGGAAACACGT
CTCTGTGAGTTTGCAATTCATTTGGCTTGGAGCCCTGGCTCGATGCCCTCATGGATCTTTCTCCCAAGGAGGGAC
GTCTTGAGGGGTCCGAGCCTCAGGCCAAGGACCCCTGATGCAGACTCTGGAATCCCTGGCCCAAGGCCTGTCTG
GGCCCATCTGGGGCTGAGGACACACAGATACATAATGACACCTGCAGAAATGTATTCTCTGAGGACACTTAGAAT

1507/6881
FIGURE 1394B

ATGAGGAAGAGGGTGTGGCCCAACCTCACTTCACCTGGGGAGGGGCTTCTTCCGGACAGTAGACACCCTGCCCC
TGCAGAGAGATGTCATGGGGGCACCTGCTCTCCCTGATAGATGCTGAGAGCATCCAGAACTTCCAGACCAGCCC
TCTCACACACCCAGAAGAGGCCTTTCCCATCTGGAGAGAAGCTTCCAGACCAGCCCTTACACACCACAGCCAG
GAGGGGCCTTTCCACCTGGAGAGAACTTCCAGACCAGCCCTCATAACACAGCCAAGAGGGGCCTTTCTCACC
TGGAGAGAAATTTCCAGACCATCCCCTCTCACCACAGCCAGGAGAGGCCTTTCCACCGGTAGAGAACTTCCAG
ACCAGCCCTCACACCACAGCCAAGAGAAGCCTTTCCAGCCTGGAGAGAACTTCCAGACCAGCCCTCTCACTAC
AGCCAGGAGAGGCCTTTCCCGCCTGGAACTTCCGGACAAGCCTCTCACACACCACAGCCAGGAGAGGCCTTTCC
CACCTGGACAGAACTTCCAGACCAGCCCTCTCACCACAGCCAGGAGAGGCCTTTACCACCTGGAGAGAAGCTT
CCAGACCAGCCCTCACACCACAGCCAGGAGAGGCCTTTCCACCTGGAGAGAACTTCCAGACCAGCCCTCAT
ACCACAGCCAAGAGGGGCCTTTCTCACCTGGAGAGAACTTCCAGACCAGCCCTCACACCACCGCCAGGAGAGG
CCTTTCCACCGGGAGAGAACTTCCAGACCAGCCCTCACACCACAGCCAGGAGAGGCCTTTCCACCGGGAGA
GAACTTCCAGACCAGCCCTCTCACTACAGCCAGAAGAGGCCTTTCCACCGGGAGAGGAAGCTTCCAGACCAGCC
CCTCACACCACAGCCAGGAGAGGCCTTTCCCGCCTGGAGAGAAGCTTCAGGCCAGCTCCTCACACCACAGCCAGG
AGAGACCTTTTCTGCCTGGAGAGAACTTTCCAGACCAGCCCTCACACCACAGCCAGGAGAGGCCTTCCCTGCCT
GGAGAGAAAGCTTCCAGACCAGCCCTTACACCACAGCCAGGAGAGGCCTTTCCACCTGGAGAGAACTTCCAGA
CCAGCCCTCTCACACCACAGCCAGGAGAGGCCTTCCACCTGGAGGGAAAATTGCTCCTTTGATGGAGGTTAGGG
ACTGTCAACCTCAGCACTGTGAACATAACGGGCGAGATCATTCTTCAGGGGAAGGAGCTGCCCAGAGCATCACAG
GATGTTCCAGTGTCCCTGGTCTCTGCCCCACAGATGCCAGCACTCCCACCATTCGTGGCAACCAAGGATGTCTCC
AGACACTGCCCCGTGTCCATGGGGTTATCACCCACTGTGCTGAGTCAAAGGGTGCCTTGCCCTGGTCTAATCCAG
GACATAGCCGTGGATACGTCCAAAAATCCCCAGAACCTAGTGAGCCCTCTGGCTCTGGGAGCCCTATCTCAGGA
ATTTTCAGGGTCATTTGTGACTTTTCATTTCTTAAACCTGAAATAGACTCTCTTAGAAAACAAGTGACTCCTTCC
CAGTGGCCAAAACCTTAATCATCAGAGCGCTTCCCTCAGTTCCCTCACCCATCAGCCAGTGGGCTCTCCAAAGTTAA
CCAACAGCTCCCTCTTGTGGTTCACTAAAAAACTTGGTTATTCCATGGAGTTGTGCAAAGCTATGGCTTCCTTGG
TGCAATATTCTTAAACCTGCTTTGCATAGAAATCACTTTTGCCAGGCTGGAGTGCAGTGGCGTGATCTCGGCT
CATGGCAATCTCCATCTCCCGGTTCAAGCGATTTTCCTGCCTCAGCCTCCCCAGTAGCTGGGACTACAGACGTG
TGCCACCACGCCTGGCTAAATCTTTTTTGTATTTTATTTTAGTAGAGACGGGGTTTACCATACTGGCCAGGCTG
CTCTCGAACTCCTGACCTCATCGTCCACCTGCCTCGGCCTCCCCAAAGTGTGAGATTAGGCGTTAGCCACCGCG
CCCGGCCAGAAATCACTTTTATATTGTCACATGGGCCCTCTGCACAGAGTCCGATGGCTCCTCCCGGGGAAGCCT
GATTTTGTGACGTGTGTATAGTAAATGCAGGCCCTCTGGCAGCACCATAATTGGTCCGTTACCCTGAGCCAGAG
CTCTGAAAGCATCTGTGGAATGATCACGGGACCCTTCTCCTCTGAGAAGGCTCCCGGCTGCCTCCCCGCCACCGA
GCTTGTAGCCTGAATGCCTGGCTGTGCGATGGAGCATTTTGTCTCTGGGGTGTCTTCCTTAGCCAAAAGGGAACGT
GTCATTTGCTCGACCCTGGCCACCCCTTGCCGCCAGCTGTTGTGCTGGGCACAGTCTGGGGCACAGGCCTCCAT
GATGAAGACGCGTGGGCTGTGCGTGCTTTTCATCCGTCACAACTGGCACCTGTACCTGCCAGCAGGAGCATGATG
GGGACTTCCATGCTGGAATTGCTCCCTGATTAAAATGAGATATGGCTATTTGGAAGACACTGCATTTTAGCCAGT
GTACCTGGGCACAGACTCGGGGCTGCCCTGAAGCTGATGAAGGCTTGAAGGACGGAAGGGCTGAGCCACATGAAG
GCAGCACTCAGGGCCAGGGGAGAGAGAAGAGGATCAGCAGTGCAGCCCCAGGATGCCTCGCAGACGTGCCTTCTG
CCATGATTGTGAAGTTCTAGCCACGTGGAACCTCTCTCGGAAGAAGTGGTTGTTAAAGAGCACCTCTGCCTTCTTC
CTCTGTTGCCATGTGATCTCTGCACACGCTAGCTCTCCTTCGCCTTCTGCCATGCTGGAAAGTAGCCTGAGGCCCT
CACCAGAAGCAGACGCTGGCACCGTGCTGCTTGTACAGCCTGCAGAGCCGTGAGCCAAGTAAACCTCTTTAATTA
CCCAGCCTCAGGTGCTCCGGGAACGCCTTCCGCGGAATGAAGCGGCCCATGCCCTTGTTGACGTTGATGTTTCCG
TCTTCAAAGACGATCTTGCCCTGGCTGATGACCACTAGTGGGGAGCCGTGGCACTCCATACCCCTCGAAGATGTTG
TACTCCACCGCCTGCACCAACAGCCTCAGCGTTACTTCCAGGATTTGCTCTGCCCCAAACGAGCTGTTTATAAC
AGCGATTTTGCCTAACATTATATCATAAGCGTGTTCCAATGTTTTTTTTTCTCTCTAAAAATACCTTTTATTGAC
TGTAATATTCCACTGTATGGTCCACAGTGTATATAACCAACAACCTCACCGTTGCGCATGTAGGCTGCCGGTGGCT
TTCTATAATCAAATCAATATTGTTCTGGGGCATCACAAAGAGGAAGGGGGTCCCCXGGGGTTATGCAATGTGGC
TGCTTTGACTGTACTGGACATAAAAAATAAGTAAAATGTTCTTCACTTTTACTTAAAATGTGTCTTTAAATAAAATT
TTTTTCTAGGTT

1508/6881
FIGURE 1395

MARGGAACKSDARLLLGRDALRPAPALLAPAVLLGAALGLGLGLWLGCRAQRQTRHQKDDTQNLKKNLESNAQT
PSETGSPSRRRKREVMQSKDKEAVDECEPPSNSNITAFALKAKVIYPINQKFRPLADGSSNPSIHENLKQAVLPH
QPVEASPSSSLGSLSQGEKDDCSSSSSVHSATSDDRFLSRTFLRVNAFPEVLACESVDVDLCIYSLHLKDLLHLD
TALRQEKHMMFIQIFKMCLLDLLPKKKSDDELYQKILSKQEKDLEEEKGLQVKLSNTEMSGAGDSEYITLADVE
KKEREYSEQLIDNMEAFWKQMANIQHFLVDQFKCSSSKARQLMMTLTERMIAAEGLLCDSQELQALDALERTMGR
AHMAKVIEFLKLQVQEETRCRLAAISHGLELLAGEGKLSGRQKEELLTQQHKAFWQEAERFSREFVQRGKDLVTA
SLAHQVEGTAKLTLAQEEEQRSFLAEAOPTADPEKFLEAFHEVLERQRLMQCDLEEEENVRATEAVVALCQELYF
STVDTFQKFVDALFLQTLPGMTGLPPEECDYLRQEVQENAAWQLGKSNRFRQQWKLFQELLEQDQQVWMEECAL
SSVLQTHLREDHEGTIRGVLGRLGGLTEESTRCVLQGHDLRLSALRRLALRGNALATLTQMRLSGKKHLLQELR
EQRALEQGSSQCLDEHQWQLLRALEARVLEEASRLEEEAQQTRLQLQORLLAEAEVQGQLLQQHMECAIGQALLV
HARNAATKSRAKDRDDFKRTLMEAAVESVYVTSAGVSRLVQAYYQQIGRIMEDHEERKLQHLKTLOGERMENYKL
RKKQELSNPSSGSRTAGGAHETSQAVHQRMLSQQKRFLAQFPVHQQMRLLHAQQQQAGVMDLLEAQLETQLQEAEO
NFI SELAALARVPLAESKLLPAKRGLLEKPLRTKRRKKPLPQERGD LGVPNNEDLASGDQTSGLSLSKRLSQESE
AGDSGNSKKMLKRRSNL

1509/6881
FIGURE 1396

CCGATCCGGGCGGTGCTGGCAGCCGGAGCGGCGGGCGGGCCGAGCAGCCGGGGCAGCCGCGCGTGGGCATCC
ACGGGCGCCGAGCCTCCGTCCGTGTCTCTATCCCTCCCGGGCCTTTGTTCAGCGCGCCCGCTGGGAGCGGGGCCGA
GAGCGCCGTTCCAGTCAGACAGCCCCGAGGTCAGCGGCCGGGCGAGGGCGCCAGAGGGGGCCATGTCGTACC
AGGGCAAGAAGAGCATCCCGCACATCACGAGTGACCGACTCCTCATCAAAGGTGGACGGATCATCAACGATGACC
AATCCCTTTATGCTGACGTCTACCTGGAGGATGGACTTATCAAACAAATAGGAGAGAACTTAATCGTTCCTGGTG
GAGTGAAGACCATTGAAGCCAACGGGCGGATGGTTATTCCCGGAGGTATTGATGTCAACACGTACCTGCAGAAGC
CCTCCAGGGGATGACTGCGGCTGATGACTTCTTCCAAGGGACCAGGGCGGCCTGGTGGGCGGGACCACGATGA
TCATTGACCATGTTGTTCTGAACCTGGGTCCAGCCTACTGACCTCTTTCGAGAAGTGGCACGAAGCAGCTGACA
CCAAATCCTGCTGTGATTACTCCCTCCACGTGGACATCACAAGCTGGTACGATGGCGTTTCGGGAGGAGCTGGAGG
TGCTGGTGCAGGACAAAGGCGTCAATTCCCTCCAAGTCTACATGGCCTATAAGGATGTCTACCAAATGTCCGACA
GCCAGCTCTATGAAGCCTTTACCTTCCTTAAGGGCCTGGGAGCTGTGATCTTGGTCCATGCAGAAAATGGAGATT
TGATAGCTCAGGAACAAAAGCGGATCCTGGAGATGGGCATCACGGGTCCCGAGGGCCATGCCCTGAGCAGACCTG
AAGAGCTGGAGGCCGAGGCGGTGTTCCGGGCCATCACCATTGCGGGCCGGATCAACTGCCCTGTGTACATCACCA
AGGTCATGAGCAAGAGTGCAGCCGACATCATCGTCTGGCCAGGAAGAAAGGGCCCTAGTTTTTGGAGAGCCCA
TTGCCGCCAGCCTGGGGACCGATGGCACCCATTACTGGAGCAAGAACTGGGCCAAGGCTGCGGCGTTCGTGACTT
CCCCTCCCCTGAGCCCCGACCCTACCACGCCCCGACTACTTGACCTCCCTACTGGCCTGTGGGGACTTGCAGGTCA
CAGGCAGCGGCCACTGTCCCTACAGCACTGCCCAGAAGGCGGTGGGCAAGGACAACCTTTACCTGATCCCCGAGG
GTGTCAACGGGATAGAGGAGCGGATGACGGTCGTCTGGGACAAGGCGGTGGCTACTGGCAAAATGGATGAGAACC
AGTTTGTGCTGTACACCAGCACCAATGCAGCCAAGATCTTTAACCTGTACCCAAGGAAAGGGCGGATTGCCGTGG
GCTCGGATGCCGACGTGGTCATCTGGGACCCCGACAAGTTGAAGACCATAACAGCCAAAAGTCACAAGTCGGCGG
TGGAGTACAACATCTTCGAGGGTATGGAGTGCCACGGCTCCCCACTAGTGGTCATCAGCCAGGGCAAGATCGTCT
TTGAAGACGGAACATCAACGTCAACAAGGGCATGGGCCGCTTCATTCCGCGGAAGGCGTTCCCGGAGCACCTGT
ACCAGCGCGTCAAAATCAGGAATAAGGTTTTTGGATTGCAAGGGGTTTCCAGGGGCATGTATGACGGTCCTGTGT
ACGAGGTACCAGCTACACCCAAATATGCAACTCCCGCTCCTTCAGCCAAATCTTCGCCTTCTAAACACCAGCCCC
CACCCATCAGAAACCTCCACCAGTCCAACCTTCAGCTTATCAGGTGCCCAGATAGATGACAACAATCCCAGGCGCA
CCGGCCACCGCATCGTGGCGCCCCCTGGTGGCCGCTCCAACATCACCAGCCTCGGTGACAGTGGATGCGCGGAG
GAGCTAGCCTGAAGGATTCTGGGAATCATGTCCATCCCTTTTCTGTGATGTTTTTGAACCCACAGTTTTTAGT
TGGTGTGATGGAGGGAGGGGGAAGTCGAAGGATGCTCTTTCCCTTTTCTGTTTAGGAAGAAGTGGTACTAGTGT
GGTGTGTTTGCTTGAAATTCCTTGCCCCACAGTTGTGTTTCATGCTGAATCCACCTCGGAGCATGGTGTTCAT
TCCCCCTTCTAGTGAACCACAGGTTTTAGCATTGTCTTGTTCTGTCCCTTCCACTTCTAACTCCACTGGCTCCA
TGATTCTCTGAGTGGTGGTTCCCTTGCACCCTGTAGATGTTCTAGGATAGTTGATGCATGTTACTAAATTACGTA
TGCAAGTCTGTGAGTGGTCTGAGGGGACATCGCCAAGGACTGACTGAGACACGATGCCGAGACCTCAAGCCCTG
AGGGGCAGTCCCAAAACCCCTTACAGTGAAGATGTTTACTCATTGCCCCCACCTCTGGTCCACACTAGAAAGAAGC
TCGCCCCACCTCCACCTGTGAGATCCGTGAATTCTCGGAATGGCAGGGGAAGCCTTGCACTAGGTTGCAGAGAAG
CATCCTCCACATCCTGTGTGAGAAACCCCTGGTCTCCGTGGCACTTGTAACCTACCGTGTGTCTTCTGGTCTGTG
TGTGTTCTTCAAGCCAGCTCTAGGCTTCAGGCCGAGCCAGGTTCACTCAGAAAGAGGTCTCCCCATCCCCATT
CGGGGCTGACGATGGGGGGCTGATGGCTGCCCTGCGTGGCCTGAGTCCCTGGTCCCTCTGAGGCAGTTGACGGGG
CAGTCAGATTTTTTAAAGTTTTGTACAAAGTTTTCTTTGTAATCACTCCCATTTTTTACTTAACAACCACTTGT
GTGGCTCTTATTTCTGAATTCAAAGCTTGTGAAAAATAAAGAAAAATGAACCTGCCCACTGAAAAAAAAAAAAAA
AAA

1510/6881
FIGURE 1397

MSYQGKKSIPHITSDRLLIKGGRIINDDQSLYADVLEDGLIKQIGENLIVPGGVKTIEANGRMVIPGGIDVNTY
LQKPSQGMTAADDFFQGTRAALVGGTTMIIDHVVPEPGSSLLTSFEKWHEAADTKSCCDYSLHVDITSWYDGVRE
ELEVLVQDKGVNSFQVYMAYKD VYQMSDSQLYEAF TFLKGLGAVILVHAENGDLIAQE QKRILEMGITGPEGHAL
SRPEELEAEAVFRAITIAGRINCPVYITKVMSKSAADI IALARKKGPLVFGEPIAASLGTDGTHYWSKNWAKAAA
FVTSPPPLSPDPTTPDYLTSLACGDLQVTGSGHCPYSTAQKAVGKD NFTLIPEGVNGIEERM TVVWDKAVATGKM
DENQFVAVTSTNAAKIFNLYPRKGRIAVGSDADVVIWDPDKLKTITAKSHKSAVEYNIFEGMECHGSPLVVISQG
KIVFEDGNINVNKGMGRFIPRKAFPEHLYQRVKIRNKVFG LQGVSRGMYDGPVYEV PATPKYATPAPSAKSSPSK
HQPPFIRNLHQSNFSLSGAQIDDNNPRRTGHRIVAPPGGRSNITSLG

1511/6881
FIGURE 1398A

TTTCTCCTTGGACCAAGATGACTGATGGAAAACCTCTCCACCTCTACAAATGGCGTAGCCTTCATGGGTATTCTGG
ATGGTCGACCAGGAAACCCCTTCAGAACCTGCAACACGTCAATCTCAAGGCGCCCCGACTCCTCTCCGCGCCTG
AGTACGGGCCCCAAGCTGAAACTCAGGGCTTTAGAAGACCGGCACAGCCTCCAGTCCGTGGACTCGGGGATTCTTA
CCCTGGAGATCGGGAACCCGGAGCCTGTACCTGCAGCGCGGTCCACGTGAGGAGGAAGCAGTCCGACTCCGACC
TCATCCCCGAGCGGGCCTTCCAGAGCGCCTGCGCGCTGCCATCCTGTGCGCCACCAGCTCCTAGCAGCACCGAGC
GGGAACAGAGCGTGCGCAAATCCTCCACGTTTCCCAGGACAGGCTATGACTCGGTAAAGCTCTATAGCCCCGACCT
CCAAAGCCCTGACCCGCAGCGATGATGTCTCCGTCTGCAGCGTGTCCAGTCTTGGGACAGAGCTGTCCACCACGC
TGTCCGTGAGCAATGAGGACATCTTGGACCTTGTGGTCACGAGCAGCTCCAGTGCCATTGTGACCCTGGAGAATG
ACGATGACCCACAGTTTACCAACGTCACCTTGAGCTCTATCAAGGAAACCCGTGGCTTACACCAGCAGGACTGTG
TTCATGAAGCTGAGGAGGGGAGTAAATTGAAAATATTGGGGCCATTTAGTAACTTCTTTGCAAGGAACCTTGCTTG
CTAGAAAACAAAGTGCAAGGCTTGACAAACACAATGACTTGGGATGGAAGTTATTTGGGAAAGCGCCACTCCGAG
AGAATGCCCAGAAGGATTCAAAGAGAATACAGAAGGAATATGAAGACAAGGCTGGAAGACCTAGCAAGCCACCCCT
CTCCAAAGCAGAATGTGAGGAAGAATCTTGACTTTGAACCACTTTCCACCACCCGCACTCATCCTCGAGGACAGAC
CAGCAAATCTCCAGCAAAACCAGCTGAAGAAGCTCAGAAGCACAGACAGCAGTATGAAGAAATGGTGGTTTCAGG
CCAAAAGCGAGAGCTGAAAGAAGCCAGCGAAGGAAGAAGCAGCTGGAAGAAAGATGCAGAGTCGAGGAAAGCA
TTGGAACGCTGTGCTCACCTGGAATAATGAGATCTTACCTAACTGGGAAACAATGTGGTGCTCTAGAAAAGTTC
GAGATTTATGGTGGCAGGGAATCCCTCCAAGTGTGAGAGGCAAAGTCTGGAGCTTAGCCATTGGCAACGAGTTAA
ATATCACCCACGAGCTCTTTGACATCTGTCTTGCCGAGCCAAGGAGAGGTGGCGGTCCCTTAGCACAGGAGGCT
CTGAAGTGGAGAACGAAGATGCTGGTTTTTTCAGCAGCAGACAGAGAAGCCAGTCTGGAGCTTATTAACTGGACA
TTTCTAGAACATTTCTAATCTCTGCATTTTCCAGCAAGGTGGTCCATATCATGACATGTTGCACAGTATTTTGG
GCGCTTATACTTGTTACCGGCCAGATGTGGGTTATGTCCAGGGCATGTCTTCATAGCAGCAGTGTGATCTTGA
ACTTAGATACTGCAGATGCCTTTTATTGCCTTTTCTAACCTTCTGAATAAACCTGTCAAATGGCGTTTTTTAGAG
TGGACCATGGCCTTATGTTGACTTATTTTGTGCTGCAATTTGAAGTATTCTTTGAAGAAAATTTGCCGAAATTATTTG
CGCATTTCAAGAAGAACAACCTAACTCCAGATATCTACCTAATTGATTGGATCTTTACCTTATATAGTAAATCTC
TGCCCCCTCGACCTGGCCTGTCTGTATCTGGGACGTGTTCTGTGCGGATGGGGAAGAGTTCCGTGTTCCGCACGGCCC
TGGGCATCCTGAAGCTGTTTCGAGGACATCCTGACCAAGATGGACTTCATTACATGGCCCAGTTCCTGACCCGGC
TGCCCGAGGACCTGCCCGCCGAGGAGCTGTTTGCCCTCCATCGCCACGATCCAGATGCAGAGCCGAAACAAGAAGT
GGGCTCAGGTACTGACTGCATTGCAGAAAGACAGCCGGGAAATGGAGAAGGGAAGTCCGTCCCTCCGACACTGAG
GCTGCAGCGGGAATTGCACTCGGCACCAATCAGAGCCCCATGCCGCGGCCCTCTGTTGTTTCAGACTGACACC
CGGGCAGCCGAGAAGAACAGACGCTCTTTAAGTTTGATTCTTAACACTGGAGTTGGCCTTAAACAAAACAAACAC
AAAAACTTTTTAAAGAATTAAACCAAGGCTTAGCCTTAAGCAGCTCAGTGAAGGATGAGCTGCTGCGGACCACAG
CCAGCCACTGCATCTGCTGCACAGTTGAACGATGGGCAGTGGCTCACCCCCACTCCTTTATTTAGCAAAAGCTA
ATTAAATTGTAATGTTTCTATGTCAACTACTGGGAAGTATGTTACAGTCTTAGCCAGGATGCATGAGAGATGTTA
TTTGGGAGACTTGAGATGCTTTGGCTGATATTTACATGTTTTTCGATAAGAAAAGGGATCGCTGATTGAGTTATTGA
GATAGTTTTTCCAGAGCTGGAGGTCACGTTTCTAAAACCTACCTACGAAAGATAGCATTAAAGGAACAGGGGCTC
TCTGAGGATGGCCACTGATGTGTGTTTGTGGATACCTGGGCATCGACCCAGCCTGCAGGTGAGCTCTGGGCCATG
TTGCCCTGACACAGTCACAGTGTAGAGGCTGCAGGTGCACACGTGGGCTCCAGTGGGACTGCGCTCTGGGAGACT
GCTCCCTGGCATCGGTCTGCGGAGGTGGAAAGTTCGAGAGGAGGAGCTATTTGCGAGGAAGCCCTGTGGCAATA
GAGATAGGCTTAAAAGCGGAGAGAAACACAGAGTGGAATCAGCCCCCTGTAAGTAAAAGGGTAGAGAAAGAGATGT
GTGGCTGGGCCCCTCTCCACCTGCCTGTTTCAGTGGAGGCCAGGGCAGCAGCCAGAACAGCACATGTGGGGGAGG
TGGCCCCCTGTGCCAGCAGTGGCTCCTCTCTGCCCTTGAGCCCTGCACAGCTGGACCCATCCTAAGTGCCAGTGA
GTCCCTCACACATTTGACTTTAGAACGTGTGCTTCATGACCCGTTGTACAGACGGAGGAGCGAGCAACACACGTC
TAACAGCCTAGACAATCTCGTCAGATGCTCATACTGGACCATCAGCCTCCCCATTTAGCTGACTTTCCAGGGT
CGTTGGCAAATTTTTGTTCTGTCTTTTCCCTTGACTAATTGTAGAACTTTGTGTGAGGACTTTGGTTATCCAAAA
TCACAGAAATGAACGTTTTTGAGCTGCGCAGTCTAAAGGGCAGGCCAGTGTCTGGAAGCAGGGCCACGTGGCG
GTCCGCTGGCAGGCTGGTCTGGGGAGCATTCTGCGGACCCGGTCACGGGCTTGGTTAGTCATGCGTACATGTGT
GCCTTGGGGTGCTCTGCACTCCACGGCCCTTCTCAGCCACACTTCCCACCCAGGGGGTGCCCCAGGCTGATCT
CATTTCTGATGTTGAGGGCTGTTTGGCTCTGTCTGTATAGCTTGTAACAGGAGCCTTGGGCTAGGGGCTGGGGAA

1512/6881
FIGURE 1398B

GGAAAGCCGAGCTGGCATTCTGTTCTCTGGACTTTTTATGCCTGCCATACCCGCTAATGCTCCTCGAGGTGCAGGA
GCAGGTTGCTGAGCCAGTGGCTGCCCCGTGCCCTCCTTCCCAGCACTATCATGTGTACGTTTCCCGGACTCTGC
CCCTACATCTCAGCTGAATCTCCAGGGAGGCTGCAGAGCATCGTGGAGACCACTTTCTGCCTCGGCCTTTAAATG
CTGACTCACCTCCTCTCGGAGGAGGCGTCCTGTCTTCACGGGGGGGTCCCGGTGGCCTCCAGACGTAGCCATTTCT
CTGACATCAAGATGTTGAATGTAATCTGGTCTGAGCTGGGCCTGTGGGAGGGGCCGCTGAGGCCTGTGCGCTGT
TGTCTCGCAGATGTACTTATTTTTGTTTCATGATACGGGCGTTCCGTTTCCTTAAAGATGTATATATTTTTCTTACT
GTACATAAAGATGTTTCCTTAAGTCGTACAGAAGGTGGCGCGGCAAAGGGCCTCGTGCAGTGTGTTTCAGATTGCCC
CTGGGGATCTTCTGTGTCTTCAGCGCCCAGCCCTGCGTGTTCCTGGTGAAGCAGTTTCACATCAGTCTCTCCAGA
TAGCACTACGATGTATTCCGCTTCTGAACAGGATCCCATGCCAGTGTGGAACACCTTCCCAATCTTAGTTTCAGAA
GTGGCTTGTATGACCTGTTTCAGGGGTCACATGAGGTCTCGCCAGTTTCCTGGGTCTCTTCAGAGGCCAGAAAGT
TCTAAGTTCTGAGTCCCCGCCAGGGTCCCTTAACACCTCGGCACAGAGGCTGTTGGCAAGTGTAGAGGCTGCCT
CTGTGTGTGGTTTAAAGTAAACTGGAAATGAGACATTGACGTGCTGCTCCTCCAGAGGTCTGCACACTCCACTTCA
CATGCCGTTGACTCTCACAGTCTAAGACTTCAGGGCCGGGACCTTTGTCCAGCCTGCACAGTAGAGTGAGGCTGC
CTCTCCCGCCAGGCATTGGGATCCCATTTAGAAACGGCATTCACTTCAGAAGGTACTTTTTAACTGCTCAGTTTT
TGACTATTTTTAAATAGTTTGTCTGAAAACCTCTGATAACACTTGCTACATATCATGTTTTAATTGCTTGTACAGTT
AACCTTTAATTTTTATTTAGTAAAGTGTATCAAAGTAGGACTTTTTTGAATTGTAAATAGGTGGTTTTATTAAATA
AAAGTCAATGTAAAATTGTT

1513/6881
FIGURE 1399

MTDGKLSTSTNGVAFMGILDGRPGNPLQNLQHVNLKAPRLLSAPEYGPKLKLRALEDHRHSLQSVDSGIPTLEIGN
PEPVPCSAVHVRRKQSDSDLIPERAFQSACALPSCAPPAPSSTEREQSVRKSSTFPRTGYDSVKLYSPTSKALTR
SDDVSVCSVSSLGTELSTTLVS NEDILDLVVTSSSSAIVTLENDDDPQFTNVTLS SIKETRGLHQDCVHEAEE
GSKLKILGPFPSNFFARNLLARKQSARLDKHNDLGWKLF GKAPLRENAQKDSKRIQKEYEDKAGRPSKPPSPKQNV
RKNLDFEPLSTTALILEDRPANLPAKPAAEEAQKHQQYEEMVVQAKKRELKEAQRKKQLEERCERVEESIGNAVL
TWNNEILPNWETMWCSRKVRLWWQGIPPSVRGKVWSLAIGNELNITHELF DICLARA KERWRSLS TGGSEVENE
DAGFSAADREASLELIKLDISRTFPNLCIFQGGPYHMLHSILGAYTCYRPDVGYVQGMSFIAAVLILNLD TAD
AFIAFSNLLNKPCQMAFFRVDHGLMLTYFAAFEVFFEEENLPKLF AHFKNNLTPDIYLDWIFTLYSKSLPLDLA
CRIWDVFCRDGEEFLFRTALGILKLFEDILTKMDFIHMAQFLTRLPEDLP AEELFASIATIOMQSRNKKWAQVLT
ALQKDSREMEKGSPLRH

1514/6881
FIGURE 1400

GCT**ATC**GCGGTGGACATCACGCTGCTATTCCGGGCCAGCGTCAAGACCGTGAAGACGCGGAACAAGGCGCTGGGA
GTGGCGGTGGGCGGCGGGGTCGATGGCAGCCGGGACGAGCTGTTCCGCCGAGCCCCCGGCCAAGGGCGACTTC
TCCAGCCGGGGCCCGCGAAGTGATTTCTCACATTGGCAAACCTGAGAGATTTTCTTCTGGAACACAGGAAAGATTAT
ATTAATGCTTATAGCCATACCATGTCTGAATATGGGAGGATGACAGACACAGAACGAGACCAGATAGACCAGGAT
GCCCAGATATTCATGAGGACCTGTTTCAAGCAATTCAGCAACTACGAACAGAAGCTCACAAGGAGATACATTCC
CAGCAAGTGAAGGAGCACAGGACCGCTGTTTTGGATTTCATTGAAGATTACTTGAAAAGAGTATGTAAACTTTAC
TCAGAACAGAGAGCCATCCGAGTTAAAAGAGTGGTGGATAAGAAAAGATTATCTAAGCTGGAACCAGAACCAAAT
ACAAAGACAAGAGAATCCACATCTTCTGAGAAAGTTTCACAGAGTCCTTCAAAAGACTCTGAAGAAAACCTGCC
ACTGAAGAACGTCCAGAAAAAATTTGGCTGAAACACAACCTGAATTGGGAACGTGGGGAGATGGCAAAGGCGAA
GATGAGTTATCCCCAGAAGAAATACAAATGTTTGAACAGGAAAATCAGCGACTAATTGGTGAAATGAACAGCTTG
TTTGATGAAGTGAGGCAAATCGAAGGGAGAGTGGTTGAGATTTCCAGACTCCAAGAGATATTCACGGAAAAGGTT
TTGCAACAGGAAGCTGAGATTGACAGCATTACACAGTTAGTTGTGGGGGCAACTGAAAATATCAAGGAAGGCAAC
GAAGACATAAGAGAGGCCATTAAAAACAACGCTGGCTTCCGCGTGTGGATCCTCTTCTTCTCGTGATGTGCTCC
TTCTCCTTGCTCTTCTCGACTGGTACGACAGCT**TAG**CCAGGGCCACGGGGGCCAGCACGAGAGTCCTCATGGGC
ACTCACAGACTGCGTGCTTTTCATGTACTTCCAGTGCTGGAGCATGGTATGACCAGATTTTATCACAGTGCCATTT
GAAGGGAAAGGAGTTCAGACAGACAGACGTATTTCCCCAAAAGGGATACCCCAGGCCGATGGTGTTTCAGCCATTT
AGCAGCTGAAAAAGGAAACAGTGCACACCAATGGGAGGCAGCCTGCGTAGCCCTCATCAGGCAAGACAGACTGAA
TGCAGGAGTGGGTGATTAGCTGCTCCTTGAACCTGAGGCTGCCTTGGCAGCAGGGGCACAGCAGGCCTCAAGAGC
CCCTAATTGTCTCAGGGTTCAAAGGAAGACACTGACCTTTCCCATCCCGGTAGCTTCAGGGAAGATCATAGTTAA
TAACGTCTCTCAACAAATGATTACTTCTTTGTTTCCTTGTTGGCTTCTTGTCTGTCTGAGTCAACGAATACACAGA
CTTACTGGATTATAGAAGAGAAAATTCACATCTGCCTTGTTAATCTAATAAATATAATTACAGCCCCTTAAAAAA
AAAAA

1515/6881
FIGURE 1401

MAVDITLLFRASVKTVKTRNKALGVAVGGGVDGSRDELFRRSPRPGDFSSRAREVISHIGKLRDFLLEHRKDYI
NAYSHTMSEYGRMTDTERDQIDQDAQIFMRTCSEAIQQLRTEAHKEIHSQQVKEHRTAVLDFIEDYLKRVCKLYS
EQRAIRVKRVVDKKRLSKLEPEPNTKTRESTSSEKVSQSPSKDSEENPATEERPEKILAETQPELGTWGDGKGED
ELSPEEIQMFEQENQRLIGEMNSLFDEVQRQIEGRVVEISRLQEIFTEKVLQQEAEIDSIHQLVVGATENIKEGNE
DIREAIKNNAGFRVWILFFLVMCŠFSLLFLDWYDS

1516/6881
FIGURE 1402

AGCTTAGAGGCAAAGTTAAGAGACTCATCAGATTCTGAGCTGCTGCGGGATATTTTGAGAAGACGTGCTGTATT
GCCCAGAAGCCATCGTGTCACTGGTCGGGGTCCTGCGGAGGCTGGCTGCCTGCCGGGAGCACAAAGCAGGCTCCTG
AGGTCTACCTGGCCTTTACCGTCCGCAACCCAGAGACGTGCCAGCTGTTCACCACCGAGCTAGGCTGGACTGGGA
TCAGATGGGAAGTGGGAAGCTCATCATGACCAGAACTGTTTCCCTACAGAGAGCACTTGGAGATGGCAATGCTGA
ACCTCACACTGTAGGACTCACACACGACTCCAACGGGCTTGTGAGAATTAAGTCACTCTCGTGGGAAGAATTTTT
ATATGGGAAAGCGGATAAACTTTTCATTGCACTGGAATGTTTGGAAAATGTTAAATTCCAAATCAGGAACCACAA
ACTGCCCTCTAATAAGACATTGGCTATCTAAGCATGTGGGTGCCCCCTTTCTGCCAGCAGTTCTGGTTCCTAAGA
AAATCACCATAAATCAGACATGAAAATTCTGGCTCCAAAAATAGCATTTTCTTTGTGCAATAAAAAACGAGTGTA
TCAAGTATGACGTTCCCCAACGTGGACACACTTGTTTCCCTCAGAAAGCCAAACCTGCTGCAGCTGCCACATCCC
TGGACACACTCGTTTTCTCACAAAGCCAAGCCCGCTACAGCTGCCACATCCCTGGACACACTCGGTTCCCTCACAA
AGCCAAGCCCGCTGCAGCTGCCACATTCCCTGGGCTTATGGTGCAGCAGGTGCTTTTTTCAAGACAGGAATCAAAG
TGTAAGGAACATGGCAGAAAGGTGACACCTGGAGACCAATGCAGGATGAGGAGTACTGCAGAGGTACACAGGGAA
GTCACAGAACAGTAATACGCTGGCAGGGGCATGGGGCATGAAGAACAGAAGAAGACATTTGAGAAAAGCATCTGC
AAAATACTAAAGAGCAGAGCTTACCTCATTTTCTGTCCCCACCCCATCCAGGTACCCACCTGGCTGACCCCAGG
TCCCCGACCCAACAACAACCCCTCCCAAGTCCCTAACTCCCTTACCTGGACTTGAGACCCCTTACACCCCAGCAG
TGCTCCGCTCCAACCTTGACATCATGCTTTCTGGAACTTCCCCGTGTGTCCCACTTTCCACACTTGTTGCGCT
GGAGCACCTTCCGGCTCTACATGCTGTACGTTCCCTGTGAGCACCTCCTCTCGGCCTCTGGCCAACACAGTC
CCACCCATCTGTGGGTAACAAGGGGTGTGGGTGTTCTTTTCAGCCTTGCTAAACTGTCTGAATCAAGGATCACA
AACTACAGCCTTCAGGCCAAATCCAGCCACAGCCTGTGTTTGTAAATAAAGCTTTATTGGAACAAAGCCACACC
CCTTAATCTACAGATGATCTGTGGCTACTTTCACGCCACAACAGAGTACCATGGTTCTGACAGAGACTGGGGGAC
CCAGTCTAAATGACTTCCGACCTGGACCTTTACTGAAAATCCTCCCAATCATTCTGTTGACAAGAATGATGTATT
ACTTTTTGCAATAAGAAACAAGTAACATTTGCAGAATTCCACCCATCTTTCAAGGCTGGTCCCAGAAGTTCCTT
TGCCCACACACCTACCTGATCCTGACAACTTCCTAAACTGCAGCCCTGCCACCCGGCTCCAGCATCATTTGTGG
AGTGTGAGCTCCATAAATCCAGAGGGCAGGTGGGGGTGTGTCCTAACATTCCCGAGCCTACTGTACCGAAACGGG
ACAGCAGAGTAGGCCAGCATCTGTGACTTCTGCTCCCTCACTAGCTTTTCCACCAGACCCACATGTTACCACCC
TGGCTGTGGGAAGCAGGGATCAGGGAGTGTGGCTCGGTGCCCGTCTCCAGAACCCTGCCACCCCTGGCGTGGTGG
CAGACATGGTTACCTGCAGCTGAGCTGCCAGTTCCCTCTGAGTCCTCAAAGACCAGGCCGTTTTCTTCATGTTTCA
CTAGCTCATGTAACTGCAGAGAGAACCAAGGGAGCCTGAGAGCTGCCTGGGGAAGACACCAGACCCCTGGGGTG
CCCAGCTTGCTCCACCCACCCACGCTCAAGCCAGGCTGGGGGTGGAACAGGGGGTGTGGTTTCTGGGAGCT
GGTTCTTAGATTTGGCATCTGAAGCATATAAAGGTCTGGGGGAGTGCACATCAAAATGGCCAAATCAATTTGAGG
AGGGAGCCTTAAGGAAGGTTGTACGTTCTGTGCTGGATGCTCTTCAAGTACTGAAGAATTATTTTTGCATGTTT
TTCTTAATTCCATGGCCATGGAACAAGTAAAGGCAACCCCTGGGGACTGGTTCAGCACATAAAAGATGACTTTT
CTAGGACACC

1517/6881
FIGURE 1403

MAPEENAGTELWLQGFERRFLAARSLRSFPWQSLEAKLRDSSDSELLRDILQKTVKHPVCVKHPPSVKYARCFLS
ELIKKHEAVHTEPLDELYEVLAETLMAKESTQGHRSYLLPSGGSFTLSEITAIISHGTTGLVTWDATLYLAEWAI
ENPAAFTNRGBVLELGSGAGLTGLAICKMCRPQAYIFSDCHSRVLEQLRGNVLLNGLSLEADITANLDAFG

FIGURE 1404

TTGTCCTGGCTTCTCTGAGAAGAAAAGTTGAAAAAGGGTAAAAGTTTTTCAGGAATATTCGGGCTCTCTATTGCT
AAGCATAGCGAGTGTTCGGTTTTCTCTCTCCAACAGACATCGCTATTGCGGTTCCGAGGCAGTGGGAAGAGATCCG
GCCCCGACATCGTCGAGCTGGCGGAACCGGAGGAAGTGGAGGTGCTGGAGCCCGAGGAGGATTTTCGAGCAGTT
TCTGCTCCCGGTTCATCAACGAGATGCGCGAGGACATCGCGTCGCTGACGCGCAGACACGGGCGGGCGTACCTGCG
GAACCGGAGCAAGCTGTGGGAGATGGACAATATGCTCATCCAGATCAAAACGCAGGTGGAGGCCTCGGAGGAGAG
CGCCCTCAACCACCTCCAGAACC CGGGCGACGCGGCCGAGGGCCGGGCGGCCAAGAGGTGCGAGAAGGCCGAGGA
GAAGGCCAAGGAGATTGCGAAGATGGCAGAGATGCTGGTGGAGCTGGTCCGGCGGATAGAGAAGAGCGAGTCGTC
GTGAGCGCGGTTCGGCGGTTTCCAGCCAATGGATTCTGGTCAACTGGTGGAGATTGGCTGACACCCTGGAGAAGCC
GAAACCAGAGAGCCTTTTGTTTTCTCTTTTTTCTGTCTATGCTCTGTCTCACTTAACACTACGTTTTTCTGCTAT
GGTCTGTGGTTGATGACCTCAATATGAGTTTCGATTGTTAACGTGTTTTTGTTTGGGAAGTAATTTTGTTTGAAA
ATGCTCTCACATACAGGAATTAGGGCCTAGATTGTAAGCTCTTGACGAGTCACATTTGTTCCCGGGCTTTGGTG
GTTATTTCTAAATTTTTGAGGTGCTTTGCTATTTCTTGTGTGACCTGATAGCTCCCTGGAACCTTTGGGTCTGTGT
GTGACACATGAGACTCACAGTTGGAGTTCTCCAGCTCTGGAGGTGCTGAAGGAGCTGCATTAATTCTGGAAGACG
ACTCCATGCAGCAACTACTGAAGAAAAGGACCAGACTTCAACGGGGAGTGTGGAATGGGCCGACCTGGCTGGGACTG
GTGAATCTGGAGAAGAGCTGGAGAATGGATAGTATTGTCTGTATTTGGAGACTTTAATTTCTGTGTGAGACCAA
GGAGGAGAGATGTGTTTTGTTCAAAATTTAAATTTGTTGTGTGTACACTATCTTATGTAACCTGTCTGGTGAGTTT
GTTTGGACAACCTAACTCAGCTTTATTTGACATGGAACCTAAAATAGAAGATAAGATCTTGATATTCTGTACAAG
TTGATGTAATACCCTGATGCGTTTTAGAGGACTTGGCATAAAATGAAAGATTGGCAAAGGCCCTTGAGGGGCTTG
GGGATGACAGTATGGAACCTGTCTGCATTGGACCCTAAACTGGACTAGAAGAGGCATCTTCAAGGTTTCATACGTTG
TCCAGCTGTAAGTTTCAATTTGAGTAGCAGACCTAACAAATATTTGAGGTGAGAACCCTACCATGTTAAACAAACA
AAAACCTTACCATGTTAATAAAAGTATTCATTTGC

1519/6881
FIGURE 1405

MRPLDIVELAEPEEEVEVLEPEEDFEQFLLPVINEMREDIASLTREHGRAYLRNRSKLWEMDNMLIQIKTQVEASE
ESALNHLQNPGDAAEGRAAKRCEKAEEKAKEIAKMAEMLVELVRRIEKSESS

1520/6881
FIGURE 1406

GTTGGGGCAACCTGTTGCTAGTCTGGTCGTTGGTGACAGCGAGGCTTCCGCGCTCGCTGCTGGTGAGCAGCCCCG
GCGTGCCCCGCGGGCTGGAAGAGGCGGCGGCGTGATGCGGCCCGTGGACGCGGACGAGGCGCGGGAGCCCCGCGA
GGAGCCGGGCAGCCCGCTGAGCCCCGCGCCCCGCGCCGCGGAGAACCTGGCCTCCCTGGAGCGCGAGCGCGC
CCGGGCGCACTGGCGGGCCCCGAGGAAGCTGCTGGAGATCCAGAGCCTGCTCGACGCCATCAAGAGTGAGGTGGA
GGCAGAGGAGCGGGGCGCCCCGGGCCCCAGCACCCCGCCGCTGCGGAGGCTGAGGAGCGGGTGGCTCGGCTGTG
CGCCGAAGCAGAGAGGAAGGCTGCGGAGGCGGCGCGGATGGGCAGGCGGATCGTGGAGCTGCACCAGCGGATCGC
CGGCTGCGAGTGTCTGCTGAGCCGGCGAGGCCGCGCGGGTCTGGAGCGGAGCGCGGGCGGGAGTGTCCGCGTGGA
AGGCGCTGGGTAGGCAGGGAGGGGAGCGCAGAGCCGTGCCACGCTCTCCGCGGAGTTGGTTTCATTCTTTTTTCA
TAGGTAATTAGAGAAAATAATTTGATATGTTGTTGTAAAGAGTCATGACCACTGGAAGTATTTTCAGGACGTAGA
CCTGGTGGGTCACTACGTGGGGGGAGAGAGGTGTGAAGCGGAGGTACATGCTGGAAACGTGTGAATGTTGTTACG
AGATTGGAGCATTGCGATGACCTTCCTGCAGGTGGAAGCATTGTGCACAGGTGGTTGGGTTTGTGTTGACTCCCG
GATATGAGAATATCAAGCTCAAAATTTATGTTGTGATGATGAATTTCTCCCACTTGTACTTTAGGTGGCCAAC TG
ACGAACTGTGTTACCTGATAAGGAGTCGTGGCTGCTTGGACAGGCTCAAACCAAGAGAGCCTTTCGTTTTGTCT
CCCCTGTTTTTCTGCCTGCGTTTTTCTCCACATTAGCCACTCAATTTCCAGTACCATCCTGGCGGATGACTTCAGC
ATTAGATGGTCAGGTGTATTTTTTTTATTAATAGGCGCATTAGTTTGGAAAAGACAGCTTTTCATTAATGTCCCA
CGTAAAGGAATATGGCCTATACAGTACGTACGCTGCTGCGTGGTCATATTTGTTCCCTGTGATCTTATTGTATTTT
CAAAGTTTGGAAGTATACTCGTGTGCTTTGCTGTTTTTTTTATGCTTCCTGGAATTTGGGGACTCATGAGAGACTT
GAGGTTAGAGTTCTGCAAGTGAGAAGACACTACATGGTTGCAGCTGCCACATGAAGAACCCAAGCTCCTGTCAA
GTTGTGAATGCGACTTTGGATGAGATTAAGAAGGCCAGTGGACGGTTGGTCTTGAAGAGTGGCAGTGTGTGGAT
TTGAGGACCTCTGCAGACCATCAGATCAAAGGAGGGAGAGCTGTTTTGGGTGTTTTGTGTTTTTTTTGTTTTTATAG
CATTTTGCTTTTTTCTTGGAATGTAATTTTCTATGGCATGTTAACTGGTGCACATCGTGTAACTGTCTGGTGAG
CAACCTACAATTGGGATGAGTTCTAGGTACATGTGTTTGCTGACTTTGGGGTAAACAACTTTGTGTTATAATACAGT
CTCTGCCACAGATGCATGTGACCTCTTCAGGGGCCAGAGTGGCTGAGGAAGGAAAGCTTCAAGCTGGCCATGGG
GGTCCCAAACAGTCATTCCAGGCTTAGATGATGACTAGCCTAGGTCATCAGAGCCCAGACTCCACAGAGACTAAA
ATCAGAGCTCTGTCTTGTTATGATAAATTTCAATTTGCTTGGAAAAAGAAATGCTGAAAGCCAGTGTGTTAGAATCT
TTGTGCAGATGACCAAAGCAATTGACTTGGCCAAGAAAAGGTAAGGTAAATAAACATTTTTTCAAATGAAAAAA
AAAAAAAAAAAA

1521/6881
FIGURE 1407

MRPVDADEAREPREEPGSPLSPAPRAGRENLASLERERARAHWRARRKLEIQSLDDAIKSEVEAEERGARAPAP
RPRAEAEERVARLCAEAERKAAEAARMGRRIVELHQRIAGCECC

1522/6881
FIGURE 1408

ATGACCCACACCGTGCAAGGCTTGGATGTGGCTGGTCTTCTGAAAGCACTTCCTCCCATTAAACTTCATTCCCTGT
TCAGCAGAAACAGACGAGGACCGTCAGGAACACCTGGGAAGGAACGAGAATGGAAGAGCAGAGCAAGGGGCAAGG
CATAACAGCCCTGCAGGGAACCCAGAAGGCAGCCATCCCTGACAGTGAGAGCAGCTCTTGTCCTGGGAAGGCAGAT
GGGTCCCTGCCAGAAGCCTGGGCCTGGCCTTGTTGGCCTCACCGGCAAGCTCAAGCTTGCCCCCAGCTGCTGATC
AAGCAAGACATCGTGTCCCTTCTTAGCAACTTTGTCACCAGGCTGTGCTTCCAGAGCTGCTGTCACCGCAGTTT
TTTGTGCAGGAGCCACAACACCTACCCATGCAGTCCATGGACTTCTCAGGTCTCTGGGGCCCCCTCCTGGCTGTG
GCCTCCCCCGGGCTGGGTTTCTGGTGGCCCTCTGGAGTGCAAGAGACCTGGACTGGGCCGACTGGACCGTCCCA
CACCTGACCAACTGCTTATGCCTCGCATGTGTCACAACGTTAACAGAGTTATTTGTATATTTGGCCCACAGTT
AAAGAACCTCCTACAGATGTTACTCCCACTTTCTTGACAACAGGGGTGCTCAGTACTTTACGCCAAGCTGATTTT
GAGGCCCATAACATTCTCAGGGAGTCTGGGTATGCTGGGAAAATCAGCCAGATGCCGGTGATTTTGACACCATTA
CATTTTGATAGGGACCCACTTCAAAGCAGCCTTCATGCCAGAGATCTGTGGTTATTCGAACCTTTATTACTAGT
GACTCCCTGACTGGTATACCTGCAACACCTGGCAATGAGATCCCTGTAGAGGTGGTATTAAAGATGGTCACTGAG
ATTAAGAAGATTCCTGGTATTTCTCGAATTATGTATGACTTAACATCAAAGCCCCAGGAAGTACTGAGTGGGAG
TAA

1523/6881
FIGURE 1409

MTHTVQGLDVAGLLKALPPIKLHSCSAETDEDROEHLGRNENGRAEQGARHTALQGTQKAAIPDSESSSCPGKAD
GSCQKPGPGLVGLTGKLKLAPOLLIKQDIVSLLSNFVTRLCFPELLSPQFFVQEPQHLPMSMDFSGLWGPLLAV
ASPGLGFLVALWSARDLDWADWTVPHPDQLLMPRMCHNVNRVICIFGPPVKEPPTDVTPTFLTGTGVLSTLRQADF
EAHNILRESGYAGKISQMPVILTPLHFDRDPLQKQPSQQRSVVIRTFITSDSLTGIPATPGNEIPVEVVLKMOVTE
IKKIPGISRIMYDLTSKPPGTTEWE

1524/6881
FIGURE 1410

GAGCGGCGCCGGCCTCGGCGGCTGAGGAAAGCAGGAGGAGGTGGTGGCGGCGGGAAGATGCCGCTCTTTGGCGTA
AATTGCAATCGATTAGGGATCGTTTTCTCAGAATCAAGTTAGAAGTGAGAGTTCAGATAAGTGAGGCCGCCATTGC
TGCTTTGAACACCTCAGAAGGGGAGAAATGGATTATCAGGAGTGAAAAAGAAGAGCTTGCTGGGAGTCAAAGAAA
ATAATAAAAAAGTCCAGCACTAGGGCCCCCTTACCTACCAAACGCAAAGACCGCTCAGATGAGAAAGTCCAAGGATC
GCTCAAAAAGATAAAGGGGCCACCAAGGAGTCGAGTGAGAAGGATCGCGGCCGGGACAAAACGCGAAAGAGGCACA
GCGCTTCCAGTGGTAGCAGCAGTACCAGGTCTCGGTCCAGCTCGACTTCCAGCTCAGGCTCCAGCACCAGCACTG
GCTCAAGCAGTGGCTCCAGCTCTTCCTCAGCCTCCAGCCGCTCAGGAAGCTCCAGCACCTCCCGCAGCTCCAGCT
CTAGCAGCTCTTCTGGCTCTCCAAGTCCTTCTCGGCGCAGACACGACAACAGGAGGCGCTCCCGCTCCAAATCCA
AACCACCTAAAAGAGATGAAAAGGAGAGGAAAAGGCGGAGCCCATCTCCTAAGCCCACCAAAGTGCACATTGGGA
GACTCACCAGGAATGTGACAAAGGATCACATCATGGAGATATTTTCCACCTATGGGAAAATTAAATGATTGACA
TGCCCGTGGAAGGATGCATCCCCATCTGTCCAAAGGCTATGCGTGCGTAGAGTTTGAGAATCCAGATGAAGCTG
AGAAGGCGCTGAAGCACATGGATGGAGGACAAATTGATGGCCAGGAGATCACTGCCACCGTCGTGCTGGCCCCCT
GGCCTAGGCCAACCCCCAGGAGATTCAGCCCTCCCAGGAGAATGTTGCCACCACCGCCTATGTGGCTCAGGTCTC
CCCCACGGATGAGGAGAAGGTCCCGCTCCCCGAGGCGCAGGTCCCCCGTGCGCCGGAGATCACGGTCCCCGGGCC
GCCGCCGCCACAGGAGCCGCTCCAGCTCCAACCTCTCCCAATAAACAGGCCACTGAAGCTCTCGCCCCCTGTAAC
TATACGCCACCCAGCTCAGTTTTGTCACTTTTCTAGCCAAAGCAAGACCAGTAGGAAAGCAAACCCCTGACTCTG
GCAGGATTTGCAGGCAGCAGGCAGCACCCCTCTGCCAGCCGGGCTCCGGCTGCAGAAGTGCTGTTGGCTTGATG
CTGTGTGCCTGTCAAGATTCCTTCCGGTTTTCTGGCTAGAAAGCTCACCCGTTTCCGGTTTTAAGAGTCAGTTCA
GTGGCAGAGCCACCAGGGACAAGTGAGGCTCTTGGGGGTGGTTTGACCCTGCTTACCTGGGAGCACACTTTTCCC
TTCCCCGATGACCTGGGATGGTGGCCAGGCCGTGCCCTTGCTGTTGCTGGGCAGTGTCTTTTTGGAAAGGGAGCT
GCCCCAGGCTTTAGTGCAGCTGCCAACGCTGTTAGGCCTGGCCTCTCGAGGCCTCTTCTGACTTCAAGGGTCACA
GCCCCCAAAGATCCTCTCACCCATGGTAGTTGCTGCTCATGGTTCTGTCTGTCCGTGCACCGATGCATACACCA
CACCCACCCGCTGTACTCTGAAATTGGCGAGTGAGTTGAGAGCCAGCTCTGCGGGGTATCACGCAGCCATGGTT
GTGCCTGTCTTTCATGGTGGTCTTTTCAGGTTATCTTGGCAACATGTACATTGCTTTTATTTTTTTCTTTTTTGC
TTTTATTGTACAGTCAGTTCTATAAAATTTCTCTTTTGAGTTTTATACCTTTGTAGCATTTTAGATGACATTGTG
TTTGTACTTTGTTGTGTAGAGTGGAAGAATTGTGTTGAATAAACCAAGATCGGAATGC

1525/6881
FIGURE 1411

MDLSGVKKKSLLGVKENKKSSSTRAPSPTRKDRSDEKSKDRSKDKGATKESSEKDRGRDKTRKRHSASSGSSST
RSRSSSTSSSGSSTSTGSSSGSSSSSASSRSGSSSTSRSRSSSSSSSGSPSPSRRRHDRRRRSRSKSKPPKRDEKE
RKRRSPSPKPTKVHIGRLTRNVTKDHIMEIFSTYGKIKMIDMPVERMHPLSKGYACVEFENPDEAEKALKHMDG
GQIDGQEITATVVLAPWPRPTPRRFSPPRMLPPPPMWLRSPPMRRRRSRSPRRRSPVRRRSRSPGRRRHRSS
SNSSQ

1526/6881
FIGURE 1412

CTCCACCCTGTGGGCTGTAAGCAAGCTCAGGCTAGTCTCCCCACTGGGGGCTGTGCCCCTCCCTGGGACGGTTCC
GTGGGCAGCCCCATCACTGTGTTCAATAGTGTGAGAATGTAGCTGCGTGGGGACAATCCATCGTGGAGTGTTC
TCAGCTTAGGTCTGGACAGGAGACTTGGCGGGAGATGCTCCAGGATGTGGGTGATTCTGTACCTGGGGAGGCTAT
CTCTGACCTCCCGACAGGGGACACTCCCAGGCCAGCCCAGGGGTCAGGGGCAGAGGTGCACACCTCAGCATGAGC
CAAGACTGGGGTCAGGGAGCAGGTGTGGTTTGAGCCAGGACCTGGGGCGGGGTGGGGCCGGGGCCTTTCTGCCT
CATTTGCTTTCAATGAAAGCCTCAAAGCAGCCAAAACCAGGCTTTCCCCCTTCCTCGAGTTTGAATATCCAGAAT
CTTTTGTAATTCTTGTGGTTAAATTGTTTATTTTGTAAAAATAAAATAAAATTAGTTAATAA

1527/6881
FIGURE 1413

ATAGAAGACTACTCGGAGAGCGCTGCCTCTGGGTTGGCGGGCTGGCAGGCTGTAGCCGAGCGCGGGCAGGACTCG
TCCCGGCAGGGTTCCAGAGCCATGGGAGCGGAAAAGGAGGCTGCTGTGCGATTAAAGGAGGCCTTTTCGGCTGGCGCAG
CAGCCGCACCCAGAACCAGGCGAAGCTGGTGGTGGCGCTGAGCCGCACCTACCGCACGATGGATGATAAGACAGTT
TTTCATGAGGAGTTTCATTACCTTAAATATGTTATGGTGGTCTATAAACGTGAACCAGCTGTGGAGAGGGTA
ATAGAATTTGCAGCAAAGTTTGTTACCTCATTTCACCAATCAGATATGGAAGATGATGAGGAAGAGGAAGATGGT
GGCCTTTTAAATTATTTGTTTACTTTTCTCTTAAAGTCTCATGAAGCAAACAGCAATGCAGTGAGATTTAGAGTG
TGCCTGCTCATAAACAAGCTTTTGGGAAGTATGCCAGAAAAATGCTCAGATTGATGATGATGTGTTTGATAAAATT
AATAAAGCCATGCTTATTAGATTGAAAGATAAGATTCCAAATGTGAGAATACAGGCAGTTCTGGCGCTTTCACGA
CTTCAGGATCCCAAGGATGATGAATGCCAGTGGTTAATGCATATGCTACTTTGATTGAAAATGATTCAAATCCA
GAAGTTAGACGGGCAGTGTTATCATGTATTGCACCATCAGCAAAGACTTTGCCAAAAATTTAGGGCGCACCAAG
GATGTGAAAGAGGCTGTGAGAAAGCTGGCTTATCAGGTTTTAGCTGAAAAGGTTTCATATGAGAGCTATGTCCATT
GCTCAGAGAGTAATGCTCCTTCAACAAGGTCTTAATGACAGATCAGATGCTGTGAAACAAGCTATGCAGAAGCAT
CTTCTTCAAGGCTGGTTACGGTTCTCTGAAGGAAATATCTTAGAGTTGCTCCATCGGTTGGATGTAGAAAATTCT
TCTGAAGTGGCAGTCTCTGTTCTCAATGCCTTGTTTTCAATAACTCCTCTCAGTGAACCTGGTGGGACTCTGTAAA
AACAAATGATGGCAGGAAATTGATTCCAGTGGAACATTAACCTCCTGAAATTGCTTTGTATTGGTGTGCCCTTTGT
GAATATTTGAAATCAAAGGAGATGAAGGTGAAGAATTTTATAGAGCAGATTTTGCCAGAGCCTGTAGTATATGCA
GACTATTTATTGAGTTACATCCAGAGCATTCCAGTTGTTAATGAAGAACACAGAGGTGATTTTTCTATATTGGA
AATTTGATGACAAAAGAATTCATAGGTCAACAATTGATTCTAATTATTAAGTCTTTGGATACCAGTGAAGAAGGA
GGAAGAAAAAACTGCTGGCTGTTTTACAGGAGATTCTTATTTTACCCACAATCCCAATATCCCTGGTTTTCTTT
CTTGTTGAAAGACTACTCCACATCATTATAGATGATAATAAGAGAACACAAATTGTTACAGAAATTATCTCAGAG
ATTCGGGCGCCCATTTGTTACTGTTGGTGTAAATAACGATCCAGCTGATGTAAGAAAGAAAGAACTCAAGATGGCT
GAAATAAAAGTTAAGCTTATCGAAGCCAAAGAAGCTTTGGAAAATTGCATTACCTTACAGGATTTTAAATCGGGCA
TCAGAATTAAGAAGAAATAAAAGCATTAGAAGATGCCAGAATAAACCTTTTGAAAGAGACAGAGCAACTTGAA
ATTAAAGAAGTCCACATAGAGAAGAATGATGCTGAAACATTGCAGAAATGTCTTATTTTATGCTATGAACTGTTG
AAGCAGATGTCCATTTCAACAGGCTTAAGTGCAACCATGAATGGAATCATCGAATCTTTGATTCTTCCTGGAATA
ATAAGTATTCATCCTGTTGTAAGAAACCTGGCTGTTTTATGCTTGGGATGCTGTGGACTACAGAATCAGGATTTT
GCAAGGAAACACTTCGTATTACTATTGCAGGTTTTGCAAAATGATGATGTGACAATAAAAATAAGTGCTTTAAAG
GCAATCTTTGACCAACTGATGACGTTTCGGGATTGAACCATTTAAACTAAAAAATCAAACACTTCATTGTGAA
GGTACAGAAATAAACAGTGATGATGAGCAAGAATCAAAGAAGTTGAAGAGACTGCTACAGCTAAGAATGTTCTG
AAACTCCTTTCTGATTTCTTAGATAGTGAGGTATCTGAACTTAGGACTGGAGCTGCAGAAGGACTAGCCAAGCTG
ATGTTCTCTGGGCTTTTGGTCAGCAGCAGGATTCTTCTCGTCTTATTTTGTATGTTACAATCCTGTGACTGAA
GAGGATGTTCAACTTCGACATTGCCTAGGCGTGTTCTTCCCCGTGTTTGCTTATGCAAGCAGGACTAATCAGGAA
TGCTTTGAAGAAGCTTTTCTTCCAACCCTGCAAACTGGCCAATGCCCTGCATCTTCTCCTTTAGCTGAAATT
GATATCACAAATGTTGCTGAGTTACTTGTAGATTTGACAAGACCAAGTGGATTAAATCCTCAGGCCAAGACTTCC
CAAGATTATCAGGCCCTTAACAGTACATGACAATTTGGCTATGAAAATTTGCAATGAGATCTTAACAAGTCCGTGC
TCGCCAGAAATTCGAGTCTATACAAAAGCCTTGAGTTCTTTAGAACTCAGTAGCCATCTTGCAAAAGATCTTCTG
GTTCTATTGAATGAGATTCTGGAGCAAGTAAAAGATAGGACATGTCTGAGAGCTTTGGAGAAAATCAAGATTCAG
TTAGAAAAAGGAAATAAAGAATTTGGTGACCAAGCTGAAGCAGCACAGGATGCCACCTTGACTACAACTACTTTC
CAAAATGAAGATGAAAAGAATAAAGAAGTATATATGACTCCACTCAGGGGTGTAAGCAACCCAAGCATCAAAG
TCTACTCAGCTAAAGACTAACAGAGGACAGAGAAAAGTGACAGTTTCAGCTAGGACGAACAGGAGGTGTCAGACT
GCTGAAGCCGACTCTGAAAGTGATCATGAAGTTCCAGAACCAGAATCAGAAATGAAGATGAGACTACCAAGACGA
GCCAAACCGCAGCACTAGAAAAAGTAACTTAACCTTGCCCAATTTCTCAATGAAGATCTAAGTTAGGAAAAGA
CGATGGAGGTGGAATCCTTTAAGATTATGTCCAGTTATTTGCTTTAATAAGAAGAAGTTACCTTGTCAAAATC
AG

1528/6881
FIGURE 1414

GGCACGAGAACA**ATG**CGGGCTCCACTAGGGGGTATGTTTTCTGGGCAGCCACCCGGTCCCCCTCAGGCCCCGCCGG
GCCTTCCGGGCCAAGCTTCGCTTCTTCAGGCAGCTCCAGGCGCTCCTAGACCTTCCAGCAGTACTTTGGTGGACG
AGTTGGAGTCATCTTTTCGAGGCTTGCTTTGCATCTCTGGTGAGTCAGGACTATGTCAATGGCACCGATCAGGAAG
AAATTTCGAACCGGTGTTGATCAGTGTATCCAGAAGTTTCTGGATATTGCAAGACAGACAGAATGTTTTTCTTAC
AAAAAAGATTGCAGTTATCTGTCCAGAAACCAGAGCAAGTTATCAAAGAGGATGTGTCAGAACTAAGGAATGAAT
TACAGCGGAAAGATGCACTAGTCCAGAAGCACTTGACAAAGCTGAGGCATTGGCAGCAGGTGCTGGAGGACATCA
ACGTGCAGCACAAAAAGCCCGCCGACATCCCTCAGGGCTCCTTGGCCTACCTGGGAGCAGGCATCTGCCAACATC
CCTGCACCTCTGAAGCCAACGTGAGCAAAGGGCAGAGGCAGTTGGCCTATGAGTGGGCTGATGCG**TGA**GGXTGGC
CACACATTCTTCTGTGGACTTGACATTTTTGGAAGAACTCTTTGCCAGATAATGAGTTCATTTTAGTTTTATG
CTCCCATGAAAAATTTTCCACTATTTTTATAAGCTGTTAATTTCTTGAGTACTTTATAACATGTCTGTAGCTTG
GATAAACCAAGTAAGTATTTAAAAAAAAAAAAAAAAAAAA

1529/6881
FIGURE 1415

MAAPLGGMFSGQPPGPPQAPPGLPGQASLLQAAPGAPRPSSSTLVDELESSFEACFASLVSQDYVNGTDQEEIRT
GVDQCIQKFLDIARQTECFFLQKRLQLSVQKPEQVIKEDVSELRNELQRKDALVQKHLTKLRHWQQVLEDINVQH
KKPADIPQGSLAYLGAGICQHPCTSEANVSKGQRQLAYEWADA

1530/6881
FIGURE 1416

CCTAGACGCACGTCCGCTCGCCCGGCGCCCGAGCCAGTCCGCGCGCACGCCGTCTGCGCCCCGAAAGCCCCGCC
CAAGGCGCGCCCGCCACCGCTCTCCACGTGCTCGCTGGAGGGCGGTGCGAGGGGCCGAGCCGACAAGATGTTCT
TGCTGCCTCTTCCGGCTGCGGGGCGAGTAGTCGTCCGACGTCTGGCCGTGAGACGTTTCGGGAGCCGGAGTCTCT
CCACCGCAGACATGACGAAGGGCCTTGTTTTAGGAATCTATTCCAAAGAAAAAGAAGATGATGTGCCACAGTTCA
CAAGTGCAGGAGAGAATTTTGATAAATTGTTAGCTGGAAAGCTGAGAGAGACTTTGAACATATCTGGACCACCTC
TGAAGGCAGGGAAGACTCGAACCTTTTATGGTCTGCATCAGGACTTCCCCAGCGTGGTGCTAGTTGGCCTCGGCA
AAAAGGCAGCTGGAATCGACGAACAGGAAAACCTGGCATGAAGGCAAAGAAAAACATCAGAGCTGCTGTTGCAGCGG
GGTGCAGGCAGATTCAAGACCTGGAGCTCTCGTCTGTGGAGGTGGATCCCTGTGGAGACGCTCAGGCTGCTGCGG
AGGGAGCGGTGCTTGGTCTCTATGAATACGATGACCTAAAGCAAAAAAGAAGATGGCTGTGTCGGCAAAGCTCT
ATGGAAGTGGGGATCAGGAGGCTTGGCAGAAAGGAGTCTGTTTGCTTCTGGGCAGAACTTGGCAGCCCAATTGA
TGGAGACGCCAGCCAATGAGATGACGCCAACCAGATTTGCTGAAATTATTGAGAAGAATCTCAAAAGTGCTAGTA
GTAAAACCGAGGTCCATATCAGACCCAAGTCTTGGATTGAGGAACAGGCAATGGGATCATTCCCTCAGTGTGGCCA
AAGGATCTGACGAGCCCCAGTCTTCTTGAAATTCATAAAAGGCAGCCCCAATGCAAACGAACCAACCCCTGG
TGTTTGTTGGGAAAGGAATTACCTTTGACAGTGGTGGTATCTCCATCAAGGCTTCTGCAAATATGGACCTCATGA
GGGCTGACATGGGAGGAGCTGCAACTATATGCTCAGCCATCGTGTCTGCTGCAAAGCTTAATTTGCCCATTAATA
TTATAGGTCTGGCCCCCTCTTTGTGAAAATATGCCAGCGGCAAGGCCAACAAAGCCGGGGGATGTTGTTAGAGCCA
AAAACGGGAAGACCATCCAGGTTGATAACACTGATGCTGAGGGGAGGCTCATACTGGCTGATGCGCTCTGTTACG
CACACACGTTTAACCCGAAGGTCATCCTCAATGCCGCCACCTTAACAGGTGCCATGGATGTAGCTTTGGGATCAG
GTGCCACTGGGGTCTTTACCAATTTCATCCTGGCTCTGGAACAACTCTTCGAGGCCAGCATTGAAACAGGGGACC
GTGTCTGGAGGATGCCTCTCTTCGAACATTATACAAGACAGGTTGTAGATTGCCAGCTTGCTGATGTTAACAACA
TTGGAATAACAGATCTGCAGGAGCATGTACAGCTGCAGCATTCCCTGAAAGAATTTCGTAACCTATCCTAAGTGGG
CACATTTAGACATAGCAGGCGTGATGACCAACAAAGATGAAGTTCCCTATCTACGGAAAGGCATGACTGGGAGGC
CCACAAGGACTCTCATTGAGTTCTTACTTCGTTTCAGTCAAGACAATGCTTAGTTTCAGATACTCAAAAATGTCTT
CACTCTGTCTTAAATTGGACAGTTGAACTTAAAAGGTTTTTGAATAAATGGATGAAAATCTTTTAACGGAGACAA
AGGATGGTATTTAAAAATGTAGAACACAATGAAATTTGTATGCCTTGATTTTTTTTTTCATTTACACAAAGATTT
ATAAAGGTAAAGTTAATATCTTACTTGATAAGGATTTTTAAGATACTCTATAAATGATTAAAATTTTAGAACTT
CCTAATCACTTTTCAGAGTATATGTTTTTCATTGAGAAGCAAAATTGTAACCTCAGATTTGTGATGCTAGGAACAT
GAGCAAACCTGAAAATTACTATGCACTTGTCAGAAACAATAAATGCAACTTGTTGTG

1531/6881
FIGURE 1417

ATTTCGGAGCTGCGGGAGCCGGGCTGGCAGGAGCAGGATGGCGGCGGGCGGGCTGCAGGCGAGGCGCGCCGGGTG
CTGGTGTACGGCGGCAGGGGCGCTCTGGGTTCTCGATGCGTGCAGGCTTTTCGGGCCCCGCAACTGGTGGGTTGCC
AGCGTTGATGTGGTGGAGAATGAAGAGGCCAGCGCTAGCATCATTGTTAAAATGACAGACTCGTTCACTGAGCAG
GCTGACCAGGTGACTGCTGAGGTTGGAAAGCTCTTGGGTGAAGAGAAGGTGGATGCAATTCTTTGCGTTGCTGGA
GGATGGGCCGGGGGCAATGCCAAATCCAAGTCTCTCTTTAAGAAGTGTGACCTGATGTGGAAGCAGAGCATATGG
ACATCGACCATCTCCAGCCATCTGGCTACCAAGCATCTCAAGGAAGGAGGCCTCCTGACCTTGGCTGGCGCAAAG
GCTGCCCTGGATGGGACTCCTGGTATGATCGGGTACGGCATGGCCAAGGGTGCTGTTACCAGCTCTGCCAGAGC
CTGGCTGGGAAGAACAGCGGCATGCCGCCCCGGGGCAGCCGCCATCGCTGTGCTCCCGGTTACCTGGATACCCCG
ATGAACAGGAAATCAATGCCTGAGGCTGACTTCAGCTCCTGGACACCCTTAGAATTCCTAGTTGAAACTTTCCAT
GACTGGATCACAGGGAAAAACCGACCGAGCTCAGGAAGCCTAATCCAGGTGGTAACCACAGAAGGAAGGACGGAA
CTACCCCCAGCATATTTTTAGGCCTCATCTCAGTGCCTATGAGGGGCCTGCCAGAAAAGTCACTAACCTGTCTCA
GTGTGGCCTTGTCAGCCTTGTTGTTTTCTGTAACCCCTGTTTGTTGGTACGAGATAATGAGTCCTATTTTTCTCTC
ACATAATATGCATTTGCTCTCCTAGGACAGTGTAATACATTTATGTGAAGTAAAGACATGCGAGACTGGTGGCCT
GCAAATAGCATCCGTTGATCTGTGTTAACTGCATAGGGAGGGCTCTGCATAGCACCTGCTATAGCGGTGTCATGT
TGGATCGCTTTTGACTGTTTCATCTGTCCTTGACAGTGGCTGTCATCTTGACTACTTTGTTGATTTGTTGGTAT
TGGGGACATTTTAAAGGCTGAGTTATTTTTGAATGTCATGTTTATGTCATAGACGTAGTTTTTCGCATCCTTGAAT
TAACTGCCTTAACTCCTTTTGTTGGTATAAGCAAACTACATGGACTCTGTCCTGGTATCCTTTTCCTGTGTGGT
TGCCCCGTGTCCTCTGGCCTAGGGTTAAGTGTGCAAGATAACTACTCGTGAGTATTCAGAATGTTGTTCCCTAATA
AATGCACTTGTTGTCTGTCTTCTTTAATCAAATCACATCTTATATACAGCAGTCAGAGATGAGTATACTAGAATC
ATGGATTGCTGGAGGTCTTTTAATCTGATGTTCTCAGAAGGGGGTGGATTTAAATCCTGAAATAAATATTTCAAC
AC

1532/6881
FIGURE 1418

ACAGTCCCTCCGGGTGGCGGGGCGCCCCGAGCGTGGCAGCGCGCTAGGCGGCAGCAGCGGGCGCGGAGCGGGGCG
CGGCCGCCGCGCGTTCCCTCTTGGCGGGGTTGGCCGGCCGGGGCGGGGCGCGGCGCTCGGGCTCGAGGCATTTCGG
AGCTGCGGGAGCCGGGCTGGCAGGAGCAGGATGGCGGGCGGGCGGGCTGCAGGCGAGGCGCGCCGGGTGCTGGTG
TACGGCGGCAGGGGCGCTCTGGGTTCTCGATGCGTGACAGGCTTTTCGGGCTCGCAACTGGTGGGTTGCCAGCGTT
GATGTGGTGGAGAATGAAGAGGCCAGCGCTAGCATCATTGTTAAAATGACAGACTCGTTCACTGAGCAGGCTGAC
CAGGTGACTGCTGAGGTTGGAAAGCTCTTGGGTGAAGAGAAGGTGGATGCAATTCTTTGCGTTGCTGGAGGATGG
GCCGGGGGCAATGCCAAATCCAAGTCTCTCTTTAAGAACTGTGACCTGATGTGAAGCAGAGCATATGGACATCG
ACCATCTCCAGCCATCTGGCTACCAAGCATCTCAAGGAAGGAGGCCTCCTAACCTTGGCTGGCGCAAAGGCTGCC
CTGGATGGGACTCCTGGTATGATCGGGTACGGCATGGCCAAGGGTGCTGTTACACAGCTCTGCCAGAGCCTGGCT
GGGAAGAACAGCGGCATGCCGCCCGGGGCGAGCCGCCATCGCTGTGCTCCCGGTTACCCTGGATACCCCGATGAAC
AGGAAATCAATGCCTGAGGCTGACTTCAGCTCCTGGACACCCTTAGAATTCCTAGTTGAAACTTTCCATGACTGG
ATCACAGGGAAAAACCGACCGAGCTCAGGAAGCCTCATCTCAGTGCCATGAGGGGCCTGCCAGAAAAGTCACTA
ACCTGTCTCAGTGTGGCCTTGTCAGCCTTGTTGTTTTCTGTAAACCCTGTTTGTGGTACGAGATAATGAGTCCTA
TTTTTCTCTCACATAATATGCATTTGCTCTCCTAGGACAGTGTAATACATTTATGTGAAGTAAAGACATGCGAGA
CTGGTGGCCTGCAATAGCATCCGTCAATCTGTGTAACTGCATAGGGAGGCTCTGCATAGCACCTGCTATAGCG
GTGTCATGTTGGATCGCTTTTGTGACTGTTTCATCTGTCCTTGACAGTGGCTGTCATCTTGACTACTTTGTTGATT
TGTTGGTATTGGGGACATTTTAAAGGCTGAGTTATTTTTGAATGTCATGTTTATGTCATAGACGTAGTTTTTCGCA
TC

1533/6881
FIGURE 1419

GGCACGAGCGCAACCACAGCGCGCAGGGCAGGGCGGAGCTGGCCTCTGAGCCCCGGCCTCGGACCGCCCACTCCA
CTCCCCGGCACGCCCCGGTGCCGCCTTCCGGCTCCAGTCCCCGGGCTCGGCCTCGGCGAGGTGTAATTCGCAGCGCG
GGCCGGCCCCGGAGGCTCTCGGCGAGCGCGGCGCGGTAACAAGTGGGCGAGG**ATG**CCGTACGAGATCAAGAAGGT
GTTTCGCCAGCCTCCCGCAGGTGGAGAGGGGCGTCTCCAAGATCATCGGCGGCGACCCTAAGGGCAACAATTTTCT
GTACACCAATGGAAAGTGCCTCATCCTAAGGAACATCGACAACCCAGCCCTTGCTGACATCTACACAGAGCACGC
CCATCAGGTGGTGGTGGCCAAGTATGCGCCAGCGGATTCTACATTGCCTCCGGAGATGTGTCTGGGAAGCTGAG
GATCTGGGATACCACGCAGAAGGAGCACCTGTTGAAGTATGAGTACCAGCCTTTTCGCTGGGAAGATCAAAGACAT
TGCTTGGACTGAAGACAGTAAGAGGATCGCCGTGGTTCGGGGAAGGAAGGGAGAAGTTTGGAGCAGTCTTCCTCTG
GGATAGTGGCTCTTCTGTGGGCGAGATTACAGGACACAACAAGTCAACAGCGTGGACATCAAGCAGAGCCG
GCCATACCGGCTGGCCACGGGAAGCGATGATAACTGCGCGGCATTCTTTGAGGGACCCCCATTCAAGTTCAAGTT
CACAATTGGCGACCACAGCCGCTTTGTCAACTGTGTGCGATTCTCTCCTGATGGGAACAGATTTCGCCACAGCCAG
TGCTGACGGCCAGATATACATCTATGACGGGAAGACTGGGGAGAAGGTGTGCGCGCTGGGCGGAAGCAAGGCCCA
CGACGGTGGGATTTACGCAATTAGTTGGAGTCCCGACAGCACCCATTTGCTTTCTGCTTCTGGGGACAAAACCTC
CAAGATTTGGGACGTACGCGTGAACCTCCGTGGTACGACATTTCCCATGGGCTCCACGGTTCTGGACCAGCAGCT
GGGCTGCCTATGGCAGAAGGACCACCTGCTCAGTGTCTCCCTGTCCGGGTACATCAACTATCTGGACAGAAACAA
CCCCAGCAAGCCCTGACGTCATCAAGGGTCACAGTAAATCGATCCAGTGTCTGACGGTGCATAAAAAACGGCGG
CAAGTCCTACATTTACTCTGGGAGCCACGACGGACACATTAATTACTGGGATTACAGACGGGGGAGAACGACTC
CTTCGCTGGGAAAGGCCACACGAACCAGGTGTCCAGGATGACCGTGGATGAGTCGGGGCAGCTCATCAGCTGCAG
CATGGACGACACCGTGCCTGACACAGCCTCATGCTGCGGGACTACAGCGGACAAGGAGTTGTGAAACTGGACGT
TCAGCCAAAGTGCGTAGCCGTGCGCCCCGGGGGATACGCCGTGGTCTGTGTCATTGGACAGATTGTCTCTGCTGAA
GGATCAGAGGAAGTGCTTCAGCATCGACAACCCCGGCTACGAGCCCGAAGTTGTGGCAGTGCACCCCGGCGGGGA
CACGGTGGCAATTGGGGGTGTGGACGGCAACGTCCGCCTGTATTCCATCCTGGGCACCACGCTGAAGGATGAGGG
CAAGCTCCTAGAGGCCAAGGGCCCCGTGACCGACGTGGCCTACTCCACGACGGCGCCTTCTCTCGCGGTGTGCGA
CGCCAGCAAGGTGGTCACAGTGTTCAGCGTTGCTGACGGCTACTCGGAGAACAATGTTTTTTATGGACACCATGC
AAAAATCGTCTGCCTGGCCTGGTCCCCAGACAATGAACACTTTGCCTCCGGTGGCATGGACATGATGGTGTATGT
TTGGACCTGAGTGACCCGAAACCAGAGTCAAGATCCAAGATGCACACCGGCTGCACCATGTCAGCAGCCTGGC
CTGGCTGGACGAGCACACGCTGGTCACGACCTCCCATGATGCCTCTGTCAAGGAGTGGACAATCACCTACT**AGAGG**
AGCCCCACCCCCGCTCTGGATGGACCGAATCAGGCACTAGAGTTTAACTGCAGCGGAACATGTCATTTCTCTAT
TTCTGTGACGCGCCCCCATGCCCCACCCACCAAGAGGGCAGGAGGGCCAGTCATGACCTCGTCTCTGCAG
GGTGTCTGTACACGTTCTTCTGAAAGCTTTAGACAGTAACAGTTTGCACATGAAAAATAAAGCGAGCACCTAAAC
AATGTGTGGAGCATAACTAAAACCCACAGCCCAACCAAACCTTGAGAATGCGAAACATTCCAGAGGCGAGTAGCCT
CCAAAGCACACAGAGCCCTGGCCCCCGCGGGCTCTCACTATCTGTACAGGGGAGGTTGTACAGGTGAATGAGCC
GGGGGGCTCATGTTCTGCCTGCAGAACATTTCTGTACTAGTGAGAAGAGGGAATATGCATTGCAGTTCAGCAA
GCCGGAATTCTGTGTTGAACAGATGTCTGTCTCCCTAGTGTGTGACTCACACCTTGTGGCTGCCTTCAGAGCGCC
ACCTCCAGATCAGATGGGGACACACAACCCCTGGATATGTTTCATTGTGAGATTTTGTGCTTGATTTTAAGAATG
GAATTGTGGGTATCTTTCCTTTTTTTTTTAATGTATCTTAAGTGTGCTGTCAGTGTTTACAACTAGTGCGTTG
ACGGCACCGTGTCCAAGTTTTTAGAACCTTGTAGCCAGACCGAGGTGTCCTGGTCAACGTTTCACCATCATGC
TTTGATGTTCCCTGTCTTTCCCTCTTCTGCTCTCAAGAGCAAAGGTTAATTTAAGGACAAAGATGAAGTCACTG
TAACTAATCTGTCAATTGTTTTTACCTTCCTTTTCTTTTTCAGTGCAGAAATTAAAAGTAAGTATAAAGCACCGT
GATTGGGAGTGTTTTTGCGTGTGTGGAATCACTGGTAAATGTTGGCTGAGAACAATCCCTCCCCTGCACTTGT
GAAAACACTTTGAGCGCTTTAAGAGATTAGCCTGAGAAATAATTAAATATCTTTTCTCTTCAAAAAAAAAAAAAA
AAAA

1534/6881
FIGURE 1420

MPYEIKKVFASLPQVERGVSKIIGGDPKGNNFLYTNGKCVILRNIDNPALADIYTEHAHQVVVAKYAPSGFYIAS
GDVSGKLRIWDTTQKEHLLKYEQPFAGKIKDIAWTEDSKRIAVVGEKREKFGAVFLWDSGSSVGEITGHNKVIN
SVDIKQSRPYRLATGSDDNCAAFFEGPPFKFKFTIGDHSRNVNCFVSPDGNRFATASADGQIYIYDGKTGEKVC
ALGGSKAHDGGIYAIWSPDSTHLLSASGDKTSKIWDVSVNSVSTFFPMGSTVLDQQLGCLWQKDHLLSVSLSGY
INYLDRNNPSKPLHVIKGHKSISQCLTVHKNGGKSYIYSGSHDGHINYWDSETGENDSFAGKGHTNQVSRMTVDE
SGQLISCSMDDTVRYTSLMLRDYSGQGVVKLDVQPKCVAVGPGGYAVVVCIGQIVLLKDQKCFSIDNPGYEPEV
VAVHPGGDTVAIGGVVDGNVRLYSILGTTLKDEGKLEAKGPVTDVAYSHDGAFLAVCDASKVVTVFSVADGYSEN
NVFYGHHAIVCLAWSPDNEHFASGGMDMMVYVWTLSDPETRVKIQDAHRLHHVSSLAWLDEHTLVTTSHDASVK
EWTITY

1535/6881
FIGURE 1421

GGCACGAGCGCAACCACAGCGCGCAGGGCAGGCGGAGCTGGCCTCTGAGCCCCGGCCTCGGACCGCCCACTCCA
CTCCCCGGCACGCCCCGGTGCCGCCTTCCGGCTCCAGTCCCCGGGCTCGGCCTCGGCGAGGTGTAATTCGCAGCGCG
GGCCGGCCCCGGAGGCTCTCGGCGAGCGCGGCGCGGTAACAAGTGGGCGAGGATGCCGTACGAGATCAAGAAGGT
GTTTCGCCAGCCTCCCGCAGGTGGAGAGGGGCGTCTCCAAGATCATCGGCGGCGACCCTAAGGGCAACAATTTTCT
GTACACCAATGGAAAAGTGCCTCATCTAAGGAACATCGACAACCCAGCCCTTGCTGACATCTACACAGAGCACGC
CCATCAGGTGGTGGTGGCCAAGTATGCGCCAGCGGATTCTACATTGCCTCCGGAGATGTGTCTGGGAAGCTGAG
GATCTGGGATACCACGCAGAAGGAGCACCTGTTGAAGTATGAGTACCAGCCTTTCGCTGGGAAGATCAAAGACAT
TGCTTGGACTGAAGACAGTAAGAGGATCGCCGTGGTGGGGAAGGAAGGGAGAAGTTTGGAGCAGTCTTCTCTG
GGATAGTGGCTCTTCTGTGGGCGAGATTACAGGACACAACAAAGTCATCAACAGCGTGGACATCAAGCAGAGCCG
GCCATACCGGCTGGCCACGGGAAGCGATGATAACTGCGCGGCATTCTTTGAGGGACCCCCATTCAAGTTCAGTT
CACAAATTGGCGACCACAGCCGCTTTGTCAACTGTGTGCGATTCTCTCTGATGGGAACAGATTTGCCACAGCCAG
TGCTGACGGCCAGATATACATCTATGACGGGAAGACTGGGGAGAAGGTGTGCGCGCTGGGCGGAAGCAAGGCCCA
CGACGGTGGGATTTACGCAATTAGTTGGAGTCCCAGACAGCACCCATTGCTTTCTGCTTCTGGGGACAAAACCTC
CAAGATTTGGGACGTCAGCGTGAACCTCCGTGGTCAGCACATTTCCCATGGGCTCCACGGTTCTGGACCAGCAGCT
GGGCTGCCTATGGCAGAAGGACCACCTGCTCAGTGTCTCCCTGTCCGGGTACATCAACTATCTGGACAGAAACAA
CCCCAGCAAGCCCCCTGCACGTATCAAGGGTCACAGTAAATCGATCCAGTGTCTGACGGTGCATAAAACGGCGG
CAAGTCCTACATTTACTCTGGGAGCCACGACGGACACATTAATTACTGGGATTCAGAGACGGGGGAGAACGACTC
CTTCGCTGGGAAAGGCCACACGAACCAGGTGTCCAGGATGACCGTGGATGAGTCGGGGCAGCTCATCAGCTGCAG
CATGGACGACACCGTGCAGGTACACCAGCCTCATGCTGCGGGACTACAGCGGACAAGGAGTTGTGAAACTGGACGT
TCAGCCAAAGTGCCTAGCCGTGGGCCCCGGGGGATACGCCGTGGTCTGTGTCATTGGACAGATTGTCTCTGTA
GGATCAGAGGAAGTGCTTCAGCATCGACAACCCCGGCTACGAGCCCCGAAGTTGTGGCAGTGCACCCCGGCGGGGA
CACGGTGGCAATTGGGGGTGTGGACGGCAACGTCCGCTGTATTCCATCCTGGGCACCACGCTGAAGGATGAGGG
CAAGCTCCTAGAGGCCAAGGGCCCCGTGACCGACGTGGCCTACTCCCACGACGGCGCCTTCCTCGCGGTGTGCGA
CGCCAGCAAGGTGGTTCAGTGTTCAGCGTTGCTGACGGCTACTCGGAGAACAATGTTTTTTTATGGACACCATGA
AAAAATAAGCGAGCACCTAAACAATGTGTGGAGCATAACTAAACCCACAGCCCAACCAACCTTGAGAATGCGA
AACATTCCAGAGGCAGTAGCCTCCAAAGCACACAGAGCCCCCTGGCCCCGCGCGGCTCTCACTATCTGTGAGGGG
AGGTTGTACAGGTGAATGAGCCGGGGGGCTCATGTTCTGCTGCCTGCAGAACATTTCTGTACTAGTGAGAAGAGGGA
ATATGCATTGCAGTTCAGCAAAGCCGGAATTCTGTGTTGAACAGATGTCTGTCTCCCTAGTGTGTGACTCACACC
TTGTGGCTGCCTTCAGAGCGCCACCTCCAGATCAGATGGGGACACACAACCCCTGGATATGTTTCATTGTCAGAT
TTTGTGCTTGATTTTAAGAATGGAATTGTGGGTATCTTTCCTTTTTTTTTTAATGTATCTTAAGTGTGCTGTCA
GTGTTTACAACTAGTGCCTTGACGGCACCGTGTCCAAGTTTTTAGAACCTTGTTAGCCAGACCGAGGTGTCT
GGTCACCGTTTACCATCATGCTTTGATGTTCCCTGTCTTTCCTCTTCTGCTCTCAAGAGCAAAGGTTAATTT
AAGGACAAAGATGAAGTCACTGTAACTAATCTGTCAATTGTTTTTACCTTCCTTTTCTTTTTCAGTGCAGAAAT
AAAAGTAAGTATAAAGCACCGTGATTGGGAGTGTGTTTTCGTGTGTCGGAATCACTGGTAAATGTTGGCTGAGAA
CAATCCCTCCCTTGCACTGTGAAAACACTTTGAGCGCTTTAAGAGATTAGCCTGAGAAATAATTAAATATCTT
TTCTCTTCAAAAAAAAAAAAAAAAAAAAA

1536/6881
FIGURE 1422

MPYEIKKVFASLPQVERGVSKIIGGDPKGNNFLYTNGKCVILRNIDNPALADIYTEHAHQVVVAKYAPSGFYIAS
GDVSGKLRIWDTTQKEHLLKYEQPFAGKIKDIAWTEDSKRIAVVGE GREKF GAVFLWDSGSSVGEITGHNKVIN
SVDIKQSRPYRLATGSDDNCAAFFEGPPFKFKFTIGDHSR FVNCVRFSPDGNRFATASADGQIYYIDGKTGEKVC
ALGGSKAHDGGIY AISWSPDSTHLLSASGDKTSKIWDVSVNSVVSTFPMGSTVLDQQLGCLWQKDHL LSVSLSGY
INYLD RNNPSKPLHVIKGH SKSIQCLTVHKNGGKSYYISGSHDGHINYWDSETGENDSFAGKGHTNQVSRMTVDE
SGQLISCSMDDTVRYTSLMLRDYSGQGVVKLDVQPKCVAVGPGGYAVVVCIGQIVLLKDQRKCF SIDNPGYEPEV
VAVHPGGDTVAIGGVDGNVRLYSILGTTLKDEGKLLEAKGPVTDVAYSHDGAFLAVCDASKVVTVF SVADGYSEN
NVFYGHHEK

1537/6881
FIGURE 1423

ATTTTAGCTGTTGGTTCCGGCCGCACCGTGTGGGCTGTAGTAGCGGGAGGGGTGGGGGTCTCCAGAGTTAAGTG
GCTGTCTCGACTGTGCCCATACAGCAGCCAGCTTTCTTCCTTAATAACTGCCCGTTTGAAGAGTGCAGAGGATGT
CCAAGCGGCACCGGTTGGACCTAGGGGAGGATTACCCCTCTGGCAAGAAGCGTGCGGGGACCGATGGGAAGGATC
GAGATCGAGACCGGGATCGTGAAGATCGGTCTAAAGATCGAGACCGAGAACGTGATAGAGGAGATAGAGAGCGAG
AGAGGGAGAAAAGAAAAGGAGAAGGAGTTGCGAGCTTCAACAAATGCTATGCTTATCAGTGCTGGATTACCACCTT
TGAAAGCTTCCCATTCAGCTCACTCAACCCACTCAGCACATTCAACGCATTCAACACATTCTGCTCATTCAACGC
ATGCCGGACATGCAGGTACACGTCACCTCCACAGTGCATTAATCCGTTACCAACTTACCCCATACTCCTCGAT
ACTATGATATTCTAAAGAAACGTCTTCAGCTCCCTGTTTGGGAATACAAGGATAGGTTTACAGATATTCTGGTTA
GACATCAGTCCCTTGTACTGGTTGGTGAGACTGGGTCTGGTAAAACAACACAGATTCCACAGTGGTGTGTGGAGT
ACATGCGATCATTACCAGGACCCAAGAGAGGAGTTGCCTGTACCCAACCCAGGAGAGTGGCTGCAATGAGTGTGG
CTCAGAGAGTTGCTGATGAGATGGATGTGATGTTGGGCCAGGAAGTTGGTTACTCCATTTCGATTTGAAGACTGCA
GTAGTGCAAAAACCATTTCTTAAGTATATGACTGATGGGATGTTACTTCGTGAAGCTATGAATGATCCCTCCTGG
AGCGTTATGGTGTAATAATTCTTGATGAGGCTCATGAGAGGACACTGGCTACAGATATTCTAATGGGTGTTCTGA
AGGAAGTTGTAAGACAGAGATCAGATTTAAAGGTTATAGTTATGAGCGCTACTCTAGATGCAGGAAAATTCAGA
TTTACTTTTGATAACTGTCTCTCTCTAACTATTCTGGGCGTACACATCCTGTTGAGATCTTCTATACTCCAGAAC
CAGAGAGAGATTATCTTGAAGCAGCAATTGCAACAGTTATCCAGATTTCATATGTGTGAAGAGGAAGAGGGAGATC
TTCTTCTTTTCTTAAGTGGTCAAGAGGAAATTGATGAAGCCTGTAAGAGAATAAAGCGTGAAGTTGATGATTTGG
GCCCTGAAGTTGGTGACATTAATAATCATTCCATTGTATTCTACACTTCCACCTCAGCAGCAGCAACGCATTTTTG
AGCCTCCACCTCCCAAAAAACAGAATGGAGCAATTGGAAAGAAAGGTAGTTGTGTCAACTAACATAGCAGAGACGT
CTTTGACAATAGATGGTGTGGTGTGTTGTGATTGATCCTGGATTTGCGAAACAGAAGGTCTACAATCCTCGAATCA
GAGTTGAGTCCCTTTTGGTGACAGCTATTAGTAAAGCTTCAGCTCAGCAAAGGGCTGGTCGAGCTGGACGTACCA
GACCTGGAAAATGCTTCAGACTTTACACAGAGAAAGCTTATAAAACAGAAATGCAGGATAACACCTATCCTGAGA
TTTTGCGTTCTAATTTAGGATCAGTTGTGTTACAATTGAAGAACTTGGTATTGATGACTTGGTACATTTTGATT
TTATGGATCCACCAGCTCCTGAAACTCTGATGAGAGCCCTGGAACTTTGAATTACCTGGCTGCTTTAAATGATG
ATGGAGATCTGACTGAATTGGGATCCATGATGGCAGAGTTTCCTCTAGATCCACAGCTCGCAAAAATGGTTATTG
CAAGTTGTGACTACAACGTGTTCTAATGAGGTCCTATCTATTACTGCTATGTTGTGTCAGTCCCACAGTGTGTTGTT
GCCCCACGGAGGCCAAGAAAGCCGCAGATGAGGCCAAGATGAGATTTGCCACATAGATGGAGATCATCTGACAC
TGCTGAACGTCTACCATGCTTTTAAACAAAATCATGAATCGGTTTCAGTGGTGTGTTATGACAACCTTCATTAAC
GGTCCCTGATGTCCGCAGACAATGTACGCCAGCAGCTATCTCGAATTATGGACAGATTTAATTTGCCTCGTCGAA
GTACTGACTTTACAAGCAGGGACTATTATATTAATATAAGAAAAGCTTTGGTTACTGGGTATTTTATGCAGGTGG
CACATTTAGAACGAACAGGGCATTACTTAACTGTGAAAGATAACCAGGTGGTTCAGTTGCATCCCTCTACTGTT
TTGACCACAAACCTGAATGGGTGCTTTATAATGAGTTTGTCTAACAACAAAGAATTACATCCGGACATGTACAG
ATATCAAGCCAGAATGGTTGGTGAAAATTGCCCTCAATATTATGACATGAGCAATTTCCACAGTGTGAAGCAA
AGAGACAGTTGGACCGCATCATTGCCAACTTCAATCCAAGGAATATTCACAGTACTGAATTCAGTGCTTAGAAC
TGAAGTTATTGAGAGGACAGCTTTAAAGATGAATGAACTCAAAAGTTCGAGTTGTGCTCTTCACGTTGGTTTCGA
TAATGGCCTTTATTTGAAAGCTTTTTAATTTTTCTTTACAGTAAATATTCCATTCTGATTTTATAAATTAAACAT
TTATGCCTCCCTTTTGTGTTGACACTGTAGCTCATACTGGAAAAGTCGATCAATGTTTTGCAGTTTATTGAAAGT
AGTTCTATATATAACAATGTTATAAGCATTTCTTTAGAAATGGTTGAAAATGCTTCTAAAATGTGATTATCGACC
ATGGTATGCATGATCGTTGTAATTGTTGACATTCTTTTAGAAGTTGTGAAATGTTACAACCTTGTGCTTATGTAG
ACACAATCTTCTGTCTCAGTACAGAGGCACTGACTTCAATAAAGTCTATTTATACT

1538/6881
FIGURE 1424A

AGGATTTTAAAGAGTGGACTTGGTATTACCATAATTCCTATGAATGTAGCAAATGTAAAGCAAAGTGGACCGAACTG
TGAAACAATCTTTTGAATAATCACTCCCTACAGGAGTTTCAGCTTTACAGCCGAGACTGAAAAGGAGAAACAAG
ACTGGATTGAAGCTGTGCAGCAATCAATAGCAGAACTCTCTCTGATTATGAAGTAGCTGAGAAGATTGGTTCA
ATGAATCCAACAGGAGCTGTGCAGATTGTAAAGCCCCAGATCCTGACTGGGCATCCATCAATCTCTGTGTTGTCA
TCTGTAAGAAGTGTGCAGGACAGCATAGATCTTTAGGACCAAAGATTCCAAGGTTAGAAGTCTAAAAATGGATG
CTAGCATTGGAGCAATGAAGTCAATCGAGCTTTTATTGTCTATTGGAAACAAAAGAGCAAATGACTTTTGGGCTG
GTAATCTTCAAAGGATGAAGAATTACATATGGACTCACCAGTAGAAAAGAGAAAAAACTTTATTACTCAGAAAT
ATAAAGAAGGAAAATTCAGAAAACTCTTTTGGCATCTCTCACCAAAGAAGAATTAAATAAGGCTCTATGTGCTG
CTGTAGTGAAACCGGATGTTCTAGAAACAATGGCTTTGCTGTTGAGTGGAGCAGATGTCATGTGTGCCACCGGAG
ACCCCGTGATAGCACCCCTATCTGCTAGCCAAGAAAGCTGGGCAAAGTCTGCAAATGGAATTTCTCTACCATA
ACAAATTCTCAGATTTCCCTCAACATGATATTCAATCCGAGGGTGTATTAAGTCAAGAGTCTTCCAGTCCACAT
TCCTCTGTGACTTTTTATATCAAGCTCCTTCTGCTGCTTCTAACTCTCTTCAGAGAAAAAACTGCTTGAAGAGA
CAAATAAAAAATGGTGTGTTTTGGAAGGAGGCTTCTTGAGTTACTATGAAAATGATAAGTCTACCACACCTAATG
GCACCATTAATATCAATGAAGTTATCTGCCTGGCTATACACAAAGAGGACTTCTATTTAAATACTGGGCCCATCT
TTATCTTTGAGATCTACTTACCCTCCGAACGTGTGTTTTTATTGGAGCTGAAACATCTCAAGCTCAAAGAAAAT
GGACAGAGGCAATAGCCAAGCATTGTTTCCCTTATTTGCTGAAAACCTAACAGAAGCTGACTATGATTTGATTG
GTCAACTCTTCTACAAAGACTGCCATGCCCTGGATCAGTGGAGAAAAGGCTGGTTTGCTATGGACAAAATCCAGCT
TGCATTTTTGCCTTCAAATGCAAGAAGTTCAGGGAGATAGAATGCACCTAAGAAGACTGCAAGAGCTAACAAATCA
GCACAATGGTTCAAATGGGGAAAACTGGATGTTTTACTCTTGGTAGAAAAAGGGAGAACATTATACATCCATG
GGCATACCAAGTTGGATTTACAGTCTGGCATACTGCAATTGAAAAGCAGCAGGTACAGATGGTAATGCTTTAC
AAGATCAGCAGCTCAGCAAAAATGACGTTCCCATATAGTGAACAGCTGTATAGCATTTGTTACACAGTATGGTT
TAGGATGCAAATATATCTATCAAAAGAATGGTGATCCTTTGCATATAAGTGAACCTCTGGAGAGTTTCAAAGG
ATGCAAGAAGCTTTAAATTGAGGGCTGGAAAACATCAGCTTGAAGATGTGACGGCTGTGTTGAAAAGTTTTCTCT
CTGACATTGATGATGCACCTGCTTACTAAGGAGCTCTACCCATATTGGATCTCTGCTTTAGATACGCAAGATGACA
AGGAAAGAATTAATAATATGGAGCATTATACGTTCTCTTCCAGGGGTCAACCGAGCAACACTAGCAGCTATCA
TTGAACACCTGTATAGGGTTCAAGAAATGCTCAGAAATCAATCACATGAATGCCATAATTTGGCCTTGGTCTTTT
CATCCTGTTTGTTCAAACGAAGGGACAACTAGTGAAGAAGTGAATGTAATTGAGGACCTAATTAATAATTATG
TAGAAATATTTGAGGTTAAAGAAGATCAAGTCAAACAAATGGACATAGAAAATAGCTTTATTACCAAGTGGAAG
ACACCCAAGTTTCCAGGCTGGAGATTTGTTAATTGAAGTATATGTAGAAAGGAAGGAACCCGACTGTAGTATTA
TAATTCGATATCTCCTGTGATGGAAGCAGAAGAATTAATAATGATATATTAGCGATAAAAAATATTATTCCTA
CAAAAGGTGATATTTGGGCCACATTTGAAGTCATTGAAAATGAAGAGCTAGAGCGTCTCTTCACTACAAGGAAA
ATGTACTGGAGCAGGTGCTTCGGTGGAGTTCATTAGCTGAACCTGGCTCTGCTTACCTGGTGGTGAAGAGATTCT
TAACCGCTGACACAATTAACACTGCAGTGACCGGAGTACACTGGGAAGCATCAAAGAAGGAATCTTGAAAATCA
AAGAAGAACCATCCAAAATACTATCTGGAAATAAGTTTCAAGACCGGTATTTTGTGTTTACGAGATGGGTTTCTCT
TTCTTTACAAGGATGTGAAGAGTAGTAAACATGACAAGATGTTTTCTCTCAGTTCCATGAAGTTTTATCGTGGAG
TGAAAAGAAAATGAAGCCTCCAACAAGCTGGGGATTGACCGCATATTCTGAGAAACATCACTGGCACCTGTGTT
GTGATAGTTCACGAACTCAGACGGAGTGGATGACCAGTATCTTTATTGCCAGCATGAATATGATATATGGCCAC
CAGCTGGAAAGGAACGAAAACGTTCAATAACCAAAAATCCCAAAATTTGGAGGTTTGCCTCTGATTCTATACAGC
ATGAGGGGAATGCAACCTTGGCCCGAAAAATATTGAGAGTGCAAGAGCAGAACTTGAAAGGCTGCGGCTCAGTG
AAAAGTGTGATAAAGAGTCCGTGGACTCTAGCTTAAAGGAGAGAGCTTCCATGGTGGCCCACTGCCTGGAGCACA
AGGACGATAAACTTCGAAATCGACCCCGAAAACATCGGAGTTTCAACTGCCTGGAGGACACAGAGCCTGAAGCCC
CACTTGGGCAACCAAAAGGCCATAAAGGCCTAAAGACATTGAGGAAGACTGAGGACAGGAATAGCAAAGCTACTT
TGGACTCTGATCATAAGTTACCATCAAGGGTAATTGAAGAAGTAAATGTGGTTCTACAACGGTCAAGAACCCCTC
CAAAAGAATTACAGGATGAGCAGATTTTGAAGTAGGAAATAAAATGAATTGCTCCCAGATTATTTTTTTAATAT
TGTATGCAATCTTTATGTGTAAGTCCAAAAGTGAAGTATAAGATAATTCATAAGAATTTGCCTATTGATAGGCAA
ATTTGTCTATGCTTAGGCATTTAAGGAGCATTTAAAAATATGTATATATGTGACTGAATGTAAGATTAACTTTAT
TTTGGTCTGAACAAACCTTGTAAGTTCCATTGTATTAAAGTGTGTAAGAAGACATTGGGTTACTTAGGTGGTCA
GTCCTTTTAAAGTAGTTGTCTGTAAAGTGGTATAATTTATGAGCAGAAATCTCAAAGTGTACTGTATTGTATAAA

1539/6881
FIGURE 1424B

ATGCTGTGTTTAAATGAAGCCTAAGAACTATCTGTAACATATTTTGCACCTTGAGAAACCTTGTATATTAAATT
ACCATATGTTTTTAGGTTTACAGAAGTTCTACCTTAGGGAAAAAGAAAGGGAAGTAAATTGAAAAAGGGGGGAGAA
TTTATTGTAGTGGCTGCCTAAAAACCACTGGAGTTTTTAAAAAGCAAGGAGTTAAATGTCTGCAAAAACAAGG
AAGTGAGCTAAGATTCACTTCTAGTTCACTAATGACCAGAACTTGTCAATGAGAAACCACTTGTTAAGAAAAAGTC
CAGTGTTTTATTCTCAAGAGTAATATTTCGGCCAACAGATGTAAATAATAGCACTAGCCACTCTTATTAATATTTA
TAGTGTTAGAAAACCAGCCACATTACAGATTCAGTTCGTTGAGCTCATTGTTGGTGGCTGCTAAGAGGAACTT
ACACTGCATTGGAGAGGTTGTGTACACAGGACCTGGCTGGATGCTGATTGCACTGTCATTGTATGCAAGCATT
TGTCTTTTTTCAGAATTTCTGACTATACTTTTGGTACGAACAAAATTCATCACCACAGGGTCCTGTTGTTTTGTT
TGATTTTTTAGATTTTTTAAATTATTATTAAGGTTGTAATGTTTTTCTCCGAGTTGTCAGAAATAACTGGAAGAA
TACAATATATGGCCATTATGGAGCCAGGGGCTAGTTGGTGGTTTACTATACATTTGGGGGCTACCTGGTCACATT
TAATCTAGGTTTTTTTTCTTTTTTAAAGTAAAGGTGTGGTCTCTTCCCTGTACTTATGAATAAGGACAAAGCCC
TATTTTTGTTTCCACATAAAGATCAGCTACTGAATTGGTGAATTCCTGACAGACAATGCTATCTAACCATAGTT
CATGTTAGGGGAAGCATTTTTCCATCAGTTTCTTTAAATTTGGATTGTCTGGTGAGTTTTGATATTAAACATTAT
GTAGCTAAGTTTTTTTTTTTAGCATTTCTTTTTTATTTTTCAATCTATATTCACAGGCCCATACTTCAGTCAGT
CCAATCATAGTACAGTGATGTGGTGGTAGATGCTATGAATTTCTTCATTGTAAAATACGGATCATTGTATTTTG
GGGTGATAAAATAGTTCACCATGGGTATGAGATATTTATTCTTTAAATCAAAGTAAATTAGAATTTTTAAAAAGC
ACAAAAGTGCAGGACAGTTTATGAAATAGGTGGCACTATTAGGGGAATCTTCTTTAAAGCAAGAAATCATGTTAT
TTAGAAAGAAAACTAATCTTAAACATACTATTTCTAATAAATATTTATATTTTTATGAAATAAAGAGGTATGTG
GAAATTAATATTTGGTGATGTTGGACAGTGGAAGTATCTAGAGTTTTTACCTGCCTTATCTGAATTCCTTCTG
AACTTGAGCTTAACTCTAATAGCTGTTTCCCTTTCTATTCTGAACAACGTCTCCATTTTTCAAGTGTGAGAG
ATAAGGGCTAATGATGACATCTCATTTATTTTTGAGTAAACATTAAATTTGTTTTACAAGTCTACTTG

1540/6881
FIGURE 1425

TTCTTTCTTTGCTGCGTCTACTGCGAGAATGAAAGACTATTCTCAGCAATCAGACTGTGACATTCCAGAAAATGT
CGACATTACTCTGAAGGGACGCACAGTTATCGTGAAGGGCCCCAGAGGAACCCTGCGGAGGGACTTCAATCACAT
CAATGTAGAACTCAGCCTTCTTGGAAGAAAAAAAAAGAGGCTCCGGGTTGACAAATGGTGGGGTAAACAGAAAGGA
ACTGGCTACCGTTCGGACTATTTGTAGTCATGTACAGAACATGATCAAGGGTGTTACACTGGGCTTCCGTTACAA
GATGAGGTCTGTGTATGCTCACTTCCCATCAACGTTGTTATCCAGGAGAATGGGTCTCTTGTTGAAATCCGAAA
TTTCTTGGGTGAAAAATACATCCGCAGGGTTCGGATGAGACCAGGTGTTGCTTGTTAGTATCTCAAGCCCAGAA
AGATGAATTAATCCTTGAAGGAAATGACATTGAGCTTGTTTCAAATTCAGCGGCTTTGATTCAGCAAGCCACAAC
AGTTAAAAACAAGGATATCAGGAAATTTTTGGATGGTATCTATGTCTCTGAAAAAGGAAGTTCAGCAGGCTGA
TGAATTAAGATCTAAGAGTTACCTGGCTACAGAAAGAAGATGCCAGATGACACTTAAGACCTACTTGTGATATTTA
AATGATGCAATAAAAGACCTATTGATTGGACCTTCTTCTT

1541/6881
FIGURE 1426

MKTILSNQTVDIPENV DITLKGRTVIVKGPRGTLRRDFNHINVELSLLGKKKKRLRVDKWWGNRKELATVRTICS
HVQNMIKGVTLGFRYKMRSVYAHFPINVVIQENGLVEIRNFLGEKYIRRVMRPGVACSVSQAQKDELILEGND
IELVSNSAALIQQATTVKNKDIRKFLDGIYVSEKGTVQQADE

1542/6881

FIGURE 1427A

GTCCTTGCTTCTTTTTTTCATTGATGTAAATTTTTTTAACTTAATATGAAAACCTCTCCAAGTCTTGATCATCAGCC
AGGATTTTGCCACAGCAATTTTCATTCTCTTATCGGAGCTTGTATGTGTCAAAGTATACTTCAGAGTGCAAACATT
AAGCAAGTAATATATTTTACCTACAGATACTTATGAAGACATTCTTTTCGCTATCGTGAGTAAAAGTATATAAAGC
TGTTTCTAACTGAAAATGCTTGAAATAAGCCTGTAATAGAAATATTTTTTCATTTTTTAAAAAAGGGCGGAATTC
CCAGACTGTCTTCGCCTTCTTGCACCTTCGCGGGAGAAGTTGTTGGCGGAATGGATCCTGAGCCTCGATAACAGA
TTCTCAACCGGCCACCCGCCAGCCAGCCAGCGCCTTCATCCTGGGGCTGCGATGACATTCCGAAATTCCTTG
GAGTAATACCAAGTGGAAGAACTTGTAAGTGAAACAGTAAAGAAGAATGAGAAAACAAAGTCTGATGAAGAAA
CTTTAAAGCAAAGAAAGGAATAAAGGAAATCAAGGTAAATAGCTCCCGTAAAGAGGATGACTTCAAACAAAAGC
AACCAAGCAAGAAAAAGAGGATCATCTATGATTTCAGATTTCAGAGTCAGAGGAGACGTTGCAGGTAAAAAATGCCA
AAAAGCCACCAGAAAAACTGCCAGTATCTTCTAAACCTGGTAAAATTTACGGCAGGATCCTGTTACATACATTT
CAGAAACAGATGAAGAAGATGACTTTATGTGTAAGAAGCGGCCTCTAAATCAAAGAGAATGGAAGATCTACAA
ATAGTCATCTTGGAACATCAAACATGAAAAAGAATGAAGAAAACACTAAGACCAAGAATAAGCCTTTATCACCAA
TAAACTTACACCCACATCAGTACTTGATTATTTTGAACTGGAAGTGTCCAAAGATCTAATAAGAAGATGGTGG
CAAGCAAAAAGAAAAGAGCTTTCACAAAATACAGATGAGTCTGGATTAAATGATGAAGCCATCGCCAAGCAATTAC
AGCTTGATGAAGATGCGGAGCTGGAGAGGCAGTTGCATGAAGATGAAGAGTTTGCCAGAACATTAGCCATGTTGG
ATGAAGAACCCAGACCAAAAAGGCTCGAAAGGACACAGAAGCGGGAGAAAACGTTTTTCATCTGTCCAAGCCAATT
TAAGTAAAGCAGAAAAACATAAATATCCTCATAAAGTAAAAACAGCACAAAGTTTCAGATGAAAAGAAAAGAGCTACA
GTCCTAGGAAGCAAAGTAAATATGAAAGTTCAAAAAGAAATCTCAGCAACATTCCAAGTCATCAGCTGACAAAATAG
GAGAAGTCTCTTCTCCCAAGGCCAGTTCTAAGCTGGCAATTATGAAAAGAAAAGAAGAGAGCTCTTATAAAGAAA
TAGAGCCTGTGGCCTCAAAAAGAAAAGAAAATGCCATTAAATTGAAAGGAGAGACAAAAACTCCTAAGAAAACCA
AAAGTTCTCCAGCTAAAAAGAGTCTGTAAGTCTGAAAGATTCTGAAAAGAAACGCACTAATTATCAAGCTTATC
GAAGCTACTTAAATCGAGAAGGTCCCAAGGCTCTGGGCTCCAAAGAAATACCAAGGGAGCTGAAAATTGCTTGG
AAGGCCTTATATTTGTAATCACAGGCGTGCTGGAGTCTATTGAACGAGATGAGGCCAAGTCTCTAATTGAACGTT
ATGGGGGAAAAGTAACAGGAAATGTCAGCAAGAAAACAAATTATCTTGTCTATGGGTGCTGATAGTGGACAGTCCA
AGAGTGATAAGGCCGCAGCCTTGGGGACAAAATTATTGATGAAGATGGCCTGTTGAATCTGATTTCGGACTATGC
CAGGCAAGAAATCCAAGTATGAAATAGCAGTTGAACTGAGATGAAGAAAGAGTCCAACTGGAGAGAACACCCC
AAAAAATGTCCAAGGAAAAAGAAAATTAGTCCATCTAAAAAGGAATCAGAATCTAAAAAGAGCAGGCCGACTT
CCAAAAGGGACAGTTTGGCAAAGACAATAAAAAAGGAAACAGATGTGTTTTGGAAAAGCCTGGATTTCAGGAGC
AGGTGGCTGAGGAGACAAGTGGTGACAGCAAGGCTAGGAATTTGGCTGATGACAGCAGTGAAAACAAAGTGGA
ATTTGCTCTGGGTGGATAAATATAAGCCAACCTCGCTCAAGACCATAATTGGACAGCAAGGTGACCAGAGCTGTG
CCAACAACTCCTACGCTGGCTCCGAACTGGCAAAAGAGTTCTTCCGAAGATAAAAAACACGCAGCAAAAGTTTG
GTAAATTTTCCGGCAAAGATGATGGCTCTAGTTTTAAAGCAGCGTTGCTGTGAGGCCCTCCTGGTGTGGCAAAA
CCACCACAGCTTCCCTGGTGTGTGTCAGGAGTTGGGATACAGCTACGTGGAAGTGAATGCAAGTGACACCCGAGTA
AGAGCAGTTTGAAGGCGATTGTTGCTGAGTCACTGAACAATACCAGCATCAAAGGCTTTTATTCAAATGGAGCAG
CCTCTTCAGTAAGCACGAAACATGCTCTCATCATGGATGAAGTAGATGGCATGGCAGGCAATGAGGATAGGGGAG
GAATTCAGGAATTAATTGGCCTGATAAAACATACTAAAAATTCCCATTTATTGTATGTGCAATGATAGAAATCATC
CCAAGATTGCTCTCTGGTTCAATTATTGTTTTGATCTTCGTTTTTCAAAGACCTCGGGTTGAACAGATTAAGGGTG
CTATGATGTCTATTGCATTTAAAGAAGGTTTAAAGATTCCCCCTCCAGCTATGAATGAAATAATTTTGGGAGCCA
ATCAAGATATCAGACAGGTTTTACATAATCTGAGTATGTGGTGTGCACGAAGTAAAGCATTAAACCTATGACCAGG
CCAAAGCTGATTCTCACAGAGCCAAAAAGGATATCAAAATGGGCCCATTTGATGTTGCCCGGAAAAGTGTGTCAG
CTGGAGAGGAGACTGCTCACATGTCACTTGTGGACAAGTCAGATCTCTTTTTTTCATGATTATTCAATAGCACCCC
TCTTCGTCCAGGAAAATTACATACACGTGAAGCCTGTAGCAGCAGGGGTGACATGAAAAGCACCTGATGCTTT
TAAGCAGAGCAGCAGACAGCATATGCGATGGTGACCTAGTGACAGCCAGATCCGGAGTAAGCAAACTGGAGTC
TTCTGCCTGCGCAGGCCATTTATGCCAGTGTCTTCTCGAGAGTTGATGAGGGGTACATGACCCAGTTTCCCA
CCTTCCCAAGCTGGCTGGGGAAGCACTCGTCTACAGGCAAACATGATCGTATTGTTTCAGGACCTGGCCTTGATA
TGAGTCTCAGAACTTACTCCAGCAAAGGACTGTAAACATGGATTATCTGTCTGCTTCTAAGGGATGCACTTGTAC
AGCCCTTGACCTCACAAGGAGTAGACGGAGTACAGGATGTTGTTGCACTTATGGACACATATTATTGATGAAG
AAGACTTTGAGAATATCATGGAAATCAGCAGCTGGGGTGGCAACCTAGTCCCTTTTCAAAGCTGGATCCCAAGG

1543/6881
FIGURE 1427B

TGAAAGCAGCCTTCACAAGAGCTTACAATAAGGAAGCCCACCTTACTCCATACTCACTTCAAGCTATAAAGGCAT
CTAGACACAGCACAAAGCCCATCCCTGGATTTCGGAATACAATGAAGAATTAAATGAAGATGACTCTCAATCTGATG
AGAAAGACCAAGATGCTATAGAACTGATGCCATGATCAAGAAAAAGACAAAATCTTCAAAGCCTTCAAAACCAG
AAAAAGATAAGGAGCCCAGAAAAGGAAAAGGAAAAAGTTCGAAGAAATGAACCATTCTTCACTAGCGACAGCCA
CTTTTTACTCTCCCTCCTGACCAGTCCAGCTGGTCTAGAGAAAGCCTTGTTTTTTCCAGAGCAACCATGTTTTA
GCATAATGGGATGACCTGGTGTCCCATTTATAAATAAAGGGTGGTATGGCTAGAAGGGTATGAGCAGTAGGCTTAT
GTACACCTCTTATAGAGGTTGATAGGACTGCTTGGGTCTCCACTGTCCTCTGTCAATCTAGTTAGACGTGCTTC
TGAATGACTGTAGAATTGGAAGTACAACTACACCTGGGCTTTGGAGTCAGATTTTAGTTAACAATAATGAGCCT
GGAGCAGTAGTACTAAGGCGTCTTTTGTAGGCTTAAGAATTTATCCTAATGGCCTTTATAGGACCAATGCTGATT
TTTTTTAAAGGCAGTTCCTATTATGTGGTGAAATTTTGTAATAAATGATTATACAAAACAGTCACCACCTAGAA
CTGGGTATTCTTTGTACATTGTCAGATATCTTTCAAAGTATAAATTAGGAATAAAAATGTTCCACATGATATGTG
TACAAATTCCTTTTAAGATTGTCATCTTGTACAGCAAAATATTATGTTGGTATATTACTTCCTTATTAATTTGCA
AATGATTGGATTAAAAAAGCTCACTGTATTCCTTACTAACCTGTTGTGTGAAACATAACATTGGCAGTCGAGGAG
TCAGAACTCGGATTCCCAGCCTCACTCCCTCTGTGTGTGTTGACCACGTCTCTGCTGTGAATAGGATTTTCATGCA
GTGGTCTGTTATGGGGCTTTGCAGCGTGGGGGGCTGCAGAAGATTCTCAGACATTCTTATCCTTCTGGAGTCTCA
ACCCATCAGGTTTCAGACCAGTAGGAACCAGGCTGGGTGAGGCTCTTAATTTCACTACGGTGGGGGACAAAATGAA
CACTGGCTTTTGTTCACCTTGCCCTGAGAGATCTAGTCCTGTCTGTGATGGCTTCCACAAACCTGTTGGAAG
TTTGGGTATTCTTATAACTGTATGTGTTGAGTGGCCGTGACGTATGGACCTAGCCTGGAATTTAGATGTCTAGC
TATTTTTTAATCTTGTGGTAAATGCTCAGAGGTCTGTGCTACCTCTGTGAGGTATATACTAAAATGAATGTAAA
ATAAGGATCGTATTCCTGCTTTAAGGAACTGGTAGTCTTGTTGGGTGATGAGACAAAGTTCTTGAGACATTTA
AACTGTATTTACCAGTGTGAAAAATGTCATTTATGGAGATTAATTCATTATGGAATAAAACATTGCCTAAGCCC
TTGCCTGCTG

1544/6881
FIGURE 1428

MDIRKFFGVIPSGKKLVSETVKKNEKTKSDEETLKAKKGIKEIKVNSSRKEDDFKQKQPSKKKRRIIYDSDSESEE
TLQVKNAKKPPEKLPVSSKPGKISRQDPVTYISETDEEDDFMCKKAASKSKENGRSTNSHLGTSNMKKNEENTKT
KNKPLSPIKLTPTSVLDYFGTGSVQRSNKKMVASKRKELSQNTDESGLNDEAIAKQLQDDEDAELERQLHEDEEF
ARTLAMLDEEPPKTKKARKDTEAGETFSSVQANLSKAEKHKYPHKVKT AQVSDERKSYSPRKQSKYESSKESQQHS
KSSADKIGEVSSPKASSKLAIMKRKEESSYKEIEPVASKRKENAIKLKGETKTPKKT KSSPAKKESVSPEDSEKK
RTNYQAYRSYLNREGPKALGSKEIPKGAENCLEGLIFVITGVLESIERDEAKSLIERYGGKVTGNVSKKTNLYVM
GRDSGQSKSDKAAALGTKIIDEDGLNLIRTMPGKKSKEYEIAVETEMKKESKLERTPQKNVQGKRKISPSKKESE
SKKSRPTSKRDSLAKTIKKETDVFWKSLDFKEQVAEETSGDSKARNLADDSSSENKVENLLWVDKYKPTSLKTIIG
QQGDQSCANKLLRWLRNWQKSSSEDKKHAAKFGKFSGKDDGSSFKAALLSGPPGVGKTTTASLVCQELGYSYVEL
NASDTRSKSSLKAIVAESLNNTSIKGFYSNGAASSVSTKHALIMDEV DGMAGNEDRGGIQELIGLIKHTKIP IIC
MCNDRNHPKIRSLVHYCFDLRFQRPRVEQIKGAMMSIAFKEGLKIPPPAMNEIILGANQDIRQVLHNLSMWCAR'S
KALTYDQAKADSHRAKDKIKMGPFDVARKVFAAGEETAHMSLVDKSDLFFHDYSIAPLFVQENYIHVKPVAAGGD
MKKHLMLLSRAADSICDGLVDSQIRSKQNWSLLPAQAIYASVLPGELMRGYMTQFPTFP SWLGKHSSTGKHDRI
VQDLALHMSLR TYSSKRTVNMDYLSLLRDALVQPLTSQGV DGVQDVVALMDTY YLMKEDFENIMEISSWGGKPS
FSKLDPKVKAAFTRAYNKEAHLTPYSLQAIKASRHSTSPSLDSEYNEELNEDDSQSDEKDQDAIETDAMIKKKTK
SSKPSKPEKDKEPRKGKGKSSKK

1545/6881
FIGURE 1429A

ATAGTTTCGCGTAGCGGCTCGAGCGTGGAGATGAAGCGTATTTTCTCACTGCTAGAAAAGACTTGCGTTGGCGCAC
CAATACAGTTTGGCTGGCAAAAACATCAGGAACTACCTTGCAGTAACAGGAGCTGATTATATTGTGAAAATCT
TTGATCGCCATGGTCAAAAAAGAAGTGAAATTAACCTACCTGGTAACCTGTGTTGCCATGGATTGGGATAAAGATG
GAGATGTCCTAGCAGTGATTGCTGAGAAATCTAGCTGCATTTATCTTTGGGATGCCAACACAAATAAGACCAGCC
AGTTAGACAATGGCATGAGGGATCAATGTCTTTCCTTCTTTGGTCAAAAGTTGGAAGTTTCTGGCTGTTGGAA
CTGTTAAAGGAAATTTGCTTATTTATAATCATCAGACATCTCGAAAGATTCTGTCTTGGAAAACATACTAAGA
GAATCACTTGTGGATGTTGGAATGCAGAAAATCTGCTTGTCTTAGGTGGTGAAGATAAAATGATTACAGTTAGTA
ATCAGGAAGGTGACACGATAAGACAGACACAAGTGAGATCAGAGCCTAGCAACATGCAGTTTTTCTTGATGAAGA
TGGATGACCGAACCTCTGCTGCTGAAAGCATGATAAGTGTGGTGTCTGGCAAGAAAACCTTTGTTTTTTTTAAATC
TGAATGAACCAGATAACCCAGCTGATCTTGAATTTAGCAGGACTTTGGCAACATTGTCTGTCTATAATTGGTATG
GTGATGGCCGCATCATGATTGGTTTTTCATGTGGACATTTTGTGGTCATTTCTACTCATACTGGAGAGCTTGGTC
AAGAGATATTTAGGCTCGTAACCATAAAGATAATCTAACCAGCATTGCAGTATCACAGACTCTTAACAAAGTTG
CTACATGTGGAGATAACTGCATTAATAATCCAAGACTTGGTTGACTTAAAGACATGTATGTTATACTCAACCTGG
ATGAGGAAAATAAAGGATTGGGTACCTTGTCTGGACTGATGATGGCCAGTTGCTAGCACTCTCTACCCAAAGGG
GCTCACTTCATGTTTTCTGACCAAGCTTCCCATACTTGGGGATGCCTGCAGCACAAGGATTGCCTATCTCACCT
CCCTCCTTGAAGTCACCGTAGCCAACCTGTTGAAGGAGAGCTACCAATCACAGTTTCTGTTGATGTGGAACCCA
ACTTTGTGGCAGTAGGTCTTTATCATCTGGCTGTAGGAATGAATAATCGAGCTTGGTTTTATGTCTTGGAGAAA
ATGCTGTGAAAAAATTGAAAGATATGGAGTATCTGGGAACAGTAGCCAGTATTTGCCTTCACTTCTGACTATGCTG
CTGCATTTTTTGAAGGCAAAGTCCAGTTACATTTGATAGAAAAGCGAAATCTTGGATGCTCAAGAAGAACGTGAGA
CTCGGCTTTTTCCAGCAGTGGATGATAAGTGCCGTATCTTATGCCATGCCTTAACTAGTGATTTCTCATCTATG
GTACAGATACTGGTGTCTGTTTCACTATTTCTACATTGAAGACTGGCAATTCGTTAATGATTATCGACATCCTGTCA
GTGTGAAAAAGATTTTTCCCGACCCAAATGGGACCAGATTAGTTTTTCATTGATGAAAAAGTGATGGATTGTTTT
ACTGTCCAGTCAATGACGCTACCTATGAGATTCCAGATTTTTTCACCAACCATTAAAGGTGTTCTTTGGGAAAAC
GGCCAATGGATAAAGGTGTATTTATTGCTTATGATGATGATAAGGTGTACACTTATGTCTTTCACAAGGACACTA
TACAAGGAGCCAAGTTATTTTGGCTGGTAGCACCAAAGTCTCTTTTGCTCATAAACCTTTGCTGCTATATAATG
GAGAGCTGACCTGCCAAACACAGAGTGGAAAAGTAAACAACATCTACCTTAGCACCCATGGCTTTCTCAGCAACT
TAAAAGATACGGGGCCTGACGAAGTACGACCAATGCTGGCACAGAATTTAATGCTAAAGAGGTTTTCTGATGCTT
GGGAAATGTGCAGGATTCTGAATGATGAGGCTGCCTGGAATGAGTTGGCCAGAGCTTGTCTACATCACATGGAAG
TGGAGTTTGAATCCGTGTTTTATCGGAGAATTGGAATGTTGGCATAAGTATGTCTTGGAAACAAATAAAGGGAA
TAGAGGACTACAATCTTTTGGCAGGACACCTTGCCATGTTTACCAACGATTATAACCTGGCTCAGGACTTGTACC
TTGCATCCAGCTGTCTTATTGCTGCCCTGGAGATGAGAAGGGATTTACAGCATTGGGACAGTGCTCTACAACCTGG
CAAAGCATTGTGGCCCCAGACCAGATACCTTTTATATCAAAAAGAAATATGCTATTACAGCTTGAATTCGCGGGTGATT
ATGTAAATGCTTTGGCTCATTATGAGAAAGGAATAACAGGTGATAATAAGGAACATGATGAAGCTTGTCTGGCTG
GAGTGGCCAGATGTCCATAAGAATGGGAGACATACGTGAGGGGTTAACCAAGCCCTCAAGCATCCCAGCAGGG
TCCTTAAAAGAGACTGTGGAGCCATATTGGAGAATATGAAGCAATTTTCAGAAGCGGCCCACTGTATGAAAAAG
GTCTCTACTACGATAAAGCAGCATCTGTTTACATCCGCTCTAAGAATTGGGCAAAAGTTGGTGATCTTCTGCCCC
ACGTTTTCTTCTCCTAAGATCCATTGTGAGTATGCCAAAGCCAAGGAAGCAGATGGAAGATACAAAGAAAGCTGTTG
TAGCTTATGAAAATGCAAAACAGTGGCAAAAGTGTAATCCGCATCTATCTGGATCACCTCAATAATCCTGAAAAAG
CTGTCAATATTGTTAGAGAGACCCAGTCTCTGGATGGAGCCAAAATGGTAGCCAGGTTTTTTCTACAGCTTGGTG
ACTATGGGTCTGCCATCCAGTTTTCTGTCTATGTCCAAATGCAACAATGAAGCTTTTCACTGGCTCAGCAACACA
ACAAAATGGAATCTATGCAGATATTATTGGTTCTGAAGACACTACTAATGAAGACTATCAAAGCATTGCCTTAT
ACTTTGAAGGAGAAAAAGAGATATCTTACAGGCTGGAAAATTCTTCTTGTGTGTGGCCAATATTACAGGACTTTA
AACACTTCTGAAATGCCAAAGCTCGGAAGATAATGTGGCAATAGAAATGGCAATTGAAACTGTTGGTCAGGCCA
AAGATGAAGTCTGACCAATCAGCTGATAGACCATCTCCTGGGGGAGAACGATGGCATGCCTAAGGATGCCAAGT
ACCTGTTCCGCTTGTACATGGCTCTGAAGCAATACCGAGAAGCTGCCAGACTGCCATCATCATTGCCAGAGAAG
AGCAGTCTGCAGGCAACTACCGGAATGCACACGATGTTCTCTTCACTATGTATGCAGAACTGAAATCCCAGAAGA
TCAAAATTCCTCCGAGATGGCCACCAACCTCATGATTCTGCACAGCTATATACTAGTAAAGATTTCATGTTAAAA
ATGGAGATCACATGAAAGGGGCTCGCATGCTCATTGCGGTGGCCAACAACATCAGCAAATTTCCATCACACATTG

1546/6881
FIGURE 1429B

TACCCATCCTGACGTCAACTGTGATTGAGTGTACAGGGCAGGCCTGAAGAACTCTGCTTTCAGCTTCGCAGCTA
TGTTGATGAGGCCTGAATACCGCAGCAAAATAGATGCCAAATACAAAAGAAGATCGAGGGAATGGTCAGGAGAC
CCGATATATCTGAGATAGAAGAGGCCACGACTCCATGTCCATTCTGCAAATTTCTTCTCCCAGAGTGTGAACTCC
TCTGTCCTGGATGTAAAAACAGTATCCCATATTGCATTGCAACAGGTCGACACATGTTGAAAGATGACTGGACGG
TGTGTCCACATTGTGACTTCCCTGCTCTATACTCAGAATTGAAGATCATGCTAAACACTGAAAGCACATGTCCTA
TGTGTTTCAGAAAGATTAAACGCTGCTCAGCTGAAAAAGATTTTCAGACTGTACCCAGTACCTGCGAACGGAGGAGG
AACTGTGATTGGCACGTGCAGATACAATGCTCCTGAGAAGACAGCATTTTCCACAGGAGGCTGTTTCCCTCCCCTG
GTGGATTTAAGAGACGGTCCTTTCTGGATACAGAGAAATGAAACAACGGTGACCTCTCCAGGTCGGCACTTTCCA
CTTCTGTACGGTGGCAAAACGATGACATGTAACCTTGCTGTTTATTGTACTTTGTATATTATTTCCCTCTTCAAAG
TCTTTCTTACACACTCTATCCTCTGCACTGTTAATAGTAACCTATGACATAATTGTAAATATTCAGCTTTTGTCT
AACTTTTGTATTTTGAAAACTTTAAAAATAAAATTGTTGACTAG

1547/6881
FIGURE 1430

GGCACGAGGCCTGGGCGGCTCCGCTAGCTGTTTTTCGTCTTCCCTAGGCTATTTCTGCCGGGCGCTCCGCGAAGA
TGCAGCTCAAGCCGATGGAGATCAACCCGAGATGCTGAACAAAGTGCTGTCCCGGCTGGGGGTGCGCGGCCAGT
GGCGCTTCGTGGACGTGCTGGGGCTGGAAGAGGAGTCTCTGGGCTCGGTGCCAGCGCCTGCCTGCGCGCTGCTGC
TGCTGTTTTCCCTCACGGCCAGCATGAGAACTTCAGGAAAAAGCAGATTGAAGAGCTGAAGGGACAAGAAGTTA
GTCCTAAAGTGTA~~CT~~TCATGAAGCAGACCATTGGAATTCCTGTGGCACAATCGGACTTATTCACGCAGTGGCCA
ATAATCAAGACAAACTGGGATTTGAGGATGGATCAGTTCTGAAACAGTTTCTTTCTGAAACAGAGAAAATGTCCC
CTGAAGACAGAGCAAAATGCTTTGAAAAGAATGAGGCCATACAGGCAGCCCATGATGCCGTGGCACAGGAAGGCC
AATGTCGGGTAGATGACAAGGTGAATTTCCATTTTATTCTGTTTAACAACGTGGATGGCCACCTCTATGAACCTG
ATGGACGAATGCCTTTTCCGGTGAACCATGGCGCCAGTTCAGAGGACACCCTGCTGAAGGACGCTGCCAAGGTCT
GCAGAGAATTCACCGAGCGTGAGCAAGGAGAAGTCCGCTTCTCTGCCGTGGCTCTCTGCAAGGCAGCCTAATGCT
CTGTGGGAGGGACTTTGCTGATTTCCCTCTTCCCTTCAACATGAAAATATATACCCCCCATGCAGTCTAAAAT
GCTTCAGTACTTGTGAAACACAGCTGTTCTTCTGTTCTGCAGACACGCCTTCCCCTCAGCCACACCCAGGCACTT
AAGCACAAGCAGAGTGACAGCTGTCCACTGGGCCATTGTGGTGTGAGCTTCAGATGGTGAAGCATTCTCCCCAG
TGTATGTCTTGTATCCGATATCTAACGCTTTAAATGGCTACTTTGGTTTCTGTCTGTAAGTTAAGACCTTGGATG
TGGTTTAATTGTTTGTCTCAAAAGGAATAAACTTTTCTGCTGATAAGATAAAAAAAAAAAAAAAAAAAAA

1548/6881
FIGURE 1431

MQLKPMEINPEMLNKVLSRLGVAGQWRFDVLGLEEESLGSVPAPACALLLLFPLTAQHENFRKKQIEELKGQEV
SPKVYFMKQTIGNSCGTIGLIHAVANNQDKLGFEDGSVLKQFLSETEKMSPEDRAKCFEKNEAIQAADAVAQEG
QCRVDDKVNHFHILFNNVDGHLIELDGRMPFPVNHGASSEDLLKDAAKVCREFTEREQGEVRFSAVALCKAA

1549/6881
FIGURE 1432

GCCAAACACCAGAGCACCCCTAGAAGGTTTAACTAAAAGAATGCTCATGTTTGACCCAGTTCCTGTCAAGCAAGAG
GCCATGGACCCTGTCTCAGTGTCTATACCCATCTAATTACATGGAATCCATGAAGCCTAACAAGTATGGGGTCATC
TACTCCACACCATTTGCCTGAGAAGTTCTTTTCAGACCCCGAGAAGGTCTGTGCGACGGAATACAGATGGAGCCAGTG
GACCTCACGGTGAACAAGCGGAGTTACCCCCCTTCGGCTGGGAATTCGCCCTCCTCTCTGAAGTTCCCGTCCCTCA
CACCGGAGAGCCTCGCCTGGGTTGAGCATGCCTTCTTCCAGCCCACCGATAAAAAAATACTCACCCCCTTCTCCA
GGCGTGCAGCCCTTCGGCGTGCCGCTGTCCATGCCACCAGTGATGGCAGCTGCCCTCTCGCGGCATGGAATACGG
AGCCCGGGGATCCTGCCCCTCATCCAGCCGGTGGTGGTGCAGCCCGTCCCCTTTATGTACACAAGTCACCTCCAG
CAGCCTCTCATGGTCTCCTTATCGGAGGAGATGGAAAATTCCAGTAGTAGCATGCAAGTACCTGTAATTGAATCA
TATGAGAAGCCTATATCACAGAAAAAATTAAAAATAGAACCTGGGATCGAACCACAGAGGACAGATTATTATCCT
GAAGAAATGTCACCCCCCTTAATGAACTCAGTGTCCCCCGCAAGCATTGTTGCAAGAGAATCACCCCTTCGGTC
ATCGTGCAGCCTGGGAAGAGACCTTTACCTGTGGAAATCCCGGATACTCAAAGGAAGCGGAGGATACACAGATGT
GATTATGATGGATGCAACAAAGTGTACACTAAAAGCTCCCACTTGAAAGCACACAGAAGAACACACACAGGAGAA
AAACCCCTACAAATGTACATGGGAAGGGTGCACATGGAAGTTTGCTCGGTCTGATGAACTAACAAGACATTTCCGA
AAACATACTGGAATCAAACCTTTCCAGTGCCCGGACTGTGACCGCAGCTTCTCCCGTTCTGACCATCTTGCCCTC
CATAGGAAACGCCACATGCTAGTCTGATTGCCTCTGTGTCCTGCCTCAGCGTGACTCCCCACTCACCTGGCTCTC
TCTCTGTCCTGCCTCCATTATCTAACACATTTTTTACATGTACATTTTAATTTGATTTCAGCTGGTCTGAATCTC
TGAATTTATATCATCCAAACTTCCATATGGTCAGTAGTAGATGTTCTCTAATCCTCCCTCTCCTTACCACGGGT
CAGACCTAAAGAATGTGAACACTTTTTT

1550/6881
FIGURE 1433

CCTTTCCGTCCTGGCGGCAGCCATCAGGTAAGCCAAGATGGGTGCATACAAGTATATCCAGGAGCTATGGAGAAAG
AAGCAGTCTGATGTCACGCGCTTTCTTCTGAGGGTCCGCTGCTGGCAGTACCGCCAGCTCTCTGCTCTTCACAGG
GCTCCCCGCCCCACCCGGCCTGATAAAGCGCGCCAACTGGGCTACAAGGCCAAGCAAGGTTACGTTATACATAGG
ATTTGTGTTAGCCGTGGTGGCCGAAAACGCCCAGTTCCTAAGGGTGCAACTTACGGCAAGCCTGTCCATCATGGT
GTTAACCAGCTAAAATTTTGCTCGAAGCCTTCAGTCCGTTGCGGAGGAGCGAGCTGGACGCCACTGTGGGGCTCT
GGGAGTCCTGAATTCTTACTGGGTGGTGAAGATTCCACATACAAATTTTTTGAGGTTATCCTCATTGATCCATT
CCATAAAGCTATCAGAAGAAATCCTGACACCCCATGGATCACCAAACCAGTCCACAAGCACAGGGAGATGCGTGG
GCTGACATCTGCAGGCCGAAAGAGCCGTGGCCTTGGAAGGGCCATAAGTTCCACCACACTATTTGTGGTTCTCG
CCGGGCAGCTTGGAGAAGGCGCAATACTCTCCAGCTCCACCGTTACCGCTAATACAAGTAAAGTTTGTAATAATC
ATACCTAATAAGTCTGCAGATGTTTCTTGAATGC

1551/6881
FIGURE 1434

CAGCCATCAGGTAAGCCAAGATGGGTGCATACAAGTATATCCAGGAGCTATGGAGAAAGAAGCAGTCTGATGTCA
CGCGCTTTCTTCTGAGGGTCCGCTGCTGGCAGTACCGCCAGCTCTCTGCTCTTCACAGGGCTCCCCGCCCCACCC
GGCCTGATAAAGCGCGCCAAC TGGGCTACAAGGCCAAGCAAGGTTACGTTATACATAGGATTTGTGTTAGCCGTG
GTGGCCGTAACCAGCTAAAATTTTGCTCGAAGCCTTCAGTCCGTTGCGGAGGAGCGAGCTGGACGCCACTGTGGG
GCTCTGGGAGTCCTGAATTCTTACTGGGTTGGTGAAGATTCCACATACAAATTTTTTGAGGTTATCCTCATTGAT
CCATTCCATAAAGCTATCAGAAGAAATCCTGACACCCCATGGATCACCAAACCAGTCCACAAGCACAGG

1552/6881
FIGURE 1435

GCCGCTGCCACCGCACCCCGCCATGGAGCGGCCGTCGCTGCGCGCCCTGCTCCTCGGCGCCGCTGGGCTGCTGCT
CCTGCTCCTGCCCCCTCTCCTCTTCCCTCCTCTTCGGACACCTGCGGCCCTGCGAGCCGGCCTCCTGCCCCGCCCT
GCCCCCGCTGGGCTGCCTGCTGGGCGAGACCCGCGACGCGTGCGGCTGCTGCCCTATGTGCGCCCGCGGCGAGGG
CGAGCCGTGCGGGGGTGGCGGCGCCGGCAGGGGGTACTGCGCGCCGGGCATGGAGTGCCTGAAGAGCCGCAAGAG
GCGGAAGGGTAAAGCCGGGGCAGCAGCCGGCGGTCCGGGTGTAAGCGGCGTGTGCGTGTGCAAGAGCCGCTACCC
GGTGTGCGGCAGCGACGGCACCACCTACCCGAGCGGCTGCCAGCTGCGCGCCGCCAGCCAGAGGGCCGAGAGCCG
CGGGGAGAAGGCCATCACCCAGGTCAGCAAGGGCACCTGCGAGCAAGGTCCTTCCATAGTGACGCCCCCAAGGA
CATCTGGAATGTCACTGGTGGCCAGGTGTACTTGAGCTGTGAGGTCATCGGAATCCCGACACCTGTCTCATCTG
GAACAAGGTAAAAAGGGTCACTATGGAGTTCAAAGGACAGAACTCCTGCCTGGTGACCGGGACAACCTGGCCAT
TCAGACCCGGGGTGGCCAGAAAAGCATGAAGTAACTGGCTGGGTGCTGGTATCTCCTCTAAGTAAGGAAGATGC
TGGAGAATATGAGTGCCATGCATCCAATTCCCAAGGACAGGCTTCAGCATCAGCAAAAATTACAGTGGTTGATGC
CTTACATGAAATACCAGTGAAAAAGGTGAAGGTGCCGAGCTATAAACCTCCAGAATATTATTAGTCTGCATGGT
TAAAGTAGTCATGGATAACTACATTACCTGTTCTTGCCCTAATAAGTTTCTTTTAATCCAATCCACTAACACTTT
AGTTATATTCACTGGTTTTACACAGAGAAATACAAAATAAAGATCACACATCAAGACTATCTACAAAAATTTATT
ATATATTTACAGAAGAAAAGCATGCATATCATTAACAAATAAAATACTTTTTATCACAAAAAAAAAAAAAAAAA

1553/6881
FIGURE 1436

MERPSLRALLLGAAGLLLLLLPLSSSSSSDTGCPCEPASCPEPLPPLGCLLGETRDACGCCPMCARGEGEPCGGGG
AGRGYCAPGMECVKSRKRRKGKAGAAAGGPGVSGVCVCKSRYPVCSDGTTYPSCQLRAASQRAESRGEKAITQ
VSKGTCEQGPSIVTPPKDIWNVTGAQVYLSCEVIGIPTPVLINWKVRGHYGVQRTELLPGDRDNLAIQTRGGPE
KHEVTGWVLVSPLSKEDAGEYECHASNSQGQASASAKITVVDALHEIPVKKGEGAEI

1554/6881
FIGURE 1437

GGCACGAGGCTCGGGTCAAATGCGCGCCTCGGACCCCTAGTGC GCGTGC GCGCTGGTGGCTCCGCCCCCTTTGGAGC
TACTTCCTCATGCTGCCCCGCTCGCCTACCGTTCAGGCTGCTGAGCCTTTTCCTTCGTGGATCCGCTCCCACGGCA
GCGCGCCATGGCCTCCGGGAGCCGCTCCTGGAGAGGAGGTGCGCTGCCGCTCCTCCTTCAGCACTCATCGAGT
CTGGGACGCGAGCTTCCTTATGACCCCGTGGACACGGAGGGCTTTGGAGAAGGTGGTGACATGCAGGAGCGTTTTT
CTGTTCCCGGAGTACATCCTGGATCCGGAGCCGCAACCCACCCGCGAAAAGCAGCTGCAGGAGCTCCAGCAACAG
CAGGAGGAGGAGGAGCGACAGAGGCAGCAGCGGCGGGAGGAGCGGCGACAGCAAAACCTACGGGCCAGGTCCCGG
GAGCACCCGGTCGTGGGGCACCCGGACCCGGCATTGCCGCCAGCGGCGTGAAGTGTCTCGGGCTGCGGGGCAGAG
CTGCACTGCCAGGACGCCGGAGTGCCCGGCTACCTGCCCGAGAGAAGTTCTCCGCACGGCGGAGGCAGACGGC
GGGCTGGCACGGACCGTGTGCCAGCGCTGCTGGCTGCTGTGCGACCAACGGCGCGCTCTACGCCTGCAGGTGAGC
CGCGAGCAGTACCTGGAGCTGGTGAGCGCCGCTTGCGGCGGCCCCGGCCCCCTCCCTGGTGCTCTACATGGTGAGC
CTGCTGGACCTGCCCGACGCCCTGCTGCCCCGACTTGCCCCGCGCTGGTGGGCCCCAAGCAGCTGATCGTGCTGGGA
AACAAAGTGGACCTCCTGCCCCAGGATGCTCCTGGCTACCGGCAGAGGCTGCGGGAGCGACTGTGGGAGGACTGT
GCCCCGCGCCGGGCTCCTGCTGGCCCCCTGGCCACCAAGGGCCACAGCGCCCCGTCAAGGACGAGCCACAGGACGGG
GAGAATCCGAATCCGCCGAAGTGGTCCCGCACAGTGGTCAGGGACGTGCGGCTGATCAGCGCCAAGACCGGCTAT
GGAGTGAAGAGTTGATCTCTGCCCTTCAGCGCTCCTGGCGCTACCGTGGGGACGTCTACTTAGTGGGCGCCACC
AACGCCGGCAAATCCACTCTCTTTAACACGCTCCTGGAGTCCGATTACTGCACTGCCAAGGGCTCCGAGGCCATC
GACAGAGCCACCATCTCCCTTTGGCCAGGTACTACATTAAACCTTCTGAAGTTTCCTATTTGCAACCCAACTCCT
TACAGAAATGTTTAAAGGCATCAAAGACTTAAAAAAGATTCAACTCAAGCTGAAGAAGATCTTAGTGAGCAAGAA
CAAAATCAGCTTAATGTCTCAAAGCATGGTTATGTGCTAGGAAGAGTTGGAAGGACATTCTTGTTATTTCAGAA
GAACAGAAGGATAACATTCCCTTTGAGTTTGATGCTGATTCACTTGCCTTTGACATGGAAAATGACCCTGTTATG
GGTACACACAAATCCACCAACAAGTAGAATTGACTGCACAAGATGTGAAAGATGCCCACTGGTTTTATGACACC
CCTGGAATTACAAAAGAAAATTGTATTTTAAATCTTCTAACAGAAAAAGAAGTAAATATTGTTTTGCCAACACAG
TCCATTGTTCCAAGAACTTTTGTGCTTAAACCAGGAATGGTTCTGTTTTTGGGTGCTATAGGCCGCATAGATTTT
CTGCAGGGAAATCAGTCAGCTTGGTTTACAGTCGTGGCTTCCAACATCCTCCCTGTGCATATCACCTCCTTGGAC
AGGGCAGACGCTCTGTATCAGAAGCATGCAGGTCATACGTTACTCCAGATTCCAATGGGTGGAAGAAGAACGAATG
GCAGGATTTCTCCTCTTGTGCTGAAGACATTATGTTAAAAGAAGGACTGGGGGCATCTGAAGCAGTGGCCGAC
ATCAAGTTTTCTCTGCAGGTTGGGTTTCAGTAACACCTAATTTTAAAGGACAGACTGCATCTCCGAGGCTATACA
CCTGAAGGAACAGTTTTGACCGTCCGGCCCCCTCTCTTGCCATATATTGTTAACATCAAAGGACAGCGCATCAAG
AAAAGTGTGGCCTATAAAACCAAGAAGCCTCCTTCCCTTATGTACAACGTGAGGAAGAAGAAAGGAAAGATAAAT
GTATGAGACCGACCTTGTTCACTCCAGATATTAAGTATTGAACACAACAAAATACATTGAATTTGTATTAAAC
ATATAACGCATAAATAAAGCTCCCATTCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

1555/6881
FIGURE 1438

MLPARLPFRLLSLFLRGSAPTAARHGLREPLLEERRCAAASSFQHSSSLGRELPYDPVDTEGFGEggDMQERFLFP
EYILDPEPQPTREKQLQELQQQOEEEEERQORQORREERRQQNLRARSREHPVVGHDPDPALPPSGVNCSCGAE LHC
QDAGVPGYLPREKFLRTAEADGGLARTVCQRCWLLSHHRRALRLQVSREQYLELVSAALRRPGPSIVLYMVDLLD
LPDALLPDLPALVGPKQLIVLGNKVDDL PQDAPGYRQRLRERLWEDCARAGLLLAPGHQGPQRPVKDEPQDGENP
NPPNWSRTVVRDVRLISAKTGYGVEELISALQRSWRYRGDVYLVGATNAGKSTLFNTLLES DYCTAKGSE AIDRA
TISPWP GTTLNLLKFPICNPTPYRMFKRHQRLKKDSTQAEEDLSEQEQNLNVLKKHGYVVGRVGR TFLYSEEQK
DNIPFEFDADSLAFDMENDPVMGTHKSTKQVELTAQDVKDAHWFYDTPGITKENCILNLLTEKEVNIVLPTQSIV
PRTFVLKPGMVLF LGAIGRIDFLOGNQSAWFTVVASNILPVHITSLDRADALYQKHAGHTLLQIPMGGKERMAGF
PPLVAEDIMLKEGLGASEAVADIKFSSAGWVS VTPNFKDRHLRLRGYTPEGTVLTVRPPLLPYIVNIKGQRIKKS V
AYKTKKPPSLMYNVRKKKGKINV

1556/6881
FIGURE 1439

GAAAGCTGTATTTGCTGCACGTGGAAATCTCCGTTATTTTCCAGCACCCAACAGTAGCGTAATGGGAGTAACGGA
CTTAACCTCATTTCTCTTTTCAGAGCATTAGCCTTCATATGCCCTTCCCTGCATGCTTCCCCCAGGCCGTCAAGA
CTTGAGTTCTGCCTCGCTTCCCGGCGCGGTGCGAGCCCTCAGCCCACTTAGGATAATGGCGACAGCTGAGGTACT
GAACATTGGTAAAAAATTATATGAGGGTAAAACAAAAGAAGTCTACGAATTGTTAGACAGTCCAGGAAAAGTCCT
CCTGCAGTCCAAGGACCAGATTACAGCAGGAAATGCAGCTAGAAAAACCACCTGGAAGGAAAAGCTGCAATCTC
AAATAAAATCACCAGTTGTATTTTTCAGTTATTACAGGAAGCAGGTATTAAAACTGCCTTACCAGAAAATGTGG
GGAGACAGCTTTCATTGCACCGCAGTGTGAAATGATTCCAATTGAATGGGTTTGCAGAAGAATAGCAACTGGTTC
TTTTCTCAAAAAGAAATCCTGGTGTCAAGGAAGGATATAAGTTTTACCCACCTAAAGTGGAGTTGTTTTTCAAGGA
TGATGCCAATAATGACCCACAGTGGTCTGAGGAACAGCTGATTGCTGCAAAATTTTGCTTTGCTGGACTTCTTAT
AGGCCAGACTGAAGTGGATATCATGAGTCATGCTACACAGGCTATATTGAAATACTGGAGAAAATCCTGGTTGCC
CCAGAATTGTACACTGGTTGATATGAAGATTGAATTTGGTGTGATGTAACCACCAAAGAAATGTTCTTGCTGA
TGTTATTGACAATGATTCTGGAGACTCTGGCCATCAGGAGATCGAAGCCAACAGAAAGACAAACAGTCTTATCG
GGACCTCAAAGAAGTAACTCCTGAAGGGCTCCAAATGGTAAAGAAAACTTTGAGTGGGTTCAGAGAGAGTAGA
GTTGCTTTTGAAATCAGAAAGTCAGTGCAGGGTTGTAGTGTGATGGGCTCTACTTCTGATCTTGGTCACTGTGA
AAAAATCAAGAAGGCCTGTGGAAATTTTGGCATTCCATGTGAACCTCGAGTAACATCTGCGCATAAAGGACCAGA
TGAAACTCTGAGGATTAAAGCTGAGTATGAAGGGGATGGCATTCTACTGTATTTGTGGCAGTGGCAGGCAGAAG
TAATGGTTTGGGACCAGTGATGTCTGGGAACACTGCATATCCAGTTATCAGCTGTCTCTCCCTCACACCAGACTG
GGGAGTTCAGGATGTGTGGTCTTCTCTTCGACTACCCAGTGGTCTTGGCTGTTCAACCGTACTTTCTCCAGAAGG
ATCAGCTCAATTTGCTGCTCAGATATTTGGGTTAAGCAACCATTGGTATGGAGCAAACTGCGAGCAAGCATT
GAACACATGGATTTCTTGAAGCAGGCTGACAAGAAAATCAGAGAATGTAATTTATAAGAAAAGATGCCATTGAA
TTTTTTAGGGGAAAACTACAAATTTCTAATTTAGCTGAAGGAAAATCAAGCAAGATGAAAAGGTAATTTTAAAT
TAGAGAACACAAATAAAATGTATTAGTGAATAAATGCTTCTCTAGATCCATATTAATAAACATGAGCATCTAACC
CCTCCTTTCTTAGGCTAGACACCAAGATATTTAGCCAGCCTTTATCATTCTCTTACTTTATCCTTTTTCTTA
AGTATTGGTGGTCACTACTATTGAGTTTCTTCTTAACACTGATTAAATGATCTTAACCTCCCTCAGCTAAACTG
GCATTACTGACTCCCAGCTATATTTCTCCAGACTTGCATTTTTTTTTTTTTTTTTTGGAGACAGGGTCTCACTGTG
CCCAGGCTGGAGTGCAGTGGCGTGATCTCAGTTCAGTCTGCTTTCCCTCCTGGGCTCAAGCAGTCTCTCCACCT
CAGCCTCTCGACTAACAGGGACTATAATCTTGACAGCACCATGCCGAGCTAATTTTATTTTGTAGAGATGAGCT
CTCACTATGTACCCAGGTTCTGCTCAAACCTGAACCCTAGTAATTTCTCTATCTCAGCCTCCCAAAGTGCTA
GGGTACAGACATGAGCCACTGTGCTGTCTAGACTTGTACTTTCAACTGTCCATTTCTCCCTGTCTGTCCCATG
GGCACTCATGAAAAACAGAATGCTCCCAACTTTATTCATCTTCCAAGCCTGTAGCTCTTGGTATACTCACTGTT
GCAAGTCAGAAGCTTGATTTTCATCATTGATGTTTTTCTCACGTTTTCACATCTCACTCATCACCAGTCATGTTGG
TGTTAATTTCTGATTAAACCCTTGAATTTACCGTCTTCTCATCCTCTGTACAAAAGCCTCAAGTGAGGGTCAAAT
CAACATTATCCTGATCTAGACAGCCCCCATTTCTCAATCCACCCTTTTCCAAGTTGATTGCCCAAGGACTTCTAAC
AATAAACTCTCTTTTGACACACAGACTTCTTTGAAAATATACATGCTGTTGACCCTCTCTGTAGAAAACCGCACA
CATAAACTTACCAACAGATTTTCATTGGTTCTTGGGTTCTCCCGAAGCCTATCCATGGTTTATAGATTAAGAATT
GATGAGGTAGCTGGGCACAGTGGCTCACACCTACGATCACAGCACTTCGGGAGGCTGAAGCAAGCAGATCACTTG
AGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAGTAGCCAGC
CGTGATGACAGGCACCTGTAATCCAGCTACTCGGGAGGCTGAGGCATGAGAATTGCTTGAACCCGGGAGGCGGA
GGTTGCAGTGAGCCTAGATCATGCCACTGCCTCCAACCTGGGCAGCAGAGCAAGACTCTGTCTCAAAGGGGAA
AAAAAAAATTGCTGATGTGACCCATGAAGGGAACCTCATTTTCTCGTAATTTTGGACTGCCACACATTGGTACCT
TTAGTTCTCTGAAGGCCACGTTTTTATCATTAAAGACCTATTTGTTAGCTAGTAGAGCTTTATGTTGCTGTCCA
TGAAACCTTCTGTAACCACAGTGACTACAAGTAGTTCTTTCTCTATTGAATTATTAGGTCCAGAATAGAAGATGT
CATTGTACACTTTATTTCCCTCACACTGTGTTATGCTCTGATGTGCTATGCTTAGCTATCTGTGAGAGATTAGTA
AATTATAAACTCATGTGTACTACTTAAGTTTATATCTTATGCTAGTTTATAAGAACAATTAAAGGACTTAGAA
GATTAA

1557/6881
FIGURE 1440A

TCGGGAAGGAAGAGCCTGTCGCGAGCGCGAGCTTCTGAGCTCGACGGGCCGAGCTGGCAGCTGGTTGGTGCTTAC
ACCTTGCCCGCAGCGGCAGGTCCTTCCACGTGCTTTTCGGCGGCACATGGAGCTGGAGGAGTTGGGGATCCGAGA
GGAATGTGGCGTGTTCGGGTGCATCGCCTCAGGAGAGTGGCCACGCAGCTGGATGTACCGCATGTGATCACTCT
GGGACTCGTGGGGCTGCAGCACCGGGGTCAGGAGAGTGTGGTATTGTGACTAGTGATGGGAGTTCGGTGCCAAC
ATTCAAATCACACAAGGGAATGGGTCTTGTAATCACGTCTTTACTGAAGACAATTTGAAAAAATTATATGTTTC
AAATCTTGGAATTGGACACACCAGGTATGCCACCACAGGAAAATGTGAAGTAGAAAATTGTCAGCCCTTCGTTGT
TGAAACACTTCATGGGAAGATAGCTGTGGCACATAATGGCGAATTGGTAAATGCTGCTCGATTAAAGGAAAAGCT
TCTGCGTCATGGTATTGGTCTGTCTACAAGTCTGTAGTGAATGATTACCCAGTTACTGGCGTATACCCCTCC
TCAGGAACAAGATGACACCCAGACTGGGTAGCCAGGATTAAAACTTGATGAAGGAAGCACCCACAGCATACTC
CCTGCTTATAATGCACAGAGATGTTATTTATGCAGTACGAGATCCTTATGGAAATCGTCCCTTATGCATTGGTCTG
TCTTATTCCAGTGTCTGATATAAATGACAAAAGAGAAAAAACATCAGAAACAGAAGGATGGGTGGTGTCTTCAGA
ATCTTGTAGCTTCTTATCTATTGGTGCAAGATATTACCGTGAAGTCTTGCTGGAGAAATGTGGAAATATCCAG
ACACAATGTCCAAACTCTTGATATTATATCAAGGTCTGAAGGAAACCCAGTGGCTTTTTGTATCTTTGAATATGT
TTATTTTGCAAGACCAGACAGTATGTTTGAAGACCAAATGGTTTATACAGTAAGATACCGTTGTGGCCAGCAGCT
AGCGATTGAAGCACCTGTGGATGCAGATTTGGTTAGCACTGTTCCAGAATCTGCTACGCCTGCTGCTCTTGCTTA
CGCAGGAAAGTGTGGACTTCCATATGTGGAGGTGCTGTGTAAAAACCGGTATGTAGGGAGAACCTTCATTCAGCC
AAACATGAGGTTAAGACAACCTTGGTGTGCAAAAAAATTTGGAGTATTGTTCAGACAACCTTTAAAGGCAAAAGAAT
TGTTCTTGTAGATGATTCAATTGTTCAGAGGCAATACCATCTCACCTATAATAAAACTGCTCAAAGAATCTGGTGC
AAAAGAGGTACACATTCGAGTAGCTTCACCACCAATTAATATCCATGCTTCATGGGAATAAACATTCCTACAAA
AGAAGAGCTCATTGCCAATAAACAGAAATTTGATCACCTTGAGAATATCTAGGAGCAAACAGTGTTGTGTATCT
GTCAGTAGAAGGACTGGTTTCATCTGTACAAGAAGGGATAAAGTTTAAAAAACAGAAAGAGAAAAAGCACGATAT
TATGATCCAAGAAAATGGAAATGGTCTGGAATGTTTTGAAAAGAGTGGTCATTGTACAGCTTGTCTCACTGGAAA
ATATCCTGTAGAATTAGAATGGTAGCTGGTAGGGTTGGATGTGTGTAGTTTCAAGATAGAAAGTTGGTCAAGAAG
TTATAGTGGTCACACCTCATCTATTTACTGTTACTCAGTTGGTACAATGTAAAATGCCATGCTTATGTTTTATAAG
TTTTGAGATTTTTTTTTTTTTCTGAAAAGGATACCAAAGTGCAGTAACTGAACATTTCCAATTGCATATAATACAA
CAATATGTGGTGTCTTTTTTTTTTACACAAGCATTGGCTAGCCTTTTTTAACCTGGTCAGAGAAGGCAGGTGGTCAC
TGACATTTCCCAAGTCCATGCTTTAAAGGGTTTGCAAGAAGTTAGGGTTAAGGAGAGGTGATGCCAACAAGACAG
GTGAGTTAAATATACCATTTACACAAAAGTTGAATAGAATACATTATACCTCATAGGTGTCTAGCCTCTACAGT
TCTGGCTGTAGTTATGACCTTGGCTTCCCTGTCTAACTGTAGACAAATCTTTAAAAAAAATAATAATAATCTGG
TGCTCAGTTTCCCCACATGTGCAATGGGATACTTATTAATAATTAATAAGAATGTGAATAAGTGTCACTACTTT
TGTGATTTGAGCCATCATTTCACTTCTGATTTTAAGACAACCTCATGATTGTTAGCTTTCAGAAAGCTAATGATTG
TTAACTTTTTGAAATTAGTTTACAATTAATTAAGATTTTATTATGATGGAAGGAGACATAATTGGCAGATCTTTG
CCATCTCTCTTTGAGATGTCTTAAAAAGGGTTGTAAAAATCTGTGAAAAAGTTTTTCCTACATTTGACTAGAAAA
TGTGATCCATAGTATTTAGTGCCCTGATACTATAAGCTCAGCAAGTAACCTGGTACATTTGAAATAAAAAACCAA
TTTTTAGATTCAAACAATCCCTTTATCCTTAATTTAATTAATTATCATATGCTTTTTTTAATGAAGTGCTTGATC
ACTTGCAAACATATATACATGTAGATGTACATATACATGTACACATACACATAAATATTATTGCAATTAAGTGAT
CAAGTACAGACACAATAGGGGCCAGTTTTGTTTAAGGATCAAAGAGACAACCACTTTGGGGAATTAGTATCAACT
TACAATCCAAGTCCAAGTATCATCTTATAATCACTTTTTTCTACTATATTAAGATCTAATGAATTTGATTTCTTT
TTTGAAGTTTTTTCTTGTAACATCTGAGATTAGAAGTTTAAGATGACTTGACCCCAAACCTTTGTTTATGTAAGA
ATTTTTAAACATAAAAGTGTTTGTCTGTTATGTTACCATAAATTTGATGTATATAGTGTCCAGATCCATTTAGA
AATTTAATATTTATTAATAACTGAACTGTTTGTCTTCCCTTTGGTATATAGTCTCGCATATTATATTATAGCAGG
CCAAGATAAAATTTGACAGCTCTTTAAGCCACATGCAGCAGTGGGTCAGATAACCTGTGGCAGTGACACGGG
CAAATTGGCATTGTAATAAGCCCTGGGACCACCTCAACATGCGTAGCCTCTTGTCTTAAATGTACTCCCCATGG
CAGCATGGAGGAGGCAAGACCTGTGGGTCAATTTGAACTGGCCTTACTTTGATTTTTAAACAAGAGACTCAGG
GAAAGTACTAAACCAAAATCTCTGATTTTACTTTGCGTTTTCTGTAGTTTTGTGTTTACTGAGATGCTTTTGTA
AGGAAAATAATACTGTGACAGTTTAGTAATCTACAGATTCTTAATATTTCTCCATCATGGCCTTTTACTTCACA
ATTTCTGAAGTCTGAATTCAATTACAATTTTTTTTTTACCAATTAATCTCAAATGTTGTTTAACTGCTTTAAAT
TCATATACGTAGAGTATTATAAAGTGCAGAGATGAAAAATGTGTTTTACGGGATTATATTGTGAAGTAACTA

1558/6881

FIGURE 1440B

AGCCTACTTTTTGTGACTTATTTGTGATGCCTTGTTGATAAATATGTGTAATAAGTATGTTT

1559/6881
FIGURE 1441

CTCTTTCCCATCTTGCAAGATGGCGGGTGAAAAAGTTTAGAAGCCAGATACTAAAGAGAAGAAACCCGAAGCCAA
GAAGACTGATGCTGGTGGCAAGGTGAAAAAGGGTAACCTCAAAGCTAAAAAGCCCAAGAAGGGGAAGCCCCGTTG
CAGCCGCAACCCTGTCCTTGTCAGAGGAATTGGCAGGTATTCCCGATCTGCCATGTATTCCAGAAAGGCCATGTA
CAAGAGGAAGTACTCAGCCGCTAAATCCAAGGTTGAAAAGAAAAAGAAGGAGAAGGTTCTTGCAACTGTTACAAA
ACCAGTTGGTGGTGACAAGAACGGCGGTACCCGGGTGGTTAACTTCGCAAAATGCCTAGATATTATCCTACTGA
AGATGTGCCTCGAAAGCTGTTGAGCCACGGCAAAAAAAAAACCCCTCAGTCAGCACGTGAGAAAACTGCGAGCCAG
CATTACCCCGGGACCATTCTGATCATCCTCACTGGACGCCACAGGGGCAAGAGGGTGGTTTTCTGAAGCAGCT
GGCTAGTGGCTTATTACTTGTGACTGGACCTCTGGTCCTCAATCGAGTTCCTCTATGAAGAACACACCAGAAATT
TGTCATTGCCACCTCAACCAAAATCGATATCAGCAATGTAAAAATCCCAAAACATCTTACTGATGCTTACTTCAA
GAAGAAGCAGCTGCGGAAGCCCAGACACCAGGAAGGTGAGATCTTCGACACAGAAAAGGGAAATATGAGATTAC
GGAGCAGCGCAAGATTGATCAGAAAGCTGTGGACTCACAAATTTTATCAAAAATCAAAGCTATTCTCAGCTCCA
GGGCTAGTTGCGATCTGTGTTTGCCCTGACGAATGGAATTTATCCTCACAAATTGGTGTTCTAAATGTCCTTAAGA
ACCTAATTAATAGCTGACTAC

1560/6881
FIGURE 1442

GTTTTTAGTTTGTAGCTGCCTGGAGTGTTATTTTAAGAAAGCAGAAGCACCATCATTGTCACACTCCTTATAGA
TCACACACCTTAACCCTGACTTTTTTTGCTCCAGTTTTTTCAGAAGAAGTGAAGTCAAGATGAAGAACCATTGCT
TTTCTGGGGAGTCCTGGCGGTTTTTATTAAGGCTGTTTCATGTGAAAGCCCAAGAAGATGAAAGGATTGTTCTTGT
TGACAACAAATGTAAGTGTGCCCGGATTACTTCCAGGATCATCCGTTCTTCCGAAGATCCTAATGAGGACATTGT
GGAGAGAAACATCCGAATTATTGTTCTCTGAACAACAGGGAGAATATCTCTGATCCCACCTCACCATTGAGAAC
CAGATTTGTGTACCATTGTTCTGACCTCTGTAAAAAATGTGATCCTACAGAAGTGGAGCTGGATAATCAGATAGT
TACTGCTACCCAGAGCAATATCTGTGATGAAGACAGTGCTACAGAGACCTGCTACACTTATGACAGAAACAAGTG
CTACACAGCTGTGGTCCCACTCGTATATGGTGGTGAGACCAAAATGGTGGAAACAGCCTTAACCCCAGATGCCTG
CTATCCTGACTAATTTAAGTCATTGCTGACTGCATAGCTCTTTTTCTTGAGAGGCTCTCCATTTTGATTCAGAAA
GTTAGCATATTTATTACCAATGAATTTGAAACCAGGGCTTTTTTTTTTTTTTGGGTGATGTAAAACCAACTCCCT
GCCACCAAAATAATTTAAATAGTCACATTGTTATCTTTATTAGGTAATCACTTCTTAATTATATGTTCACTACTCT
AAGTATCAAAATCTTCCAATTATCATGCTCACCTGAAAGAGGTATGCTCTCTTAGGAATACAGTTTCTAGCATT
AACAAATAAACAAGGGGAGAAAATAAACTCAAGGACTGAAAATCAGGAGGTGTAATAAAATGTTCTCGCATT
CCCCCGCTTTTTTTTTTTTTTTTGACTTTGCCTTGGAGAGCCAGAGCTTCCGCATTTTCTTTACTATTCTTTTT
AAAAAAGTTTCACTGTGTAGAGAACATATATGCATAAACATAGGTCAATTATATGTCTCCATTAGAAAAATAAT
AATTGGAACATGTTCTAGAACTAGTTACAAAAATAATTTAAGGTGAAATCTCTAATATTTATAAAAGTAGCAA
AATAAATGCATAATTTAAATATATTTGGACATAACAGACTTGGAAGCAGATGATACAGACTTCTTTTTTTCATAA
TCAGGTTAGTGTAAGAAATTGCCATTTGAAACAATCCATTTTGTAACCTTATGAAATATATGTATTTTCAT
GGTACGTATTCTCTAGCACAGTCTGAGCAATTAAATAGATTTCATAAGCATA

1561/6881
FIGURE 1443

GGTGCTGCAAGACTCTCTGGTAGAAAAATGAAGAGGGTCCTGGTACTACTGCTTGCTGTGGCATTGACATGCT
TTAGAGAGAGGCCGGGATTATGAAAAGAATAAAGTCTGCAAGGAATTCTCCCATCTGGGAAAGGAGGACTTCACA
TCTCTGTCACTAGTCCGTGTACAGTAGAAAATTTCCAGTGGCACGTTTGAACAGGTCAGCCAACTTGTGAAGGAA
GTTGTCTCCTTGACCGAAGCCTGCTGTGCGGAAGGGGCTGACCCTGACTGCTATGACACCAGGACCTCAGCACTG
TCTGCCAAGTCCGTGTGAAAGTAATTCTCCATTCCCCGTTCACCCAGGCACTGCTGAGTGCTGCACCAAAGAGGGC
CTGGAACGAAAGCTCTGCATGGCTGCTCTGAAACACCAGCCACAGGAATTCCTACCTACGTGGAACCCACAAAT
GATGAAATCTGTGAGGCGTTTCAAGGAAAGATCCAAAGGAATATGCTAATCAATTTATGTGGGAATATTCCACTAAT
TACGGACAAGCTCCTCTGTCACTTTTAGTCAGTTACACCAAGAGTTATCTTTCTATGGTAGGGTCCTGCTGTACC
TCTGCAAGCCCAACTGTATGCTTTTTGAAAGAGAGACTCCAGCTTAAACATTTATCACTTCTCACCCTCTGTCA
AATAGAGTCTGCTCACAATATGCTGCTTATGGGGAGAAGAAATCAAGGCTCAGCAATCTCATAAAGTTAGCCCAA
AAAGTGCCTACTGCTGATCTGGAGGATGTTTTGCCACTAGCTGAAGATATTACTAACATCCTCTCCAAATGCTGT
GAGTCTGCCTCTGAAGATTGCATGGCCAAAGAGCTGCCTGAACACACAGTAAACTCTGTGACAATTTATCCACA
AAGAATTCTAAGTTTGAAGACTGTTGTCAAGAAAAAACAGCCATGGACGTTTTTGTGTGCACTTACTTCATGCCA
GCTGCCCAACTCCCCGAGCTTCCAGATGTAGAGTTGCCACAAACAAAGATGTGTGTGATCCAGGAAACACCAAA
GTCATGGATAAGTATACATTTGAACTAAGCAGAAGGACTCATCTTCCGGAAGTATTCCTCAGTAAGGTACTTGAG
CCAACCCTAAAAAGCCTTGGTGAATGCTGTGATGTTGAAGACTCACTACCTGTTTTAATGCTAAGGGCCCTCTA
CTAAAGAAGGAAGTATCTTCTTTCATTGACAAGGGACAAGAACTATGTGCAGATTATTCAGAAAATACATTTACT
GAGTACAAGAAAAAACTGGCAGAGCGACTAAAAGCAAAATTGCCTGATGCCACACCCACGGAAGTGGCAAAGCTG
GTTAACAAGCACTCAGACTTTGCCTCCAAGTCTGTTCCATAAACTCACCTCCTCTTTACTGTGATTTCAGAGATT
GATGCTGAATTGAAGAATATCCTGTAGTCCTGAAGCATGTTTATTAACCTTGACCAGAGTTGGAGCCACCCAGGG
GAATGATCTCTGATGACCTAACCTAAGCAAAACCACTGAGCTTCTGGGAAGACAAGTAGGATACTTTCTACTTTT
TCTAGCTACAATATCTTCATACAATGACAAGTATGATGATTTGCTATCAAAATAAATTGAATATAATGCAAACC
AT

1562/6881
FIGURE 1444

MKRVLVLLLAFAFGHALERGRDYEKNKVCKEFSHLGKEDFTSLSLVLYSRKFPSGTFEQVSQLVKEVVS LTEACC
AEGADPDCYDTRTSALSAKSCESNSPFPVHPGTAECCTKEGLERKLCMAALKHQ PQEFP TYVEPTNDEICEAFRK
DPKEYANQFMWEYSTNYGQAPLSLLVSYTKSYLSMVGSCCTSASPTVCFLKERLQLKHL SLLTTLSNRVCSQYAA
YGEKKSRLSNLIKLAQKVPTADLEDVLP LAEDITNILSKCCESASEDCMAKELPEHTVKLCDNLSTKNSKFEDCC
QEK TAMDVFVCTYFMPAAQLPELPDVELPTNKDVCDPGNTKVMDKYTFELSRRTHLPEVF LSKVLEPTL KSLGEC
CDVEDSTTCFNAKGPLLKKELSSFIDKGQELCADYSENTFTEYKKKLAERLKAKLPDATPTELAKLVNKH SDFAS
NCCSINSPPLYCDSEIDAELKNIL

1563/6881
FIGURE 1445

AGCTTTTCTCTTCTGTCAACCCACACGCCTTTGGCACAAATGAAGTGGGTAACCTTTATTTCCCTTCTTTTTCTC
TTTAGCTCGGCTTATTCCAGGGGTGTGTTTCGTCGAGATGCACACAAGAGTGAGGTTGCTCATCGGTTTAAAGAT
TTGGGAGAAGAAAAATTTCAAAGCCTTGGTGTGATTGCCTTTGCTCAGTATCTTCAGCAGTGTCATTTGAAGAT
CATGTAAAATTAGTGAATGAAGTAACTGAATTTGCAAAAACATGTGTTGCTGATGAGTCAGCTGAAAAATTGTGAC
AAATCACTTCATACCTTTTTTGGAGACAAATTATGCACAGTTGCAACTCTTCGTGAAACCTATGGTGAAATGGCT
GACTGCTGTGCAAAACAAGAACCTGAGAGAAATGAATGCTTCTTGCAACACAAAGATGACAACCCAAACCTCCCC
CGATTGGTGAGACCAGAGGTTGATGTGATGTGCACTGCTTTTCATGACAATGAAGAGACATTTTTGAAAAAATAC
TTATATGAAATTGCCAGAAGACATCCTTACTTTTATGCCCCGGAACCTCCTTTTCTTTGCTAAAAGGTATAAAGCT
GCTTTTACAGAATGTTGCCAAGCTGCTGATAAAGCTGCCTGCCTGTTGCCAAGCTCGATGAACTTCGGGATGAA
GGGAAGGCTTCGTCTGCCAAACAGAGACTCAAGTGTGCCAGTCTCCAAAAATTTGGAGAAAGAGCTTTCAAAGCA
TGGGCAGTAGCTCGCTGAGCCAGAGATTTCCCAAAGCTGAGTTTGCAGAAGTTTCCAAGTTAGTGACAGATCTT
ACCAAAGTCCACACGGAATGCTGCCATGGAGATCTGCTTGAATGTGCTGATGACAGGGCGGACCTTGCCAAGTAT
ATCTGTGAAAAATCAAGATTCGATCTCCAGTAAACTGAAGGAATGCTGTGAAAAACCTCTGTTGGAAAAATCCCAC
TGCATTGCCGAAGTGGAATGATGAGATGCCTGCTGACTTGCCTTCATTAGCTGCTGATTTTGTGAAAGTAAG
GATGTTTGCAAAAACTATGCTGAGGCAAAGGATGTCTTCTTGGGCATGTTTTTGTATGAATATGCAAGAAGGCAT
CCTGATTACTCTGTCTGTGCTGCTGCTGAGACTTGCCAAGACATATGAAACCACTCTAGAGAAGTGCTGTGCCGCT
GCAGATCCTCATGAATGCTATGCCAAGTGTTTCGATGAATTTAAACCTCTTGTGGAAGAGCCTCAGAATTTAATC
AAACAAAATTGTGAGCTTTTTTGAGCAGCTTGGAGAGTACAAATTCAGAATGCGCTATTAGTTCGTTACACCAAG
AAAGTACCCCAAGTGTCAACTCCAACCTCTTGTAGAGGTCTCAAGAAACCTAGGAAAAGTGGGCAGCAAATGTTGT
AAACATCCTGAAGCAAAAAGAATGCCCTGTGCAGAAGACTATCTATCCGTGGTCCTGAACCAGTTATGTGTGTTG
CATGAGAAAACGCCAGTAAGTGACAGAGTCACCAAATGCTGCACAGAATCCTTGGTGAACAGGCGACCATGCTTT
TCAGCTCTGGAAGTCGATGAAACATACGTTCCCAAAGAGTTTAATGCTGAAACATTACCTTCCATGCAGATATA
TGCACACTTTCTGAGAAGGAGAGACAAATCAAGAAACAACTGCACTTGTGAGCTCGTGAAACACAAGCCCAAG
GCAACAAAAGAGCAACTGAAAGCTGTTATGGATGATTTTCGAGCTTTTGTAGAGAAGTGCTGCAAGGCTGACGAT
AAGGAGACCTGCTTTGCCGAGGAGGGTAAAAAAGCTTGTGCTGCAAGTCAAGCTGCCTTAGGCTTATAACATCAC
ATTTAAAAGCATCTCAGCCTACCATGAGAATAAGAGAAAGAAAATGAAGATCAAAGCTTATTCATCTGTTTTTC
TTTTTCGTTGGTGTAAGCCAACACCCTGTCTAAAAAACATAAATTTCTTTAATCATTTTGCCTCTTTTCTCTGT
GCTTCAATTAATAAAAAATGGAAAGAATCTAATAGAGTGGTACAGCACTGTTATTTTTCAAAGATGTGTTGCTAT
CCTGAAAATTCTGTAGGTTCTGTGGAAGTTCCAGTGTTCTCTTATTCCACTTCGGTAGAGGATTTCTAGTTTC
TTGTGGGCTAATTAATAAATCATTAACTCTTCTAAGTT

1564/6881
FIGURE 1446

TCCATATTGTGCTTCCACCACTGCCAATAACAAAATAACTAGCAACCATGAAGTGGGTGGAATCAATTTTTTTTAA
TTTTCTACTAAATTTTACTGAATCCAGAACACTGCATAGAAATGAATATGGAATAGCTTCCATATTGGATTCTT
ACCAATGTACTGCAGAGATAAGTTTAGCTGACCTGGCTACCATATTTTTTGCCAGTTTGTTCAGAAGCCACTT
ACAAGGAAGTAAGCAAAATGGTGAAAGATGCATTGACTGCAATTGAGAAACCCACTGGAGATGAACAGTCTTCAG
GGTGTTTAGAAAACCAGCTACCTGCCTTTCTGGAAGAACTTTGCCATGAGAAAGAAATTTTGGAGAAGTACGGAC
ATTCAGACTGCTGCAGCCAAAGTGAAGAGGGAAGACATAACTGTTTTCTTGACACAAAAAGCCCCTCCAGCAT
CGATCCCCTTTTCCAAGTTCCAGAACCTGTCACAAGCTGTGAAGCATATGAAGAAGACAGGGAGACATTTCATGA
ACAAATTCATTTATGAGATAGCAAGAAGGCATCCCTTCCTGTATGCACCTACAATTCTTCTTTGGGCTGCTCGCT
ATGACAAAATAATTCATCTTGCTGCAAAGCTGAAAATGCAGTTGAATGCTTCCAAACAAAGGCAGCAACAGTTA
CAAAAGAATTAAGAGAAAGCAGCTTGTTAAATCAACATGCATGTGCAGTAATGAAAAATTTGGGACCCGAAGTT
TCCAAGCCATAACTGTTACTAACTGAGTCAGAAAGTTTACCAAAGTTAATTTTACTGAAATCCAGAACTAGTCC
TGGATGTGGCCCATGTACATGAGCACTGTTGCAGAGGAGATGTGCTGGATTGTCTGCAGGATGGGGAAAAAATCA
TGTCTACATATGTTCTCAACAAGACACTCTGTCAAAACAAAATAACAGAATGCTGCAAACTGACCACGCTGGAAC
GTGGTCAATGTATAATTCATGCAGAAAATGATGAAAAACCTGAAGGTCTATCTCCAAATCTAAACAGGTTTTTAG
GAGATAGAGATTTTAACCAATTTTCTTCAGGGGAAAAAATATCTTCTTGCAAGTTTTGTTTCATGAATATTCAA
GAAGACATCCTCAGCTTGCTGTCTCAGTAATTCTAAGAGTTGCTAAAGGATACCAGGAGTTATTGGAGAAGTGTT
TCCAGACTGAAAACCTCTTGAATGCCAAGATAAAGGAGAAGAAGATTACAGAAATACATCCAGGAGAGCCAAG
CATTGGCAAAGCGAAGCTGCGGCCTCTTCCAGAACTAGGAGAATATTACTTACAAAATGCGTTTTCTCGTTGCTT
ACACAAAGAAAGCCCCCAGCTGACCTCGTCGGAGCTGATGGCCATCACCAGAAAAATGGCAGCCACAGCAGCCA
CTTGTTGCCAACTCAGTGAGGACAACTATTGGCCTGTGGCGAGGGAGCGGCTGACATTATTATCGGACACTTAT
GTATCAGACATGAAATGACTCCAGTAAACCCTGGTGTTGGCCAGTGCTGCACTTCTTCATATGCCAACAGGAGGC
CATGCTTCAGCAGCTTGGTGGTGGATGAAACATATGTCCTCCTGCATTCTCTGATGACAAGTTCATTTTCCATA
AGGATCTGTGCCAAGCTCAGGGTGTAGCGCTGCAAACGATGAAGCAAGAGTTTCTCATTAACCTTGTGAAGCAAA
AGCCACAAATAACAGAGGAACAACCTGAGGCTGTCATTGCAGATTTCTCAGGCCTGTTGGAGAAATGCTGCCAAG
GCCAGGAACAGGAAGTCTGCTTTGCTGAAGAGGGACAAAACTGATTTCAAAAACCTCGTGCTGCTTTGGGAGTTT
AAATTACTTCAGGGGAAGAGAAGACAAAACGAGTCTTTCATTCCGTGTGAAGTTTCTCTTTAATTTTAACTGAT
TTAACTTTTTGTGAATTAATGAAATGATAAAGACTTTTATGTGAGATTTCTTATCACAGAAATAAAATATCT
CCAAATG

1565/6881
FIGURE 1447

MKWVESIFLIFLLNFTESRTLHRNEYGIASILDSYQCTAEISLADLATIFFAQFVQEATYKEVSKMVKDALTAIE
KPTGDEQSSGCLENQLPAFLEELCHEKEILEKYGHSDCCSQSEEGRHNCFLAHKKPTPASIPLFQVPEPVTSC
YEEDRETFMNKFIYEIARRHPFLYAPTILLWAARYDKIIPSCCKAENAVECFQTKAATVTKELRESSLLNQHACA
VMKNFGTRTFQAITVTKLSQKF TKVNFTEIQKLVLDAHVHEHCCRGDVLDCLQDGEKIMSYICSQQDTLSNKIT
ECCKLTTLERGQCIIHAENDEKPEGLSPNLNRFLGDRDFNQFSSGEKNIFLASFVHEYSRRHPQLAVSVILRVAK
GYQELLEKCFQTENPLECQDKGEEELQKYIQESQALAKRSCGLFQKLGEYYLQNAFLVAYTKKAPQLTSSELMAI
TRKMAATAATCCQLSEDKLLACGEGAADIIIGHLCIRHEMTPVNPVGVCCTSSYANRRPCFSSLVVDETYVPPA
FSDDKFIHKLDCQAQGVALQTMKQEFLLINLVKQKPQITEEQLEAVIADFSGLLEKCCQGQEQEVCFAEEGQKLI
SKTRAALGV

1566/6881
FIGURE 1448A

TCACCTTGCCCTGATATTTCCAGTGTGACAGGGACACAGCCAACTGGGGTCCCTTCTAGGCTGACAGCCGCTCTCC
AGCCACTGCCGCGAGCCCGTCTGCTCCCGCCCTGCCCGTGCACCTCTCCGAGCCGCCCTCCGCCAAGCCCCAGCG
CCCGCTCCCATCGCCGATGACCGCGGGGAGGAGGATGGAGATGCTCTGTGCCGGCAGGGTCCCTGCGCTGCTGCT
CTGCCTGGGTTTCCATCTTCTACAGGCAGTCCTCAGTACAACCTGTGATTCCATCATGTATCCCAGGAGAGTCCAG
TGATAACTGCACAGCTTTAGTTTACAGACAGAAGACAATCCACGTGTGGCTCAAGTGTCAATAACAAAGTGTAGCTC
TGACATGAATGGCTATTGTTTGCATGGACAGTGCATCTATCTGGTGGACATGAGTCAAACTACTGCAGGTGTGA
AGTGGGTTTACTGGTGTCCGATGTGAACACTTCTTTTAAACCGTCCACCAACCTTTAAGCAAGAATATGTGGC
TTTGACCGTGATTCTTATTATTTTGTCTTATCACAGTCGTCCGTTCCACATATTATTTCTGCAGATGGTACAG
AAATCGAAAAAGTAAAGAACCAGGAAGGAATATGAGAGAGTTACCTCAGGGGATCCAGAGTTGCCGCAAGTCTG
AATGGCGCCATCAAACCTTATGGGCAGGGATAACAGTGTGCCTGGTTAATATTAATATTTCCATTTTATTAATAAT
ATTTATGTTGGGTCAAGTGTAGGTCAATAACACTGTATTTAATGTACTTGAAAAATGTTTTTATTTTGTGTTT
ATTTTGTACAGACTATTTGCTAATGTATAATGTGCAGAAAAATTTAATATCAAAAGAAAATTGATATTTTATA
CAAGTAATTTCTGAGCTAAATGCTTCATTGAAAGCTTCAAAGTTTATATGCCTGGTGCACAGTGTCTAGAAAGTA
AGCAATTTCCAGGTCATAGCTCAAGAATTGTTAGCAAAATGACAGATTTCTGTAAGCCTATATATATAGTCAAATC
GATTTAGTAAGTATGTTTTTATGTTTCTCAAATCAGTGATAATTGGTTTGACTGTACCATGGTTTGATATGTAG
TTGGCACCATGGTATCATATATTAACAATAATGCAATTAGAATTTGGGAGAAGCAAATATAGGTCTCTGTGTTA
AACACTACACATTTGAAACAAGCTAACCTGGGGAGTCTATGGTCTCTTCACTCAGGTCTCAGCTATAATTCGT
TATATGAGGGGCAGTGGACAGTTCCTATGCCAACTCAGACTCCTACAGGTACTAGTCACTCATCTACCAGATT
CTGCCTATGTAATAATGAATTGAAAAACAATTTTCTGTAATCTTTTATTTAAGTAGTGGGCATTTTCATAGCTTCAC
AATGTTCCCTTTTTTGTATATTACAACATTTATGTGAGGTAATTATGTCTAACAGACAATTAGAAAAAAGTCCAC
ACTTGAAGCCTAAATTTGTGCTTTTTAAGAATATTTTTAGACTATTTCTTTTTTATAGGGGCTTTGCTGAATTCTA
ACATTAAATCACAGCCCAAATTTGATGGACTAATTATTATTTTAAAATATATGAAGACAATAATTCTACATGTT
GTCTTAAGATGGAATAACAGTTATTTTCATCTTTTATTCAAGGAAGTTTAACTTTAATACAGCTCAGTAAATGGC
TTCTTCTAGAATGTAAAGTTATGTATTTAAAGTTGTATCTTGACACAGGAAATGGGAAAAAAGTAAAAATTAAT
ATGGTGTATTTTTCCAAATGAAAAATCTCAATTGAAAGCTTTTAAAATGTAGAACTTAAACACACCTTCCTGTG
GAGGCTGAGATGAAAACTAGGGCTCATTTTCTGACATTTGTTTATTTTTTGGAAAGAGACAAAGATTTCTTCTGC
ACTCTGAGCCCATAGGTCTCAGAGAGTTAATAGGAGTATTTTTGGGCTATTGCATAAGGAGCCACTGCTGCCACC
ACTTTTGGATTTTATGGGAGGCTCCTTCATCGAATGCTAAACCTTTGAGTAGAGTCTCCCTGGATCACATACCAG
GTCAGGGAGGATCTGTTCTTCTCTACGTTTATCTTGGCATGTGCTAGGGTAAACGAAGGCATAATAAGCCATGG
CTGACCTCTGGAGCACCAGGTGCCAGGACTTGTCTCCATGTGTATCCATGCATTATATACCCTGGTGAATCACA
CGACTGTCTATCTAAAGTCTTGGCCCTGGCCCTTACTATTAGGAAAAATAAACAGACAAAAACAAGTAAATATATAT
GGTCATATACATATTGTATATATATTTATATACAAACATGTATGTATACATGACCTTAATGGATCATAGAATTGC
AGTCATTTGGTGTCTGTCTAACCATTTATATAAACTTAAAAACAAGAGAAAAGAAAAATCAATTAGATCTAAAC
AGTTATTTCTGTTTCTTATTTAATACAGCTGAAGTCAAAATATGTAAGAACACATTTTAAATACTCTACTTACAG
TTGGCCCTCTGTGGTTAGTTCCACATCTGTGGATTCAACCAACCAAGGACGGAAAATGCTTAAAAAATAATACAA
CAACAACAAAAAATACATTATAACAACCTATTTACTTTTTTTTTTTTTCTTTTTGAGATGGAGTCTCGCTCTGTTGC
CCAGGTTGGAGTGCAGTGGCAGATCTCGGCTCACTGCAACCTCACCTCCCGGGTTCAAGAGATCCTCCTGCCTC
AGCCTCCTGAGCAGCTGGGACTACAGGCGCATGCCACCATGCCAGCTAATTTTTGTATTTTTTAGTAGAGGCGGG
GTTTCACCATGTTGGCCAGGATGGTCTCAATCTCCTAACCTTGAGATCCACCTCCACAGCCTCCCAAAGTCTG
GGATTACAGGTGTGAGCCACCGCACGTAGCATTTACATTAGGTATTACAAGTAATGTAAAGATGATTTAAGTATA
CAGGAGGATGTGAATAGGTTATATGCAAGCACTATGCCCTTTTATATAAGTGACTTGAACATCTGTGCCCGATT
TAGTATGTGAGGGGGGCGATCTGGGAATCAGTCCCCTGTGGATACCAAGGTACAAGTATTTTATTAACGCTTA
CTAGATGTGAGGAGAGTCTGAATATTTTCAGTGATCTTGGCTGTTTCAAAAAAATCTATTGACTTTTCAATAAAT
CAGCTGCAATCCATTTATTTTCAATTTACAAAAGATTTATTGTAAGCATCTCAATCTTGGTTTGTGAGTTTATCTTA
AGCATGTCAATTCATAAAAAACAAGTCATTTTGTATTTTTCATCTTTAAGAATGCTTAAAAAAGCTAATCCCTAA
AATAGTTAGATCTTTGTAAATGCATATTAAATAATAAAGTATGACCCACATTACTTTTTATGGGTGAAAATAAGA
CAAAAAATAAGTTTTAGTGAGGATGGTGTGAGTAAACATAAAAACTGATTTGCTCTCAGCTGATGTGTCCTGT
ACACAGTGGGAAGATTTTAGTTACACTTAGTCTAACTCCCCATTTTACAGATTTCTCACTATATATATTTCTA

1567/6881
FIGURE 1448B

GAAGGGGCTATGCATATTCAATGTATTGAGAACCAAAAGCAACCACAAATGCATAAATGCATAATTTATGGTCTTC
AACCAAGGCCACATAATAACCCAGTTAACTTACTCTTTAACCAGGAATATTAAGTTCTATAACTAGTACTCAAGG
TTTAACCTTAAAAATTAAGATTTCCCTTAACCTTAACCTTAAAAATTGATATTATATTAAACATACATAATACAATGT
AACTCCACTGTTCTCCTGAATATTTTTTGCTCTAATCTCTCTGCCGAAAGTCAAAGTGATGGGAGAATTGGTATA
CTGGTATGACTACGTCTTAAGTCAGATTTTTATTTATGAGTCTTTGAGACTAAATTCAATCACCACCAGGTATCA
AATCAACTTTTATGCAGCAAATATATGATTCTAGTGTCTGACTTTTGTTAAATTCAGTAATGCAGTTTTTAAAAA
CCTGTATCTGACCCACTTTGTAATTTTTGCTCCAATATCCATTCTGTAGACTTTTGAAAAAAAAGTTTTAATTT
GATGCCCAATATATTCTGACCGTTAAAAAATTCCTTGTTCAATATGGGAGAAGGGGGAGTAATGACTTGTACAAACA
GTATTTCTGGTGTATATTTTAATGTTTTTAAAAAGAGTAATTCATTTAAATATCTGTTATTCAAATTTGATGAT
GTTAAATGTAATATAATGTATTTTCTTTTTATTTTGCACTCTGTAATTGCACTTTTTAAGTTTGAAGAGCCATTT
TGGTAAACGGTTTTTATTAAAGATGCTATGGAACATAAAGTTGTATTGCATGCAATTTGAAGTAACTTATTTGAC
TATGAATGTTATCGGATTACTGAATTGTATCAATTTGTTTGTTCAATATCAGCTTTGATAATTGTGTACCTTA
AGATATTGAAGGAGAAAATAGATAATTTACAAGATATTATTAATTTTTATTTATTTTCTTGGGAATTGAAAAAA
ATTGAAATAAATAAAAAATGCATTGAACATCTTGCAATTCAAAATCTTCACTGAC

1568/6881
FIGURE 1449

CCCGCGAGCGGACGCGGCAGCGCCTCTGTCTCGCTTTTCTTATTTTTCCCCCTTTCCCCTTTCTTTTTTTTTT
TTTCTTTTCTTTTCTCCCCCTCCCCCTTTTACCATTTCCTTCGGAGGCGCTTTCCCCGGGCAGGGCAGAGCC
GGTCTCACCCCCCGCCTCTCCCCGGCCCCCGCCGCTTATGGCGAGAGGGAGCCCCCTCCAACCCGGGCTCGAG
CGGCGGCGGCCTCAGGCCGGGGGTTCATCATGGAACATAATTCGCTGACCGACCCAGCGGCCGAGCCGTGCGTCCC
GCTCGAGCGCCAGCGCCCGCGCCCGCGCCCCCGATCCGCTTCCCCTTTCTCCCTCCTCAGTTGGCCGAGTCGTC
CCGCGCGCACCCGCTCCGCGCGCCTATGAGAATGAGGTGGTAACGGGCCCCCGGATGACCCCGCGTCACCACTGT
GAGGCCTACAGCTCTGCCGGGGAGGAGGAGGAGGAAGAGGAGGAGAAGGTAGCTACAGCAAGCTGGGTAGCA
GGCAGATCCAAAGGATATCATGAAGTTTCCAGGGCCTTTGGAAAACCAGAGATTGTCTTTCCTGTTGGAAAAGGC
AATCACTAGGGAAGCACAGATGTGGAAAGTGAATGTGCGGAAAATGCCTTCAAATCAGAATGTTTCTCCATCCCA
GAGAGATGAAGTAATTCAATGGCTGGCCAAACTCAAGTACCAATTCAACCTTTACCCAGAAACATTTGCTCTGGC
TAGCAGTCTTTTGGATAGGTTTTTAGCTACCGTAAAGGCTCATCCAAAATACTTGAGTTGTATTGCAATCAGCTG
TTTTTTCCTAGCTGCCAAGACTGTTGAGGAAGATGAGAGAATTCCAGTACTAAAGGTATTGGCAAGAGACAGTTT
CTGTGGATGTTTCCTCATCTGAAATTTTGAGAATGGAGAGAATTATTCTGGATAAGTTGAATTGGGATCTTCACAC
AGCCACACCATTTGGATTTTCTTCATATTTTCCATGCCATTGCAGTGTCAACTAGGCCTCAGTTACTTTTCAGTTT
GCCCCAAATTGAGCCCATCTCAACATTTGGCAGTCCTTACCAAGCAACTACTTCACTGTATGGCCTGCAACCAACT
TCTGCAATTCAAGAGGATCCATGCTTGCTCTGGCCATGGTTAGTCTGGAAATGGAGAAACTCATTCTGATTGGCT
TTCTCTTACAATTGAACTGCTTCAGAAAGCACAGATGGATAGCTCCCAGTTGATCCATTGTGCGGGAGCTTGTGGC
ACATCACCTTTTCTACTCTGCAGTCTTCCCTGCCTCTGAATTCCGTTTATGTCTACCGTCCCCCTCAAGCACACCTT
GGTGACCTGTGACAAAAGGAGTGTTTCAAGATTACATCCCTCCTCTGTCCCAGGCCAGACTTCTCCAAGGACAACAG
CAAGCCAGAAGTGCCAGTCAGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGAC
CTCTACTAAACGCAAAAGTAGAGGAAATGGAAGTGGATGACTTCTATGATGGAATCAAACGGCTCTATAATGAAGA
TAATGTCTCAGAAAAATGTGGGTTCTGTGTGTGGCACTGATTTATCAAGACAAGAGGGACATGCTTCCCCTTGTCC
ACCTTTGTCAGCCTGTTTCTGTCTATGTAGTTTCAACAAGTGCTACCTTTGAGTGTAACTAAGGTAGACTACTTTG
GGAATGAGAACATGCAAAATCAGGAAAGGCTGTAGAAGGAAATATACCTTAACAGGCTGATTTGGAGTGAGCCAG
AAAAAAAAAATAAACTCTCATTATTTGTGTGGCTAATTATAATTCAGCGTTATTTAAGCACATAAAGACCAAAA
AAAAAAAAAAAAAAAA

1569/6881
FIGURE 1450

MKFFGPLENQRLSFLLEKAITREAQMWKVNVRKMPSNQNVSPSQRDEVIQWLAKLKYQFNLYPETFALASSLLDR
FLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSFCGCSSEILRMERIILDKLNWDLHTATPLDF
LHIFHAIHAVSTRPQLLFSLPKLSPSQHLAVLTKQLLHCMACNQLLQFRGSMALAMVSLEMEKLIPDWLSLTIEL
LQKAQMDSSQLIHCRELVAAHHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNSKPEVPV
RGTAIFYHHLPAASGCKQTSTKRKVEEMEVDDEFYDGIKRLYNEDNVSENVGSVCGTDLSRQEGHASPCPPLQPV
VM

1570/6881
FIGURE 1451

CCTGGACTCAGAGCTCAAGTCTGAACTCTACCTCCAGACAGAATGAAGTTCATCTCGACATCTCTGCTTCTCATG
CTGCTGGTCAGCAGCCTCTCTCCAGTCCAAGGTGTTCTGGAGGTCTATTACACAAGCTTGAGGTGTAGATGTGTC
CAAGAGAGCTCAGTCTTTATCCCTAGACGCTTCATTGATCGAATTCAAATCTTGCCCCGTGGGAATGGTTGTCCA
AGAAAAGAAATCATAGTCTGGAAGAAGAACAAGTCAATTGTGTGTGTGGACCCTCAAGCTGAATGGATACAAAGA
ATGATGGAAGTATTGAGAAAAAGAAGTTCTTCAACTCTACCAGTTCAGTGTTTAAGAGAAAGATTCCCTGATGC
TGATATTTCCACTAAGAACACCTGCATTCTTCCCTTATCCCTGCTCTGGATTTTAGTTTTGTGCTTAGTTAAATC
TTTTCCAGGAAAAAGAACTTCCCATACAAATAAGCATGAGACTATGTAAAAATAACCTTGCAGAAGCTGATGGG
GCAAACCTCAAGCTTCTTCACTCACAGCACCCCTATATACACTTGGAGTTTGCATTCTTATTCATCAGGGAGGAAAG
TTTCTTTGAAAATAGTTATTTCAGTTATAAGTAATACAGGATTATTTTGATTATATACTTGTGTTTAAATGTTTAA
AATTTCTTAGAAAACAATGGAATGAGAATTTAAGCCTCAAATTTGAACATGTGGCTTGAATTAAGAAGAAAATTA
TGGCATATATTTAAAAGCAGGCTTCTATGAAAGACTCAAAAAGCTGCCTGGGAGGCAGATGGAACCTTGAGCCTGTC
AAGAGGCAAAGGAATCCATGTAGTAGATATCCTCTGCTTAAAACTCACTACGGAGGAGAATTAAGTCCTACTTT
TAAAGAATTTCTTTATAAAATTTACTGTCTAAGATTAATAGCATTTCGAAGATCCCCAGACTTCATAGAATACTCA
GGGAAAGCATTTTAAAGGGTGATGTACACATGTATCCTTTCACACATTTGCCTTGACAACTTCTTTCACTCACAT
CTTTTTCACTGACTTTTTTTGTGGGGGGCGGGGCCGGGGGGACTCTGGTATCTAATTCTTTAATGATTCCCTATAA
ATCTAATGACATTCAATAAAGTTGAGCAAAACATTTTACTT

1571/6881
FIGURE 1452

ATGGTTTATCAGACATCACTTTGTTCTTGTTCTGTAAACATCCGAGTGCCCAACAGACATTTTGCTGCTGCTACA
AAGTCTGCAAAGAAAACAAAAAAGGTGCTAAAGAAAAAACACCAGATGAGAAAAAGATGAAATAGAAAAAATA
AAAGCATATCCCTATATGGAAGGCGAACCTGAGGATGATGTCTATTTAAAACGCTTATACCCGAGACAGATATAT
GAGGTGGAGAAAGCTGTTCACTTACTTAAGAAATTTCAAATTCCTTGACTTTACTAGTCCAAAGCAAAGTGTTTAT
CTTGATTTGACACTGGATATGGCACTGGGAAAGAAGAAAAACGTGGAGCCATTTACCAGTGTTCTTAGTTTGCCA
TACCCATTTGCTTCCGAAATCAATAAAGTTGCTGTATTTACAGAGAATGCATCAGAGGTCAAAATAGCGGAAGAA
AATGGAGCTGCATTTGCAGGAGGCACTAGTCTGATACAGAAGATTTGGGATGATGAAATTGTTGCAGACTTTTAC
GTAGCTGTTCCAGAAATAATGCCTGAACTTAATCGATTAAGGAAGAACTGAATAAAAAATATCCAAAGCTTTCT
CGAAATTCCATTGGCCGTGACATCCCCAAAATGCTTGAATTATTTAAAAATGGACATGAAATTAAGGTAGATGAA
GAAAGGGAGAAGTTTCTCCAGACCAAAATAGCAACATTGGATATGTCAAGTGACCAGATAGCTGCCAATCTGCAA
GCAGTTATTAATGAAGTTTGTAGGCACAGACCGCTGAATTTGGGTCCCTTTGTGGTACGTGCTTTCCTTCGTAGT
TCAACAAGTGAAGGTTTATTACTGAAGATTGATCCATTGTTGCCTAAAGAAGTAAAAAATGAAGAAAGTGAAAAA
GAAGATGCCTAA

1572/6881
FIGURE 1453

GTGGGAAGAGCTGAAGCAGGCGCTCTTGGCTCGGCGCGGCCCGCTGCAATCCGTAGAGGAACCCGCCGCCGAGCC
ACCATCATGCCTGGGCACTTACAGGAAGGCTTCGGCTGTGTGGTCACCAACCGATTTCGACCAGTTATTTGACGAC
GAATCGGACCCCTTCGAGGTGCTGAAGGCAGCGGAGAACAAGAAAAAGAAGCCGGCAGGGGTGGCGTTGGGGGC
CCTGGGGCCAAGAGCGCAGCTCAGGCGGCGGCCAGACCAACTCCAACGCGGCAGGCAAACAGCTGCGCAAGGAG
TCCCAGAAAGACCGCAAGAACCCGCTGCCCCGAGCGTTGGCGTGGTTGACAAGAAAGAGGAGACGCAGCCGCC
GTGGCGCTTAAGAAAGAAGGAATAAGACGAGTTGGAAGAAGACCTGATCAACAACCTTCAGGGTGAGGGGAAAATA
ATTGATAGAAGACCAGAAAGGCAACCACCTTGTGAACGAAGATTGAAAAGCCACTTGAAGAAAAGGGTGAAGGA
GGCTTAATTTTTCAGTTGATAGACCGATTATTGACCGACCTATTTCGAGGTGCTGGTGGTCTTGGAAGAGGTCGAGGG
GGCCGTGGACGTGGAATGGGCCGAGGAGATGGATTTGATTCTCGTGGCAAACGTGAATTTGATAGGCATAGTGGA
AGTGATAGATCTTCTTTTTTACATTACAGTGGCCTGAAGCACGAGGACAAACGTGGAGGTAGCGGATCTCACAAC
TGGGGAAGTGTCAAAGACGAATTAAGTACTTGGATCAATCAAATGTGACTGACGAAACACCTGAAGGTGAAGAA
CATCATCCAGTGGCAGACACTGAAAATAAGGAGAATGATGTTGAAGAGGTAAAAGAGGAGGGTCCAAAAGAGATG
ACTTTGGATGAGTGGAAGGCTATTCAAATAAGGACCGGGCAAAAGTAGAATTTAATATCTGAAAACCAAATGAA
GGTGCTGATGGGCAGTGGAAGAAGGGATTTGTTTTCATAAATCAAAGAGTGAAGAGGCTTATGCTGAGGATTCAG
TTATGGACCATCATTTCCAGAAGCCAGCAAATGATATAACGTCTCAGCTGGAGATCAATTTTGGAGACCTTGGCC
GCCCAGGACGTGGCGGCAGGGGAGGACAAGGTGGACATGGGCGTGGTGGGCGCCCAAACCGTGGCAGCAGGACCG
ACAAGTCAAGTACTTCTGCTCCTGATGTGGATGACCCAGAGGCATTCCCAGTTCTGGCTTAAGTGGATGCCATAA
GACAACCCCTGGTTCCTTCGTGAACCCCTTCTGTTCAAAGCTTTTGCATGCTTAAGGATTCCAAATGACAAATTA
AAAAAAGACTGTCATTTCATACCATTCACACCTAAAGACTGAATTTTATCTGTTTCAAAAATGAACTTATCT
CGCTACACAGAAGTAACAAATATGGTAGTCAGTTTTGTATTTAGAAATGTATTGGTAGCAGGGATGTTTTATAA
TTTTCAGAGATTATGCATTCTTCATGAATACTTTTGTATTGCTGCTTGCAAATATGCATTTCCAACTTGAAATA
TAGGTGTGAACAGTGTGTACCAGTTTAAAGCTTTCACTTCATTTGTGTTTTTAATTAAGGATTTAGAAGTTCCC
CCAATTACAACTGGTTTTAAATATTGGACATACTGGCTTTAATACATGCTTTGCATATTCACACATGATCAACT
GGGACATGTTAACTTTGATTTGTCAAATTTTATTCTGTGTGGAATACTAATATATGATTTTTAACTTAGTTTT
AATATTTTCATTTTTTGGGGAAAAATCTTTTTTCACTTCTCATGATAGCTGTTATATATATATGCTAAATCTTTAT
ATACAGAAATATCAGTACTTGAAGAAA

1573/6881
FIGURE 1454

MPGHLQEGFGCVVTNRFDQLFDDESDPFVVLKAAENKKKEAGRGGVGGPGAKSAAQAAAQTNNAAGKQLRKESQ
KDRKNPLPRSVGVVDKKEETQPPVALKKEGIRRVGRRPDQQLQEGEKIIDRRPERQPPCERRFEKPLEEKGEGG

1574/6881
FIGURE 1455

AGACGCAGTCTCCGTCGTTGACGTTAGTCGCAGTCTTCGCTGCTAACGTTTTGTTATGAGTTGCTAAAATGGTGA
AATGCTGCTCCGCCATTGGATGTGCTTCTCGCTGCTTGCCAAATTCGAAGTTAAAAGGACTGACATTTACGTAT
TCCCCACAGATGAAAACATCAAAAGGAAATGGGTATTAGCAATGAAAAGACTTGATGTGAATGCAGCCGGCATT
GGGAGCCTAAAAAAGGAGATGTGTTGTGTTTCGAGGCACTTTAAGAAGACAGATTTTGACAGAAGTGCTCCAAATA
TTAAACTGAAACCTGGAGTCATACCTTCTATCTTTGATTCTCCATATCACCTACAGGGGAAAAGAGAAAACTTC
ATTGTAGAAAAAATTCACCTCAAAACCGTTCCAGCCACTAACTACAATCACCATCTTGTTGGTGCTTCCTCAT
GTATTGAAGAATTCCAATCCCAGTTCATTTTTGAACATAGCTACAGTGTAAATGGACAGTCCAAAGAACTTAAGC
ATAAATTAGATCATGTGATCGGCGAGCTAGAGGATACAAAGGAAAGTCTACGGAATGTTTTAGACCGAGAAAAAC
GTTTTCAGAAATCATTGAGGAAGACAATCAGGGAATTAAAGGATGAATGTCTGATCAGCCAAGAAACAGCAAATA
GACTGGACACTTTCTGTTGGGACTGTTGTGAGGAGAGCATAGAACAGGACTATATTTTCATGAAATAATTTTCATGT
TACGTTCCACCTAAAATTGTCAATTGGTACAAATTTTTATAAAATCTCATTACCATCACTAAATAATATCCATCA
TTTAAAGTGCTGCTTTGGATTCTCTGGAGCATTATGCATTATAGTTGTTATCCAAAGACTTTTTTGAAAAATATGC
AGAAATTTGTGGTAATTATGTATTTGTGTCTTGTGACAATTATGTTTTATAGACCTACACTAGTGCCAGGTCAC
ATTGTAAGATGTTAAATCTCAAGAAAATTTACAGAGCTAAAAGAAATGATGTCAAATTAGTCACATTAAGCTAT
AGTAGAAGGAATTGGACACTTCTCCAGATATTTGGCTTCAAAGGAGTACCTTTACTTACATGTGCTTTATGGTAA
GTACATTGAATTTTACTTTAAATGCATTTTACTACAAAGCACAATTCATTTGTAATGCATATCCATCTTGGATTC
AATCCAAGGTGCTTTAGCTATCAGTAGTACCAAAGGATCTTTTTACAAGGCTTCCTGTGGTATTGACTCTGAGAA
TAACACATAGTGAAGATCTGTGGGCTTTTTAAATTTGTTTACAGCCAATTTAAGAAGACCCCTCATGAAGTCTCAG
TTTTCAGTACAGTACATCATTCCTCCTCACTAGGAGCACTTTGATGTAAACCAGAATAGCTTTAAAAAGACAAAA
AGGATCGTAGATCTGATTTTTAAATGGTTGGTTGCTCTGACAGATCTGAACACTTTGCTTCATGACTATTTTCGTC
ATAAAGGTATATGTTTTAAATCTGAATGGCAGTACTAGCTCTATACTTTTAATACTGCTTTGTATTTTATATGTA
AAGTAGTATTGCTGACATTTTAAAAAATACAAAATACAAAAGAAACCATTAGAAATTAATAACTGTGGCTCTTC
CAGTTGAAATAGGAATTGGAGAGAAAGGATTAGAATATTTTAATTAGGGGAGTAGATTATTGTCCAAAGGCTTTT
ATTTAGAGAAACGGGTAATTAAAACAGCAGCTTTAGAATAGCTTCTTACTGAATATGCAAAGAATAATTCCTTG
TTATTTCCCTAATTGATCCAAGTCTCATAAATTTAGCTTTTGTGATAATTCCTTACCGAAAACAACCTGAAATTGAG
AGTCATAAATACTGTGGGTAGAAATAAAAACCATTTGCCAAAGCAACACTCTACTTAGAAGCACATGTACATACA
TGGACCTCATTGAGAAAGTCCATGTTGTAGCAGTTAGAATTTGAGTATCAGCCATTTTCATTGTAGTAACAAAAAT
GAATTGCATTTTGTGCTCAGTTGTTTATTGTAATTTTATTTTGTGTTACATTAATATTAGTTAAGATATGGTCACT
TGAATTTTTTGTATTTAAGAATTTTCTGTTTTAATGCATGTTATACTTTTATGTAGGATTCCAAACCTTCCCTCT
AAATGGGATTTAACCACATCTGCGAGATCAGCGTTATGCTAAGAGGAAATCACTGAGGCCATATCTTTTTACAA
TCTGAAAAAAAGTAGTAAAAAGGTAGTTAAAAA

1575/6881
FIGURE 1456

CGGCGCCATTAAAGCGAGGAGGAGGCGAGAGCGGCCGCCGCTGGTGCTTATTCTTTTTTAGTGCAGCGGGAGAGA
GCGGGAGTGTGCGCCGCGCGAGAGTGGGAGGCGAAGGGGGCAGGCCAGGGAGAGGCGCAGGAGCCTTTGCAGCCA
CGCGCGCGCCTTCCCTGTCTTGTGTGCTTCGCGAGGTAGAGCGGGCGCGCGGCAGCGGCGGGGATTACTTTGCTG
CTAGTTTCGGTTCGCGGCAGCGGCGGGGTGTAGTCTCGGCGGCAGCGGCGGAGACACTAGCACTATGTCGGAGGAG
CAGTTCGGCGGGGACGGGGCGGCGGCAGCGGCAACGGCGGCGGTAGGCGGCTCGGCGGGCGAGCAGGAGGGAGCC
ATGGTGGCGGCGACACAGGGGGCAGCGGCGGCGGCGGGAAGCGGAGCCGGGACCGGGGGCGGAACCGCGTCTGGA
GGCACC GAAGGGGGCAGCGCCGAGTCCGAGGGGGCGAAGATTGACGCCAGTAAGAACGAGGAGGATGAAGGCCAT
TCAAACCTCCTCCCCACGACACTCTGAAGCAGCGACGGCACAGCGGGAAGAATGGAAAATGTTTATAGGAGGCCTT
AGCTGGGACACTACAAAGAAAGATCTGAAGGACTACTTTTCCAAATTTGGTGAAGTTGTAGACTGCACTCTGAAG
TTAGATCCTATCACAGGGCGATCAAGGGGTTTTGGCTTTGTGCTATTTAAAGAATCGGAGAGTGTAGATAAGGTC
ATGGATCAAAAAGAACATAAATTGAATGGGAAGGTGATTGATCCTAAAAGGGCCAAAGCCATGAAAACAAAAGAG
CCGGTTAAAAAAATTTTTGTTGGTGGCCTTTCTCCAGATACACCTGAAGAGAAAATAAGGGAGTACTTTGGTGGT
TTTGGTGAGGTGGAATCCATAGAGCTCCCCATGGACAACAAGACCAATAAGAGGCGTGGGTTCTGCTTTATTACC
TTTAAGGAAGAAGAACCAGTGAAGAAGATAATGGAAAAGAAATACCACAATGTTGGTCTTAGTAAATGTGAAATA
AAAGTAGCCATGTGCAAGGAACAATATCAGCAACAGCAACAGTGGGGATCTAGAGGAGGATTTGCAGGAAGAGCT
CGTGGAAGAGGTGGTGACCAGCAGAGTGTTATGGGAAGGTATCCAGGCGAGGTGGTTCATCAAAATAGCTACAAA
CCATACTAAATTATTCCATTTGCAACTTATCCCCAACAGGTGGTGAAGCAGTATTTTCCAATTTGAAGATTCATT
TGAAGGTGGCTCCTGCCACCTGCTAATAGCAGTTCAAACCTAAATTTTTTGTATCAAGTCCCTGAATGGAAGTATG
ACGTTGGGTCCCTCTGAAGTTTAAATTCTGAGTTCTCATTAAAGAAATTTGCTTTTCATTGTTTTATTTCTTAATT
GCTATGCTTCAGAATCAATTTGTGTTTTATGCCCTTTCCCCAGTATTGTAGAGCAAGTCTTGTGTTAAAAGCCC
AGTGIGACAGTGTGATGATGTAGTAGTGCTTACTGGTTTTTTAATAAATCCTTTTGTATAAAAATGTATTGGCT
CTTTTATCATCAGAATAGGAAAAATTGTCATGGATTCAAGTTATTTAAAGCATAAGTTTGGAAGACAGGCTTGCC
GAAATTGAGGACATGATTAATAATTGCAGTGAAGTTTGAAATGTTTTTAGCAAAATCTAATTTTTGCCATAATGTG
TCCTCCCTGTCCAAATTGGGAATGACTTAATGTCAATTTGTTTGGTGGTTGTTTAATAATACTTCCTTATGTAG
CCATTAAGATTTATATGAATATTTCCCAAATGCCAGTTTTTGCTTAATATGTATTGTGCTTTTTAGAACAAAT
CTGGATAAATGTGCAAAAGTACCCCTTTGCACAGATAGTTAATGTTTTATGCTTCCATTAAATAAAAAGGACTTA
AAATCTGTTAATTATAATAGAAATGCGGCTAGTTCAGAGAGATTTTTAGAGCTGTGGTGGACTTCATAGATGAAT
TCAAGTGTTGAGGGAGGATTAAAGAAAT

[illegible]

1577/6881
FIGURE 1457B

CAGAAGGATTGACCATGCATACCCACATAGTTAGCACCAGCAACTTCAGTGAGACCTCTGCTTTTCATGCCAGTTC
TCAAAGTTGTTCTCAGCCAGGCAATAAGCTGGGTGTCTAAAAGGACAGCTTCTCTTCCACTCAATATTGCCATT
TTTCAAAGAAACATGTTAAAAAATAAATAAGACATGGACTAGTCCTCATTAGCATGTTTGCATAGCAACC
AGTCAAGAGCATTACACTATTTCTGCTGATATACTCACCTTAGAACTGCTCAGAACCCTGGTGCTTTATTTTG
TTTTAATCTTTTGTTGCCAGTGATGATTTTCCTATTCTGCAAATAGTGTATTTCTGGATTACACATAGTATGGT
TTCCTGAAGTATTCTGATAAAATGTGTTTTTTAAACCTCAATATACTTTTAGAAAAGGAGCATCTGGTTATGC
ATAAAGCAGAGCTAAACTAAATTTCTTTCATGTCCTCCCTACTTCCTCAGTGTCAATCAGATTAAAGTGTGTAA
TCCT

1578/6881
FIGURE 1458

MKLKEVDRTAMQAWSPAQNHP IYLATGTSAQQLDATFSTNASLEIFELDLSDPSLDMKSCATFSSSHRYHKLIWG
PYKMDSKGDVSGVLIAGGENGNII LYDPSKIIAGDKEVVIAQNDKHTGPVRALDVNIFQTNLVASGANESEIYIW
DLNNFATPMTPGAQTQPPEDISCIAWNRRQVQHILASASPSGRATVWDLRKNEPIIKVSDHSNRMHCSEGLAWHPDV
ATQMVLA SEDDRLPVIQMWDLRFASSPLRVLENHARGILAIASWMADEP ELLLSGCKDAKILCSNPNTGEVLYELP
TNTQWCFDIQWCPRNPAVLSAASFDGRISVYSIMGGSTDGLRQKQVDKLSSSFGNLDPFGTGQPLPPLQIPQQT
QHSIVLPLKKPPKWIRRPVGASFSGGKLVTFENVRMP SHQGAEQQQQHHVFI SQVVTEKEFLSRSDQLQQAVQ
SQGFINYCQKKIDASQTEFEKNVWSFLKVNFEDDSRGKYLELLGYRKEDLGKKIALALNKVDGANVALKDSQVA
QSDGEESPAAEQQLLGEHIKEEKEESEFLPSSGGTFNISVSGDIDGLITQALLTGNFESAVDLCLHDNRMA DAI I
LAIAGGQELLARTQKKYFAKSQSKITRLITAVVMKNWKEIVESCDLKNWREALAAVLTYAKPDEFSA LCDLLGTR
LENEGDSL LQTQACLCYICAGNVEKLVACWTKAQDGSHP LSLQDLIEKVVILRKAVQLTQAMDTSTVGVLLAAKM
SQYANLLAAQGSIAAALAF LPDNTNQPNIMQLRDRLCRAQGE PVAGHESPKIPYEKQQLPKGRPGPVAGHHQMPR
VQTQQYYPHGENPPPPGFIMHGNVNPNASGQLPTSPGHMHTQVPPYPQPYQPAQPYPF GTGGSAMYRPQQPVA
PPTSNAYPNTPYISSASSYTGQS QLYAAQHQA SSPTSSPATSFPPPPSSGASFQHG GPGAPPSSSAYALPPGTG
TLPAASELPASQRTGPQNGWNDPPALNRVPKKKKMPENFMPPVPITSPIMNPLGDPQSQMLQQQPSAPVPLSSQS
SFPQPHLP GGQPFHGVQQPLGQTGMPPSFSKPNIEGAPGAPIGNTFQHVQSLPTKKITKKPIPDEHLILKTTFED
LIQRCLSSATDPQTKRKLDDASKRLEFLYDKLREQTLSP TITSGLHNIARSIETRNYSEGLTMHTHIVSTSNFSE
TSAFMPVLKVVL TQANKLGV

1579/6881
FIGURE 1459

GCAGAGCACAGCATCGTCGGGACCAGACTCGTCTCAGGCCAGTTGCAGCCTTCTCAGCCAAACGCCGACCAAGGA
AAACTCACTACCA**ATG**AGAATTGCAGTGATTTGCTTTTGCCCTCCTAGGCATCACCTGTGCCATACCAGTTAAACAG
GCTGATTCTGGAAGTTCTGAGGAAAAGCAGCTTTACAACAAATACCCAGATGCTGTGGCCACATGGCTAAACCCCT
GACCCATCTCAGAAGCAGAATCTCCTAGCCCCACAGACCCCTCCAAGTAAGTCCAACGAAAGCCATGACCACATG
GATGATATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGACTCTGATGAT
GTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGATGAATCTGATGAACTGGTCACTGAT
TTTCCACGGACCTGCCAGCAACCGAAGTTTTCACTCCAGTTGTCCCCACAGTAGACACATATGATGGCCGAGGT
GATAGTGTGGTTTATGGACTGAGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACA
GACGAGGACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTTGCCCAGGAC
CTGAACGCGCCTTCTGATTGGGACAGCCGTGGGAAGGACAGTTATGAAACGAGTCAGCTGGATGACCAGAGTGCT
GAAACCCACAGCCACAAGCAGTCCAGATTATATAAGCGGAAAGCCAATGATGAGAGCAATGAGCATTCCGATGTG
ATTGATAGTCAGGAACTTTCCAAAGTCAGCCGTGAATTCCACAGCCATGAATTTACAGCCATGAAGATATGCTG
GTTGTAGACCCCCAAAAGTAAGGAAGAAGATAAACACCTGAAATTTCTGATTTCTCATGAATTAGATAGTGCATCT
TCTGAGGTCAAT**TAAA**AGGAGAAAAAATAAATTTCTCACTTTGCATTTAGTCAAAAGAAAAAATGCTTTATAGC
AAAATGAAAGAGAACATGAAATGCTTCTTTCTCAGTTTATTGGTTGAATGTGTATCTATTTGAGTCTGGAAATAA
CTAATGTGTTTGATAATTAGTTTAGTTTGTGGCTTCATGGAAACTCCCTGTAAACTAAAAGCTTCAGGGTTATGT
CTATGTTTCATTCTATAGAAGAAATGCAAACTATCACTGTATTTTAATATTTGTTATTCTCTCATGAATAGAAATT
TATGTAGAAGCAAAACAAAATACTTTTACCCACTTAAAAAGAGAATATAACATTTTATGTCACTATAATCTTTTGT
TTTTTAAGTTAGTGTATATTTTGTGTGATTATCTTTTGTGGTGTGAATAAATCTTTTATCTTGAATGTAATAA
GAATTTGGTGGTGTCAATTGCTTATTTGTTTTCCACGGTGTCCAGCAATTAATAAAACATAACCTTTTTTACT
GCCTAAAAA

1580/6881
FIGURE 1460

MRIAVICFCLLGITCAIPVKQADSGSSEEKQLYNKYPPDAVATWLNPDPSQKQNLAPQTLPSKSNESHDMDDMD
DEDDDDHVDSQDSIDSNDSDDVDDTDDSHQSDSHHSDSEDELVTDFPTDLPATEVFTPVVPTVDITYDGRGDSVV
YGLRSKSKKFRRPDIQYPDATDEDITSHMESEELNGAYKAIPVAQDLNAPSDWDSRGKDSYETSQ LDDQSAETHS
HKQSRLYKRKANDESNEHSDVIDSQELSKVSREFHSHEFHSHEDMLVVDPKSKEEDKHLKFRISHELDSASSEVN

1581/6881
FIGURE 1461

CTCCAGCACAGCGTTGGTGCTGCCTGGGTATCAGAAAGCAAGCTCACATTGCTCTCCAGTACGTGTAAGCCTTTT
CTTTTCAAGATGCCTGAGGAAGTGCACCATGGAGAGGAGGAGGTGGAGACTTTTGCCTTTCAGGCAGAAATTGCC
CAACTCATATCCCTCATCATCAATACCTTCTATTCCAACGAGGAGATTTTCCCTTCAGGAGTTGATCTCTAATGCT
TCTGATGCCTTGGACAAGATTGCTATGAGAGCCTGACAGACCCTTCAAAGTTGGACAGTGGTAAAGAGCTGAAA
ATTGACATCATCCCCAACCCCTCAGGAACGTACCCTGGCTTTGGTAGACACAGGCATTGGCATGACCAAAGCTGAT
CTCATAAATAATTTGAGAACCATTGCCAAGTCTGGTACTAAAGCATGCATGGAGGCTCTTCAGGCTGGTGCAGAC
ATCTCCATGATTGGGCAGTTTGGTGTGGCTTTTTTCTGCCTACCTGGTGGCAGAGAAACTGGTTGTGATCACAA
AGCACAACGATGATGAACAGTATGCTTGGGAGTCTTCTGCTGGAGGTTCCCTTCACTGTGCATGCTGATCATGGTG
AGCCCATTTGGCAGGGGTACCAAAGTGATCCTCCATCTTAAAGAAGATCAGACAGAGTACTTAGAAGAGAGGCGGG
TCAAAGAAGTAGTGAAGAAGCATTCTCAGTTTCATAGGCTATCCCATCACCCCTTTATTTGGAGAAGGAACAAGACA
AGGAAATTAGTGATGATGAGGCAGAAGAAGAGAAAGGTGAGAAAGAAGAGGAAGATAAAGATGACGAAGAAAAGC
CCAAGATCAAAGATGTGGGTTTCAGATGAGGAGGATGACAGCAGTAAGGATAAGAAGAAGAAAACCTAAGAAGATCA
AAGAGAAATACATTGACTAGGAAGAATAACAAGACCAAGCCTATTTGGACCAGAAACCATGATGACATCACCC
AAGAGGAGTATGGAGAATTCTATAAGAGCCTCACCAAGTACTGGGAAGACCCTTGGCAGTCAAGCACTTTTCTG
TAGAAGGTCAGTTGGAATTCAGGGCATTGCTATTTCAGTCCCTCGTCGGGCTCCCTTTGACCTTTTGGAGAACAAGA
AGAAAAAGAACAACATCAAACCTGTATGTCCGCCGTGTGTTTCATCATGGACAGCTGTGATGAGTTGATACCAGAGT
ATCTCAATTTTATCCATGGTGTGGTTGACTCTGAGGATCTGCCCTGAACATCTCCCGAGAAATGCTCCAGCAGA
GCAAAATCTTGAAAGTCATTGCAAAAACATTGTTAAGAAGTGCCCTGAGCTCTTCTCTGAGCTGGCAGAAGACA
AGGAGATTATAAGAAATCTATGAGGCATTTTCTAAAAATCTCAAGCTTGAATCCACGAAGACTCCACTAACC
CCACCGCCTGTCTGAGCTGCTGCGCTGTACACCTCCAGTCTGGAGATGAGATGACATCTCTGTGCTAGTATGT
TTCTCACATGAAGGAGACACAGAAGTCCACCTATTACATCACTGGTGAGAGCAAAGAGCAGGTGGCCAACTCTGC
TTTTGTGGAGCGAGTGCGGAAACAGGGCTTCGAGGTGGTATATATGACTGAGCCATTGACGAGTACTGTGTGCA
GCAGCTCAAGGAGTTTGATGGGAAAAGCCTGGTCTCAGTTACCAAGGAGGGTCTGGAGCTACCTGAGGATGAGGA
GGAGAAGAAGAAGATGGAAGAAAGCAAGGAAAAGTTTGAGAACCTCTGCAAGCTCATGAAAGAAATCTTAGATAA
GAAGGTTGAGAAGGTGACAATCTCCAATAGACTTGTGTCTTACCCTGCTGCATTGTGACCAGCACCTACGGCTG
GACAGCCAATATGGAGCAGATCATGAAAGCCAGGCATTCGGGACAACCTCCACCATGGGCTATATGATGGCCAA
AAAGCACCTGGAGATCAACCCCGACACCCCATCATGGAGACGCTGCGGCAGAAGGCTGAGGCCGACAAGAATGA
TAAGGCAGTTAAGGACCTGGTGGTGTGCTGCTGTTTGAACCGCCCTGCTATCTTCGGGCTTTTCCCTTGAGGATCC
CCAGACCCACTCCAACCACATCTACCACATGATCAAGCTAGGTCTAGGTACTGATGAAGATGAAGTGGCAGCAGA
GGAACCCAGTGATGCAGTTCCCTGATGAGATCCCCCTCTTGAGGGTGATGAGGATGCGTCTCGCATGGAAGAAGT
CGATTAGGAGTTTCATAGTTGGAACCTTGTGCCCTTGTATAGTGTCCCATGGCTCCCACTGCAGCCTCGAGTGC
CCCTGTCCACCTGGCTGCTGGTGTCTAGTGTTTTTTCCCTCTCCTGTCTTGTGTTGAAGGCAGGAAACCAAG
GGTGTCAAGCCCCATTCCCTCTCTACTCTTGACAGCAGGATTGGATGTTGTGTATTGTGGTTTATTTTATTTCT
TCATTTTGTCTGAAATTAAGAATGTAAATAAAGAATATGCCGTTTTTATAC

1582/6881
FIGURE 1462

MKETQKSTYYITGESKEQVANSASFVERVRKQGFEVVYMTEPIDEYCVQQLKEFDGKSLVSVTKEGLELPEDEEEK
KKMEESKEKFENLCKLMKEILDKKVEKVTISNRLVSSPCCIVTSTYGWTANMEQIMKAQALRDNSTMGYMMAKKH
LEINPDHPIMETLRQKAEADKNDKAVKDLVVLLFETALLSSGFSLEDPQTHSNHIYHMIKLGGLGTDEDEVAEEEP
SDAVPDEIPPLEGDEDASRMEEVD

1583/6881
FIGURE 1463

CTCTCAAGTCACTCCAGCACAGCGTTGGTGCTGCCTGGGTATCAGAAAGCAAGCTCACATTGCTCTCCAGTACGT
GTAAGCCTTTTCTTTTCAAGATGCCTGAGGAAGTGCACCATGGAGAGGAGGAGGTGGAGACTTTTGCCTTTCAGG
CAGAAATTGCCCAACTCATATCCCTCATCATCAATACCTTCTATTCCAACGAGGAGATTTTCTTCAGGAGTTGA
TCTCTAATGCTTCTGATGCCTTGGACAAGATTGCTATGAGAGCCTGACAGACCCTTCAAAGTTGGACAGTGGTA
AAGAGCTGAAAATTGACATCTCCATGATTGGGCAGTTTGGTGTTGGCTTTTTTCTGCCTACCTGGTGGCAGAGAA
ACTGGTTGTGATCACAAAGCACAAACGATGATGAACAGTATGCTTGGGAGTCTTCTGCTGGAGGTTCTTCACTGT
GCATGCTGATCATGGTGAGCCCATTTGGCAGGGGTACCAAAGTGATCCTCCATCTTAAAGAAGATCAGACAGAGTA
CTTAGAAGAGAGGCGGGTCAAAGAAGTAGTGAAGAAGCATTCTCAGTTCATAGGCTATCCCATCACCCTTTATTT
GGAGAAGGAACAAGACAAGGAAATTAGTGATGATGAGGCAGAAGAAGAGAAAGGTGAGAAAGAAGAGGAAGATAA
AGATGACGAAGAAAAGCCCAAGATC

1584/6881
FIGURE 1464

GAGCAGCAGAATTTCAACTCCAGTAGACTTGAATATGCCTCTGGGCAAAGAAGCAGAGCTAACGAGGAAAGGGAT
TTAAAGAGTTTTTCTTGGGTGTTTGTCAAACCTTTTATTCCCTGTCTGTGTGCAGAGGGGATTCAACTTCAATTTT
TCTGCAGTGGCTCTGGGTCCAGCCCCTTACTTAAAGATCTGGAAAGCATGAAGACTGGGCTTTTTTTTCTATGTC
TCTTGGGAACTGCAGCTGCAATCCCGACAAATGCAAGATTATTATCTGATCATTCCAAACCAACTGCTGAAACGG
TAGCACCTGACAACACTGCAATCCCCAGTTTAAAGGGCTGAAGCTGAAGAAAATGAAAAAGAAACAGCAGTATCCA
CAGAAGACGATTCCCACCATAAGGCTGAAAAATCATCAGTACTAAAGTCAAAAGAGGAAAGCCATGAACAGTCAG
CAGAACAGGGCAAGAGTTCTAGCCAAGAGCTGGGATTGAAGGATCAAGAGGACAGTGATGGTCACTTAAGTGTGA
ATTTGGAGTATGCACCAACTGAAGGTACATTGGACATAAAAGAAGATATGAGTGAGCCTCAGGAGAAAAAACTCT
CAGAGAACACTGATTTTTTGGCTCCTGGTGTAGTTCCCTTCACAGATTCTAACCAACAAGAAAGTATCACAAAGA
GAGAGGAAAACCAAGAACAACCTAGAAATTATTACATCATCAGTTGAACAGGAGCAGTAAACATAGCCAAGGCC
TAAGGGATCAAGGAAACCAAGAGCAGGATCCAAATATTTCCAATGGAGAAGAGGAAGAAGAAAAAGAGCCAGGTG
AAGTTGGTACCCACAATGATAACCAAGAAAGAAAGACAGAATTGCCAGGGAGCATGCTAACAGCAAGCAGGAGG
AAGACAATACCCAATCTGATGATATTTTGGGAAGAGTCTGATCAACCAACTCAAGTAAGCAAGATGCAGGAGGATG
AATTTGATCAGGGTAACCAAGAACAAGATAACTCCAATGCAGAAATGGAAGAGGAAAATGCATCGAACGTCA
ATAAGCACATTCAAGAACTGAATGGCAGAGTCAAGAGGGTAAAACCTGGCCTAGAAGCTATCAGCAACCACAAAAG
AGACAGAAGAAAAGACTGTTTCTGAGGCTCTGCTCATGGAACCTACTGATGATGGTAATACCACGCCCAGAAATC
ATGGAGTTGATGATGATGGCGATGATGATGGCGATGATGGCGGCACTGATGGCCCCAGGCACAGTGCAAGTGATG
ACTACTTCATCCCAAGCCAGGCCCTTCTGGAGGCCGAGAGAGCTCAATCCATTGCCATCACCTCAAAATTGAGG
AGCAAAGAGAAAAAGTACATGAAAAATGAAAATATAGGTACCACTGAGCCTGGAGAGCACCAAGAGGCCAAGAAAAG
CAGAGAACTCATCAAATGAGGAGGAAACGTCAAGTGAAGGCAACATGAGGGTGCATGCTGTGGATTCTTGCATGA
GCTTCCAGTGTAAGAGAGGCCACATCTGTAAGGCAGACCAACAGGGAAAAACCTCACTGTGTCTGCCAGGATCCAG
TGACTTGTCTCCCAACAAAACCCCTTGATCAAGTTTGTGGCACTGACAATCAGACCTATGCTAGTTTCTGTCTATC
TATTCGCTACTAAATGCAGACTGGAGGGGACCACAAAAGGGGCATCAACTCCAGCTGGATTATTTTGGAGCCTGCA
AATCTATTCTTACTTGTACGGACTTTGAAGTGATTAGTTTCTCTACGGATGAGAGACTGGCTCAAGAATATCC
TCATGCAGCTTTATGAAGCCAACCTCTGAACACGCTGGTTATCTAAATGAGAAGCAGAGAAATAAAGTCAAGAAAA
TTTACCTGGATGAAAAGAGGCTTTTTGGCTGGGGACCATCCCATTTGATCTTCTCTTAAGGGACTTTAAGAAAACT
ACCACATGTATGTGTATCCTGTGCACTGGCAGTTTAGTGAACCTTGACCAACACCCCTATGGATAGAGTCTTGACAC
ATTCTGAACCTTGCTCCTCTGCGAGCATCTCTGGTGCCCATGGAACACTGCATAACCCGTTTCTTTGAGGAGTGTG
ACCCCAACAAGGATAAGCACATCACCCCTGAAGGAGTGGGGCCACTGCTTTGGAATTAAAGAAGAGGACATAGATG
AAAACTCTTGTGTTTGAACGAAGATTTTAAAGAACTCAACTTTCCAGCATCCTCCTCTGTTCTAACCCTTCAGA
AATATATGCAGCTGTGATACCTTGTAGATTTATATTTAGCAAAATGTTAGCATGTATGACAAGACAATGAGAGTAA
TTGCTTGACAACAACCTATGCACCAGGTATTTAACATTAACTTTGGAAACAAAAATGTACAATTAAGTAAAGTCA
ACATATGCAAAATACTGTACATTGTGAACAGAAGTTTAATTCATAGTAATTTCACTCTCTGCATTGACTTATGAG
ATAATTAATGATTAACTATTAATGATAAAAAATAATGCATTTGTATTGTTTCATAATATCATGTGCACTTCAAGAA
AATGGAATGCTACTCTTTTGTGGTTTACGTGTATTATTTTCAATATCTTAATACCCTAATAAAGAGTCCATAAAA
ATCC

1585/6881
FIGURE 1465

CTTCGCCGCGTGGATGGCCTATTACATCAATCACCCCTCTCTACACTCCCCCTACCTACGGAGCTCAGCAGGTGAA
ACTGGCGCTCGCCATCTTTGTGATCTGCCAGCTCGGCAACTTCTCCATCCACATGGCCCTGCGGGACCTGCGGCC
CGCTGGGTCCAAGACGCGGAAGATCCCATACCCCACCAAGAACCCCTTCACGTGGCTCTTCCTGCTGGTGTCTCTG
CCCCAACTACACCTACGAGGTGGGGTCCTGGATCGGTTTCGCCATCATGACGCAGTGTCTCCCAGTGGCCCTGTT
CTCCCTGGTGGGCTTCACCCAGATGACCATCTGGGCCAAGGGCAAGCACC GCAGCTACCTGAAGGAGTTCCGGGA
CTACCCGCCCCTGCGCATGCCATCATCCCCTTCCTGCTCTGAGCGCTCACCCCTGCTGAGGCTCAGCCCCCTCAA
CCCGGTGGCATTCTGGGGGAGGAGTGGGGCCCACAGCTCTCCAGCACCCGGAATAAAGCCCGCCTGCCCCAGTCG
GGA

1586/6881
FIGURE 1466

GAGGGCGGGCCTGTTTCCGGGAGGCGCGTGGGGCTTGAGGCCGAGAACGGCCCTTGCTGCCACCAACATGGGAGAC
TTTGTACCGTGTCCCGTTCTTAGTGCTCGAATGTCCCAACCTGAAGCTGAAGAAGCCGCCCTGGTTGCACATGCC
GTCGGCCATGACTGTGTATGCTCTGGTGGTGGTGTCTTACTTCCTCATCACCGGAGGAATAATTTATGATGTTAT
TGTTGAACCTCCAAGTGTCGGTTCTATGACTGATGAACATGGGCATCAGAGGCCAGTAGCTTTCTTGGCCTACAG
AGTAAATGGACAATATATTATGGAAGGACTTGCATCCAGCTTCCTATTTACAATGGGAGGTTTAGGTTTCATAAT
CCTGGACCGATCGAATGCACCAAATATCCCAAACTCAATAGATTCCCTTCTTCTGTTCAATTGGATTTCGTCTGTGT
CCTATTGAGTTTTTTTCATGGCTAGAGTATTCATGAGAATGAAACTGCCGGGCTATCTGATGGGTTAGAGTGCCTT
TGAGAAGAAATCAGTGGATACTGGATTGCTCCTGTCAATGAAGTTTTAAAGGCTGTACCAATCCTCTAATATGA
AATGTGGAAAAGAATGAAGAGCAGCAGTAAAGAAATATCTAGTGAAAAACAGGAAGCGTATTGAAGCTTGGAC
TAGAATTTCTTCTTGGTATTAAAGAGACAAGTTTTATCACAGAATTTTTTTTCTGCTGGCCTATTGCTATACCAA
TGATGTTGAGTGGCATTTCCTTTTAGTTTTTCATTAAAATATATCCATATCTACAATAATATCAAATAAA
GTGATTATTTTTTACAACCCCTCTTAACATTTTTTGGAGATGACATTCTGATTTTCAGAAATTAACATAAAATCC
AGAAGCAAGATTCCGTAAGCTGAGAACTCTGGACAGTTGATCAGCTTACCTATGGTGCTTTGCCTTTAACTAGA
GTGTGTGATGGTAGATTATTCAGATATGTATGTAAACTGTTTCCTGAACAATAAGATGTATGAACGGAGCAGA
AATAAATACTTTTTCTAATTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

1587/6881
FIGURE 1467

METLYRVPFLVLECPNLKLLKKPPWLHMPSAMTVYALVVVSYFLITGGIIYDVIVEPPSVGSMTDEHGHQRPVAFLL
AYRVNGQYIMEGLASSFLFTMGGLGFIILDRSNAPNIPKLNRFLLLFIGFVCVLLSFFMARVFMRMKLPGYLMG

1588/6881
FIGURE 1468

ATGCCCCAACTCTCCGGAGGAGGTGGCGGCGGGGGGGGACCCGGAACCTCTGCGCCACGGACGAGATGATCCCC
TTCAAGGACGAGGGCGATCCTCAGAAGGAAAAGATCTTCGCCGAGATCAGTCATCCCGAAGAGGAAGGCGATTTA
GCTGACATCAAGTCTTCCTTGGTGAACGAGTCTGAAATCATCCCGGCCAGCAACGGACACGAGGTGGCCAGACAA
GCACAAACCTCTCAGGAGCCCTACCACGACAAGGCCAGAGAACACCCCGATGACGGAAAGCATCCAGATGGAGGC
CTCTACAACAAGGGACCCCTCCTACTCGAGTTATTCCGGGTACATAATGATGCCAAATATGAATAACGACCCATAC
ATGTCAAATGGATCTCTTTCTCCACCCATCCCGAGAACATCAAATAAAGTGCCCGTGGTGCAGCCATCCCATGCG
GTCCATCCTCTCACCCCCCTCATCACTTACAGTGACGAGCACTTTTCTCCAGGATCACACCCGTCACACATCCCA
TCAGATGTCAACTCCAAACAAGGCATGTCCAGACATCCTCCAGCTCCTGATATCCCTACTTTTTATCCCTTGTCT
CCGGGTGGTGTGGACAGATCACCCACCTCTTGGCTGGCAAGGTCAGCCTGTATATCCCATCACGGGTGGATTCT
AGGCAACCCTACCCATCCTCACTGTCACTCGACACTTCCATGTCCAGGTTTCCCATCATATGATTCCCGGTCCT
CCTGGTCCCCACACAACCTGGCATCCCTCATCCAGCTATTGTAACACCTCAGGTCAAACAGGAACATCCCCACACT
GACAGTGACCTAATGCACGTGAAGCCTCAGCATGAACAGAGAAAAGGAGCAGGAGCCAAAAAGACCTCACATTAAG
AAGCCTCTGAATGCTTTTATGTTATACATGAAAGAAATGAGAGCGAATGTCGTTGCTGAGTGTACTCTAAAAGAA
AGTGCAGCTATCAACCAGATTCTTGGCAGAAGGTGGCATGCCCTCTCCCGTGAAGAGCAGGCTAAATATTATGAA
TTAGCACGGAAAGAAAGACAGCTACATATGCAGCTTTATCCAGGCTGGTCTGCAAGAGACAATTATGGTAAGAAA
AAGAAGAGGAAGAGAGAGAAACTACAGGAATCTGCATCAGGTACAGGTCCAAGAATGACAGCTGCCTACATCTGA

1589/6881
FIGURE 1469

TGGCCACAACACCGACACAGTAGCATTGTGCCAGTTTCTGGTTGGAATGGTGACAACACGCTGGAGCCAAGTGC
TAACATGCCCTTGGTTCAAGGGATGGAAAAGTCACCCGTAAGGATGGCAATGCCAGTGGAACCACGCTGCTTGAGGC
TCTTGACTGCATCCTACCACCAACTCGTCCAAGTGAAGCCCTTGTGCCTGCCTCTCCAGGATGTCTACAAAAT
TGGTGGTATTGGTACTGTTTCTGTTGGCTGAGTGGAGACTGGTGTCTCAAACCTGGTATGGTGGTCACCTTTGC
TCCAGTCAACGTTGCAACAGAAGTAAAATCTGTTGAAATGCACCATGAAGCAGAAGGCTAAATAAATATTATCCC
TACTACCTGCCACCCCACTGTTAATCAGTGGTGGAGAATGGTCTCAGAAGTGTGTTTCAATTGGCCATTGAA
GTTTAGTAGTAAAAGACTGGTTAATGATAACAATGCATCATAAACCTTCAGAAGGAAAGGAGAATGTTTTGTGG
ACCACTTTGGTTTTCTTTCTTTGCATGTGGCAGTTTTAAGTTATTAGTTTTTAAAATCAGTACTTTTTACTGGAA
ACAACCTTGACCAAAAATTTGTCACAGAATTTTGAGACCCATTAAAAAGTTTAATGAAAAAA

1590/6881
FIGURE 1470

AAGCCAGAACGAGAAAGGAAAAGACTCATATCAACACTGTGATCATCGGACACGTAGATTCTGGGCAAGTCCACCA
CTACTGGCCATCTGATCTACAAATGCGGTGGCGTCGACAAAAGAACCATCGAAAAATTTGAGAAGGAGGCTGCTG
AGATGGGAAAGTGCTCCTTCAAGTATGCCTGGGTCTTGGATAAACTGAAAGCTGAGCGTGAACATGGTATCACCA
TTGATATCTCTTTGTGGAAATTTGAGACCAGCAAGTACTATGGGACAATGTGGGCTTCAATGTCAAGAATGTGTC
TGTCAAGGATGTTTCGTCGTGGCAACGTTGCTGGTGACAGCAAAAAGGACCCACCAATGGAAGCAGCTGGCTTCAC
TGCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGTGCTGGCTATGCCCCTGTATTGGATTGCCACACGGC
TCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGACTGATCGCCATTCTGGTAAAAAGCTGGAAGATGGCCC
TAAATTCTTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCCTGGCAAGCCCGTGTATGTTGAGAGCTTCTC
AGACTATCCACCTTTGGGTCGCTTTGCTGTTTCATGATATCAGACAGACAGTTGCGGTGGGTGTCATCAAAGCAGT
GGACAAGAAGGCTGCTGGAGCTGGCAAGGTCACCAAGTCTGCCCAGAAAGCTCAGAAGGCTAAATAAATATTATC
CCTA

1591/6881
FIGURE 1471

AAATTGTTAAGGAAGTCAGCACTTACATTAAGAAAATTGGCCACAACACCGACACAGTAGCATTGTGCCAGTTT
CTGGTTGGAATGGTGACAACACGCTGGAGCCAAGTGCTAACATGCCTTGGTTCAAGGGATGGAAAGTCACCCGTA
AGGATGGCAATGCCAGTGGAACCACGCTGCTTGAGGCTCTTGACTGCATCCTACCACCAACTCGTCCAAGTACA
AGCCCTTGTGCCTGCCTCTCCAGGATGTCTACAAAATTGGTGGTATTGGTACTGTTCTGTTGGCTGAGTGGAGA
CTGGTGTCTCAAACCTGGTATGGTGGTCACCTTTGCTCCAGTCAACGTTGCAACAGAAGTAAAAATCTGTTGAAA
TGCACCATGAAGCTTTGAGTGAAGTTCTTCCTGGGGACAATGTGGGCTTCAATGTCAAGAATGTGTCTGTCAAGG
ATGTTTCGTGCTGGCAACGTTGCTGGTGACAGCAAAAAGGACCCACCAATGGAAGCAGCTGGCTTCACTGCTCAGG
TGATTATCCTGAACCATCCAGGCCAAATAAGTGTGGCTATGCCCTGTATTGGATTGCCACACGGCTCACATTG
CATGCAAGTTTGCTGAGCTGAAGGAAAAGACTGATCGCCATTCTGGTAAAAAGCTGGAAGATGGCCCTAAATTCT
TCTTTGGGTCGCTTTGCTGTTTCATGATATCAGACAGACAGTTGCGGTGGG

1592/6881
FIGURE 1472

GTGAACATGGTATCACCATTGATATCTCTTTGTGGAAATTTGAGACCAGCAAGTACTATGTGACTATCATTGATG
CCCCAGGACACAGAGACCTCATCAAAAACATGATTACAGGGACATCTCAGGCTGACTGTGCTGTCTTGATTGTTG
CTGCTGGTTTTTGGTGAATTTGAAGCTGGTATCTCCAAGAATGGGCAGACCCGAGAGCACGCCCTTCTGGCTTACA
CACTGGGTGTGAAACAACATAATTGTTGGTGTAAACAAAATGGATTCCACTGAGCCACCCTACAGCCATAAGAGAT
ATGAGGAAATTGTAAAGGAAGTCAGCACTTACATTAAGAAAATTTGGCCACAACACCGACACAGTAGCATTTGTGC
CAGTTTCTGGTTGGAATGGTGACAACACGCTGGAGCCAAGTGCTAACATGCCTTGGTTCAAGGGATGGAAAGTCA
CCCGTAAGGATGGCAATGCCAGTGGAACCAGCCTGCCTCTCCAGGATGTCTACAAAATTGGTGGTATTGGTACTG
TTCCTGTTGGCTGAGTGGAGACTGGTGTCTCAAACCTGGTATGGTGGTCACCTTTGCTCCAGTCAACGTTGCAA
CAGAAGTAAATCTGTTGAAATGCACCATGAAGCTTTGAGTGAAGTTCTTCCTGGGGACAATGTGGGCTTCAATG
TCAAGATGTGTCTGTCAAGGATGTTTCGTTCGTGGCAACGTTGCTGGTGACAGCAAAAAGGACCCACCAATGGAAG
CAGCTGGCTTCACTGCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAA

1593/6881
FIGURE 1473

GAAAAATTTGAGAAGGAGGCTGCTGAGATGGGAAAGTGCTCCTTCAAGTATGCCTGGGTCTTGGATAAACTGAAA
GCTGAGCGTGAAACATGGTATCACCATTGATAATCTCTTTGTGGAAATTTGAGACCAGCAAGTACTATGTGACTATC
ATTGATGCCCCAGGACACAGAGACCTCATCAAAAACATGATTACAGGGACATCTCAGGCTGACTGTGCTGTCTTG
ATTGTTGCTGCTGGTTTTTGGTGAATTTGAAGCTGGTATCTCCAAGAATGGGCAGACCCGAGAGCACGCCCTTCTG
GCTTACACACTGGGTGTGAAACAACATAATTGTTGGTGTTAACAAAATGGATTCCACTGAGCCACCCTACAGCCAT
AAGAGATATGAGGAAATTGTTAAGGAAGTCAGCACTTACATTAAGAAAATTGGCCACAACACCGACACAGTAGCA
TTTGTGCCAGTTTCTGGTTGGAATGGTGACAACACGCTGGAGCCAAGTGCTAACATGCCTTGGTTCAAGGGATGG
AAAGTCACCCGTAAGGATGGCAATGCCAGTGGAACACGCTGCTTGAGGCTCTTGACTGCATCCTACCACCAACT
CGTCCAAC TGACAAGCCCTTGTGCCTGCCTCTCCAGGATGTCTACAAAATTGGTGGTATTGGTACTGTTCTCTGTT
GGCTGAGTGGAGACTGGTGTTC TCAAACCTGGTATGGTGGTCACCTTTGCTCCAGTCAACGTTGCAACAGAAGTA
AAATCTGTGTCAAGGATGTTTCGTCTGGCAACGTTGCTGGTGACAGCAAAAAGGACCCACCAATGGAAGCAGCTG
GCTTCACTGCTCAGGTGATTATCCTG

1594/6881
FIGURE 1474A

GGTGGTTCGCAGAAGCAGCAGTGAAGAGAAGCTACTGTGTTTGGTGCGGGAGCGAGCTGGCCACACCTGTGAGGC
TGCAGTGATTGTGATTCTCATCCTGGTGTGGGAAGGAATCCCGCTGTCTCTGGCTGACAACTCTACTCGGAGCT
TACCGAGACGCTGAGGAAATACGGCACGCTCACCAATCGCCGGTGTGCCTTGAATGAAGAGAGAACTTGCGCCTG
TCAGGGGCTGGATCCAGAAACCTGTGGTGCCTCCTTCTCTTTTGGTTGTTTCATGGAGCATGTACTACAATGGATG
TAAGTTTGGCAGAAGCAAGATCCCAAGGAAGTTTAAAGCTGCTTGGGGATGACCCAAAAGAGGAAGAGAACTGGA
GTCTCATTTGCAAAACCTGTCCACTCTTATGGCACCAACATATAAGAACTTGACCTGATGCATATAATAATCA
GATTGAATATGAACACAGAGCACCAGAGTGCCGTCTGGGTCTGAAGGAAGGCCGTCCATTCTCAGGGGTCACTGC
ATGTTTGGACTTCTGTGCTCATGCCCACAGAGACTTGCACAACATGCAGAATGGCAGCACATTGGTATGCACTCT
CACTAGAGAAGACAATCGAGAATTTGGAGGAAAACCTGAGGATGAGCAGCTTCACGTTCTGCCTTTATACAAAGT
CTCTGACGTGGATGAGTTTGGGAGTGTGGAAGCTCAGGAGGAGAAAAACGGAGTGGTGCCATTTCAGGTACTGAG
TTCTTTTCGGCGAAAAGTCAGGATGTTAGCAGAGCCAGTCAAGACTTGCCGACAAAGGAACTAGAAGCCAAGAA
AGCTGCAGCTGAAAAGCTTTCTCCCTGGAGAACAGCTCAAATAAAAATGAAAAGGAAAAGTCAGCCCCATCACG
TACAAAACAACTGAAAACGCAAGCCAGGCTAAACAGTTGGCAGAACTTTTGCGACTTTCAGGACCAGTCATGCA
GCAGTCCCAGCAGCCCCAGCCTCTACAGAAGCAGCCACCACAGCCCCAGCAGCAGCAGAGACCCCAGCAGCAGCA
GCCACATCACCTCAGACAGAGTCTGTCAACTCTTATTCTGCTTCTGGATCCACCAATCCATACATGAGACGGCC
CAATCCAGTTAGTTCCTTATCCAACTCTTCACACACTTCAGATATCTATGGAAGCACCAGCCCTATGAACCTTCTA
TTCCACCTCATCTCAAGCTGCAGGTTTCAATTTGAATTCTTCTAATCCCATGAACCCTTACCCTGGGCTTTTGAA
TCAGAATACCCAATATCCATCATATCAATGCAATGGAAACCTATCAGTGGACAACTGCTCCCCATATCTGGGTTC
CTATTCTCCCCAGTCTCAGCCGATGGATCTGTATAGGTATCCAAGCCAAGACCCTCTGTCTAAGCTCAGTCTACC
ACCCATCCATACACTTTACCAGCCAAGGTTTGGAAATAGCCAGAGTTTACATCTAAATACTTAGGTTATGGAAA
CCAAAATATGCAGGGAGATGGTTTTCAGCAGTTGTACCATTAGACCAAATGTACATCATGTAGGGGAAATTGCCTCC
TTATCCCCTCATGAGATGGATGGCCACTTCATGGGAGCCACCTCTAGATTACCACCCAATCTGAGCAATCCAAA
CATGGACTATAAAAATGGTGAACATCATTACCTTCTCACATAATCCATAACTACAGTGCAGCTCCGGGCGATGTT
CAACAGCTCTCTTCATGCCCTGCATCTCCAAAACAAGGAGAATGACATGCTTTCCACACAGCTAAATGGGTTATC
AAAGATGCTTCCAGCTCTTAACCATGATAGAACTGCTTGTGTCCAAGGAGGCTTACACAAATTAAGTGATGCTAA
TGGTTCAGGAAAAGCAGCCATTGGCACTAGTCCAGGGTGTGGCTTCTGGTGCAGAGGACAACGATGAGGTCTGGTC
AGACAGCGAGCAGAGCTTCTGGATCCTGACATTGGGGGAGTGGCCGTGGCTCCAACCTCATGGGTCAATTCTCAT
TGAGTGTGCAAAGCGTGAGCTGCATGCCACAACCCCTTTAAAGAATCCCAATAGGAATCACCCACCAGGATCTC
CCTCGTCTTTTACCAGCATAAGAGCATGAATGAGCCAAAACATGGCTTGGCTCTTTGGGAAGCCAAAATGGCTGA
AAAAGCCCGTGAGAAAGAGGAAGAGTGTGAAAAGTATGGCCAGACTATGTGCCTCAGAAATCCCATGGCAAAAA
AGTGAAACGGGAGCCTGCTGAGCCACATGAACTTCAGAGCCACTTACCTGCGTTTCATCAAGTCTCTTGCCGA
AAGGACCATGTCCGTGACCACAGACTCCACAGTAACATACATCTCCATATGCCTTCACTCGGGTCACAGGGCCTTA
CAACAGATATATATGATATCACCCCTTTTGTGGTTACCTCACTTGAAAAGACCACAACCAACCTGTCAGTAGT
ATAGTTCTCATGACGTGGGCAGTGGGGAAGGTCACAGTATTCATGACAAATGTGGTGGGAAAAACCTCAGCTCA
CCAGCAACAAAAGAGGTTATCTTACCATAGCACTTAATTTTCACTGGCTCCCAAGTGGTCACAGATGGCATCTAG
GAAAAGACCAAAGCATTCTATGCAAAAAGAAGGTGGGGAAGAAAGTGTTCGCAATTTACATTTTAAACACTGG
TTCTATTATTGGACGAGATGATATGTAAATGTGATCCCCCCCCCGCTTACAACCTCTACACATCTGTGACCACT
TTTAATAATATCAAGTTTGCATAGTCATGGAACACAAATCAAACAAGTACTGTAGTATTACAGTGACAGGAATCT
TAAAATACCATCTGGTGCTGAATATATGATGTACTGAAATACTGGAATTATGGCTTTTGAATGCAGTTTTTAC
TGTAATCTTAACTTTTATTTATCAAAATAGCTACAGGAAACATGAATAGCAGGAAAACACTGAATTTGTTTGGAT
GTTCTAAGAAATGGTGCTAAGAAAATGGTGTCTTTAATAGCTAAAAATTTAATGCCTTTATATCATCAAGATGCT
ATCAGTGTACTCCAGTGCCCTTGAATAATAGGGGTACCTTTTCACTCAAGTTTTTATCATAATTACCTATTCTTA
CACAAGCTTAGTTTTTAAATGTGGACATTTTAAAGGCCTCTGGATTTTGTCTCATCCAGTGAAGTCCTTGTAGGA
CAATAACGTATATATGTACATATATACACAAACATGTATATGTGCACACACATGTATATGTATAAATATTTTAA
ATGGTGTTTTGAAGCACTTTGTCTACCTAAGCTTTGACAACTTGAACAATGCTAAGGTACTGAGATGTTTAAAA
AACAAGTTTACTTTTCAATTTTGAATGCAAAGTTGATTTTTTTAAGGAAACAAAGAAAGCTTTTTAAATATTTTGT
CTTTTAGCCATGCATCTGCTGATGAGCAATTGTGTCCATTTTTAACACAGCCAGTTAAATCCACCATGGGGCTTA
CTGGATTCAAGGGAATACGTTAGTCCACAAAACATGTTTTCTGGTGTCTCATCTCACATGCTATACTGTAAACAG

FIGURE 1474B

[illegible]

1596/6881
FIGURE 1475

MAPTYKKLAPDAYNNQIEYEHRAPCECLGLKEGRPFSGVTACLDCAHAHRDLHNMQNGSTLVCTLTREDNREFG
GKPEDEQLHVLPLYKVSDVDEFGSVEAQEEKKRSGAIQVLSSFRKVRMLAEPVKTCRQRKLEAKKAAAEKLSSL
ENSSNKNEKEKSAPSRKQTENASQAKQLAELLRLSGFVMQQSQQPQLQKQPPQPPQQQQRPPQQQPHHPQTESV
NSYSASGSTNPYMRPNPVSPYPNSSHTSDIYGSTSPMNFYSTSSQAAGSYLNSSNPMNPYPGLLNQNTQYPSYQ
CNGNLSVDNCSPLYGSPQSQPMDLYRPSQDPLSKLSLPPHTLYQPRFGNSQSFTSKYLGYNQNMQGDGFS
SCTIRPNVHHVGKLPYPPTHEMDGHFMGATSRLLPNLSNPNMDYKNGEHHSPSHIHNYSAAPGMFNSSLHALHL
QNKENDMLSHTANGLSKMLPALNHDRTACVQGGLHKLSDANGQEKQPLALVQGVASGAEDNDEVWSDSEQSFLDP
DIGGVAVAPTHGSILIECAKRELHATTPLKNPNRNHPTRISLVFYQHKS MNPKHGLALWEAKMAEKAREKEEEEC
EKYGPDYVPQKSHGKKVKREPAEPHETSEPTYLRFIKSLAERTMSVTTDSTVTTSPYAFTRVTGPYNRYI

1597/6881
FIGURE 1476

AGGCACAGGCAGCCTGCATACACTCCTTTTCTGGTGTCAACATTATTTAAAGCATGGGAAATAGTAATGAGAC
AGTGTCTTCTTTCATTAGAACCTTAGGAGTCTACTAGATTTCTTCATCTCTATTTGTTGTTATTAGTAGCCAAACT
GTGCAAAAAACACGGTCTTGAGAAATGACAGCACAGTATCTTAGAGGGAAAGGAAATGTAGGATGCCAGTGTGGG
GACAAATTTCTGATTGCCAGTGATTGTTGTGAGCATAACAATAATTTTCATGAACATTAAAGCCTCTATTGAGGGC
AGCTGCAGTTGTAAAGGAAAAAAATGGTCCTGAACATTTAAACTACACTGGTGTACATCATAATCAAACAAAG
TAAACAGAAAAAATTTAACTTTTGCTAAAAAAGCAGAAAGCACTTGATCTTTAGGAAGGCACGCAGTTGC
TTATTATGAATCATTCTAGAGTCCGATGCATTTTCAAAGCCGGTTACAGTCATTACGAAGCACACCCTTGTGAG
GTAAGTGTATCATCACCTTTGGTTCATAAATAAAAAAGCTGAGACGCCGAGCGATTAAAGTCACTCGCCTAAGGAG
AATGAGTCAACGTCAAGAGTCATAGTTGACCCGGCCTAAAGACTCCAGACCATCAGTCCAGGGCTTAGTCAGCGG
GGCCCGGAGTGGCTTCCCTGGCTGGCATCTGGACTTAGGCTATTTCCGTGCACGTAAAAGCGGAATATTGGAACG
GTTGCACAGAACTTCCAAATAATTTTTACCGCCACGCAAGATTTAGCCCTGAGGTCTTAATCTCAGGATTTGGGA
CAGTAAAAGCTGTCTGTCCTTCCCTCCCTCGTCCAGCCGGTGGCAAGCGGGTACTGCGGGCGGTTCCGTCCGTCCCT
TTCGCAGAAATGGCAACGAATGACCACCAGCATTAGCTGAGCCAGGGGACGTGGGAGGGTTGATTGCCTAAACGA
CTCTGCATCGCCGCCTCTTTTTGAACTAAGAGAAAATGGTGGGAGATCAAAAGAAAACTAAATAAACACACAGG
CACTTGTCTGGGACCTCAACTAAGCAAAATGAAGCCTTATTGTGTGTGCTGAGCCTGCAGTTCCCAACCTTCCG
GGGAAGATGGGAGGACAGGGCGACAAAGGGCACAGTAGGCTTGCCTGGCAGTAAGTGTGACCGCAGCTATCCAGG
CGGAAGAGCAGAGGACTGAAACCACCCTCCAGCAAGCGAGTGTCCGCCGCGTTGAGAACCGCGCACCTACCCAT
CGGCCACGTGACCAGTCTTTTTAAAAAATTTCTTTACCTTAAAAAAGGTGGGGGAGAG
ACTCCACTTCCCAGAAGCCTCTCGTTACTCACGCAGCCGAGTCTTGGCGAGGTGCCGCCAGGGCCAAACGGACA
TATCCGTACAGTGGCCAGAAGCTGGCCAATCCGGTTTGAATCTCATTTTTTCTCTTACCCCCCTTCTGGAGC
GGTTGTGCGATCAGATCGATCTAAGATGGCGACTGTGCAACCGGAAACCACCCCTACTCCTAATCCCCGACTAC
AGAAGAGGAGAAAACGGAATCTAATCAGGAGGTTGCTAACCAGAACTATATTAAACATCCCCTACAGAACAG
ATGGGCACTCTGGTTTTTTTAAAAATGATAAAGCAAACTTGGCAAGCAAACTGCGGCTGATCTCCAAGTTTGA
TACTGTTGAAGACTTTTGGGCTCTGTACAACCATATCCAGTTGTCTAGTAATTTAATGCCTGGCTGTGACTACTC
ACTTTTTAAGGATGGTATTGAGCCTATGTGGGAAGATGAGAAAAACAAACGGGGAGGACGATGGCTAATTACATT
GAACAAACAGCAGAGACGAAGTGACCTCGATCGCTTTTGGCTAGAGACACTTCTGTGCCTTATTGGAGAATCTTT
TGATGACTACAGTGATGATGTATGTGGCGCTGTTGTTAATGTTAGAGCTAAAGGTGATAAGATAGCAATATGGAC
TACTGAATGTGAAAACAGAGAAGCTGTTACACATATAGGGAGGGTATACAAGGAAAGGTTAGGACTTCCCTCAA
GATAGTGATTGGTTATCAGTCCCACGCAGACACAGCTACTAAGAGCGGCTCCACCCTAAAAATAGGTTTGTGT
TTAAGAAGACACCTTCTGAGTATTCTCATAGGAGACTGCGTCAAGCAATCGAGATTTGGGAGCTGAACCAAAGCC
TCTTCAAAAAGCAGAGTGGACTGCATTTAAATTTGATTTCCATCTTAATGTTACTCAGATATAAGAGAAGTCTCA
TTCGCCCTTTGTCTTGTACTTCTGTGTTCATTTTTTTTTTTTTTTTTTTGGCTAGAGTTTCCACTATCCCAATCAA
AATTACAGTACACATCCCAGAATCCATAAATGTGTTCTTGGCCACTCTGTAATAGTTTCAAGTATGATGATGATG
AATTACATACAGATTTTACCTATCCACAATAGTCAGAAAACAACTTGGCATTCTTATACTTTACAGGAAAAAA
TTCTGTTGTTCCATTTTATGCAGAAGCATATTTTGTGTTTGAAGATTATGATGCATACAGTTTCTAGCAAT
TTTCTTTGTTTCTTTTACAGCATTGTCTTTGCTGTACTCTTGCTGATGGCTGCTAGATTTTAATTTATTTGTTT
CCCTACTTGATAATATTAGTGATTCTGATTTTCAGTTTTTCATTTGTTTTGCTTTTGTTTTTTCTCATGTAA
TTGGTGAAGGATCCAGGAATATGACACAAAGGTGGAATAAACATTAATTTTGTGCATTCTTTGGTAATTTTTTT
GTTTTTTGTAACACAAAGCTTTGCTACAAATTTATGCATTTTCATTCAAATCAGTGATCTATGTTTGTGTGATT
CCTAAACATAATTGTGGATTATAAAAAATGTAACATCATAATTACATTCCTAACTAGAATTAGTATGTCTGTTTT
TGTATCTTTATGCTGTATTTTAACTTTGTATTACTTAGGTTATTTTGTCTTTGGTTAAAAATGGCTCAAGTAGA
AAAGCAGTCCCATTCATATTAAGACAGTGTAACAACTGTAAATAAAATGTGTACAGTGAATTGTCTTTTAGACA
ACTAGATTTGTCTTTTATTTCTCCATCTTTATAGAAGGAATTTGTACTTCTTATTGCAAGGCAGTCTCTATATT
ATGTCTTCTTTTGTGGTGTCTTCCATGTGAACAGCATAAGTTTGGAGCACTAGTTTGATTATTATGTTTATTACA
ATTTTAAATAAATTGAATAGGTAGTATCATATATATGGA

1598/6881
FIGURE 1477

AGCGGCACGCACCACAGCTCGAGCACCGCCCTTCCGGTTGGAGCCATTGCAAGCCCCCCCCACGCCCCGCCCCC
TCGCTAGGCGCTCGCCACGCCCATGCCTCCGTGCTGCGCGGCCACCCCGGATGTCAGCCCCCGCGCCGACCA
GAATCCGTGAACATGGCGAACGAGGTTATCAAGTGCAAGGCTGCAGTTGCTTGGGAGGCTGGAAAGCCTCTCTCC
ATAGAGGAGATAGAGGTGGCACCCCCAAAGGCTCATGAAGTTCGAATCAAGATCATTGCCACTGCGGTTTGCCAC
ACCGATGCCTATACCCTGAGTGGAGCTGATCCTGAGGGTTGTTTTCCAGTGATCTTGGGACATGAAGGTGCTGGA
ATTGTGGAAAGTGTGTGGTGGAGGAGTTACTAAGCTGAAGGCGGGTGACACTGTCATCCCACTTTACATCCACAG
TGTGGAGAAATGCAAATTTTGTCTAAATCCTAAACTAACCTTTGCCAGAAGATAAGAGTCACTCAAGGGAAAGGA
TTAATGCCAGATGGTACCAGCAGATTTACTTGCAAGGAAAGACAATTTTGCATTACATGGGAACAGCACATTT
TCTGAATACACAGTTGTGGCTGATATCTCTGTTGCTAAAATAGATCCTTTAGCACCTTTGGATAAAGTCTGCCTT
CTAGGTTGTGGCATTTC AACCGTTATGGTGTCTGTGTGAACACTGCCAAGTTGGAGCCTGGCTCTGTTTGTGCC
GTCTTTGGTCTGGGAGGAGTCGGATTGGCAGTTATCATGGGCTGTAAAGTGGCTGGTGTCTCCCGGATCATTGGT
GTGGACATCAATAAAGATAAATTTGCAAGGGCCAAAGAGTTTGGAGCCACTGAATGTATTAAACCTCAGGATTTT
AGTAAACCCATCCAGGAAGTGCTCATTGAGATGACCGATGGAGGAGTGGACTATTCCTTTGAATGTATTGGTAAT
GTGAAGGTCATGAGAGCAGCACTTGAGGCATGTACAAAGGGCTGGGGCGTCAGCGTCGTGGTTGGAGTAGCTGCT
TCAGGTGAAGAAATTGCCACTCGTCCATTCCAGCTGGTAACAGGTCGCACATGGAAAGGCACTGCCTTTGGAGGA
TGGAAGAGTGTAGAAAGTGTCCTCAAAGTTGGTGTCTGAATATATGTCCAAAAGATAAAAGTTGATGAATTTGTG
ACTCACAATCTGTCTTTTGATGAAATCAACAAAGCCTTTGAACTGATGCATTCTGGAAAGAGCATTTCGAAGTGT
GTAAAGATTTAATTCAAAAAGAGAAAAATAATGTCCATCCTGTCTGTGATGTGATAGGAGCAGCTTAACAGGCAGGG
AGAAGCGCCTCCAACCTCACAGCCTCGTAGAGCTTCACAGCTACTCCAGAAAATAGGGTTATGTGTGTCAATTCAT
GAATCTCTATAATCAAGGACAAGGATAATTCAGTCATGAACCTGTTTTCTGGATGCTCCTCCACATAAAATAATTG
CTAGTTTATTAAGGAATATTTTAACATAATAAAAGTAATTTCTACATTTGTGTGGAAATTGTCTTGTTTTATGCT
GTCATCATTGTACCGTTTGTCTGCCATTATCTTCATTCTGCAAGGGAAAGGGAAAGGAAGCAGGGCAGTGGTG
GGTGTCTGAAACCTCAGAAACATAACGTTGAACTTTTAAGGGTCTCAGTCCCGTTGATTAAAGAACAGATCCTA
GCCATCAGTGACAAAGTTAATCAGGACCCAAGTCTGCTTCTGTGATATTATCTTGAAGGGAGGTACTGTGCCTTG
TTCATACCTGTACCCCAAAATTCCTAGGATGGCATCTGCCCTTCAGGGGGCACTAAAATGTATTATTGAAACAGCA
TTCTGGGCTTAAATAGGTGTATGTATGTGTTGGTTGTGACTGTACTATTTCTAGTATAGTGAACACTACATACTGAA
TATCCAAGTTCTCAGCACCTACTTTTGTCAAATCTTAACATTTTGCCACTTCGAGATCACATTGCCATTCTCCC
CTCCAGAGGTAACAATTATCCACAATTTGATGTTTATCATTCTGTGTGTTGTACTTTCACTGTGTATAACCTA
AACCATCTACTCTTTAGTACTGTTTTATATATTTTTAAGCCTCATACTTGCTCATTCTACAGCTTTTTTCACTCA
TTATTGTATAATTATATCTGAAGCTCTCGTTCATTAAATTTTAGTCCTGTGTAGCAGAATTCAATTACGGGAAC
CCATAATTTATCTGTTCTCCAGTTGAAGGCATGAAGTTGTTGCCAGTTTCTGTATTATAACACTGTAGTGGAACA
TTCTTCTGCATTGGGCTCACTGCGTGTACCTAAGACGTATCACAGAAATAACACATTTAGCCTTATAGACATTG
CCAAATTGCTCTTCAAAGTAAATGTGAGTTTTTGTGAATTACATGAGTATGGAATGGTGTTTTATTATGACTTTA
GTTTGCATTTTCTCAA

1599/6881
FIGURE 1478

CGCAGTTTGAATCGCGGTGCGACGAAGGAGTAGGTGGTGGGATCTCACCGTGGGTCCGATTAGCCTTTTCTCTGC
CTTGCTTGCTTGAGCTTCAGCGGAATTCGAAATGGCTGGCGGTAAGGCTGGAAAGGACTCCGGAAAGGCCAAGAC
AAAGGCGGTTTCCCGCTCGCAGAGAGCCGGCTTGCCAGTCCCAGTGGGCCGTATTCATCGACACCTAAAAATCTAG
GACGACCAGTCATGGACGTGTGGGCGCGACTGCCGCTGTGTACAGCGCAGCCATCCTGGAGTACCTCACCGCAGA
GGTACTTGAACTGGCAGGAAATGCATCAAAAGACTTAAAGGTAAAGCGTATTACCCCTCGTCACTTGCAACTTGC
TATTCGTGGAGATGAAGAATTGGATTCTCTCATCAAGGCTACAATTGCTGGTGGTGGTGTTCATTCCACACATCCA
CAAATCTCTGATTGGGAAGAAAGGACAACAGAAGACTGTCTTAAAGGATGCCTGGATTCCCTTGTTATCTCAGGACT
CTAAATACTCTAACAGCTGTCCAGTGTTGGTGATTCCAGTGGACTGTATCTCTGTGAAAAACACAATTTGCCTT
TTTGTAATTCTATTTGAGCAAGTTGGAAGTTTAATTAGCTTTCCAACCAACCAAATTTCTGCATTGAGTCTTAA
CCATATTTAAGTGTTACTGTGGCTTCAAAGAAGCTATTGATTCTGAAGTAGTGGGTTTTGATTGAGTTGACTGTT
TTTAAAAAAGTGGTTTGAATTTAATTGTGATGCAGAAGTTATAGTAACAAACATTTGGTTTTGTACAGACATTAT
TTCCACTCTGGTGGATAAGTTCAATAAAGGTCATATCCCAAACATAAAA

1600/6881
FIGURE 1479

MAGGKAGKDSGKAKTKAVSRSQRAGLQFPVGRIHRHLKSRTTSHGRVGATAAVYSAAILEYLTAEVLELAGNASK
DLKVKRITPRHLQLAIRGDEELDSLKATIAGGGVIPHIHKSLLIGKKGQOKTV

1601/6881
FIGURE 1480

AAGATGCTGAAAGGAAAGAAGGCCAAGGGAAAAGAAGGTGGCTCCGGCCCCCTGCTGTCGTGAAGAAGCAGGAGGCT
AAGAAAGTGGTGAATCCCCTGTTTGAGGAAAAGGCCTAAGAATTTTGGCATTGGACAGGACATCCAGCCCAAAGA
GACCTCACCCGCTTTGTGAAATGGCCCCGCTATATCAGGTTGCAGCAGCAGAGAGCCATCCTCTATAAGCGGCTG
AAAGTGCTCCTGCGATTAACCAGTTCACCCAGGCCCTGGACCGCCAAACAGCTACTCAGCTGCTTAAGCTGGCC
CACAAGTACAGACCAGAGACAAAGCAAGAGAAGAAGGCTGTTGGCCCAGGCCGAGAAGAAAGCTGCTGGCAAAGG
GGACGTCCCCACCAAGAGACCACCTGTCCTTTGAGCAGGAGCTGGCTGTCTTCTTGCCTGCCCTATGTCGTAAAA
TGGTGGTCCCTTAGTGATTATCAAGAGGAAGGCAAGACTGGGACGTCTCGTCCACAGGAAGACCTGCACCACTG
TCGCCTTCACACAGGTGAACTCGGAAGACAAAGGCGCTTTGGCTAAGCTGGTGGAAGCTATCAGGACCAATTACA
ATGACAGATACGATGAGATCTGCCGTCCTGGGGTGGCAACATCCTGGGTCCTAAGTCTGTGGCTCGCATTGCCA
AGCTCGAAAAGGCAAAGGCTAAAGAAGCTGCCACTAAAGTGGGTTAAATGTGCACTGTTGAGTTTTCTGTACATA
AAAATAATTAAAATAATACAAATTTTCCTTCAAAGAAAAAAAAAAAAAAAAAAAA

1602/6881
FIGURE 1481

MLKGKKAKGKKVAPAPAVVKKQEAKKVVNPLFEERPKNFGIGQDIQPKRDLTRFVKWPRYIRLQQQRAILYKRLK
VPPAINQFTQALDRQTATQLLKLAKYRPETKQEKKAVGPGREESCWQRGRPHQETTCPLSSWLSSCLPYVVKWW
SLSALSRGRQDWDVSSSTGRPAPLSPSHR

1603/6881
FIGURE 1482

CCTCTCTCCGGTCCGTGCCTCCAAGATGACAAAGAAAAGAAGGAACAATGGTCGTGCCAAAAAGGGCCGCGGCCA
CGTGCAGCCTATTCGCTGCACTAACTGTGCCCAGATGCGTGCCCAAGGACAAGGCCATTAAGAAATTCGTCATTTCG
AAACATAGTGGAGGCCGCAGCAGTCAGGGACATTTCTGAAGCGAGCGTCTTCGATGCCTATGTGCTTCCCAAGCT
GTATGTGAAGCTACATTACTGTGTGAGTTGTGCAATTCACAGCAAAGTAGTCAGGAATCGATCTCGTGAAGCCCG
CAAGGACCGAACACCCCCACCCCGATTTAGACCTGCGGGTGCTGCCCCACGTCCCCACCAAAGCCCATGTAAGG
AGCTGAGTTCTTAAAGACTGAAGACAGGCTATTCTCTGGAGAAAAATAAAATGGAAATTGTACTTA

1604/6881
FIGURE 1483

GAACCGCCATCTTCCAGTAATTCGCCAAAATGACGAACACAAAGGGAAAAGAGGAGAGGCACCCGATATATGTTCT
CTAGGCCTTTTAGAAAAACATGGAGTTATTCTTTGGCCACGTATATGCGAATCTATAAGAAAGGTGATATTGTAG
ACATCAAGGGAACGGGTACTGTTCAAAAAGGAATGCCCCACAAGTGTTACCATGGCAAACTGGAAGAGTCTACA
ATGTTACCCAGCATGCTGTTGGCATTGTTGTAAACAAACAAGTTAAGGGCAAGATTCTTGCCAAGAGAATTAATG
TGCGTATTGAGCACATTAAGCACTCTAAGAGCCGAGATAGCTTCCTGAAACGTGTGAAGGAAAATGATCAGAAAA
AGAAAGAAGCCAAAGAGAAAAGGTACCTGGGTTCAACTAAAGCGCCAGCCTGCTCCACCCAGAGCAGCACACTTTG
TGAGAACCAATGGGAAGGAGCCTGAGCTGCTGGAACCTATTCCCTATGAATTCATGGCATAGGTGTTAAAAAAA
AAAAAATAAAGGACCTCTGGGCTACAA

1605/6881
FIGURE 1484

ATGAATTTTGAACCCTTATCCTTGAGCACTGATCAATTTTCTAAAGTTACTGGGGGTGTGGAAACAGTAAAGCTT
AAACTGACACAAGATGAAATAGAAAACCTTACATTGCCCTGTCTCCATTAAGGAACTTGAAGAAGCCAAATTGGCA
GAGAATGCTTGTACCCTGGCTGACCTGACAGAGGGTCAGGTTGGCAAGCTACTCATCCGCAAGTCTGGAAGGGTG
CAACTCCTCTTGGGCAAGGTGACTCTGGACGTGACCATGGGAACTGCCTGCTCCTTCCTGCAGGAGCTGGTGTCC
GTGGGCCTTGGAGACAGTAGGACAGGGGAGATGACAGTCCTGGGACACGTGAAGCACAAACTTAGGAAGCAGCAG
CAGGGAGGAGTGGCTGTGACATCACAGCCTGTGACTCTACTGGTGCAACAAGCAGTAACCCCTCTGGGCACCTCT
AGCTCTCTCTCAGGGCCCTGGGGCCACACTGGTGAAGCAAGGCCCCGAAGGCGAGTCCCATCCCCTTTCCACCC
CGAGAAAAGCACCTTTCCCCAAAGCCACAGCCCTGCCAGGGGTTCTATCTCCTCTCTCAGGCCAAATAA

1606/6881
FIGURE 1485

GGGAAGTGCTGTTGGAGCCGCTGTGGTTGCTGTCCGCGGAGTGGAAGCGCGTGCTTTTGTTTGTGTCCCTGGCCA
TGGCGCTGCAGCTCTCCCGGGAGCAGGGAATCACCTGCGCGGGAGCGCCGAAATCGTGGCCGAGTTCTTCTCAT
TCGGCATCAACAGCATTTTATATCAGCGTGGCATATATCCATCTGAAACCTTTACTCGAGTGCAGAAATACGGAC
TCACCTTGCTTGTAAGTACTGATCTTGAGCTCATAAAATACCTAAATAATGTGGTGAACAAGTAAAGATTGGT
TATACAAGTGTTTCAGTTCAGAACTGGTTGTAGTTATCTCAAATATTGAAAGTGGTGAGGTCTGGAAAGATGGC
AGTTTGATATTGAGTGTGACAAGACTGCAAAGATGACAGTGCACCCAGAGAAAAGTCTCAGAAAGCTATCCAGG
ATGAAATCCGTTTCAGTGATCAGACAGATCACAGCTACGGTGACATTTCTGCCACTGTTGGAAGTTTCTTGTTTCAT
TTGATCTGCTGATTTATACAGACAAAGATTTGGTTGTACCTGAAAAATGGGAAGAGTCGGGACCACAGTTTATTA
CCAATTCTGAGGAAGTCCGCCTTCGTTTCACTTACTACTACAATCCACAAAGTAAATAGCATGGTGGCCTACAAAA
TTCTGTCAATGACTGAGGATGACATGAGGAAAATAATGTAATTGTAATTTTGAAATGTGGTTTTCTGAAATCA
GGTCATCTATAGTTGATATGTTTTATTTTCAATTGGTTAATTTTTACATGGAGAAAACCAAATGATACTTACTGAA
CTGTGTGTAATTGTTCTTTATTTTTTTTGGTACCTATTTGACTTACCATGGAGTTAACATCATGAATTTATTGCA
CATTGTTCAAAAGGAACCAGGAGGTTTTTTTTGTCAACATTGTGATGTATATTCCTTTGAAGATAGTAACTGTAGA
TGGA AAAACTTGTGCTATAAAGCTAGATGCTTTTCTAAATCAGATGTTTTGGTCAAGTAGTTTGACTCAGTATAG
GTAGGGAGATATTTAAGTATAAAATACAACAAAGGAAGTCTAAATATTCAGAATCTTTGTTAAGGTCTGAAAGT
AACTCATAATCTATAAACAATGAAATATTGCTGTATAGCTCCTTTTGACCTTCATTTTCATGTATAGTTTTCCCTA
TTGAATCAGTTTCCAATTATTTGACTTTAATTTATGTAACCTGAACCTATGAAGCAATGGATATTTGTACTGTTT
AATGTTCTGTGATACAGAACTCTTAAAAATGTTTTTTCATGTGTTTTATAAAATCAAGTTTTAAGTGAAAGTGAG
GAAATAAAGTTAAGTTTGTTTTAAAAAAAAAAAAAAAAAAAA

1607/6881
FIGURE 1486

MALQLSREQGITLRGSAEIVAEFFSFGINSILYQRGYIPSETFTRVQKYGLTLLVTTDLELIKYLNNVVEQLKDW
LYKCSVQKLVVVISNIESGEVLERWQFDIECDKTAKDDAPREKSQKAIQDEIRSVIRQITATVTFLPLEVSCS
FDLLIYTDKDLVVPEKWEESGPQFITNSEEVRLRSFTTTIHKVNSMVAYKIPVND

1608/6881
FIGURE 1487

CTGGGATTACAGGTGTGAGCCATCTTGCTCATTTTAGTTTAAACTTTTGAGTGGTTTGTGTCTCCTGATTGGACT
CCTACAAATACAGAATTGATGCTAGGAAGGGTACCAGGAGATAGATGCACACAGATGGGATTTGGGAGTAGGTTT
GGTTATCCAAGGAGCAGTGCTGAGCTCCTTGCTAATGGGATATGGGATGCTGGTGATTTCCAGGAAGTGACCTCA
CAATGACTCAAGCTACCACATACTGTTGATTGTGAAATGCCAGTTGAAGCATATGTCCTGCGAGCTTAGGGGTGC
TACAAGTTGACCACTGCAGCAGTAAAGATGACTCTGAAGAATGGCATGGGATGGATCCTTTGGAATGCACTTGAG
CAGCGGTCTCCAACCACAGGGCCACAGAGCTGGAGCTGGATCTACCATGAAAGACTTCTGAATCCAGGAAGAGAG
ACTGACTGGGCAACATGTTATTTCAGGTGGGACCATCCAGTTGCAGGAAAACAAGCTTAACATGCCCCACTGATTCT
ACATTATGCTCCTACCTCCCGGCAGCCTCTCCAGGCCCAGAACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCA
TGACTCACAATGGCCTATTTAGGCCCATACCCTACCTCACGGCAGTCTCCGCAGATGAGCCTACTGCCTCACAAC
AGCCTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTTTAGACCCAGCTCCTGCCTCCCAGCCTTCTCTCTAG
GCCCTGAACTTTCTGAAGTCGACCTCACCAGGCCCAGCTCATGCTTCTTTGCAGCCTCTCCAGGCCCAGCTCCTG
CATCTTGGTGGCCCCCTCCAGGCCCAGCCTCTGCCTCCCGTCGGCCTCTACAGTCCCAACATCTGCCTCATAGCAG
ATTCTTGAGGCCCAGCATCTGCCTCACTGTGGACCCCCAGACCCAGATGGTGTCTCACTGTGGCATCCTCAGGC
AAAGCTCCTGCCTTTTCGGCAGCCTCTCCAGGCCCAGCTCCTCCTGCCTCCCAGTGGCCTCTTTTCGGCCCAGCCCA
GCTCATGCCTCCCAGCGGCCTTCCCAGGCCCGCTTTTGACTTTTCGGTGGCCTCTGCAGGCCTCGACAAGGCCTG
GCCTCCTGCCTCCCGAA

1609/6881
FIGURE 1488

MLLPGSLSRPRTFSSQPLQTKLMTHNGLFRPIPYLTAVSADEPTASQQPPQQLHRYNGLFRPSSCLPAFSLGP
ELSEVDLTRPSSCFFAASPGPPLPPVGLYSPNICLIADS

1610/6881
FIGURE 1489

AGGGCCGGGGTGGGGCGCTGGCGTTTTCCGTTGCTTGGATCAGTCTAGGTGCAGCTGCGGATCCTTCAGCGTCTGC
ATCTCGGCGTCGCCCCGCGTACCGTCGCCCCGGCTCTCCGCCGCTCTCCCGGGGGTTTCGGGGCACTTGGGTCCAC
AGTCTGGTCCTGCTTCACCTTCCCCTGACCTGAGTAGTCGCCATGGCACAGGTTCTCAGAGGCACTGTGACTGAC
TTCCCTGGATTTGATGAGCGGGCTGATGCAGAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAG
AGCATCCTGACTCTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAGACTCTGTTT
GGCAGGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAAAATTTGAAAAATTAATTGTGGCTCTGATGAAA
CCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCCTTGAAGGGAGCTGGAACAAATGAAAAAGTACTGACA
GAAATTATTGCTTCAAGGACACCTGAAGAACTGAGAGCCATCAAACAAGTTTATGAAGAAGAATATGGCTCAAGC
CTGGAAGATGACGTGGTGGGGGACACTTCAGGGTACTACCAGCGGATGTTGGTGGTTCTCCTTCAGGCTAACAGA
GACCCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTTTCAGGCTGGAGAACTTAA
TGGGGGACAGATGAAGAAAAGTTTATCACCATCTTTGGAACACGAAGTGTGCTCATTGAGAAAGGTGTTTGAC
AAGTACATGACTATATCAGGATTTCAAATTGAGGAAACCATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTA
CTCCTTGCTGTTGTGAAATCTATTGCAAGTATACCTGCCTACCTTGCAGAGACCCTCTATTATGCTATGAAGGGA
GCTGGGACAGATGATCATACCCTCATCAGAGTCATGGTTTCCAGGAGTGAGATTGATCTGTTTAAACATCAGGAAG
GAGTTTAGGAAGAATTTTGCCACCTCTCTTTATTCCATGATTAAGGGAGATACATCTGGGGACTATAAGAAAGCT
CTTCTGCTGCTCTGTGGAGAAGATGACTTAACGTGTCACGGGGAAGAGCTCCCTGCTGTGTGCCTGCACCACCCCA
CTGCCTTCCTTCAGCACCTTTAGCTGCATTTGTATGCCAGTGCTTAACACATTGCCTTATTCATACTAGCATGCT
CATGACCAACACATACACGTCATAGAAGAAAATAGTGGTGCTTCTTTCTGATCTCTAGTGGAGATCTCTTTGACT
GCTGTAGTACTAAAGTGTACTTAATGTTACTAAGTTTAATGCCTGGCCATTTTCCATTTATATATATTTTTTAAG
AGGCTAGAGTGCTTTTAGCCTTTTTTAAAACTCCATTTATATTACATTTGTAACCATGATACTTTAATTAGAAG
CTTAGCCTTGAAATTGTGAACTCTTGAAATGTTATTAGTGAAGTTCGCAACTAACTAAACCTGTAAAATTATG
ATGATTGTATTCAAAGATTAATGAAAATAAACATTTCTGTCCCCCTGAATTAT

1611/6881
FIGURE 1490

MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSELTG
KFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKQVYEEYGSSEDDVVGDTSGYYQ
RMLVLLQANRDPDAGIDEAQVEQDAQALFQAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYM TISGFQIEETI
DRETSGNLEQLLLAVVKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI
KGTSGDYKKALLLLCGEDD

1612/6881
FIGURE 1491

CATAACAAGCCAAACGCCAGACCGAGAGTGCCTCCGTGCGCGAGTGCCCGGTGTGTGCGCGCCGGCGAGAGCAGG
GGCCCCGCCGGCTCCCCGCCCGCGCGGCCCGAACTCATGCAGCTCCGAGCGAGCGAGCGCGCCAGCCAGCG
CCTCGGCCGAACCCCTCCGCAGCAGGCTGCCTGCTGTTTCCCGGGGAGATCATGAAACGAGGTGCGCTTCCCAGC
AGCAGTGAGGATTCTGACGACAATGGCAGCCTGTCAACTACTTGGTCCAGAATTCCCGATCCCAGCATAGGAGA
AGCTCCTGCTCCAGACATGAAGATCGAAAGCCTTCAGAGGTGTTTAGGACAGACCTGATCACTGCCATGAAGTTG
CATGACTCCTACCAGCTGAATCCGGATGAGTACTATGTGTTGGCAGATCCCTGGAGACAGGAATGGGAGAAAGGG
GTCCAGGTGCCTGTGAGCCCGGGGACCATCCCTCAGCCTGTGGCCAGGGTTGTGTCTGAAGAGAAATCCCTCATG
TTCATCAGGCCCCAAGAAGTACATCGTGTATCAGGCTCTGAGCCTCCCGAGTTGGGCTATGTGGACATCCGGACG
CTGGCTGACAGCGTGTGTGCTATGACCTCAATGACATGGATGCTGCATGGCTGGAAGTACCAATGAAGAATTT
AAGGAGATGGGAATGCCTGAACTAGATGAATACACCATGGAGAGGGTCTTAGAGGAATTTGAGCAGCGATGCTAC
GACAATATGAATCATGCCATAGAGACTGAGGAAGGCCGTTGGGATCGAATATGATGAAGATGTTGTCTGTGATGTC
TGCCAGTCTCCTGATGGTGAGGACGGCAATGAGATGGTGTCTGTGACAAATGCAACATCTGTGTGACCAGGGCC
TGTTATGGAATCCTCAAGGTACCAGAGGGCAGCTGGCTGTGCCGGACATGTGCCCTGGGGGTTTCAGCCAAAATGT
CTGCTGTGTCCGAAGAAGGGTGGAGCTATGAAGCCCACCCGTAGCGGAACCAAGTGGGTCCACGTTAGCTGTGCT
CTGTGGATCCCTGAGGTGAGCATTGGCAGCCCAGAGAAGATGGAGCCCATCACCAAGGTGTACACATTTCCAGC
AGCCGGTGGGCGCTAGTGTGACGCTCTGCAATGAGAAGTTTGGGGCCTCTATACAGTGCTCTGTGAAGAACTGC
CGCACAGCCTTCCATGTGACCTGTGCTTTTGACCGGGGCTGGAGATGAAGACCATCTTAGCAGAGAATGATGAA
GTCAAGTTCAAGTCTATTGCCCAAAGCACAGCTCACATAGGAAACCCGAGGAGAGTCTTGCGCAAGGGGGCTGCA
CAGGAGAATGGGGCCCTGAGTGTTCCTCCCGGAATCCGCTGGAGCCCTTTGCCAGCCTTGAGCAGAACCGGGAG
GAGGCCACCGGGTGAGTGTCCGTAAGCAGAAGCTGCAGCAGTTGGAGGATGAGTTCTACACCTTCGTCAACCTG
CTGGATGTTGCCAGGGCTCTGCGGCTGCCTGAGGAAGTAGTGGATTTCTGTACCAGTACTGGAAGTTGAAGAGG
AAGGTCAACTTCAACAAGCCCCCTGATCACCCCAAAGAAAGATGAAGAGGACAATCTAGCCAAGCGGGAGCAGGAT
GTCTTATTTAGGAGGCTGCAGCTGTTACGCACCTGCGGCAGGACCTGGAGAGGGTAATGATTGACACTGACACC
TTATAGTGACTTAGAGAAGAAGATGCAAAGAGGCGAACGCTCGCCCAGAGCAAGAAATGATAGCCAGTCATATAC
TCTCAGACCCTTGTACACACCACAGCATGAGGTTGTGTTGGTTAAAAATATTTATGGGCTGGTAAACTCATTGTA
CATATGTGCAAACTGCTACTGAGTGGGGAGCTTCTTTGTGGTTTTTTTTTTTAAAAACACTTTCCCATTAATC
TTTACTGTTTTGTAAAGATCAAATGGGGTGTTCTTCCCCACCCCATTCCTTCATTCTAGAGCTAGAGTGAATGA
GCCCCAAGAAATGACCCAAGGAGTTGACTCAGGATGGTTTACAGACTGATTTAGAAAACAGAACGGATTTTCAT
TTCTAATGGAGGGGGCCAGAGATGGGAAATTTCTTGTTTTCAGTCCGGGGAAACACACCTAGGTGCTGGTGATGGG
CTTATGAAGGAAGCTAAGCACGGCTGCTCACTGGCCCCACTTTGTTTCTTGGGTAATTCACAGGGGAATTTCCCA
GTACTGTCTATGGAGCAGAGCAGGCAGTGGGTGCTGATGTGTGTGATGAGCTGTATGTACACATGCATATATCTG
TTACAGAAGATACTCCTGGCAGTGAGGTGCTAAGTCATCACTGAGGCTGTGTGTGTGTGTGTGTGCGCGTGCC
CGTGTCCATCCATGTCTCTGTTGTGTGTCTGTGTGCGGGTATGGGTGGGATTCTGGTGGACAGGGGTGTCAGAT
CTGTCTGAGGAGCCCCAGTCATGCTCAGCACGCTACAGATGTGTTGTTTGTACACTGAGATTGCTGAATGTCGT
GGCTGTTGGCTGCCGAGCCTCAGCTGCTGGCATTTCCTTCTGCTGTTTGTGCTTTTGTGCCTCCCCCACTTTCC
ATCACCTCTGGAGTCCCGTCTGGACGTCCCTTCTGCTACAGGAATAATGAGGCGTGGGCTGCCTCCCGCTAGGG
CCTCCTGCTCCCTGTAGGTAGTTTCTGGCTGAGGCTTGCTAATTGGGGATGCTTCTTAGAGCATCTTCCACATCA
ACTCCCTGCTGCTGGCTACCGATTAAATTCATTAGTGTGAAAGAGGTGGGAGTGAGGTTTTCTGGCCTGAAGC
AGTCTGCACTGAAAGGTACCCAAGTGGCCTGAAACAGTGTAGGGAAAGACCTGGGAAACACTGGACCAAAAAAGC
CTGATCTCATGGAGACCTGCATGGCCCTGTTAGAGATGGCGTAGAAGTGAAAGTCTTAAAGGGAGCATTAGAGAT
CCTTTTAATACACGACTGAGTGCCAGCTTATTTGTGATGCCCCCTCCCAGACCAGGTTAGGATTCTGGGAAGGC
CGCGGATTCCGGCCCTGGAAGAGGCAGGATCCTGGAGCAGTTTTGTGAGGCTTTTGTGCTCCCATACGCCCCCTG
GTGGTGAGTGTAAGAAGACTTTGCCTCTCACAACCTACATGTATGTGTGGCATTTTTGTAGAGATGAGAAAAGG
ATTGAGAAGGATAAACTGGAATCCTGGTAAGAAGCCTTTATGCCAGCCCGACACCTGCTGTAATTGGGGTGCATG
AGCTATGGAGTCAGATAGTTGTTGGGAGGGGGAGGACAAGAAGTCTATTGTTTGGACTGTGTTGTCTCACAATC
ACCACAAAATAAAAGTGTAGAAAATGCTTGTGGTGTACTAACTCTTTTCTGTACTTAAGTTACTCAGATTAAACAT
GCACTTCTAATTCTAAACATTTTTTTTGGAGTCATCACTGTCGCTGTTTAAGTAGAACAATGCCAACGATGTATG
AGAAACAGGGAATAAATCAGGATTTGTGTGTGT

1613/6881
FIGURE 1492

MKRGRLPSSSEDSDDNGSLSTTWSQNSRSQHRRSSCSRHEDRKPSEVFRDITAMKLHDSYQLNPDEYYVLADP
WRQEWKGVQVPVSPGTIPQVARVVSEKSLMFIRPKKYIVSSGSEPPELGYVDIRTLADSVCRYDLNDMDAAW
LELTNEEFKEMGMPELDEYTMERVLEEFQRCYDNMNHAIETEEGLGIEYDEDVVCDCQSPDGEDGNEMVFCDK
CNICVHQACYGILKVPEGSWLCRTCALGVQPKLLCPKKGAMKPTRSGTKWVHVSCALWIPEVSIQSPEKMEPI
TKVSHIPSSRWALVCSLCNEKFGASIQSVKNCRTAFHVTCAFDRGLEMKTILAENDEVKFKSYCPKHSSHRKPE
ESLGKGAQENGAPCESPRNPLEPFASLEQNREEAHRVSVRKQKLQQLLEDEFYTFVNLLDVARALRLPEEVDFL
YQYWKLKRKVNFNKPLITPKKDEEDNLAKREQDVLFRRLQLFTHLRQDLERVMIDDTL

1614/6881
FIGURE 1493

GTGAGTGTGTGTCGGTCGCACGGCGTGTGTCTCCGGCCGCGGGTTCCGCCTCCTCCCCTGCCGCCGCTGCTCACG
GTGTAAGTCAATGTGAAGCAGCAGCTCCAGCCCCGGGATAAAACATGGCGACGTCTCTGCATGAGGGACCCACGAA
CCAGCTGGATCTGCTCATTCCGGCCGTGGAAGCATCAGTTCACAGCAGTAATGCACACTGTACAGATAAGACAAT
TGAAGCTGCTGAAGCCCTGCTTCATATGGAATCTCCTACCTGCTTGAGGGATTCAAGAAGTCCTGTGGAAGTGTT
TGTTCCCTCCTTGTGTATCAACTCCAGAATTCATCCATGCTGCTATGAGGCCAGATGTCATTACAGAACTGTAGT
GGAGGTGTCAACTGAAGAGTCTGAACCCATGGATACCTCTCCTATTCCAACATCACCAGATAGCCATGAACCAAT
GAAAAAGAAAAAGTTGGCCGTAAACCAAGACCCAGCAATCACCAATTTCCAATGGGTCTCCTGAGTTAGGTAT
AAAGAAGAAACCAAGAGAAGGAAAAGGAAACACAACCTATTTGTGGGAGTTTCTTTTAGATCTACTTCAAGATAA
AAATACTTGTCCCAGGTATATTAAATGGACTCAGAGAGAAAAAGGCATATTCAAGCTGGTGGATTCAAAGGCTGT
CTCTAAGCTTTGGGGAAAGCATAAGAACAACCCAGACATGAACTATGAAACCATGGGACGAGCTTTGAGATACTA
CTACCAAAGGGGAATTTCTGCAAAGGTTGAAGGACAGAGGCTTGTATATCAGTTCAGGATATGCCGAAAAACAT
AGTGGTCATAGATGATGACAAAAGTGAACCTGTAATGAAGATTTAGCAGGAACTACTGATGAAAAATCATTAGA
ACGAGTGTCACTGTCTGCAGAAAGTCTCCTGAAAGCAGCATCCTCTGTTCGCAGTGGAAAAATTCATCCCCTAT
AACTGCTCCAGAGCAGAGAAGGGTGTAGCTAGAGTTGTGAATATCACTTCCCCTGGGCACGATGCTTCATCCAG
GTCTCCTACTACCACTGCATCTGTGTGTCAGCAACAGCAGCTCCAAGGACAGTTCGTGTGGCAATGCAGGTACCTGT
TGTAATGACATCATTGGGTCAGAAAATTTCAACTGTGGCAGTTTCACTCAGTTAATGCAGGTGCACCATTAAATAAC
CAGCACTAGTCCAACAACAGCGACCTCTCCAAAGGTAGTCATTTCAGACAATCCCTACTGTGATGCCAGCTTCTAC
TGAAAATGGAGACAAAATCACCATGCAGCCTGCCAAAATTATTACCATCCCAGCTACACAGCTTGCACAGTGTCA
ACTGCAGACAAAGTCAAATCTGACTGGATCAGGAAGCATTAAACATTGTTGGAACCCCATTTGGCTGTGAGAGCACT
TACCCCTGTTTTCAATAGCCCATGGTACACCTGTAATGAGACTATCAATGCCTACTCAGCAGGCATCTGGCCAGAC
TCCTCCTCGAGTTATCAGTGCAGTCATAAAGGGGCCAGAGGTTAAATCGGAAGCAGTGGCAAAAAAGCAAGAACA
TGATGTGAAAACCTTTGCAGCTAGTAGAAGAAAAACCAGCAGATGGAAATAAGACAGTGACCCACGTAGTGGTTGT
CAGTGCGCCCTTCAGCTATTGCCCTTCCTGTAACATATGAAAACAGAAGGACTAGTGACATGTGAGAAATAAATAG
CAGCTCCACCATGGACTTCAGGCTGTTAGTGGCAGTACTGACATAAACATTTGCAAGGGAAGTCATCAAGAAAAG
TCAAAGAAGACTTTTAAACATTTTAAATGCATATACAAAACAATCAGACTTACTGGAAATAAATTACCTATCCC
ATGTTTTCAGTGGGAAATGAACTACATATTGAGATGCTGACAGAAAACCTGCCTCTTACAGTAGGAAACAACCTGAAC
CCATCAATAAGAAAAAGGATCGAAAGGGACCAAGCAGCTCACTACGATATCAAGTTACACTAAGACTTGGAACAC
TAACATTCTGTAAGAGGTTATATAGTTTTTCACTGGGAGGGGTTGGGATGGGTAATCTCATTGTTACATATAGCAA
TTTTTGATGCATTTTATATGCATACCAGCAATTATTACTGTGTTTCGCACAGTTCCTCACTTAACCTGGTGTATGTG
AAGACTCTGCTAATATAGGTATTTTAGAATGTGAATTGAAGAATGGATCCCAAAAACCTCAGAAAGAGGATAGCA
AAAAAGATCTAGTGCATTTTATATATATATATATATATATATACATACATATATATATATATATATAGCTTAAG
CTGATTTAAACAAAGGCCCTTAGACTAATTTTCGATTTTCTTTCTTGAAATAAGCTAATGGCTTGTGTGTAAA
GCTTTTTTATTAAAGAAAAATTTTAAAAATCTTGTACCTAGCACAGTATTGTTATAGAATATACATGTAACATT
TTATAAGGTAGTTTAAAGTCTGTGAGTTTCTTAATTGTGGACAAATTAACAGTTGGCTCTGGCCTTTTGCTGTAAAC
ATGCCTGTGTCACTCACTTAGCCTTGGCATTGTGTCAGACATACCATTTTTCAGTTCTGCTGTCACTTGGAGTTT
AGGCTCAGCATGAATTTTGGCAGGTAGCTCTAATACCTGGAGTTTTCTTTGTTTTTTTTTCTTTTTTTTTAGTTG
AAGTTTATGAGGGAATACCAGTGTTTCACTTTTGAACATAATAGTTTGTATATTCAACATTTGAAGTATATTCT
ATTTTGTGTACTCTTGTTTCAAAGTGATTCAAGTAGTTTTCTGAAATATAGAAATGAAATTTATCTTCTGTT
TTGGTCTCTGGTGATATTTTAAACAATATTTAAAGTCAGTATAGAAGTGTTTTAGTTAGGAAGTGATAAAACAT
CTCTCTTCTCCTTCCCACTACTGCATGAAGAAATTTCTACTTCCATTATATTAATATTGG

1615/6881
FIGURE 1494

GCACGAGGGACTTCTGTTCCAGAGCAAAGGTCATTTCAGCCGCTTGAATCAGCCTTTTCCCCCACC CGGTCCCCA
ACTTTGTTTACCCGATAAGGAAGGTCAGCATTCAAAGTCAAGAAGCGCCATTTATCTTCCCGTGCGCTCTACAAA
TAGTTCCGTGAGAAAAGATGGCCGGGAACTCGATCCTGCTGGCTGCTGTCTCTATTCTCTCGGCCTGTCAGCAAAG
TTATTTTGCTTTGCAAGTTGGAAAGGCAAGATTAAAATACAAAGTTACGCCCCAGCAGTCACTGGGTCAACCAGA
GTTTGAGAGAGTATTTTCGGGCACAACAAAACACTGTGTGGAGTTTTATCCTATATTCATAATTACATTGTGGATGGC
TGGGTGGTATTTCAACCAAGTTTTTGCTACTTGTCTGGGTCTGGTGTACATATATGGCCGTCACCTATACTTCTG
GGGATATTGAGAAGCTGCTAAAAAACGGATCACCGGTTTCCGACTGAGTCTGGGGATTTTGGCCTTGTTGACCT
CCTAGGTGCCCTGGGAATTGCAAACAGCTTTCTGGATGAATATCTGGACCTCAATATTGCCAAGAACTGAGGCG
GCAATTCTAACTTTTTCTCTTCCCTTTAATGCTTGCAGAAGCTGTTCCCACCATGAAGGTAATATGGTATCATTT
GTTAAATAAAAATAAAGTCTTTATTCTGTAAAAA

1616/6881
FIGURE 1495

MAGNSILLAAVSILSACQQSYFALQVGKARLKYKVTPPAVTGSPEFERVFRAQQNCVEFYPIFIITLWMAGWYFN
QVFATCLGLVYIYGRHLYFWGYSEAAKKRITGFRSLGILALLTLLGALGIANSLDEYLDLNIAKKLRRQF

1617/6881
FIGURE 1496

CGCCGAGCTCCAGCCGAAGGAGAAGGGGGGTAAGTAAGGAGGTCTCTGTACCATGGCTCGTACAAAGCAGACTGC
CCGCAAATCGACCGGTGGTAAAGCACCCAGGAAGCAACTGGCTACAAAAGCCGCTCGCAAGAGTGCGCCCTCTAC
TGGAGGGGTGAAGAAACCTCATCGTTACAGGCCTGGTACTGTGGCGCTCCGTGAAATTAGACGTTATCAGAAGTC
CACTGAACTTCTGGTTCGCAAAC TTCCCTTCCAGCGTCTGGTGCGAGAAATTGCTCAGGACTTTAAAACAGATCT
GCGCTTCCAGAGCGCAGCTATCGGTGCTTTGCAGGAGGCAAGTGAGGCCTATCTGGTTGGCCTTTTTGAAGACAC
CAACCTGTGTGCTATCCATGCCAAACGTGTAACAATTATGCCAAAAGACATCCAGCTAGCACACAGCATACGTGG
AGAACGTGCTTAAGAATCCACTATGATGGGAACATTTCACTCTCCCATGGGGTCAAAGGTACCTAAGTATATG
ATTGCGAGTGGA

1618/6881
FIGURE 1497

ATGAAGAAAGGAAAGCTCATCTCTGCCACATTTCTGGAAAGCGCTGTTCCCGGTGCTCACCTATTGTCTCGCAGG
CAGGTTTCTGAAAGGATGGAGGAAATCTGCAGGAAGCACATGTTTCTGCTTAATTCCTGCCAGCTTTTGGCTGTC
AGACCCCAAATCCTTCAGCCACTAGCCTGTTTCAGGGCCCTGGTTTGATAACCCTGCAATTGCAGAGTGAGTGGG
AGGAGAAGCCTCATACCTTTGTTTTTCTGGTTCTTCCCAACACCCTGGTGGCCTACTTGGGTGTCCCACAAGCTC
TCTGTGGAAAATAGTGCATCTCATTTAGCAACAACCTCCACCTAGCACAAAGTTCTGAGCTATACTTAAACCAGTGG
GGAGAGAGTGTTGGAATGATTAAGGCTTGCATTTCGACTGTGCAAGAAGAACCATTTTCTCTTCATGGTGCTGGAG
GCAGAGATTGAGGCTCTCAAGGAGGAGCTGCTCTTCATGAAGAAGAACCACGAAGAGGAAGTAAAGGCCTACAA
GCCCAGAGTGCCAGCTCTGGTTTGACCCTGGAGGAGCTGGACAAGTATTGGTCTCAGCAGATTGAGGAGAGCGCC
ACAGTGGTCACCACGCAGCCTGCCAAGGTTGGAGCTGCTGAGATGATGCTCACAGAGCTGAGACATACAGTCCAG
TCTTTGGAGATCGACCTGGACTCCTTGAGAAATCTGAAGGCCAGCTTGGAGAACAGCCTGAATGGAGCAGCTCAA
CGGCATCCTGCTGCACCCGGAGTCAGAGCTGGCACAGACCCAGAGGGACAGTGCCAGGCCAGGAGTACGAGGCC
CTGCTGAACATCAAGGTCAAGCTGGAGGCTGAGATCACCACCTACTGCCGCCTGCTGGAAGATGACGAGGACTTC
AATCTTGTGGATGGCAAAGTGGTGTCTGAGACCAATGATACCAAAGTTCTGAGACATTTAA

1619/6881
FIGURE 1498

MKKGKLISATFLESAPGAHLLSRRQVSEEMEEICRKHMFLLNSCQLLAVRPQILOPLACSGPWFDNPAIAEWSG
RRSLIPLFFWFFPTPWPTWVSHKLSVENSASHLATTPPSTSSELYLNQWGESVGMKACIRLCKKNHFLFMVLE
AEIEALKEELLFMKKNHHEEVKGLQAQSASSGLTLEELDKYWSQQIEESATVVTTQPAKVGAAEMMLTEL RHTVQ
SLEIDLDSLRLKASLENSLNGAAQRHPAAPGVRAGTDPEGQCQAQYEALLNIKVKLEAEITTYCRLLLEDDF
NLVDGKVVSETNDTKVLRH

1620/6881
FIGURE 1499

AAAACACCAAATGGCGGATGACGCCGGTGCAGCGGGAGGGCCCGGAGGCCCTGGTGGCCCTGGGATGGGGAACCG
CGGTGGCTTCCGCGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGTCGCGGAGGCAAGGCCGAGGATAAGGAGTG
GATGCCCCGTACCAAGTTGGGCCGCTTGGTCAAGGACATGAAGATCAAGTCCCTGGAGGAGATCTATCTCTTCTC
TCTGCCCCATTAAGGAATCAGAGATCATTGACTTTTTCTGGGGGCCTCTCTCAAGGATGAGGTTTTGAAGATTAT
GCCAGTGCAGAAGCAGACCCGTGCCGGCCAGCGCACGAGGTTCAAGGCATTGCTTGCTATCGGGGACTACAATGG
CCACGTCGGTCTGGGTGTTAAGTGCTCCAAGGAGGTGGCCACCGCCATCTGTGGGGCCATCATCCTGGCCAAGCT
CTCCATTGTCCCCGTGCACAGAGGCTACTGGGGGAACAAGATCGGCAAGCCCCACACCGTCCCTTGCAAGGTGAC
AGGCCGCTGCGGCTCTGTGCTGGTGCACCTCATCCCTGCACCCAGGGGCACTGGCATCGTCTCCGCACCTGTGCC
TAAGAAGCTGCTCATGATGGCTGGTATCGATGACTGCTACACCCAGCCCAGGGCTGCACTGCCACCCCTGGGCAA
CTTCGCCAAGGCCACCTTTGATGCCATTTCTAAGACCTACAGCTATCTGACCCCTGACCTCTGGAAAGAGACTGT
ATTTACCAAGTCTCCCTATCAGGACTTCACTGACCACCTAGTCAAGACCCACACCAGAGTCTCCATGCAGCGGAC
TCAGGCTCCAGCTGTGGCTACAACGTAGGGTTTTTATACAAGAAAAATAAAGTGAATTAAGCGTGTCAAAAAAAA
AAAAAAAAAAAAAAAAAAAA

1621/6881
FIGURE 1500

TGAGAACACGCTGTGTGGCTGAAAAGTGAAGGCAAGAGCTGATTGGCCTCTGTGCTCCCTCCGCAAGGGGATC
GTTTTCTCCAGAAGAGCTGGATATTCTTTCGCCAGTTATGGCAGACAAGTTAACGAGAATTGCTATTGTCAACC
ATGACAAATGTAAACCTAAGAAATGTCGACAGGAATGCAAAAAGAGTTGTCCTGTAGTTCGAATGGGAAAATTAT
GCATAGAGGTTACACCCCAGAGCAAAATAGCATGGATTTCGAAACTCTTTGTATTGGTTGTGGTATCTGTATTA
AGAAATGCCCCTTTGGCGCCTTATCAATTGTCAATCTACCAAGCAACTTGGAAAAAGAAACCACACATCGATATT
GTGCCAATGCCTTCAAACCTTACAGGTTGCCTATCCCTCGTCCAGGTGAAGTTTTGGGATTAGTTGGAACATAATG
GTATTGGAAAGTCAACTGCTTTAAAAATTTTAGCAGGAAAACAAAAGCCAAACCTTGGAAAGTACGATGATCCTC
CTGACTGGCAGGAGATTTTGACTTATTTCCGTGGATCTGAATTACAAAATTACTTTACAAAGATTCTAGAAGATG
ACCTAAAAGCCATCATCAAACCTCAATATGTAGACCAGATTCCCTAAGGCTGCAAAGGGGACAGTGGGATCTATTT
TGGACCGAAAAGATGAAACAAAGACACAGGCAATTGTATGTCAGCAGCTTGATTAAACCCACCTAAAAGAACGAA
ATGTTGAAGATCTTTCAGGAGGAGAGTTGCAGAGATTGCTTGTGCTGTCGTTGCATACAGAAAGCTGATATTT
TCATGTTTGATGAGCCTTCTAGTTACCTAGATGTCAAGCAGCGTTTAAAGGCTGCTATTACTATACGATCTCTAA
TAAATCCAGATAGATATATCATTTGTGGTGGAAACATGATCTAAGTGTATTAGACTATCTCTCCGACTTCATCTGCT
GTTTATATGGTGTACCAAGCGCCTATGGAGTTGTCACTATGCTTTTAGTGTAAGAGAAGGCATAAACATTTTTT
TGGATGGCTATGTTCCAACAGAAAACCTTGAGATTCAGAGATGCATCACTTGTTTTTAAAGTGGCTGAGACAGCAA
ATGAAGAAGAAGTTAAAAAGATGTGTATGTATAAATATCCAGGAATGAAGAAAAAATGGGAGAATTTGAGCTAG
CAATTGTAGCTGGAGAGTTTACAGATTCTGAAATTATGGTGTATGCTGGGGGAAAATGGAACGGGTAAAACGACAT
TTATCAGAATGCTTGCTGGAAGACTTAAACCTGATGAAGGAGGAGAAGTACCAGTTCTAAATGTCAGTTATAAGC
CACAGAAAATTAGTCCCAAATCAACTGGAAGTGTTCCGCAGTTACTACATGAAAAGATAAGAGATGCTTATACTC
ACCCACAATTTGTGACCGATGTAATGAAGCCTCTGCAAATTGAAAACATCATTGATCAAGAGGTGCAGACATTAT
CTGGTGGTGAACCTACAGCGAGTAGCTTTAGCCCTTTGCTTGGGCAAACCTGCTGATGCTATTTAATTGATGAAC
CATCTGCATATTTGGATTCTGAGCAAAGACTGATGGCAGCTCGAGTTGTCAAACGTTTCATACTCCATGCAAAAA
AGACAGCCTTTGTTGTGGAACATGACTTCATCATGGCCACCTATCTAGCGGATCGCGTCATCGTTTTTGTGCTCAGCTTG
TTCCATCTAAGAACACAGTTGCAAACAGTCCTCAAACCCCTTTTGGCTGGCATGAATAAATTTTTGTCTCAGCTTG
AAATTACATTCAGAAGAGATCCAAACAACCTATAGGCCACGAATAACAAACTTAATTCAATTAAGGATGTAGAAC
AAAAGAAGAGTGGAACTACTTTTTCTTGATGATTTAGACTGACTCTGAGAATATTGATAAGCCATTTATTA
GGAGTATTTACTAGAATTTTTTGTATATAAACTTGAATCAGGATTTTATGCCCCACATACTCTGGAACCTGAA
GTATAATATACTTAATATAACATAAAAAGCCAGTTGGGTCTAAATGTAGTTGAAACACAGAAAATGCCACTTT
TCTGTTCTGAAGAGGCTCTTTTGTGCATAATATTCTAAATGAAGACATTTCAAGCTATACAAATTACTTCCAA
GTTTTTCATGATGTATGGGAAGATTTTCAGTAGGTGATTATATTACCGGTACCAAATGCTGACCAGTGTGCTCC
ATTTTTTAAATCTTGAAAAGGGTTTCTGTACTTACCTGGTTTGCCAAGTATGCCAGTGTAAATGAACTGCCCTTA
TTTTAAAAGCCAGTCAAAGATTCCACTGATTGACATTTGATAAATAAACATCAGGATTATGTTTATTGTTTGT
TCAGTCTTTGCACTATATTACCAGTATATGGTTTCCGAGGAAGATTATCTACTGCAAAACACCAGTGTGAAAA
ATAGGTATTTTTAAATTGTTTTTAATCTTTTTTGGTGCTTTTAAACATGTTTAGCAAAAACCAATTCAGTTCCAT
TCCCCGAAAAAACCCCTAACTTTACTCTGAACTTTTTTTTGTTTTTGCATTCCATGAGGTTCTGTATTAGTCAT
TCTCTAGGTAATGTCAATTTTTGTACACATATATTTATATAATCACTGATTGAGATTTAGGAAAAAGCATTCTAA
AGAATATTTGCTTCCCTTAGAACTACAGACTCGAAATCTTTAAAGATGGTGCCTAAGCATCTATGTATTTTTTT
AAGTTCACAGATTTTTCTGTTGGGAGCAAGGATTATAAACCACTTCCCTAAAGGCAACATTAATGCAAAAGT
CCCCAGATGGCAATACAAAGTATCCCCTGGTACCACATATATTCATTTGTGAGTTTGGATATAGAGCACATTATC
TAAACCATTTTTGTAGTTCCAAAAACCCATCTAAATTTCTTGAGTTCTGAATTTTGAACAGGATTACCTGGAGCC
TGGAGCCACTTTAAGTTGTACTTCTGACTAACTGGAATTATGAGTGAGGAAGAGTGTACTAAATAAATGACT
GGGGCAAGCAAAATTGAGGAGGAAATTAGAACTGTTTGACAACTTTAAGAGCTACTTGAAATAACAGAAGTCT
TGATTAATATGCAATAATGGCTAGAAAGTATGGTTTAACTGGACCCTATTATGCCTTTTTAAAAATAATTCAGT
AACCATAAATACATGTTGTAAAAAATTCAAATATACAGAATGGAATAAAAAAATGATCTCCCTTTATTACCTC
CCAAAGGTTACCAGCGTTTGAATTTAATAATGTATATTCTTTCATGCTTTTTTCTGTGCACTTACCTAAGTGTGA
ATATGTAAAGGGTTTGTGTTGTATACAAATGGGATTATACTAAAATAAGTAATGCCTATTTTTAAGGATAGGTTA
AATTTGTGAATGATCATTTCAAATATATTGAATAAATAAGCAAAAGCTATTGTTATTTACTGATCCTG

1622/6881
FIGURE 1501

MADKLTRIAIVNHDKCKPKKCRQECKKSCPVVVMGKLCIEVTPQSKIAWISSETLCIGCGICIKKCPFGALSIVNL
PSNLEKETTHRYCANAFKLHRLPIPRPGEVLGLVGTNGIGKSTALKILAGKQKPNLGKYDDPPDWQEILTYFRGS
ELQNYFTKILEDDLKAI IKPQYVDQIPKAAKGTVGSILDRKDETKTQAIVCQQLDLTHLKERNVEDLSGGELQRF
ACAVVCIQKADIFMFDEPSSYLDVKQRLKAAITIRSLINPDRIIIVVEHDLVLDYLSDFICCLYGVP SAYGVVT
MPFSVREGINIFLDGYVPTENLRFRDASLVFKVAETANEEEVKKMCMYKYPGMKKKMGEFELAI VAGEFTDSEIM
VMLGENGTGKTTFIRMLAGRLKPDEGGEVPVLNVSYKPQKISPKSTGSVRQLLHEKIRDAYTHPQFVTDVMKPLQ
IENIIDQEVQTL SGGELQ RVALALCLGKPADVYLIDEPSAYLDSEQRLMAARVVKR FILHAKKTAFVVEHDFIMA
TYLADRVIVFDGVP SKNTVANS PQTLLAGMNKFLSQLEITFRRD PNNYRPRINKLNSIKDVEQKKSGNYFFLDD

1623/6881
FIGURE 1502

AGGAAATGAGGCTGAACCTTTGTAGTGCCCTCGCTAACCTTCAGACCAGTAAACCAGATGCTGTAGAGCAGACATG
TATATTGGAATCTACAGAAATTGCTTTGCTTAACAACATCCCATATCATGAAGGCTTTAAAATGGCAATGAGCAA
AGTTTTGTCTTCACTGACTCCAGAGAACTGTATCAGACCATGGATACTCACTGTCAGAATGAGATGAGCTCTGG
AACTGGACAGAGTAATACTGTACAGAACATCCTTGAACCTTTCTACGTGTTAGATGTGTCCGAAGGCTTCTCTGT
TCTGCCTGTTATTGCTGGCACACTTGGGCAGGTTAAACCATACAGTTCTGTGGAGAAAGACCAGCATCGTATTGC
TCTGGACCTCATATCTGAAGCCAATCACTTTCTTAAAGAAACACTTGAGTTTTGGCTGAGACATGTGGAGGATGA
ATCTGCTATGTTACAAAGGCCAAAATCAGACAAGTTATGGAGCATAATTATATTGGATGTCATTGAGCCATCTGG
GCTCATTGAGCAGGAAATAATGGAAAAAGCTGCAATATCCAGGTGTTTACTACAATCTGGAGGCAAGATCTTCC
TCAGTATGTGCTGATGTTTGGGTTGCTTGTGGAATCACAGACACTCCTAGAGGAGAATGCTGTTCAAGGAACAGA
ACGTACTCTTGGATTAAATATAGCACCTTTTATTAACCAGTTTCAGGTACCTATACGTGTATTTTTGGACCTATC
CTCATTGCCCTGTATACCTTTAAGCAAGCCAGTGGAACCTTAAAGACTAGATTTAATGACTCCGTATTTGAACAC
CTCTAACAGAGAAGTAAAGGTATACGTTTGTAAATCTGGAAGACTGACTGCTATTCCATTTTGGTATCATATGTA
CCTTGATGAAGAGATTAGGTTGGATACTTCAAGTGAAGCCTCCCACTGGAAACAAGCTGCAGTTGTTTTAGATAA
TCCCATCCAGGTTGAAATGGGAGAGGAACCTTGTACTCAGCATTGAGCATCACAAAAGCAATGTCAGCATCACAGT
AAAGCAATGAAGAGCAGTTTTTCCAATGAAAACCTGTGTAAATAGAGCATCAACAAGTACAAAATTCTTGTCTTAAT
TAGTGGGGGTATATAAAAATTCCTTGTAATGGTCAAAATATTTTTTAAAATTGACATTAATAAAGCATATTTTAA
AGATTCTAAATAAAAAGGGTAGCATTATTATAGAAAATACTGCTGCAGATTTGCTTTCTGGAAAAGGATACATCACT
AGTTTTTTTAAATTAGGAACTTCTTTTGTGCTCGATTTTACAGAATAGGGATTTTAAAAGTCTTATCGTTATTGACA
TGTGTAAGTAAAGCAAAACCTTTACTTTTGTAGGCATCTTGGCCTTTTTTCTTAAATCCAAACTTGTAATTGGGAA
ACACTGAAAGGCTTCCACTGAAGACTGAGGGTTATGGTTACCTGTAAATTCCAATCTTGCTTCCTTTAAATACTC
AGTGTACATCTGAAACATCTCAGGTTTTGTTTTGAGAATGCAAGCTTGAAAAAGAATTTAAGCTATAAGCTAAAT
GTAATTTAAACAGTAAAGGAGTTAGGGAATACATCTTCAGGAGGCAGCATTTTTCTTGGTCTACTTTGGCAAAAG
AACATTTAAAAGCTGGTAACAAAACAAAGTTAAATTGAAGGAAGACTTAATCCTATACTATTTTTCAAAGTTTTG
ATTTGGATGTACAATAAGTACATTAATTGATCCAATTTTTACAACTTTTGAAATAAAGGAAGATCATTATTATG
CCTCCT

1624/6881
FIGURE 1503

MAMSKVLSSLTPEKLYQTMDTHCQNEMSSGTGQSNTVQNILEPFYVLDVSEGFSVLPVIAGTLGQVKPYSSVEKD
QHRIALDLISEANHFPKETLEFWLRHVEDESAMLQRPKSDKLWSIIILDVIEPSGLIQQEIMEKAAISRCLLQSG
GKIFPQYVLMFGLLVESQTLLEENAVQGTERTLGLNIAPFINQFQVPIRVFLDLSSLPCIPLSKPVELLRLDLMT
PYLNTSNREVKVYVCKSGRLTAIPFWYHMYLDEEIRLDTSSEASHWKQAAVVDNPIQVEMGEELVLSIQHHKSN
VSITVKQ

[illegible]

1626/6881
FIGURE 1505

MIAAQAKLVYQLNKYYTERCQARKAAIAKTIREVCKVVSDVLKEVEVQEPRFISSLSEIDARYEGLEVISPTFE
VVLYLNQMGVFNFDGSLPGCAVLKLSGGRKRSMSLWVEFITASGYLSARKIRSRFQTLVAQAVDKCSYRDVVK
MIADTSEVKLRIRERYVVQITPAFKCTGIWPRSAAQWPMHIPWPGPNRVAEVKAEGFNLLSKECYSLTGKQSSA
ESDAWVLQFGAENRLLMGGCRNKCLSVLKTLLRDRHLELPGQPLNNYHMKTLLLYECEKHPRETDWDESCLGDR
NGILLQLISCLQCRRCPHYFLPNLDFQGKPHSALESAAKQTWRLAREILTNPKSLDKL

1627/6881
FIGURE 1506

CGCGACTCCCACTTCCGCCCTTTTGGCTCTCTGACCAGCACCATGGCGGTTGGCAAGAACAAGCGCCTTACGAAA
GGCGGCAAAAAGGGAGCCAAGAAGAAAGTGTTGATCCATTTTCTAAGAAAGATTGGTATGATGTGAAAGCACCT
GCTATGTTCAATATAAGAAATATTGGAAAGACGCTCGTCACCAGGACCCAAGGAACCAAAATTGCATCTGATGGT
CTCAAGGGTCGTGTGTTTGAAGTGAGTCTTGCTGATTTGCAGAATGATGAAGTTGCATTTAGAAAATTCAAGCTG
ATTACTGAAGATGTTTCAAGGGTAAAACTGCCTGACTAACTTCCATGGCATGGATCTTACCCGTGACAAAATGTGT
TCCATGGTCAAAAAATGGCAGACAATGATTGAAGCTCACGTTGATGTCAAGACTACCGATGGTTACTTGCTTCGT
CTGTTCTGTGTTGGTTTTACTAAAAACGCAACAATCAGATACGGAAGACCTCTTATGCTCAGCACCAACAGGTC
CGCCAAATCCGGAAGAAGATGATGGAATCATGACCCGAGAGGTGCAGACAAATGACTTGAAAGAAGTGGTCAAT
AAATTGATTCCAGACAGCATTGGAAAAGACATAGAAAAGGCTTGCCAATCTATTTATCCTCTCCATGATGTCTTC
GTTAGAAAAGTAAAAATGCTGAAGAAGCCCAAGTTTGAATTGGGAAAGCTCATGGAGCTTCATGGTGAAGGCAGT
AGTTCTGGAAAAGCCACTGGGGACGAGACAGGTGCTAAAGTTGAACGAGCTGATGGATATGAACCACCAGTCCAA
GAATCTGTTTTAAAGTTCAGACTTCAAATAGTGGCAAATAAAAAGTGCTATTTGTGATGGTTTGCTTCTGAAAAAA
AAAAAAAAAAAAAAAAAAAAA

1628/6881
FIGURE 1507

MAVGKNKRLTKGGKKGAKKKVVDPFSSKDWYDVKAPAMFNIRNIGKTLVTRTQGTKIASDGLKGRVFEVSLADLQ
NDEVAFRKFKLITEDVQGKNCLTNFHGMDLTRDKMCSMVKKWQTMIEAHVDVKTTDGYLLRLFCVGFTKKRNNQI
RKTSYAQHQQVRQIRKKMMEIMTREVQTNDLKEVVNKLIPDSIGKDIEKACQSIYPLHDVFVRKVKMLKKPKFEL
GKLMELHGEGSSSGKATGDETGAKVERADGYEPPVQESV

1629/6881
FIGURE 1508

AAGTCTAC**ATG**AAAAGGATGGTTTCTTGAGCTTCCACAAACTTAAAACCATGAAACATCTATTATTGCTACTAT
TGTGTGTTTTTCTAGTTAAGTCCCAAGGTGTCAACGACAATGAGGAGGGTTTCTTCAGTGCCCGTGGTCATCGAC
CCCTTGACAAGAAGAGAGAAGAGGCTCCCAGCCTGAGGCCTGCCCCACCGCCCATCAGTGGAGGTGGCTATCGGG
CTCGTCCAGCCAAAGCAGCTGCCACTCAAAGAAAGTAGAAAGAAAGCCCCCTGATGCTGGAGGCTGTCTTCAGC
CTGACCCAGACCTGGGGGTGTTGTGTCTACAGGATGTCAGTTGCAAGAGGCTTTGCTACAACAGGAAAGGCCAA
TCAGAAATAGTGTTGATGAGTTAAATAACAATGTGGAAGCTGTTTCCAGACCTCCTCTTCTTCTTCAGTACA
TGTATTTGCTGAAAGACCTGTGGCAAAAGAGGCAGAAGCAAGTAAAGATAATGAAAATGTAGTCAATGAGTACT
CCTCAGAACTGGAAAAGCACCAATTATATATAGATGAGACTGTGAATAGCAATATCGCAACTAACCTTCGTGTGC
TTCGTTCAATCCTAGAAAACCTGAGAAGCAAAATACAAAAGTTAGAATCTGATGTCTCAGCTCAAATGGAATATT
GTCGCACCCCATGCACTGTCAAGTATTCCTGTGGTGTCTGGCAAAGAATGTGAGGAAATTATCAGGAAAG
GAGGTGAAACATCTGAAATGTATCTCATTCAACCTGACAGTTCTGTCAAACCGTATAGAGTATACTGTGACATGA
ATACAGAAAATGGAGGATGGACAGTGATTGAGAACCCTCAAGACGGTAGTGTTGACTTTGGCAGGAAATGGGATC
CATATAAACAGGGATTTGGAAATGTTGCAACCAACACAGATGGGAAGAATTACTGTGGCCTACCAGGTGAATATT
GGCTTGGAATGATAAAATTAGCCAGCTTACCAGGATGGGACCCACAGAACTTTTGATAGAAATGGAGGACTGGA
AAGGAGACAAAGTAAAGGCTCACTATGGAGGATTCACTGTACAGAATGAAGCCAACAAATACCAGATCTCAGTGA
ACAAATACAGAGGAACAGCCGGTAATGCCCTCATGGATGGAGCATCTCAGCTGATGGGAGAAAACAGGACCATGA
CCATTACAAACGGCATGTTCTTCAGCACGTATGACAGAGACAATGACGGCTGGTTAACATCAGATCCCAGAAAAC
AGTGTTCATAAAGACGGTGGTGGATGGTGGTATAATAGATGTCATGCAGCCAATCCAAACGGCAGATACTACT
GGGGTGGACAGTACACCTGGGACATGGCAAAGCATGGCACAGATGATGGTGTAGTATGGATGAATTGGAAGGGGT
CATGGTACTCAATGAGGAAGATGAGTATGAAGATCAGGCCCTTCTTCCCACAGCAAT**TAGT**CCCCAATACGTAGAT
TTTTGCTCTTCTGTATGTGACAACATTTTTGTACATTATGTTATTGGAATTTTCTTTTCATACATTATATTCTCT
AAAACCTCTCAAGCAGACGTGAGTGTGACTTTTTGAAAAAGTATAGGATAAATTACATTAAAAATAGCACATGATT
TTCTTTTGTTTTCTTCATTTCTTTGCTCACCAAGAAGTAACAAAAGTATAGTTTTGACAGAGTTGGTGTTTATA
ATTTAGTTCTAGTTGATTGCGAGAATTTTCAAATAAGGAAGAGGGGTCTTTTATCCTTGTCGTAGGAAAACCAT
GACGGAAAGGAAAACTGATGTTTAAAGTCCACTTTTAAACTATATTTATTTATGTAGGATCTGTCAAAGAAA
ACTTCCAAAAAGATTTATTAATTAACCAGACTCTGTTGCAAT

1630/6881
FIGURE 1509

MKRMVSWSFHKLKTMKHL L L L L L L L L C V F L V K S Q G V N D N E E G F F S A R G H R P L D K K R E E A P S L R P A P P P I S G G G Y R A R P
A K A A A T Q K K V E R K A P D A G G C L H A D P D L G V L C P T G C Q L Q E A L L Q Q E R P I R N S V D E L N N N V E A V S Q T S S S S F Q Y M Y L
L K D L W Q K R Q K Q V K D N E N V V N E Y S S E L E K H Q L Y I D E T V N S N I A T N L R V L R S I L E N L R S K I Q K L E S D V S A Q M E Y C R T
P C T V S C N I P V V S G K E C E E I I R K G G E T S E M Y L I Q P D S S V K P Y R V Y C D M N T E N G G W T V I Q N R Q D G S V D F G R K W D P Y K
Q G F G N V A T N T D G K N Y C G L P G E Y W L G N D K I S Q L T R M G P T E L L I E M E D W K G D K V K A H Y G G F T V Q N E A N K Y Q I S V N K Y
R G T A G N A L M D G A S Q L M G E N R T M T I H N G M F F S T Y D R D N D G W L T S D P R K Q C S K E D G G G W W Y N R C H A A N P N G R Y Y W G G
Q Y T W D M A K H G T D D G V V W M N W K G S W Y S M R K M S M K I R P F F P Q Q

1631/6881
FIGURE 1510

CTACATGAAAAGGATGGTTTCTTGGAGCTTCCACAACTTAAAACCATGAAACATCTATTATTGCTACTATTGTG
TGTTTTTCTAGTTAAGTCCCAAGGTGTCAACGACAATGAGGAGGTGAATTTTTTAAAGCATTATTATATTATTAG
TAGTATTATTAATATAAGATGTAAACATAATCATATTATGTGCTTATTTTAATGAAATTAGCATTGCTTATAGTTA
TGAAATGGAATTGTTAACCTCTGACTTATTGTATTTAAAGAATGTTTCATAGTATTTCTTATATAAGATGGCTTA
GCTAATGTAAGATGTGTTTTTCTCACTTGCTATTCTGAGTACTGTGATTTTCATTTACTTCTAGCAATACAGG

1632/6881
FIGURE 1511A

GTCTAGGAGCCAGCCCCACCCTTAGAAAAGATGTTTTCCATGAGGATCGTCTGCCTAGTTCTAAGTGTGGTGGGC
ACAGCATGGACTGCAGATAGTGGTGAAGGTGACTTTCTAGCTGAAGGAGGAGGCGTGCCTGGCCCAAGGGTTGTG
GAAAGACATCAATCTGCCTGCAAAGATTGAGACTGGCCCTTCTGCTCTGATGAAGACTGGAAGTACAAATGCCCT
TCTGGCTGCAGGATGAAAGGGTTGATTGATGAAGTCAATCAAGATTTTACAAACAGAATAAATAAGCTCAAAAAT
TCACTATTTGAATATCAGAAGAACAATAAGGATTCTCATTCGTTGACCACTAATATAATGGAATTTTGAGAGGC
GATTTTTCTCTCAGCCAATAACCGTGATAATACCTACAACCGAGTGTGAGAGGATCTGAGAAGCAGAATTGAAGTC
CTGAAGCGCAAAGTCATAGAAAAAGTACAGCATATCCAGCTTCTGCAGAAAAATGTTAGAGCTCAGTTGGTTGAT
ATGAAACGACTGGAGGTGGACATTGATATTAAGATCCGATCTTGTGCGAGGGTCATGCAGTAGGGCTTTAGCTCGT
GAAGTAGATCTGAAGGACTATGAAGATCAGCAGAAGCAACTTGAACAGGTCATTGCCAAAGACTTACTTCCCTCT
AGAGATAGGCAACACTTACCCTGATAAAAATGAAACAGTTCAGACTTGGTTCCCGGAAATTTTAAGAGCCAG
CTTCAGAAGGTACCCCCAGAGTGAAGGCATTAACAGACATGCCGCAGATGAGAATGGAGTTAGAGAGACCTGGT
GGAAATGAGATTACTCGAGGAGGCTCCACCTCTTATGGAACCGGATCAGAGACGGAAAGCCCCAGGAACCCTAGC
AGTGCTGGAAGCTGGAACCTCTGGGAGCTCTGGACCTGGAAGTACTGGAACCGAAACCCTGGGAGCTCTGGGACT
GGAGGGACTGCAACCTGGAACCTGGGAGCTCTGGACCTGGAAGTACTGGAAGCTGGAACCTCTGGGAGCTCTGGA
ACTGGAAGTACTGGAACCAAAACCCTGGGAGCCCTAGACCTGGTAGTACCGGAACCTGGAATCCTGGCAGCTCT
GAACGCGGAAGTGCTGGGCACTGGACCTCTGAGAGCTCTGTATCTGGTAGTACTGGACAATGGCACTCTGAATCT
GGAAGTTTTAGGCCAGATAGCCCAGGCTCTGGGAACGCGAGGCTTAACAACCCAGACTGGGGCACATTTGAAGAG
GTGTCAGGAAATGTAAGTCCAGGGACAAGGAGAGAGTACCACACAGAAAACTGGTCACTTCTAAAGGAGATAAA
GAGCTCAGGACTGGTAAAGAGAAGGTCACCTCTGGTAGCACAACCACCACGCGTCGTTTCATGCTCTAAAACCGTT
ACTAAGACTGTTATTGGTCCTGATGGTCACAAAGAAGTTACCAAAGAAGTGGTGACCTCCGAAGATGGTTCTGAC
TGTCCCGAGGCAATGGATTTAGGCACATTGTCTGGCATAGGTACTCTGGATGGGTTCCGCCATAGGCACCCCTGAT
GAAGCTGCCTTCTTCGACACTGCCTCAACTGGA AAAACATTCCCAGGTTTCTTCTCACCTATGTTAGGAGAGTTT
GTCAGTGAGACTGAGTCTAGGGGCTCAGAATCTGGCATCTTCACAAATACAAAGGAATCCAGTTCTCATCACCT
GGGATAGCTGAATTCCTTCCCGTGGTAAATCTTCAAGTTACAGCAAACAATTTACTAGTAGCACGAGTTACAAC
AGAGGAGACTCCACATTTGAAAGCAAGAGCTATAAAATGGCAGATGAGGCCGGAAGTGAAGCCGATCATGAAGGA
ACACATAGCACCAAGAGAGGCCATGCTAAATCTCGCCCTGTCAGAGACTGTGATGATGTCTCCAAACACATCCT
TCAGGTACCCAAAGTGGCATTTCATATCAAGCTACCGGGATCCAGTAAGATTTTTCTGTTTATTGCGATCAA
GAGACCAGTTTGGGAGGATGGCTTTTGATCCAGCAAAGAATGGATGGATCACTGAATTTTAACCGGACCTGGCAA
GACTACAAGAGAGGTTTCCGGCAGCCTGAATGACGAGGGGGAAGGAGAATTCTGGCTAGGCAATGACTACCTCCAC
TTACTAACCCAAAGGGGCTCTGTTCTTAGGGTTGAATTAGAGGACTGGGCTGGGAATGAAGCTTATGCAGAATAT
CACTTCCGGGTAGGCTCTGAGGCTGAAGGCTATGCCCTCCAAGTCTCCTCCTATGAAGGCACTGCGGGTGATGCT
CTGATTGAGGGTTCCGTAGAGGAAGGGGCAGAGTACACCTCTCACAACAACATGCAGTTTCAGCACCTTTGACAGG
GATGCAGACCAGTGGGAAGAGAAGTGTGCAGAAGTCTATGGGGGAGGCTGGTGGTATAATAACTGCCAAGCAGCC
AATCTCAATGGAATCTACTACCCTGGGGGCTCCTATGACCCAAGGAATAACAGTCCTTATGAGATTGAGAAATGGA
GTGGTCTGGGTTTCTTTAGAGGGGCAGATTATTCCTCAGGGCTGTTTCGCATGAAAATTAGGCCCTTGTGACC
CAATAGGCTGAAGAAGTGGGAATGGGAGCACTCTGTCTTCTTTGCTAGAGAAGTGGAGAGAAAATACAAAAGGTA
AAGCAGTTGAGATTCTCTACAACCTAAAAAATTCCTAGGTGCTATTTTCTTATCCTTTGTACTGTAGCTAAATGT
ACCTGAGACATATTAGTCTTTGAAAAATAAAGTTATGTAAGGTTTTTTTTATCTTTAAATAGCTCTGTGGGTTTT
AACATTTTTGTAAAGATATACCAAGGGCCATTGAGTACATCAGGAAAGTGGCAGACAGAAGCTTCTCTCTGCAAC
CTTGAAGACTATTGGTTTGAGAACTTCTCTTCCCATACCAACCCAAAATCATAATGCCATTGGAAAGCAAAAAGTT
GTTTTATCCATTTGATTTGAATTGTTTTAAGCCAATATTTAAGGTAAAACCTCACTGAATCTAACCATAGCTGAC
CTTTGTAGTAGAATTTACAACCTTATAATTACAATGCACAATTTATAATTACAATATGTATTTATGTCTTTTGCTA
TGGAGCAAATCCAGGAAGGCAAGAGAAACATTCTTTCTAAATATAAATGAAAATCTATCCTTTAAACTCTTCCA
CTAGACGTTGTAATGCACACTTATTTTTTTCCCAAGGAGTAACCAATTTCTTTCTAAAACACATTTAAATTTTA
AAACTATTTATGAATATTAAAAAAGACATAATTCACACATTAATAACAATCTCCCAAGTATTGATTTAACTTC
ATTTTTCTAATAATCATAACTATATTCTGTGACATGCTAATTATTATTAATGTAAGTCGTTAGTTTCGAAAGCC
TCTCACTAAGTATGATCTATGCTATATTCAAATTCACCCATTTACTTTGGTCAATATTTGATCTAAGTTGCAT
CTTTAATCCTGGTGGTCTTGCCTTCTGATTTTTAATTTGTATCCTTTCTATTAAAGATATATTTGTCAATTTCTC

1633/6881
FIGURE 1511B

TTGAATATGTATTAAAATATCCCAAGC

1634/6881
FIGURE 1512

MFSMRIVCLVLSVVGTAWTADSGEGDFLAEGGGVRGPRVVERHQSAACKDSDWPFCSDEDWNYKCPSGCRMKGLID
EVNQDFTNRINKLKNSLFQKNNKDSHSLTTNIMEILRGDFSSANNRDNTYNRVSEDLRSRIEVLKRKVIEKVQ
HIQLLQKNVRAQLVDMKRLEVDIDIKIRSCRGSCSRALAREVDLKDYEDQOKQLEQVIAKDLLPSRDRQHPLIK
MKPVVDLVPGNFKSQLQKVPPEWKALTDMPQMRMELERPGGNEITRGGSTSYGTGSETESPRNPSSAGSWNSGSS
GPGSTGNRNPGSSGTGGTATWKPGSSGPGSTGSWNSGSSGTGSTGNQNPSPRPGSTGTWNPGSSERGSAGHWT
ESSVSGSTGQWHSESGSFRPDSPGSGNARPNPDWGTFFEEVSGNVSPGTRREYHTEKLVTSKGDKELRGKEKVT
SGSTTTTTRRSCSKTVTKTVIGPDGHKEVTKEVVTSEDGSDCPEAMD LGT LSGIGTLDGFRHRHPDEAAFFDTAST
GKTFPGFFSPMLGEFVSETESRGSESGIFTNTKESSSHHPGIAEFPSRGKSSSYSKQFTSSTS YNRGDSTFESKS
YKMADEAGSEADHEGTHSTKRGHAKSRPVRDCDDVLQTHPSGTQSGIFNIKLPGSSKIFSVYCDQETSLGGWLLI
QQRMDGSLNFNRTWQDYKRGFGSLNDEGEGEFWLGNDYLHLLTQRGSVLRVELEDWAGNEAYA EYHFRVGSEAEG
YALQVSSYEGTAGDALIEGSVEEGA EYTSHNNMQFSTFDRDADQWEENCAEVYGGGWYNNCQAANLNGIYYPGG
SYDPRNNSPYEIEENGVVWVSFRGADYSLRAVRMKIRPLVTQ

1635/6881
FIGURE 1513

GTCTAGGAGCCAGCCCCACCCTTAGAAAAAGATGTTTTCCATGAGGATCGTCTGCCTAGTTCTAAGTGTGGTGGGC
ACAGCATGGACTGCAGATAGTGGTGAAGGTGACTTTCTAGCTGAAGGAGGAGGCGTGCGTGGCCCAAGGGTTGTG
GAAAGACATCAATCTGCCTGCAAAGATTGAGACTGGCCCTTCTGCTCTGATGAAGACTGGAATAAAATGCCCT
TCTGGCTGCAGGATGAAAAGGTTGATTGATGAAGTCAATCAAGATTTTACAAACAGAATAAATAAGCTCAAAAAAT
TCACTATTTGAATATCAGAAGAACAATAAGGATTCTCATTGCGTTGACCACTAATATAATGGAAATTTTGAGAGGC
GATTTTTCTCAGCCAATAACCGTGATAATACCTACAACCGAGTGTGAGAGGATCTGAGAAGCAGAATTGAAGTC
CTGAAGCGCAAAGTCATAGAAAAAGTACAGCATATCCAGCTTCTGCAGAAAAATGTTAGAGCTCAGTTGGTTGAT
ATGAAACGACTGGAGGTGGACATTGATATTAAGATCCGATCTTGTGAGGGTCATGCAGTAGGGCTTTAGCTCGT
GAAGTAGATCTGAAGGACTATGAAGATCAGCAGAAGCAACTTGAACAGGTCATTGCCAAAGACTTACTTCCCTCT
AGAGATAGGCAACACTTACCACTGATAAAAAATGAAACCAGTTCCAGACTTGGTTCCCGGAAATTTTAAGAGCCAG
CTTCAGAAGGTACCCCCAGAGTGGAAAGGCATTAAACAGACATGCCGCAGATGAGAATGGAGTTAGAGAGACCTGGT
GGAAATGAGATTACTCGAGGAGGCTCCACCTCTTATGGAACCGGATCAGAGACGGAAAGCCCCAGGAACCCCTAGC
AGTGCTGGAAGCTGGAACCTCTGGGAGCTCTGGACCTGGAAGTACTGGAAGCTGGAACCTCTGGGAGCTCTGGGACT
GGAGGGACTGCAACCTGGAACCTGGGAGCTCTGGACCTGGAAGTACTGGAAGCTGGAACCTCTGGGAGCTCTGGA
ACTGGAAGTACTGGAACCAAAACCCCTGGGAGCCCTAGACCTGGTAGTACCGGAACCTGGAATCCTGGCAGCTCT
GAACGCGGAAGTGCTGGGCACTGGACCTCTGAGAGCTCTGTATCTGGTAGTACTGGACAATGGCACTCTGAATCT
GGAAGTTTTAGGCCAGATAGCCCAGGCTCTGGGAACGCGAGGCCTAACCAACCCAGACTGGGGCACATTTGAAGAG
GTGTCAGGAAATGTAAGTCCAGGGACAAGGAGAGAGTACCACACAGAAAAACTGGTCACTTCTAAAGGAGATAAA
GAGCTCAGGACTGGTAAAAGAGAAGGTCACCTCTGGTAGCACAAACCACCACGCGTCGTTTCATGCTCTAAAACCGTT
ACTAAGACTGTTATTGGTCTGATGGTCACAAAGAAGTTACCAAGAAGTGGTGACCTCCGAAGATGGTTCTGAC
TGTCCCAGGCAATGGATTTAGGCACATTGTCTGGCATAGGTACTCTGGATGGGTTCCGCCATAGGCACCCCTGAT
GAAGCTGCCTTCTTCGACACTGCCTCAACTGGAAAAACATTCCAGGTTTCTTCTCACCTATGTTAGGAGAGTTT
GTCAGTGAGACTGAGTCTAGGGGCTCAGAATCTGGCATCTTCACAAATACAAAGGAATCCAGTTCTCATCACCCCT
GGGATAGCTGAATTTCCCTTCCCGTGGTAAATCTTCAAGTTACAGCAAAACAATTTACTAGTAGCACGAGTTACAAC
AGAGGAGACTCCACATTTGAAAGCAAGAGCTATAAAATGGCAGATGAGGCCGGAAGTGAAGCCGATCATGAAGGA
ACACATAGCACCAAGAGAGGCCATGCTAAATCTCGCCCTGTGAGAGGTATCCACACTTCTCCTTTGGGGGAAGCCT
TCCCTGTCCCCCTAGACTAAGTTAAATATTTCTGCACAGTGTTCCTATGGCCCTTGCATTTCTTCTTAACTCT
CTGTTACACGTCATTGAAACTACACTTTTTTGGTCTGTTTTTGTGCTAGACTGTAAGTTCCTTGGGGGCAGGGCC
TTTGTCTGTCTCATCTCTGTATTCCCAAATGCCTAACAGTACAGAGCCATGACTCAATAAATACATGTTAAATGG
ATGAATG

1636/6881
FIGURE 1514

MF SMRIVCLVLSVVGTAWTADSGEGDFLAEGGGVRGPRVVERHQSACKDS DWPFCSDEDWNYKCP SGCRMKGLID
EVNQDFTNRINKLKNSLF EYQKNNKDSHSLTTNIMEILRGDFSSANNRDNTYNRVSEDLRSRIEVLKRKVIEKVQ
HIQLLQKNVRAQLVDMKRLEVDIDIKIRSCRGSCSRALAREVDLKDYEDQQKQLEQVIAKDLLPSRDRQHLP LK
MKPV PDLVPGNFKSQLQKVPEWKALTDMPQMRMELERP GGNEITRGGSTSYGTGSETESPRNPSSAGSWNSGSS
GPGSTGNRNPGSSGTGGTATWKPGSSGPGSTGSWNSGSSGTGSTGNQNP GS PRPGSTGTWNP GS SERGSAGHWT S
ESSVSGSTGQWHSESGSFRPDSPGSGNARPNPDWGTFFEEVSGNVSPGTRREYHTEKLVTSKGDKELRTGKEKVT
SGSTTTTTRRSCSKTVTKTVIGPDGHKEVTKEVVTSEDGSDCPEAMD LGT LSGIGTLDGFRHRHPDEAAFFDTAST
GKTFFPGFFSPMLGEFVSETESRGSESGIFTNTKESSSHHPGIAEFPSRGKSSSYSKQFTSSTS YNRGDSTFESKS
YKMADEAGSEADHEGTHSTKRGHAKSRPV RGIHTSPLGKPSLSP

'1637/6881
FIGURE 1515

TGCTGACACTACAAGGCTCGGAGCTCCGGGCACTCAGACATCATGAGTTGGTCCTTGCAACCCCGGAATTTAATT
CTCTACTTCTATGCTCTTTTATTTCTCTCTTCAACATGTGTAGCATATGTTGCTACCAGAGACAACCTGCTGCATC
TTAGATGAAAGATTTCGGTAGTTATTGTCCAACCTACCTGTGGCATTGCAGATTTCTGTCTACTTATCAAACCAAA
GTAGACAAGGATCTACAGTCTTTGGAAGACATCTTACATCAAGTTGAAAACAAAACATCAGAAGTCAAACAGCTG
ATAAAAGCAATCCAACCTCACTTATAATCCTGATGAATCATCAAAACCAAATATGATAGACGCTGCTACTTTGAAG
TCCAGGATAATGTTAGAAGAAATTATGAAATATGAAGCATCGATTTTAACACATGACTCAAGTATTCGATATTTG
CAGGAAATATATAATTCAAATAATCAAAGATTGTTAACCTGAAAGAGAAGGTAGCCCAGCTTGAAGCACAGTGC
CAGGAACCTTGCAAAGACACGGTGCAAATCCATGATATCACTGGGAAAGATTGTCAAGACATTGCCAATAAGGGA
GCTAAACAGAGCGGGCTTTACTTTATTAAACCTCTGAAAGCTAACCCAGCAATTCTTAGTCTACTGTGAAATCGAT
GGGTCTGGAAATGGATGGACTGTGTTTCAGAAGAGACTTGATGGCAGTGTAGATTTCAAGAAAACTGGATTCAA
TATAAAGAAGGATTTGGACATCTGTCTCCTACTGGCACAACAGAATTTTGGCTGGGAAATGAGAAGATTCATTG
ATAAGCACACAGTCTGCCATCCCATATGCATTAAAGAGTGGAAGTGGAAAGTGGAAATGGCAGAACCAGTACTGCA
GACTATGCCATGTTCAAGGTGGGACCTGAAGCTGACAAGTACCGCCTAACATATGCCTACTTCGCTGGTGGGGAT
GCTGGAGATGCCCTTTGATGGCTTTGATTTTGGCGATGATCCTAGTGACAAGTTTTTCACATCCCATAAATGGCATG
CAGTTCAGTACCTGGGACAATGACAATGATAAGTTTGAAGGCAACTGTGCTGAACAGGATGGATCTGGTTGGTGG
ATGAACAAGTGTCACGCTGGCCATCTCAATGGAGTTTATTACCAAGGTGGCACTTACTCAAAAGCATCTACTCCT
AATGGTTATGATAATGGCATTATTTGGGCCACTTGGAACCCGGTGGTATTCCATGAAGAAAACCACTATGAAG
ATAATCCCATTCAACAGACTCACAATTGGAGAAGGACAGCAACACCACCTGGGGGGAGCCAAACAGGCTGGAGAC
GTTTAAAGACCGTTTCAAAGAGATTTACTTTTTTAAAGGACTTTATCTGAACAGAGAGATATAATATTTTCC
TATTGGACAATGGACTTGCAAAGCTTCACTTCATTTTAAGAGCAAAAGACCCCATGTTGAAAACCTCCATAACAGT
TTTATGCTGATGATAATTTATCTACATGCATTTCAATAAACCTTTTGTTCCTAAGACT

1638/6881
FIGURE 1516

MSWSLHPRNLILYFYALLFLSSTCVAYVATRDNCCILDERFGSYCPTTCGIADFLSTYQTKVDKDLQSLEDILHQ
VENKTSEVKQLIKAIQLTYNPDESSKPNMIDAATLKSRIMLEEIMKYEASILTHDSSIRYLQEIYNSNNQKIVNL
KEKVAQLEAQCQEPCKDTVQIHDIITGKDCQDIANKGAKQSGLYFIKPLKANQQFLVYCEIDGSGNGWTVFQKRLD
GSVDFKKNWIQYKEGFGHLSPTGTTEFWLGNEKIHLISTQSAIPYALRVELEDWNGRTSTADYAMFKVGPEADKY
RLTYAYFAGGDAGDAFDGFDGDDPSDKFFTSHNGMQFSTWDNDNDKFEGNCAEQDGS GWWMNKCHAGHLNGVYY
QGGTYSKASTPNGYDNGI IWATWKTRWYSMKKTTMKIIPFNRLTIGEGQQHHLGGAKQAGDV

1639/6881
FIGURE 1517

TGCTGACACTACAAGGCTCGGAGCTCCGGGCACTCAGACATC**ATG**AGTTGGTCCTTGCACCCCCGGAATTTAATT
CTCTACTTCTATGCTCTTTTATTTCTCTCTTCAACATGTGTAGCATATGTTGCTACCAGAGACAACCTGCTGCATC
TTAGATGAAAGATTTCGGTAGTTATTGTCCAACCTACCTGTGGCATTGCAGATTTCTGTCTACTTATCAAACCAAA
GTAGACAAGGATCTACAGTCTTTGGAAGACATCTTACATCAAGTTGAAAAACAAACATCAGAAGTCAAACAGCTG
ATAAAAGCAATCCAACCTCACTTATAATCCTGATGAATCATCAAAACCAAAATATGATAGACGCTGCTACTTTGAAG
TCCAGGATAATGTTAGAAGAAATTATGAAATATGAAGCATCGATTTTAACACATGACTCAAGTATTCGATATTTG
CAGGAAATATATAATTCAAATAATCAAAAGATTGTTAACCTGAAAGAGAAGGTAGCCAGCTTGAAGCACAGTGC
CAGGAACCTTGCAAAGACACGGTGCAAATCCATGATATCACTGGGAAAGATTGTCAAGACATTGCCAATAAGGGA
GCTAAACAGAGCGGGCTTTACTTTATTAAACCTCTGAAAGCTAACCAGCAATTCCTAGTCTACTGTGAAATCGAT
GGGTCTGGAATGGATGGACTGTGTTTCAGAAGAGACTTGATGGCAGTGTAGATTTCAAGAAAACTGGATTCAA
TATAAAGAAGGATTTGGACATCTGTCTCCTACTGGCACAACAGAATTTTGGCTGGGAAATGAGAAGATTCATTTG
ATAAGCACACAGTCTGCCATCCCATATGCATTAAGAGTGGAACCTGGAAGACTGGAATGGCAGAACCAGTACTGCA
GACTATGCCATGTTCAAGGTGGGACCTGAAGCTGACAAGTACCGCCTAACATATGCCTACTTCGCTGGTGGGGAT
GCTGGAGATGCCTTTGATGGCTTTGATTTTGGCGATGATCCTAGTGACAAGTTTTTCACATCCCATAAATGGCATG
CAGTTCAGTACCTGGGACAATGACAATGATAAGTTTGAAGGCAACTGTGCTGAACAGGATGGATCTGGTTGGTGG
ATGAACAAGTGTACGCTGGCCATCTCAATGGAGTTTATTACCAAGGTGGCACTTACTCAAAGCATCTACTCCT
AATGGTTATGATAATGGCATTATTTGGGCCACTTGGAACCCCGGTGGTATTCCATGAAGAAAACCACTATGAAG
ATAATCCCATTCAACAGACTCACAATTGGAGAAGGACAGCAACACCACCTGGGGGGAGCCAAACAGGTCAGACCA
GAGCACCTGCGGAAACAGAATATGACTCACTTTACCCTGAGGATGATTTG**TAG**AAAAATTAAGTCTAACTTCTA
TTGACCCACAAAGTTTCAGAAATTCTCTGAAAGTTTCTTCCCTTTTTCTCTTACTATATTTATTGATTTCAAGTC
TTCTATTAAGGACATTTAGCCTTCAATGGAAATTAAGTCTATTTAGGACTGTATTTCCAAATTACTGATATCAG
AGTTATTTAAAAATTGTTTATTTGAGGAGATAACATTTCAACTTTGTTCCATAATATATAATAATAAATGATTG
ACTTT

1640/6881
FIGURE 1518

MSWSLHPRNLILYFYALLFLSSTCVAYVATRDNCCILDERFGSYCPTTCGIADFLSTYQTKVDKDLQSLEDILHQ
VENKTSEVKQLIKAIQLTYNPDESSKPNMIDAATLKSRIMLEEIMKYEASILTHDSSIRYLQEIYNSNNQKIVNL
KEKVAQLEAQCQEPCKDTVQIHDITGKDCQDIANKGAKQSGLYFIKPLKANQQFLVYCEIDGSGNGWTVFQKRLD
GSVDFKKNWIQYKEGFGHLSPTGTTEFWLGNEKIHLLISTQSAIPYALRVELEDWNGRTSTADYAMFKVGPEADKY
RLTYAYFAGGDAGDAFDGDFDGDDPSDKFFTSHNGMQFSTWDNDNDKFEGNCAEQDGSWWMNKCHAGHLNGVYY
QGGTYSKASTPNNGYDNGIIWATWKTRWYSMKKTTMKIIPFNRLTIGEGQQHHLGGAKQVRPEHPAETEDSLYPE
DDL

1641/6881
FIGURE 1519

AGCAGCCGCCGCCAGACAGCCGCCGCCACCCGTTGCGCCGTCCCCCTGCCGCATTACACAATGCAGCCTGCTTT
TGCAAAGTGGTACGATCGAAGGGACTGTGTCTTCACTGAATCTTGTGTTGAAGACAATAAGGATGTTAATGTAA
TTTTGAAAAATCCAACTTACATTCAGTTGTCTTGGAGGAAGTGATAATTTTAAGCATTAAATGAAATTGGTCT
TTTTTACTCTATTGATCCAAATGATTCCAAGCATAAAAGAACGGACAGATCAATTTTATGTTGTTTACGAAAAGG
AGAATCTGGCCAGTCATGGCCAAGGTTAACAAAAGAAAGGGCAAAGATGATGAACAACATGGGTGGGGATGAGGA
TGTAGATTTACCAGAAGTAGATGAAGCAGGTGATGATTCACAAGACAGTGATGATGAAAAAATGCCAGATCTGGA
GTAAGAAATATTTATCACCTGGATTTTGAGAAAGAAA

1642/6881
FIGURE 1520

ATGGTAACCAATGTCAACCAGAATACAAGTGGAGCTCTGTCTTTAAATCAACTGCCACACACTCACATGTCGAAG
ATCCAAATACCCCTTGCAAATGCCTATCCCATTGCCAACGCTGATGCCCAAGGATGCACACACTGGCTGCGTGGG
CTGCCCTCAGAAAAGATGTGCCCAGGAGGAAAATTACTCCTGGGCACCAAGTACAATTACAGTGGATCAGAGGATT
GCACTGAAAGAGGTGCAAGCTACCTGGTTACTTCACAAATATCTCTACCATACATACTATTATCGACTCAACATT
AGGGTTGTCTGTGCTCAGGACACCAGAGTAAATACTGCCCCAATTCCAGAGATGTACTCCTTCTACATGTGCCCA
TGCTTCAGGCCTGAGCTCCGTGGCTACTCCATGGACACATCACTTATCAAACACCAGTGCAACCACCACTGCAAG
CAAGCCAACAGGCCAGATTCAGTGCCAAGAGAGATTCTGGCAATCTTAGCAGAAGAACTCAACAAAAACAAAGCCC
ATCTGGACCAGAAATCCAGATGATATTACTAATGAGGAGTACAGAGAATTCTACAAGAGCTTGACTAATGACTGG
GAAGATCACTTAAAGAAAAAGAACAATATCAAATTGTATGTATGCAGAGTTTTTCATCACGGATAACTGTGAGGAG
CTAATCCCTGAATACCTGAACTTCATTAGAGTGCTGGTAGACTCGGAGGATCTCCCTCTAAATATTTCCCATAAG
ATGTTACAACAAAGCAAAATTTTGAAAGTTATCAGGAAGAATTTGGTCAAAAAATGCTTAGAACTCTTTACTGAA
CTGGCAGAAGATAAAGAGAACTACAAGAAGTTCTATGAGCAGTTCTCTGAAAACATAAAGCTTGGAATACATGAA
GACTCTCAAAATCAGAAGAAGCTTTCAGAGCTGTAAAGGTACTACACATCTGCCTCTGGTGATGAGATGGTTTCT
CTCAAGGACTACTGCACCAGAATAAGGAAAAC TAGAAATGAATCTTAA

1643/6881
FIGURE 1521

MVTNVNQNTSGALSINQLPHTHMSKIQIPLANAYPIANADAQGCTHWLRGLPSERCARGGKLLLTSTITVDQRI
ALKEVQATWLLHKYLYHTYYRLNIRVVCAQDTRVNTAPIPEMYSFYMCPCFRPELRGYSMDTSLIKHQCNHHCK
QANRPDSVPREILAILAEELNKTPIWTRNPDDITNEEYREFYKSLTNDWEDHLKKKNNIKLYVCRVFITDNCEE
LIPEYLNFIIRVLVDSEDLPLNISHKMLQQSKILKVIRKNLVKKCLELFTELAEDKENYKKFYEQFSENIKLGIHE
DSQNQKKLSELLRYYTSASGDEMVS�KDYCTRIRKTRNES

1644/6881
FIGURE 1522

GATGTGGCCCGTGGCCTAGCTCGTCAAGTTGCCGTGGCGCGGAGAACTCTGCAAAACAAGAGGCTGAGGATTGCG
TTAGAGATAAACCAGTTCACGCCGAGCCCCGTGAGGGAAGCGTCTCCGTTGGGTCCGGCCGCTCTGCGGGACTC
TGAGGAAAAGCTCGCACCAGGTGGACGCGGATCTGTCAAC**ATGGG**TAAAGGAGACCCCAACAAGCCGCGGGGCAA
AATGTCTCTCGTACGCCTTCTTCGTGCAGACCTGCCGGGAAGAGCACAGAAGAAACACCCGGACTCTTCCGTCAA
TTTCGCGGAATTCTCCAAGAAGTGTTCCGAGAGATGGAAGACCATGTCTGCAAAGGAGAAGTCGAAGTTTGAAGA
TATGGCAAAAAGTGACAAAGCTCGCTATGACAGGGAGATGAAAAATTACGTTCCCTCCCAAGGTGATAAGAAGGG
GAAGAAAAAGGACCCCAATGCTCCTAAAAGGCCACCATCTGCCTTCTTCCTGTTTTGCTCTGAACATCGCCCCAA
GATCAAAAGTGAACACCCTGGCCTATCCATTGGGGATACTGCAAAGAAATTGGGTGAAATGTGGTCTGAGCAGTC
AGCCAAAGATAAAACAACCATATGAACAGAAAGCAGCTAAGCTAAAGGAGAAATATGAAAAGGATATTGCTGCATA
TCGTGCCAAGGGCAAAAAGTGAAGCAGGAAGAAGGGCCCTGGCAGGCCAACAGGCTCAAAGAAGAAGAACGAACC
AGAAGATGAGGAGGAGGAGGAGGAAGAAGAAGATGAAGATGAGGAGGAAGAGGATGAAGATGAAGAA**TAA**ATGGC
TATCCTTTAATGATGCGTGTGGAATGTGTGTGTGTGCTCAGGCAATTATTTTGCTAAGAATGTGAATTCAAGTGC
AGCTCAATACTAGCTTCAGTATAAAAAGTGTACAGATTTTGTATAGCTGATAAGATTCTCTGTAGAGAAAATAC
TTTTAAAAAATGCAGGTTGTAGCTTTTTGATGGGCTACTCATACAGTTAGATTTTACAGCTTCTGATGTTGAATG
TTCCTAAATATTTAATGGTTTTTTTTAATTTCTGTGTGTATGGTAGCACAGCAAACCTTGTAGGAATTAGTATCAAT
AGTAAATTTTGGGTTTTTTAGGATGTTGCATTTTCGTTTTTTAAAAAAAATTTTGTAAATAAAATTATGTATATTA
TTTCTATTGTCTTTGTCTTAATATGCTAAGTTAATTTTCACTTTAAAAAAGCCATTTGAAGACCAAAAAAAAAA
AA

1645/6881
FIGURE 1523

MGKGDPNKPRGKMSSYAFFVQTCREEHKKKHPDSSVNFAEF'SKKCSERWKTMSAKEKSKFEDMAKSDKARYDREM
KNYVPPKGDKKGKKKDPNAPKRPPSAFFLFCSEHRPKIKSEHPGLSIGDTAKKLGEMWSEQSAKDKQPYEQKAAK
LKEKYEKDIAAYRAKGKSEAGKKGPGRPTGSKKKNEPEDEEEEEEEEEDEEEEEDEDEE

1646/6881
FIGURE 1524

CAGCCCCCTCTGCGGCTGCCGGGCGGGCCCCGGGCGCCCCGGGGGCTGGGGGGTGGGGGGTGGGGGAGGACGCCGAG
CGCTGAGGCAGGGGCCCCGGGCCGAGGGCGCGGCGGGGCTGCGCGCACGCTGGGGCGCGTGGAGGGGCGCGGAGGG
CGAAATGAGTCTGGTAGGTGGTTTTTCCCCACCACCCGGTGGTGCACCACGAGGGCTACCCGTTTGCCGCCGCCGC
CGCCGCAGCTGCCGCCGCCGCCGCCAGCCGCTGCAGCCATGAGGAGAACCCCTACTTCCATGGCTGGCTCATCGG
CCACCCCGAGATGTCGCCCCCGACTACAGCATGGCCCTGTCCTACAGCCCCGAGTATGCCAGCGGCGCCGCCGG
CCTGGACCACTCCCATTACGGGGGGGTGCCGCCGGGCGCCGGGCCCCCGGGCCTGGGGGGGCGCGCCCGGTGAA
GCGCCGAGGCACCGCCAACCGCAAGGAGCGGCGCAGGACTCAGAGCATCAACAGCGCCTTCGCCGAACTGCGCGA
GTGCATCCCCAACGTACCCGCCGACACCAAACCTCTCCAAAATCAAGACCCTGCGCCTGGCCACCAGCTACATCGC
CTACCTCATGGACCTGCTGGCCAAGGACGACCAGAATGGCGAGGCGGAGGCCTTCAAGGCAGAGATCAAGAAGAC
CGACGTGAAAGAGGAGAAGAGGAAGAAGGAGCTGAACGAAATCTTGAAAAGCACAGTGAGCAGCAACGACAAGAA
AACCAAAGGCCGACGGGCTGGCCGCAGCACGTCTGGGCCCTGGAGCTCAAGCAGTGAGGAGGAGGAGAAGGAGG
AGGAGGAGAGCGCGAGTGAGCAGGGGCCAAGGCGCCAGATGCAGACCCAGGACTCCGGAAAAGCCGTCCGCGCTC
CGCTCTGAGGACTCCTTGCAATTTGGAATCATCCGGTTTATTTATGTGCAATTTCTTCCCCCTCTCTTTGACCCCC
TTTGAGGCATCTGCTCCCGTCTCCCCCTCCAAAAAAAAGTGGATATTTGAAGAAAAGCATTCATATTTTAAT
ACGAAGAGGACACTCCCGTGTGCAGGCCGAATCAGACCCGGCGTGGGCGAATTCAGAAGTGCCAGGGAGAGACA
AGCTAGAGGCTCTGCGGACTTCTGCGGGCGGCTGACAACGCGAGGGCGAGGGGAGAAAGCCATCAGGTCCTAGAC
GTGGAAGAAAGGAGCCTACCAAAGTGTGGAGTAAAC

1647/6881
FIGURE 1525

TTCAC TATTAAAA TATTTTCCCCCAAGTCTCAAATATTGAAGAATCTCTAACCAGAAGGCACAGATCATTTCATG
GGGATGTATAACCGAAACCAGTCCTCTCCACCGCCTGGGGATCTTCACTTTTCGCAGTCTACGACTGCCTGTGACT
CCAGAAAGACAAACTGCAGATTGGCCAAGCTGCCTGAAGACCCAGCCCGACAGCGATGCCTGTCAGCCCGCGTCG
CCCACCAGGGCAGCTGCTCTCCCAACTCGCATGGGGGGCACCACCCCGCCTCGGTGCCCTAGAGCTGAGCGCAGC
CGCGGCTCCACGGGGATCGCCAGGGCCTCAGCCCTCGCGGCCGGCGGCGGGAGTGTTGCGGGGCAGGGACCAG
AGCGCGATCAGAGCGGCCACCCCGATTTAGGTCGCCAGCTTTCCAGTCACTGCGATGGCCACTGGGGCGCCCCT
TCCATCCTGGTTAAATTCTCATTGTGATCCCCAGCCCTCTTCTCGGTTCCCCACACCCAGGAGGCCGGTTCTCCG
CCGCTCAGGCTGGGAGAGGTCACCGCTCCGGGCAGGGTGGACCCCGAGCTCCGTCTCGGAGGACCTTTCGCCGGA
GGCGAGCAGGAAGGGGTAAACCATGAGCCTCCCACCTCACCTCCCAGACCCTGGTGCCGGGCTAAGGCCTCCGC
TTCCTCCTGAGGTCTCATTAGGAAACCTCACCGCTATTTTCAACATTTCTCAATCAAGTGCCTTTAAATAGA
GCTGCACAAACAGATTGGCGGCAAAAGCGTAGATCTTGTCACGATTGAGACCAATCCAGTATTTTCAGCCTTGTTT
GCTTTGCAATTACGGGTTGGCTTGTTGGCTACGGTGCCACCGGGGCAAATCTGCAGCCGCTCGCTTTCTCCTCTGC
GCTCCGGGCGGGTGGAGGAAGCGACCCGCGGAGTCACTGCAGGGAGGAGAGGGGGACGCGCGCGGGGGGAGGCGG
CGGAGGGCGGAGGAGACTCGCTTGACCCCAAGGC

1648/6881
FIGURE 1526

GGAGGCAAACAACCCATCTCTCTTGGAGAATCCACACTTCGTTTCTTCTAGGTCCAGCCTAAATGTTACCTCCTC
CAGGGAGCCTTTCCAGATACTGCTTCTCCTCTCTCCCCAACTCCCTCCCACAAATGAAGTTTTCTCTTCTGAAT
TCCTTGCTGGTACTGTCACTTATATTCTTTTGGGTAGATCTCTGGGCATGCATATGTACCTCCTGTGACTGTGG
GTTTCTTGACAACCTAATCAATGCATTGAACAAAGGAGATGTTTAGACAACCCATATAAAATGAATAAGAGAAAT
AGGGTGAATACCGTCTACCCCAATTGCAATCAGATTAGTTTCCTTTATTTTGAAAACGATTAGAACTAGTAGAGG
AGTTAGATGTGGCCCACTAGGGAACAAATTTTCATCTCCAAGCCGTCCTCTGGCTCGATCGGGTCTGCACTGGGT
CTGCATCAACTTGCGCTGGCTCAGAGGGAGGCTCAGCCCCAGCCTGGCCTTCCTGGTGCCCACTCCCAACATCCT
GAGCAGGGCCGACTCTAGGCACCCACGATTAGCTGAGTGATCTAGGGCAAGGACCTAGGCGTCTCTAAGTCTTA
GTTTCCCCATCTGAACAATGTTGGATAATGACACGTACCTGGGGTGGGCAGGCTAGAGTAAATGGGAAAATCAAAG
CGCCAGCCAGAGCGGGTTCGCACTGTTAGTTCTGTATTTTCTCCTCCTGCCTCTGGTTTCTTCCGTTCGGTTCTA
GCTGCCTGAAGACCCAGCCCGACAGCGATGCCTGTCAGCCCGCGTCGCCCACAGGGCAGCTGCTCTCCCAACTC
GCATGGGGGGCACCACCCCGCCTCGGTGCCCTAGAGCTGAGCGCAGCCGCGGCTCCACGGGGATCGCCAGGGCCT
CAGCCCTCGCGGCGGCGGCGCGGGAGTGTTGCGGGGCAGGGACCAGAGCGCGATCAGAGCGGCCACCCCGATT
TAGGTCGCCAGCTTTCAGTCACTGCGATGGCCACTGGGGCGCCCCTTCATCCTGGTTAAATTCTCATTGTCAT
CCCCAGCCCTCTTCTCGGTTCCCCACACCCAGGAGGCCGTTCTCCGCGCTCAGGCTGGGAGAGGTCACCGCTC
CGGGCAGGGTGGACCCCCAGCTCCGTCTCGGAGGACCTTTGCGCGGAGGCGAGCAGGAAGGGGTTAACCATGAGC
CTCCCCACCTCACCTCCCAGACCTGGTGCCGGGCTAAGGCCTCCGCTTCCCTCCTGAGGTCTCATTAGGAAACC
CTCACCGCTATTTTCAACATTTCTCAATCAAGTGCCCTTTAAATAGAGCTGCACAAACAGATTGGCGGCAAAAGC
GTAGATCTTGTCACGATTGAGACCAATCCAGTATTTACGCCCTTGTTTGCTTTGCAATTACGGGTGGCTTGTTGGC
TACGGTGCCACCGGGGCAAATCTGCAGCCGCTCGCTTTCTCCTCTGCGCTCCGGGCGGGTGGAGGAAGCGACCCG
CGGAGTCACTGCAGGGAGGAGAGGGGGACGCGCGCGGGGGAGGCGGCGGAGGGCGGAGGAGACTCGCTTGCAAC
CCAGGGCCGCGGGCACGCAGAGCTGTGTTGAAGGACATACTTTTACAGGTTTCTGACAGTCACTGAGCTATACGCA
ATAATAAAGTGCGTGATTGCGGTGTGGAACCAAGTGTCGTGTCCTTACCGGCTTCCTTTTCTGTCCACCTTCCCT
CTCTCTTCTACCTCCGTCTCGCTTTTCTTCAGTGCATGTTAGCGGTTTGCTGGATTTCCCTTCTCCCTCGCTGTT
CAACTGCTAGCATGATTTGTTACATTTTCCACAGCTGTTTATTCTTGTGTTGACTTTTGTACAAAGTCACTTTAA
ATCTGCTGCAGAAAGAATAAAGCACCTAGCCCTTTGGATGGACTCCTGCAGGCGTGTGGCTGTCCCTGGCCCACT
TTTAATTCTTTGGAGATGGCTCTTCTGTGTAAATCAGCTGCTGGGTGCGTTCGGTCACCTCGTAGGCCAGCCTAG
TTTGTATCAGCAGAACAGTAGTGGACTCGACTCAGGTCGTAAGCCTTATATTTACAGACAATTAAATCTTGGCT
GCTGTTGAACAAACTGTAATATTTACTTTGTTCTATACCGAGAAGCACTTTTAAAGT

1649/6881
FIGURE 1527

MWIMTRTWGGQARVNGKIKAPARAGRTVSSCIFSSCLWFLPFRSSCLKTQPDSDACQPASPTRAAALPTRMGTT
PPRCpraersrgstgiarasalaaggagvlrgrdqsairaatpdlgrqlsshcdghwgapsilvkfsl

1650/6881
FIGURE 1528

GAAGGAGGAGGTGGCAAATCACTTATAAATGGTGCTGAAGCAGGACCCGAAGCCTAAATTCCAGGAGGGTGAGCG
AGTGCTGTGGTTTCATGGGCCTCTGCTTTATGATGCAAAGTGTGTAAAGGTTGCCATAAAGGACAAAAAGTGAAA
TACTTTATACATTACAGTGGTTGGAATAAAAAATTGGGATGAGTGGGTTCCGGAGAGCAGAGTACTCAAATATGTG
GACACCAATTTGCAGAAACAGCGAGAAGCTTCAAAAAGCCAATCAGGAGCAGTATGCAGAGGGGAAGATGAGATGG
GCTGCCCCAGGAAAGAAGACATCTGGTCTGCAACAGAAAAATATTGAAGTGAAAACAAAAAAGAACAAACAGAAA
ACACCTGGAAATGGAGATGGTGGCAGTACCAGTGAGACTCCCCAGCCTCCTCGAAAGAAAAGGGCCAGGTAGAT
CCTACTGTTGAAAATGAGGAAACATTCATGAACAGAGTTGAAGTTAAAGTAAAGATTCTCGAAGAGCTAAACCA
TGGCTTGTTGATGACTGGGACTTAATTACCAGGCAAAAACAGCTCTTCTATCTTCCTGCCGAGAAGAATGTGGAT
TCCATTCTTGAGGACTATGCAAATTACAAGAAATCTCATGGAAACACAGATAATAAGGAGTATGCAGTTAATGAA
GTTGTGGCAGGGATAAAGAATACTTCAACCTAATGTTGGGCACCCAGCTACTCAACAAATTTGAGAGACCACAG
TATGCCGAAATTCCTTGAGATTGTCCCGATGCACCCATGTCCCAGGTGTATGGAGTGCCACATCTCCTGAGATTA
TCTGTACAAATTGGAGCAATGTTGGCCTATACACCTCTGAATGAGAAGAGCCTTGCTTTTACTCAATTATCTT
CACGATTTCTAAAGTACCTGGCAAAGAATTCTGCAACTTTGTTTAGTGCCAGCGATTATGAAGTGGCTCTTCCT
GAGTACCATCGGAAAGCTGTGTGAGAGGCACTCTCACTCACTTATGTCTGGATCTCCATAAACACATTTTGTTC
TTAGTCTATCTCTTGTACAAACGATGTGCTTTGAAGATGTTAGTGTATAACAATTGATGTTTGTCTGTTTGA
TTTTAAACAGAGAAAATAAAAGGGTAATAGCTCCTTTTCTCTTTTTTTTTTTTTTTTTCATTTCAAAGTTGCTG
CCAGTGTTTTCAATGATGGACAACACAGGGATATGCTGTAGAGTGTTTTATTGCCTAGTTGACAAAGCTGCTTTT
GAATGCTGGTGGTTCTATTCTTTTAACTATGCATTTTTATAATACGTGTTAATGCTACATGACAAAATGCTCT
GATTCCTAGTGCCAAAGGTTCAATTCAGTGTATATACTGAATACACTCATCCATTTGTGCTCCTTTTTTTTTTT
AATGGTGCTTAAAGTAAAGAGCCCATCCTTTGCAAGTCATCCATGTTGCTACTTAGGCATTTTATCTTGGCTCAA
ATTGTTGAAGAATGGCTTGTTTCACAGTTTTTGTATTTGIGTCTAATGCACGTTTTAACATGATAGATGCAATGC
ATTGTGTAGCTACTTTTCTGAAAAGTCAATCTTTTAGGAATTGTTTTTCAGATCTTCATTAAATTTTTTCTTA
AATTC

1651/6881
FIGURE 1529

MRWAAPGKKTSGLQQKNIEVKTKKNKQKTPGNGDGGSTSETPQPPRKKRAQVDPTVENEETFMNRVEVKVKIPEE
LKPWLVDWDLI TRQKQLFYLP AEKNVDSILEDYANYKKSHGNTDNKEYAVNEVVAGIKEYFNLMLGTQLLNKFE
RPQYAEILADCPDAPMSQVYGVP HLLRLSVQIGAMLAYTPLNEKSLALLLN YLHDFLKYLA KNSATLFSASDYEV
ALPEYHRKAV

1652/6881
FIGURE 1530A

CTGGGCGGCCGGGCGCGGGGAGAGGGCGCGGGAGCGGCTCGTGCGGCAGGTACCATGCGGACGCGCGAGCCCCGGC
GAGGGCCCCGGCAGGCCCGGTCCCTGCTCGGGGGCGCGCTGAGACGGCGGGTGAGCTCCACGAGAGCGCCGTCGC
CACTTCGGGGCCAACTTTGCGATTCCCGACAGTTAAGCAATGGGGAGACATTTGGCTTTGCTCCTGCTTCTGCTCC
TTCTCTTTCCAACATTTTGGAGACAGTGATGGCAGCCAACGACTTGAACAGACTCCTCTGCAGTTTACACACCTCG
AGTACAACGTCACCGTGCAGGAGAAGCTCTGCAGCTAAGACTTATGTGGGGCATCCTGTCAAGATGGGTGTTTACA
TTACACATCCAGCGTGGGAAGTAAGGTACAAAATTGTTTCCGGAGACAGTGAAAACCTGTTCAAAGCTGAAGAGT
ACATTCTCGGAGACTTTTGCTTTCTAAGAATAAGGACCAAAGGAGGAAATACAGCTATTCTTAATAGAGAAGTGA
AGGATCACTACACATTGATAGTGAAAGCACTTGAAAAAATACTAATGTGGAGGCGGAACAAAGGTCAGGGTGC
AGGTGCTGGATACAAATGACTTGAGACCGTTATTCTCACCCACCTCATAACAGCGTTTCTTTACCTGAAAACACAG
CTATAAGGACCAAGTATCGCAAGAGTCAGCGCCACGGATGCAGACATAGGAACCAACGGGGAATTTTACTACAGTT
TTAAAGATCGAACAGATATGTTTGCTATTACCCAACCAAGTGGTGTGATAGTGTAACTGGTAGACTTGATTACC
TAGAGACCAAGCTCTATGAGATGGAATCCTCGCTGCGGACCGTGGCATGAAGTTGTATGGGAGCAGTGGCATCA
GCAGCATGGCCAAGCTAACGGTGCACATCGAACAGGCCAATGAATGTGCTCCGGTGATAACAGCAGTGACATTGT
CACCATCAGAACTGGACAGGGACCCAGCATATGCAATTGTGACAGTGGATGACTGCGATCAGGGTGCCAATGGTG
ACATAGCATCTTTAAGCATCGTGGCAGGTGACCTTCTCCAGCAGTTTAGAACAGTGAGGTCCTTTCCAGGGAGTA
AGGAGTATAAAGTCAAAGCCATCGGTGGCATTGATTGGGACAGTCATCCTTTCCGGCTACAATCTCACACTACAGG
CTAAAGATAAAGGAACTCCGCCCCAGTTCTCTTCTGTTAAAGTCATTACAGTGACTTCTCCACAGTTCAAAGCCG
GGCCAGTCAAGTTTGAAAAGGATGTTTACAGAGCAGAAATAAGTGAATTTGCTCCTCCCAACACACCTGTGGTCA
TGGTAAAGGCCATTCTGCTTATTCCCATTTGAGGTATGTTTTTAAAGTACACCTGGAAAAGCTAAATTCAGTT
TAAATTACAACACTGGTCTCATTCTATTTTTGAACCAAGTAAAAAGACAGCAGGCAGCCCATTTTGAACCTGAAG
TAACAACAAGTGACAGAAAAGCGTCCACCAAGGTCTTGGTGAAAAGTCTTAGGTGCAAATAGCAATCCCCCTGAAT
TTACCCAGACAGCGTACAAAGCTGCTTTTGATGAGAACGTGCCCATTGGTACTACTGTATGAGCCTGAGTGCCG
TAGACCCTGATGAGGGTGAGAACGGGTACGTGACATACAGTATCGCAAATTTAAATCATGTGCCGTTTGCGATTG
ACCATTTCACTGGTGCCGTGAGTACGTACAGAAAACCTGGACTACGAAGTATGCCTCGGGTTTATACTCTGAGGA
TTCTGTCATCAGACTGGGGCTTGCCGTACCGCCGGGAAGTCGAAGTCTTGCTACAATTACTCTCAATAACTTGA
ATGACAACACACCTTTGTTTGAGAAAATAAATTGTGAAGGGACAATTCCCAGAGATCTAGGCGTGGGAGAGCAAA
TAACCACTGTTTCTGCTATTGATGCAGATGAACCTCAGTTGGTACAGTATCAGATTGAAGCTGGAAATGAAGTGG
ATTTCTTTAGTTTAAACCCCAACTCGGGGGTATTGTCATTAAAGCGATCGCTAATGGATGGCTTAGGTGCAAAGG
TGTCTTTCCACAGTCTGAGAATCACAGCTACAGATGGAGAAAATTTTGCCACACCATTATATATCAACATAACAG
TGGCTGCCAGTCACAAGCTGGTAACTTGCAGTGTGAAGAGACTGGTGTGCCAAAATGCTGGCAGAGAAGCTCC
TGCAGGCAAATAAATTACACAACCAGGGAGAGGTGGAGGATATTTTCTTCGATTCTCACTCTGTCAATGCTCACA
TACCGCAGTTTAGAAGCACTCTTCCGACTGGTATTAGGTAAAGGAAAACCAGCCTGTGGGTTCAGTGTAATTT
TCATGAACTCCACTGACCTTGACACTGGCTTCAATGGAAAACCTGGTCTATGCTGTTTCTGGAGGAAATGAGGATA
GTTGCTTCATGATTGATATGGAAACAGGAATGCTGAAAATTTTATCTCCTCTTGACCGTGAAACAACAGACAAAT
ACACCCTGAATATTACCGTCTATGACCTTGGGATACCCAGAAGGCTGCGTGGCGTCTTCTACATGTGCTGGTTG
TCGATGCCAATGATAATCCACCCGAGTTTTTACAGGAGAGCTATTTTGTGGAAGTGAGTGAAGACAAGGAGGTAC
ATAGTGAAATCATCCAGGTTGAAGCCACAGATAAAGACCTGGGGCCCAACGGACACGTGACGTACTCAATTGTTA
CAGACACAGACACATTTTCAATTGACAGCGTGACGGGTGTTGTTAACATCGCACGCCCTCTGGATCGAGAGCTGC
AGCATGAGCACTCCTTAAAGATTGAGGCCAGGGACCAAGCCAGAGAAGAGCCTCAGCTGTTCTCCACTGTGCTTG
TGAAAGTATCACTAGAAGATGTTAATGACAACCCACCTACATTTATTCCACCTAATTATCGTGTGAAAGTCCGAG
AGGATCTTCCAGAAGGAACCGTCATCATGTGGTTAGAAGCCCACGATCCTGATTTAGGTGAGTCTGGTCAGGTGA
GATACAGCCTTCTGGACCACGGAGAAGGAACTTCGATGTGGATAAACTCAGTGGAGCAGTTAGGATCGTCCAGC
AGTTGGACTTTTGAGAAGAAGCAAGTGTATAATCTCACTGTGAGGGCCAAAGACAAGGGAAAGCCAGTTTCTCTGT
CTTCTACTTGCTATGTTGAAGTTGAGGTGGTTGATGTGAATGAGAACCTGCACCCACCCGTGTTTTCCAGCTTTG
TGAAAAGGGGACAGTGAAAAGAAGATGCACCTGTTGGTTTATTGGTAAATGACGGTGTGCGCTCATGATGAGGACG
CCAGAAGAGATGGGGAGATCCGATACTCCATTAGAGATGGCTCTGGCGTTGGTGTGTTTTCAAATAGGTGAAGAGA
CAGGTGTCTAGAGACGTCAGATCGACTGGACCGTGAATCGACCTCCCATTTATTGGCTAACAGTCTTTGCAACCG
ATCAGGGTGTGCTGCCTCTTTCATCGTTTCATAGAGATCTACATAGAGGTTGAGGATGTCAATGACAATGCACCAC

1653/6881
FIGURE 1530B

AGACATCAGAGCCTGTTTATTACCCAGAAATCATGGAAAATTCTCCTAAAGATGTATCTGTGGTCCAGATCGAGG
CATTTCATCCAGATTCGAGCTCTAATGACAAGCTCATGTACAAAATTACAAGTGGAATCCACAAGGATTCTTTT
CAATACATCCTAAAACAGGTCTCATCACAACCTACGTCAAGGAAGCTAGACCGAGAACAGCAAGATGAACACATAT
TAGAGGTTACTGTGACAGACAATGGTAGTCCCCCAAATCAACCATTGCAAGAGTCATTGTGAAAATCCTTGATG
AAAATGACAACAAACCTCAGTTTCTGCAAAAGTTCTACAAAATCAGACTCCCTGAGCGGGAAGCCAGACCGAG
AAAGAAATGCCAGACGGGAGCCGCTCTATCAGTCATAGCCACCGACAAGGATGAGGGCCCCAATGCAGAAATCT
CCTACAGCATCGAAGACGGGAATGAGCATGGCAAATTTTTCATCGAACCAGAACTGGAGTGGTTTCGTCCAAGA
GGTTTTTCAGCAGCTGGAGAATATGATATTCTTTCAATTAAGGCAGTTGACAATGGTCGCCCTCAAAAGTCATCAA
CCACCAGACTCCATATTGAATGGATCTCCAAGCCCCAACCGTCCCTGGAGCCCATTTCATTTGAAGAATCATTTT
TTACCTTTACTGTGATGGAAAGTGACCCCGTTGCTCACATGATTGGAGTAATATCTGTGGAGCCTCCTGGCATA
CCCTTTGGTTTGACATCACTGGTGGCAACTACGACAGTCACTTCGATGTGGACAAGGAACTGGAACCATCATTTG
TTGCCAAACCTCTTGATGCAGAACAGAAAGTCAAACCTCACAGTCGAGGCTACAGATGGAACCACTACTA
TCCTCACTCAGGTATTCATCAAAGTAATAGACACAAATGACCATCGTCTCAGTTTTCTACATCAAAGTATGAAG
TTGTTATTCTGAAGATACAGCGCCAGAAACAGAAATTTTGCAAAATCAGTGCTGTGGATCAGGATGAGAAAAACA
AACTAATCTACACTCTGCAGAGCAGTAGAGATCCACTGAGTCTCAAGAAATTTTCGTCTTGATCCTGCAACCGGCT
CTCTCTATACTTCTGAGAACTGGATCATGAAGCTGTTTACCAGCACACCCTCACGGTCATGGTACGAGATCAAG
ATGTGCCTGTAAAACGCAACTTTGCAAGGATTGTGGTCAATGTCAGCGACACGAATGACCACGCCCCGTGGTTCA
CCGCTTCCTCTACAAAGGGCGGGTTTATGAATCGGCAGCCGTTGGCTCAGTTGTGTTGCAGGTGACGGCTCTGG
ACAAGGACAAAGGGAAAAATGCTGAAGTGCTGTACTCGATCGAGTCAGXXXXXXXXXXGAAATATTGGAAATCTT
TTATGATTGATCCTGTCTTGGGCTCTATTAAGTCCAAAGAATTAGATCGAAGTAACCAAGCGGAGTATGATT
TAATGGTAAAAGCTACAGATAAGGGCAGTCCACCAATGAGTGAAATAACTTCTGTGCGTATCTTTGTCACAATTG
CTGACAACGCCTCTCCGAAGTTTACATCAAAGAATATTCTGTTGAACTTAGTGAACTGTCAGCATTGGGAGTT
TCGTTGGGATGGTTACAGCCCATAGTCAATCATCAGTGGTGTATGAAATAAAAGATGGAAATACAGGTGATGCTT
TTGATATTAATCCACATTCTGGAATATCATCACTCAGAAAGCCCTGGACTTTGAACTTTGCCATTTACACAT
TGATAATACAAGGAACATAACATGGCTGGTTTGTCCACTAATACAACGGTTCTAGTTCATTGTCAGGATGAGAATG
ACAACGCGCCAGTTTTTATGCAGGCAGAATATACAGGACTCATTAGTGAATCAGCCTCAATTAACAGCGTGGTCC
TAACAGACAGGAATGTCCCACTGGTGATTTCGAGCAGCTGATGCTGATAAAGACTCAAATGCTTTGCTTGTATATC
ACATTGTTGAACCATCTGTACACACATATTTTGCTATTGATTCTAGCACTGGTGCTATTTCATACAGTACTAAGTC
TGGACTATGAAGAAACAAGTATTTTCACTTTACCGTCCAAGTGCATGACATGGGAACCCACGTTTATTTGCTG
AGTATGCAGCGAATGTAACAGTACATGTAATTGACATTAATGACTGCCCCCTGTGTTTGCCAAGCCATTATATG
AAGCATCTCTTTTGTACCAACATACAAAGGAGTAAAGTGCATCAGATAAATGCTACAGATGCTGATTCAAGTG
CATTTCTCAGATTGATTTACTCCATCACCAGGGAACATCGGGGAGAAGTTTTCTATGGACTACAAGACTGGTG
CTCTCACTGTCCAAAACACAACCTCAGTTAAGAAGCCGCTACGAGCTAACCGTTAGAGCTTCGGATGGCAGATTTG
CCGGCCTTACCTCTGTCAAAATTAATGTGAAAGAAAGCAAAGAAAGTCACTAAAGTTTACCCAGGATGTCTACT
CTGCGGTAGTGAAAGAGAATTCCACCGAGGCCGAAACATTAGCTGTCACTTACTGCTATTGGGAATCCAATCAATG
AGCCTTTGTTTTATCATATCCTCAACCCAGATCGCAGATTTAAATAAGCCGCACTTCAGGAGTTCTGTCAACCA
CTGGCACGCCCTTCGATCGTGAGCAGCAGGAGGCGTTTGATGTGGTTGTAGAAGTGACAGAGGAACATAAGCCTT
CTGCAGTGGCCACGTTGTGCTGAAGGTCATTGTAGAAGACCAAAATGATAATGCGCCGGTGTGTTGTCACCTTC
CCTACTACGCCGTTGTTAAAGTGGACACTGAGGTGGGCCATGTCACTTCGCTATGTCAGTCTGTAGACAGAGACA
GTGGCAGAAACGGGGAAGTGCACTTACTACCTCAAGGAACATCATGAACACTTTCAAATTGGACCCTTGGGTGAAA
TTTCACTGAAAAAGCAATTTGAGCTTGACACCTTAAATAAAGAATATCTTGTTACAGTGGTTGCAAAAGATGGAG
GGAACCCGGCCTTTTACGCGGAAGTTATCGTTCCGATCACTGTGATGAATAAAGCCATGCCTGTGTTGAAAAAC
CTTTCTACAGTGCAGAGATTGCAGAGAGCATCCAGGTGCACAGCCCTGTGGTCCACGTGCAGGCTAACAGCCCGG
AAGGCCTGAAAGTGTTCTACAGCATCACAGACGAGACCCCTTTCAGCCAGTTCACTATTAACCTCAATACTGGAG
TTATCAATGTCATAGCTCCTCTGGACTTTGAGGCCACCCGGCATATAAGCTGAGCATACGCGCAACTGACTCCT
TGACGGGCGCTCATGCTGAAGTATTTGTGGACATCATAGTAGACGACATCAATGATAACCCCTCTGTGTTTGCTC
AGCAGTCTTATGCGGTGACCTGTCTGAGGCATCTGTAATTGGAACGTCTGTTGTTCAAGTTAGAGCCACCGATT
CTGATTGAGAACCAATAGAGGAATCTCATACCAGATGTTTGGGAATCACAGCAAGAGTCATGATCATTTTCATG

1654/6881
FIGURE 1530C

TAGACAGCAGCACTGGCCTCATCTCACTACTCAGAACCTGGATTACGAGCAGTCCCGGCAGCACACGATTTTTG
TGAGGGCAGTTGATGGTGGTATGCCACGCTGAGCAGTGATGTGATTGTCACGGTGGACGTTACCGACCTCAATG
ATAATCCACCCTCTTTGAACAACAGATTTATGAAGCCAGAATTAGCGAGCACGCCCCCTCATGGGCATTTCTGTGA
CCTGTGTAAAAGCCTATGATGCAGACAGTTTCAGACATAGACAAGTTGCAGTATTCCATTCTGTCTGGCAATGATC
ATAAACATTTTGTTCATTGACAGTGCAACAGGGATTATCACCTCTCAAACCTGCACCGGCACGCCCTGAAGCCAT
TTTACAGTCTTAACCTGTCAGTGTCTGATGGAGTTTTTAGAAGTTCCACCCAGGTTTCATGTAAGTGTAAATGGAG
GCAATTTGCACAGTCCCTGCTTTCCTTCAGAACGAATATGAAGTGGAACTAGCTGAAAACGCTCCCCTACATACCC
TGGTGATGGAGGTGAAAACCTACGGATGGGGATTCTGGTATTTATGGTCACGTTACTTACCATATTGTAAATGACT
TTGCCAAAGACAGATTTTACATAAATGAGAGAGGACAGATATTTACTTTGGAAAACTTGATCGAGAAACCCCGG
CGGAGAAAGTGATCTCAGTCCGTTTAAATGGCTAAGGATGCTGGAGGAAAAAGTTGCTTTCTGCACCGTGAATGTCA
TCCTTACAGATGACAATGACAATGCACCACAATTCGAGCAACCAAATACGAAGTGAATATCGGGTCCAGTGCTG
CTAAAGGGACTTCAGTCGTTAAAGTTCTTGCAAGTGATGCCGATGAGGGCTCCAATGCCGACATCACCTATGCCA
TTGAAGCAGACTCTGAAAGTGTAAGAGAGAATTTGGAAATTAACAAACTGTCCGGCGTAATCACTACAAAGGAGA
GCCTCATTTGGCTTGAAAAATGAATTCCTTCACTTTCTTTGTTAGAGCTGTGGATAATGGGTCTCCATCAAAGAAT
CTGTTGTTCTTGTCTATGTTAAAAATCCTTCCACCGGAAATGCAGCTTCCAAAAATTTTTCAGAACCTTTCTATACCT
TTACAGTGTGACAGGACGTCCTATTGGAACAGAGATAGATCTCATCCGAGCAGAACATAGTGGGACTGTTCTTT
ACAGCCTGGTCAAAGGGAATACTCCAGAAAGCAATAGGGATGAGTCCTTTGTGATTGACAGACAGAGCGGGGAGAC
TGAAGTTGGAGAAGAGTCTTGATCATGAGACAACCTAAGTGGTATCAGTTTTCCATACTGGCCAGGTGCACTCAAG
ATGACCATGAGATGGTGGCTTCTGTAGATGTTAGTATCCAAGTGAAAGATGCAATGACAACAGCCCGGTCTTTG
AATCTAGTCCATATGAGGCATTTCATTGTTGAAAACCTGCCAGGGGGAAGTAGAGTAATTCAGATCAGGGCATCTG
ATGCTGACTCAGGAACCAACGGCCAAGTTATGTATAGCCTGGATCAGTCACAAAGTGTGGAAGTCATTGAATCCT
TTGCCATTAACATGGAACAGGCTGGATTACAACTTTAAAGGAACCTTGACCATGAAAAGAGAGACACTTACCAGA
TTAAAGTGGTTGCATCAGATCATGGTGAAAAGATCCAGCTATCCTCCACAGCCATTGTGGATGTTACCGTCACCG
ATGTCAACGATAGTCCACCACGATTCACGGCCGAGATCTATAAAGGGACTGTGAGTGAGGATGACCCCTAGGTG
GGGTGATTGCCATCTTAAGTACCACGGATGCTGATTCTGAAGAGATCAACAGACAAGTTACATATTTTCATAACAG
GAGGGGATCCTTTAGGACAGTTTGCTGTTGAAACTATACAGAATGAATGGAAGGTATATGTGAAGAAACCTCTAG
ACAGGGAAAAAAGGGACAATTACCTTCTTACTATCACGGCAACTGATGGCACCTTCTCATCAAAAAGCGATAGTTG
AAGTGAAAGTTCTGGATGCAATGACAACAGTCCAGTTTGTGAAAAGACTTTATATTTCAGACACTATTCCTGAAG
ACGTCCTTCTTGAAAATTGATCATGCAGATCTCTGCTACAGACGCAGACATCCGCTCTAACGCTGAAATTACTT
ACACGTTATTGGGTTTCAGGTGCAGAAAAATTCAAACCTAAATCCAGACACAGGTGAACTGAAAACGTCACCCCCC
TTGATCGTGAGGAGCAAGCTGTTTATCATCTTCTCGTCAGGGCCACAGATGGAGGAGGAAGATTCTGCCAAGCCA
GTATTGTGCTCACGCTAGAAGATGTGAACGATAACGCCCCGAATTCTCTGCCGATCCTTATGCCATCACCGTGT
TTGAAAACACAGAGCCGGGAACGCTGCTGACAAGAGTGCAGGCCACAGATGCCGACGCAGGATTAAATCGGAAGA
TTTTTATACTCACTGATTGACTCTGCTGATGGGCAGTTCTCCATTAAACGAATTATCTGGAATTATTTCAGTTAGAAA
AACCTTTGGACAGAGAACTCCAGGCAGTATACACCTCTCTTTGAAAGCTGTGGATCAAGGCTTGCCAAGGAGGC
TGACTGCCACTGGCACTGTGATTGTATCAGTTCTTGACATAAATGACAACCCCCCTGTGTTTGAGTACCGTGAAT
ATGGTGCCACCGTGTCTGAGGACATTCTTGTGTTGAACTGAAGTTCTTCAAGTGTATGCAGCAAGTCGGGATATTG
AAGCAAATGCAGAAATCACCTACTCAATAATAAGTGAAATGAACATGGGAAATTCAGCATAGATTCTAAAACAG
GGGCCGTATTTATCATTGAGAATCTGGATTATGAGAGCTCTCATGAGTATTACCTAACAGTAGAGGCCACTGATG
GAGGCACGCCTTCACTGAGCGACGTTGCCACTGTGAACGTTAATGTAACAGATATCAACGATAATACCCCTGTGT
TCAGCCAAGACACCTACACGACAGTCATCAGTGAAGATGCCGTCTTGAGCAGTCTGTATCACGGTTATGGCCG
ATGATGCCGATGGACCTTCCAACAGCCACATCCACTACTCAATTATAGATGGCAACCAAGGAAGCTCGTTTACAA
TTGACCCCGTCAGGGGAGAAGTCAAAGTGACCAAACCTTCTCGACCGAGAAACGATTTTCAGGTTACACGCTCACGG
TTCAAGCTTCTGATAATGGCAGTCCACCCAGAGTCAACACGACGACCGTGAACATCGATGTGTCCGATGTCAATG
ACAACGCGCCCGTCTTCTCCAGGGGAACTACAGTGTCAATTATCCAGGAAAATAAGCCAGTGGGCTTCAGCGTGC
TGCAGCTGGTAGTAACAGATGAGGATTCTTCCATAACGGTCCACCTTCTTCTTTACTATTGTAAGTGGAAATG
ATGAGAAGGCTTTTGAAGTTAACCCGCAAGGAGTCTCTGACATCATCTGCCATCAAGAGGAAGGAGAAAGATC
ATTACTTACTGCAGGTGAAGGTGGCAGATAATGGAAGCCTCAGTTGTCATCTTTGACATACATTGACATTAGGG

1655/6881
FIGURE 1530D

TAATTGAGGAGAGCATCTATCCGCCTGCGATTTTGGCCCTGGAGATTTTCATCACCTCTTCTGGAGAAGAATACT
CAGGTGGCGTCATTGGGAAGATCCATGCCACAGACCAGGACGTGTATGATACTCTAACCTACAGTCTCGACCCCTC
AGATGGACAACCTGTTCTCTGTTTCCAGCACAGGGGGCAAGCTGATAGCACACAAAAAGCTAGACATAGGGCAAT
ACCTTCTCAATGTCAGCGTAACAGATGGGAAGTTCACGACGGTGGCCGACATCACAGTGCATATCAGACAAGTCA
CACAGGAGATGTTGAACCACACCATCGCGATCCGCTTTGCCAACCTCACTCCGGAAGAATTCGTTGGTGACTACT
GGCGCAACTTCCAGCGAGCTTTACGGAACATCCTGGGTGTGAGGAGGAACGACATACAGATTGTTAGTTTGCAGT
CCTCTGAACCTCACCCACATCTGGACGCTTACTTTTTGTAGAGAAACCAGGTAGTGCTCAGATCTCAACAAAAC
AACTTCTGCACAAGATTAACTCTTCCGTGACTGACATTGAGGAAATCATTGGAGTTAGGATACTGAATGTATTCC
AGAAACTCTGCGCGGGACTGGACTGCCCCCTGGAAAGTTCGCGATGAAAAGGTGTCTGTGGATGAAAGTGTGATGT
CAACACACAGCACAGCCAGACTGAGTTTTGTGACTCCCCGCCACCACAGGGCAGCGGTGTGTCTCTGCAAAGAGG
GAAGGTGCCCCACCTGTCCACCATGGCTGTGAAGATGATCCGTGCCCTGAGGGATCCGAATGTGTGTCTGATCCCT
GGGAGGAGAAAACACACCTGTGTCTGTCCAGCGGCAGGTTTGGTCAGTGCCAGGGAGTTTCATCTATGACACTGA
CTGGAACAGCTACGTGAAATACCGTCTGACGGAAAATGAAAACAAATTAGAGATGAAACTGACCATGAGGCTCA
GAACATATTCCACGCATGCGGTTGTCTGTATGCTCGAGGAACTGACTATAGCATCTTGGAGATTTCATCATGGAA
GGCTGCAGTACAAGTTTGACTGTGGAAGTGGCCCTGGAATTGTCTCTGTTTCAGAGCATTCAAGTCAATGATGGGC
AGTGGCACGCAGTGGCCCTGGAAGTGAATGGAACCTATGCTCGCTTGGTTCTAGACCAAGTTTCATACTGCATCGG
GCACAGCCCCAGGGACTCTGAAAACCTGAACCTGGATAACTATGTGTTTTTGGTGGCCACATCCGTCAGCAGG
GAACAAGGCATGGAAGAAGTCTCAAGTTGGTAATGGTTTCAGGGGTTGTATGGACTCCATTTATTTGAATGGGC
AGGAGCTCCCTTTAAACAGCAAACCCAGAAGCTATGCACACATCGAAGAGTCGGTGGATGTATCTCCAGGCTGCT
TCCTGACGGCCACGGAAGACTGCGCCAGCAACCTTGCCAGAATGGAGGCGTTTGCAATCCGTCACCTGCTGGAG
GTTATTACTGCAAATGCAGTGCCTTGTACATAGGGACCCACTGTGAGATAAGCGTCAATCCGTGTTCTCTCCAAGC
CATGCCTCTATGGGGGCACGTGTGTTGTGACAACGGAGGCTTTGTTTGCCAGTGTAGAGGATTATATACTGGTC
AGAGGTGTGAGCTTAGTCCATACTGCAAAGATGAACCTGTGAAGAATGGCGGAACATGCTTTGACAGTTTGGATG
GCGCCGTTTGTGAGTGTGATTGCGGTTTTAGGGGAGAAAGGTGTGAGAGTGATATCGACGAGTGCTCTGGAACCC
CTTGCCCTGCACGGGGCCCTCTGTGAGAACACGCACGGCTCCTATCACTGCAACTGCAGCCACGAGTACAGGGGAC
GTCAGTGCAGGATGCTGCGCCCAACCAGTATGTGTCCACGCCGTGGAACATTGGGTGGCGGAAGGAATTGGAA
TCGTTGTGTTTGTGTCAGGGATATTTTTACTGGTGGTGGTGTGTTGTTCTCTGCCGTAAGATGATTAGTCGGAAAA
AGAAGCATCAGGCTGAACCTAAAGACAAGCACCTGGGACCCGCTACGGCTTTCTTGCAAAGACCGTATTTTGATT
CCAAGCTAAATAAGAACATTTACTCAGACATACCACCCAGGTGCCTGTCCGGCCTATTTCTACACCCCGAGTA
TTCCAAGTGACTCAAGAAACAATCTGGACCGAAATTCCTTGAAGGATCTGCTATCCAGAGCATCCCGAATTCA
GCACTTTTAACCCCGAGTCTGTGCACGGGCACCGAAAAGCAGTGGCGGTCTGCAGCGTGGCGCCAAACCTGCCTC
CCCCACCCCTTCAAACCTCCCTTCTGACAGCGACTCCATCCAGAAGCCTAGCTGGGACTTTGACTATGACACAA
AAGTGGTGGATCTTGATCCCTGTCTTTCCAAGAAGCCTCTAGAGGAAAAGCCTTCCCAGCCATACAGTGCCCCGG
AAAGCCTGTCTGAAGTGCAGTCTCTGAGCTCCTTCCAGTCCGAATCGTGCGATGACAATGGGTATCACTGGGATA
CATCAGATTGGATGCCAAGCGTTCCTCTGCCGGACATACAAGAGTTCCCCAACTATGAGGTGATTGATGAGCAGA
CACCCCTGTACTCAGCAGATCCAAACGCCATCGATACGGACTATTACCTGGAGGCTACGACATCGAAAGTGATT
TTCTCCACCCCCAGAAGACTTCCCCGAGCTGATGAGCTACCACCGTTACCGCCCCGAATTCAGCAATCAGTTTG
AATCCATCCACCCTCCTAGAGACATGCCTGCCGCGGGTAGCTTGGGTCTTCATCAAGAAACCGGCAGAGGTTCA
ACTTGAATCAGTATTTGCCCAATTTTTATCCCTCGATATGTCTGAACCTCAAACAAAAGGCACTGGTGAGAATA
GTACTTGTAGAGAACCCCATGCCCTTACCCGCCAGGGTATCAAAGACACTTCGAGGCGCCCGCTGTGAGAGCA
TGCCCATGTCTGTGTACGCCTCCACCGCCTCCTGCTCTGACGTGTGACGCTGCTGCGAAGTGGAGTCCGAGGTCA
TGATGAGTGACTATGAGAGCGGGGACGACGGCCACTTCGAAGAGGTGACGATCCCGCCCTGGATTCCAGCAGC
ACACGGAAGTCTGACTCTCAACTCCCCCAAAGTGCCTGACTTTAGTGAACCTAGAGGTGATGTGAGTAATCCGC
GCTGTTCTTTGCAGCAGTGCTTCCAAGCTTTTTTGGTGAGCCGAATGGGCATGGCTGCGCTGGATCCTGCGCCT
CTGGACGTGCTAGCCATTCCAGTGTCCCAACTACTGTGATCGTGAGGTTTTTCATCGGCTGTGCCATTTCCCAAC
GTCTTTTGGGATTTACATCTGTCTGTGTTAAATAATCAAACGAAAAATCAGTCTGTGTTGTGACGATGATTCA
TGTATTTATATAGATTTGATTATTTTAAATTTTCTGTCTCTTTTTTTGTAAATTTTATGTACAGATTTGATTTT
TCATAGTTTTAACTAGATTTCCAAGATATTTTGTGCATTTGTTTCAACTGAATTTTGGTGGTGTGAGTCCATTA

1656/6881

FIGURE 1530E

TCTAGCACCCCTGATTTTTTTTTTTTTTACTATAACCAGGGTTTCATTCTGTCTTTTTTCCACTGAAGTGTGACATTT
TGTTAGTACATTTTCACTGTAGTCATTCATTTCTAGCTGTACATAGGATGAAGGAGAGATCAGATACATGAACATG
TCTTACATGGGTTGCTGTATTTAGAATTATAAACATTTTTCATTATTGGAAAGTGTAACGGGGACCTTCTGCATA
CCTGTTTAGAACC AAAACCACCATGACACAGTTTTTATAGTGTCTGTATATTTGTGATGCAATGGTCTTGTAAAG
GTTTTTAATGAAAACCTACCATTAGCCAGTCTTTCTTACTGACAATAAATTATTAATAAAAT

1657/6881
FIGURE 1531

GGGGCGCTGCCCCGGTGGCTCTGGCCCCGCCGGGCGGTTGGCCCAGCCCGCCGGCCCCCTGAGCTCCGGTAGCCCGC
CGCTGGAGAAGCTGTTGCCCCGGGGCGGGCCCTTGCGGACCTTCCTCGAGCGCCAGGCGGGGTCTGAAGCCCATT
TGAAGGTCAGGAGGCCCCGAGTTGCTGGCGGTGATCAAACTGCTGAACGAGAAGGAGCAGGAGCTGCGGGAGACTG
AGCACTTGCTGCACGATGAGAATGAAGGTTTAAGGAACTTGACAGAGAATGAAATCACTTTGTGTCAAAAAGAAA
TAACTCAGCTGAAGCATCAGATTATCTTACTTTTGGTTCCCTCAGAAGAAACAGATGAAAATGATTTGATCCTGG
AAGTAACTGCAGGAGTTGGAGGTCAGGAGGCAATGTTGTTTACATCAGAGATATTTGATATGTATCAGCAATATG
CTGCATTTAAAAGATGGCATTGTTGAAACCCCTGGAATATTTTCCAAGTGAAGTAGGTGGCCTTAGACATGCATCTG
CCAGCATTGGGGGTTTCAAGCCTATAGGCACATGAAATTTGAAGGAGGTGTTTACAGAGTACAAAGAGTGCCAA
AGACAGAAAAGCAAGGCTGCGTCCATACTAGCACCATGACTGTAGCAATATTACCCAGCCTACTGAGATTAATC
TGGTGATTAATCCGAAAGATTTGAGAATTGACACTAAGCGAGCCAGTGGAGCTGGGGAGCAGCATGTAAATACCA
CGGACAGTGCTGTCCGGATAGTTTATCTTCCAACAGGTGTTGTTTCTGAATGTCAACAAGAGAGATCTCAGCTGA
AAAATAAAGAGCTGGCTATGACAAAGTTACGTGCAAACTGTACAGCATGCATGTAGAAGAAGAAATAAATAAAA
GACAGAATGCTAGAAAAATTGAGATTGGAAGTAAAGGAAGATCAGAGAAAATAAGAACATATAATTTTCCACAGA
ACCGGGTCACAGATCACAGAATAACAAGACGCTGCATGATCTTGAACTTTTATGCAAGGAGATTATCTACTGG
ATGAACTTGTACAGTCATTGAAGGAATACGCCAATTATGAATCTTTAGTAGAAATTATTTCCCAAAAAGTTTAA

1658/6881
FIGURE 1532

ATGCCGCTGCGGGTTTTTGC GGCTTTCTGCCCCCGCCGCGCGGCTTTCTGACCCTGGCCTCGCCGAATTTAGCC
CCTGCCGTACGGCTTTTTGGGGCTCTTTGCCCTCGCCGCGCGGCTTTTTGCCGCCGAGCTTTTTGCATCTTT
CTCCCCCTGCCTCCGTGGCTTTTTGCCCTGAAGCCACAGCTTTTTGCCCTCGCCGCGCGGCTTTTTGCGACCT
TTTCCCCCTGCTGCCGAGCTTTTTGCCCCACCACCGCGAATTTTCTGCCGCGGCTTTTTGTCACCGCCGCC
GTGGCTTTTTATGGCTTTTGGCCCCCGGTTTTTCCCGCCGCGGCTTCCTGCCCCGAGCCCCGGCTTTTTGCGGC
TTTTTGCCGCGGTGGCTTTTGGCCCCCGCACTGTGGCTTTTTACGCCTTTTCGCCCCCGCCGCGCAGGTTTTT
CCAGCCGCGGCTTCTTGCCCCCACTGCCCGGGCTTTTTGTGTCGTTTTGCCCCCGCCGCGCGGCTTTTTGCTGC
TATTTGTCCCTGCCACCACAGCTTTTTGCCCCCGCCGCGCGGCTCCTTGCCCCCTACGTGGCTTCCTGTCCCCG
CCTCCGCGGCTTTTTATCACCCAGCCGCTTTTTGCCCCCGCCGCCACGGGTTTTTGCTCCTGCCGCCGAGGGTT
TTTGCGCTTCATGTCCCCACCGTCGTGGCTTTTTGCGGCCCTGCTTTTTGCCCCCTCTGACGCGGCTTTTTGC
GGCTTTTTACCACCTCCACCGTGGCTTTTTGCGGCTTTTGGCACCGGACGCCATGGCTTTTTCAGGCTTTTTGCC
CCGCCGCCACGGCTTTTTGCTGCCGCCACACGTTTAGCCCCACCGCGCCTTTTTGCACCCGCAGCCGCATCTT
TTTGCCGCCGCGACTTCTTACCCCGCCACCGCGGTTTTTACCGCTGAGGCTTTTTTACCCCGCCGTCGCGGGTTT
TTGCCCCACCGCGGTGGCTTTTTGCCCCACCGCCGCGGGTCTGAGGGCGGGATTGGCAGACTCGGCTGCTAGA
TCTACCGGCGTCTTGGCTAAGGCAGCGCCGACGGTCACTCCTGGTCCAGCTCTCCTGGTTCGGGGGCTGCATAGA
GCAGCGCCAAGCTCGGCCCCGATGGGAGAGAAGAAGGAGAGCGGTGGAGGGGGTGACGCGGCTATTGCGGAGGGA
GGCGCAGGGGCCGAGCCAGCCGGGTGCTGCAGCAGTGCGGGCAGCTCCAGAAGCTCATTTGGCATCTCCTTTGGC
AGCCTGCGTTGGCTGCGCACCAAGTGCCTGAGTCCAAAGACCTCACCCAGCAGGAGATACGGACCGTGCAGGAT
GAGTCCGAGGGGCTCCTAGGCACAGAGGGGGCCCTGGAGGAAGAAGAGGATGGAGAGGAGCTCATTTGAGATGGC
ATGGAAAGGTAA

1659/6881
FIGURE 1533

ATGGATGAGGACAGCTGTGTCAATGCCCAGGCCACGGGAACTCCACTTGCTAAACAGAATGTTATCCCGGAAATC
TGTGCCCTTCTCTGTATGCCTCTTGTCCCTTTTTTCACTGCCCTATTTCAGTAACTTCACAAATATATAATGAGCAC
CTGCCAAGAACCATGTTCAGGCCTGGGGCAACAAACAGCCCCTGCTGTCAAGGAACCCGCAGGCTTGTGGGGCCGT
CATGCTATCAAAAGGCAGCTCCAAGAGAGACAGTGGGATGAGTGTCAAACAGATGTTTCAGCCAAGTATGGCAGG
AGCTCAGAGGAGGCCTCATCACTTGTTGCCTGGGACAGACGTCTGGCTGGTCTGCCCACCTCCCACCCAGCCCT
CCCTGTGCGCTGCTGCCAGAATGTCTTCCTGAACACAGCTATGACTGGGCCTACTGGCCTTGGCTGTTTGATCTA
AGCAGAGGCCTAACTGAGACTGAACTAAGCATTTTTCTCTCCCAGGAATTGGAAATTTTGAACCACGAATGAGC
ACCTCTGCAGCCAAGGCCCATGAGCAATGGCACCCCTGGAGGAGAAGCCCAAGAAGCAGACCTGGTTCCAGCCCT
TTCACCGCCCGGGGTGCCACGGCCCTTTCAACGTGTATGGCAGGAGGTGTGCAGGGCATTTCAGGAGGCCTCCTGG
CTGGCACTCGACCCAATTAGTCATTCAACGCCAGGTCTGGGGCTGCTGTCTGTTGTCTCAAAGCCCATCTGTGAA
CACATGGTAGAGTCTCCAACCTGTTCCCAGATGTCCAACCTGGTCTGCGGCACTGATGGGCTCACATATACGAAT
GAATGCCAGCTCTGCTTGGCCCCGATCCTGTTTGAATTCTTCGGCCAAGTGAGGTACAGACCAGGGCCCTATGAA
CACCTGCAAGCAAGACAGCCACGCAGTTGTGGGTACCTTGGAAGAATATTGGAGAATGCAAGAGAGAACAGGGC
AGCAGTGAACCAGTTGTCCAAGACCTGGCCCAGGTTGTTGAAGAGGTCATAGGGGTTCCACAGTCTTTTCAGAAA
CTCATATTTAAGGTTTTACTATGCCCAAACAGAAATCCTGATGGGAAAGGAAAATGCCTTGCTATATCTGTAATT
TATCAACATGAAAACATTACGGTTTTAATCATAAAATTCAAGAGATTTAACTTGTTTGCCATCAGTTCTCCACCA
AGGAAAGATAAGTTGATATTGCCAGCCTTTTCATGAGCTTCCTCCTAACAGTAGGCTTATCGCCTTTGCACATTCC
TATAGCAGAGAACATAGATCTGACTGCCCTTAAGGGATACCAATTTCTCTCTCTTCAAATTCATATCCTCAGT
GGGCAAACAGAAGCCAGAAAATCCTGCCAAAAACCTTTTCATCTGGTCAGGGAGTGGAGGCCGTGCTGTGCGCGCC
CTCTTGCGGGAGCCACCAGGCAAGCATCTTAAGAGGGGCAAGCGGAAAAGGGTGTCTGTGGATCTGCCCTGTTCT
GGTGGTTTCAGGCAGCCCTGCTTTCTTCCCGCTGGCAGTCAGCAGGGGGGAGAGTCACTCAGAGCAAGATGGA
GAGCCTTAG

1660/6881
FIGURE 1534

CAGAAGAAGCCCTTTGAGGAGCACTGGAGGAAGCACACCCTGTCCTATGTGGACGTTGGCACTGGGAAGTGCACA
GCCAGAGAACAACACATCACACACAGGAAACAGTTGTGCTCATGTGATGGGGGCCTCAGCACTAGGAAGGAGTGG
ACTATTGGCACACGCAGCAGCTTGAATAAATCTGAAAGTCACTATGCTGTGTAAGAGAAGCCAAATTTAAAAAGT
GCATGCTGTGTACAGAGGGTGTCAAGAATGCCTCCTACGTGACGGAAAGCAGATCCGTGGTTGCCTGCAGACTGG
CAGGAGCAGATTCCAAAGGCACAGGAAGAAGCTTGTGGGTAGAATGTGTTTCATTACCTTCTGTGCATTATACCAT
AAAAAAGCTGGTCACAAAAATGCAACCAAAAAACAAAGGTGAACTAGGATAAGATTTCTCACCTGTGTGATTGG
TAAACGTGCAGATGTGCCGTCATGCTTTGTTTATGAAGCTGTGGGATACAAGGACTCTCATACGTCACTGTGGAA
TGCAGAATATTGCAGCCTCATGGAAGAGGATTTGGCAGCGTCTAACAAAACCTACATGGCATTGCCCCCTTGACTC
AGCAATTCTAGAATCTGCCTCAAAAAAACTCCAGCAAAGAAATGAAAGGACTTTAGGCACAGAGTTCTTTTCACA
GCCTGCATGTGTTTGCAACAAAGTTCTTCACTGTGGCGTTTGTAATGTGGGAAAAGAGAGATCAGGCTGGTAC
TGTGTCTGTGTAGAAAAGGAGGACGTAAGAAACTCCATTTTGATCTGTACCCCGAGCGATTGTTTTGCCCTGAGA
TGCTGTTAATCTGTAACTTTAGCCCCAGCCTTGAGCTCACAGAAACCTGTGTTGTATGGAATCAAGGTTTCAGGG
ATCTAGGGCTGTGCAGGACGTGCCTTGTTAAGAAAATGCTTACAGGCAGTACGCTTGGTAAAAGTTATCGCCATT
CTCCATTCTCGATAAACCAGGGGCACAATGCACTGCGGAAAGCCGCAGGGACCTCTGCCCAGGAAAGCCGGGTAC
CATCCAAGGTTTCTCCCCACTGAGATATGGCCTTGTGGGATGGGAAAGACCTGACCATCCACCAGCCCGACACCC
GTGAAGGATCTGTGCTGAGTAGGATTAGTAAAAGAGGAAGGCCTCTGTCTCCTGCCTTCCCCTGGGAACGGAATG
TCTCAGTATAAAACTGATCGTACATTTGTTCAATTCTGAGATAGGAGAAAAACCACCTGTGGTGGGAGGCGAGA
CATGTTGGCCGCAATGCTGCTGTTACTCTTTACTCCACTGAAATGTTTGGGTGGAGAGAAGCATAAATCTGGCCT
ACGTGCACATCTAGACATAGTACCTTCCCTTGAACCTTACTTGTGACACAGATTCCCTTTGCTCACATGTTTTCTTG
CTGACCTTCTCCCCACTGTCACCCTGTTCTCCTGCCACATTCCCTCTTGCTGAGATAGTGAAAATAGTAATCAATA
AATACTGAGGGAACTCAGAGACCGGTGCCAGTGCGGGTCCTCTGTATGCTGAGCGCCAGTCCCCTGGGCCCCACTT
TTCTTTTCTCT

1661/6881
FIGURE 1535

AATAAAGAAATAGTGCTTTAAGTCAATGAATTCCCTCCTTGGGACCCACTATCGAGAACTATCAGTGGTAACGTT
TTAAAAAATGACAAATTCATCTGCTCTTGACTTGTTGTGTCTTAAGATTTCCACTAAGTGTCTTCAAACCTCCCC
CTCCCCGGCTTCCTGGATAATAGAAGTTCCCGAAGGCCGCCGATTCCAGAAGATACTGTCTGGCGTGAAATTAGT
CTCAGTAGAAACATAAGTCCCGCGCGTCTTGTGCTGCGCGTGCAGCAAGCTTTTGGGCCCTCCCGAGAAAGGGAAG
TGCATTCTCGCTTCCGTAGCGGTCTCCGCCGTTGGGGGGAAGTAATTCGGTTGTTGCACCATGGCGTCCATGG
GGACCTCGCCTTCGATGAATATGGGCGCCCTTTCCCTCATCATCAAGGATCAGGACCGCAAGTCCCGTCTTATGG
GACTTGAGGCCCTCAAGTCTCATATAATGGCAGCAAAGGCTGTAGCAAATACAATGAGAACATCACTTGGACCAA
ATGGGCTTGATAAGATGATGGTGGATAAGGATGGAGATGTGACTGTAAC TAATGATGGGGCCACCATCTTAAGCA
TGATGGATGTTGATCATCAGATTGCCAAGCTGATGGTGGAACTGTCCAAGTCTCAGGATGATGAAATTGGAGATG
GAACCACAGGAGTGGTTGTCTGGCTGGTGCCTTGTTAGAAGAAGCGGAGCAATTGCTAGACCGAGGCATTACCC
CAATCAGAATAGCCGATGGCTATGAGCAGGCTGCTCGTGTGCTATTGAACACCTGGACAAGATCAGCGATAGCG
TCCTTGTTGACATAAAGGACACCGAACCCCTGATTGAGACAGCAAAAAACACGCTGGGCTCCAAAGTGGTCAACA
GTTGTCACCGACAGATGGCTGAGATTGCTGTGAATGCCGTCTCACTGTAGCAGATATGGAGCGGAGAGACGTTG
ACTTTGAGCTTATCAAAGTAGAAGGCAAAGTGGGCGGCAGGCTGGAGGACACTAACTGATTAAGGGCGTGATTG
TGGACAAGGATTTCAAGTACCCACAGATGCCAAAAAAGTGAAGATGCGAAGATTGCAATTCTCACATGTCCAT
TTGAACCAACCAACCAAAAAACAAAGCATAAGCTGGATGTGACCTCTGTGCGAAGATTATAAAGCCCTTCAGAAAT
ACGAAAAGGAGAAATTTGAAGAGATGATTCAACAAATTAAAGAGACTGGTGCTAACCTAGCAATTTGTGAGTGGG
GCTTTGATGATGAAGCAAATCACTTACTTCTTCAGAACAACTTGCCCTGCGGTTGCTGGGTAGGAGGACCTGAAA
TTGAGCTGATTGCCATCGCAACAGGAGGGCGGATCGTCCCCAGGTTCTCAGAGCTCACAGCCGAGAAGCTGGGCT
TTGCTGGTCTTGACAGGAGATCTCATTGGGACAAC TAAGGATAAAATGCTGGTCACTCGAGCAGTGTAAGAACT
CCAGAGCTGTAACCATTTTTATTAGAGGAGGAAATAAGATGATCATTGAGGAGGCGAAACGATCCCTTCACGATG
CTTTGTGTGTATCCGGAACCTCATCCGCGATAATCGTGTGGTGTATGGAGGAGGGGCTGCTGAGATATCCTGTG
CCCTGGCAGTTAGCCAAGAGGCGGATAAGTGCCCCACCTTAGAACAGTATGCCATGAGAGCGTTTGCCGACGCAC
TGGAGGTATCCCCATGGCCCTCTCTGAAAACAGTGGCATGAATCCCATCCAGACTATGACCGAAGTCCGAGCCA
GACAGGTGAAGGAGATGAACCTGCTCTTGGCATCGACTGTTTGCACAAGGGGACAAATGATATGAAGCAACAGC
ATGTCATAGAAACCTTGATTGGCAAAAAGCAACAGATATCTCTTGCAACACAAATGGTTAGAATGATTTTGAAGA
TTGATGACATTTCGTAAGCCTGGAGAATCTGAAGAATGAAGACATTGAGAAAACATATGTAGCAAGATCCACTTCTG
TGATTAAGTAAATGGATGTCTCGTGATGCATCTACAGTTATTTATTGTTACATCCTTTTCCAGACACTGTAGATG
CTATAATAAAAATAGCTGTTTGGTAACCATAGTTTCACTTGTTCAAAGCTGTGTAATCGTGGGGGTACCATCTCA
ACTGCTTTTGTATTTCATTGTATTAAAAGAATCTGTTTAAACAACCTTTATCTTCTCTCGGGTTTAAGAAACGTT
TATTGTAACAGTAATTAAATGCTGCCTTAATTG

1662/6881
FIGURE 1536

MASMGTLAFDEYGRPFLLIKDQDRKSRLMGLEALKSHIMAAKAVANTMRTSLGPNGLDKMMVDDKGDVTVTNDGA
TILSMMDVDHQIAKLMVELSKSQDDEIGDGTGTVVVLGALLEEEAEQLDRGIHPIRIADGYEQAAARVAIEHLDK
ISDSVLVDIKDTEPLIQTAKTTLGSKVVNSCHRQMAEIAVNAVLTVADMERRDVDFELIKVEGKVGGRLEDTKLI
KGVIVDKDFSHPQMPKKVEDAKIAILTCPFEPPKPKTKHKLDVTSVEDYKALQKYEKEKFEEMIQQIKETGANLA
ICQWGFDDDEANHLLLQNNLPVRWVGPEIELIAIATGGRIVPRFSELTAEKLGFAGLVQEISFGTTKDKMLVIE
QCKNSRAVTIFIRGGNKMIIEEAKRSLHDALCVIRNLIRDNRVVGGAEEISCALAVSQEADKCPTLEQYAMRA
FADALEVIPMALSENSGMNPIQTMTEVRARQVKEMNPALGIDCLHKGTNDMKQQHVIETLIGKKQQISLATQMVR
MILKIDDIRKPGESE

1663/6881
FIGURE 1537

GTATCTGTCCGGACGGAAGCAGGAAGCGGGAGCGTAGGGCCACGCCTGCGGCGCTGCTGGTTGAGGCTGTGTGGG
TCGGGGACGGGCCGAGGCG**A**TGGCGGAGAAGTTTGACCACCTAGAGGAGCACCTGGAGAAGTTCGTGGAGAACAT
TCGGCAGCTCGGCATCATCGTTCAGTGACTTCCAGCCCAGCAGCCAGGCCGGGCTCAACCAAAAGCTGAATTTTAT
TGTTACTGGCTTACAGGATATTGACAAGTGCAGACAGCAGCTTCATGATATTACTGTACCGTTAGAAGTTTTTGA
ATATATAGATCAAGGTCGAAATCCCCAGCTCTACACCAAAGAGTGCCTGGAGAGGGCTCTAGCTAAAAATGAGCA
AGTTAAAGGCAAGATCGACACCATGAAGAAATTTAAAAGCCTGTTGATTCAAGAACTTTCTAAAGTATTTCCGGA
AGACATGGCTAAGTATCGAAGCATCCGGGGGGAGGATCACCCGCCTTCT**TAA**CCAGCTCACCTCCCTGTGTGAA
GATCCCCCGGGACTGCGATGCGGCGTGAGGCTGGGACTGCGAGTGCTGACGCCACCTTCCTGCTGAGGTGGGACT
GGGCCCTGGACACACCCCTCAGCCCCTCTGTCTCATTGTTTGGCCTCATGGGACCGAGGGGCTGGAGGAGAGGC
GGAGCTGTGCCCCAGCTGTTCCAGCAGCTTGTCTGGCGTCAACTGGCTTTCAGAGTGCTGACCCCTCATCACTGT
GGGGATCATTCTCTCTGAGGGCAGATGAGGCGCAGGAAAATAGTCTTGGAATGTTAAATATGATGGGTAAATTA
AAAGTTTTTACAACATTCTACCTAATATTTTTCTTTTAACTACTTTTTCTGTTCTATTGTATTATGGGTGTCGAA
AGCTAAATAACGACTAGGAAAAATTTTTTAAAAAAGAAAAATCAGTTTAATGTGGGAAGTACTTAAGTGGTAT
TATATTTTACATTTTCAAGTATAGTGCATAAAGAATGTTTTAAATGTAAGTGTTCATGGATTTCAATTAGACA
TGCCTATAATAAACTAAGTATGTGGCTTATTCCATGTAATTATTTTTGTAATATAATAACAATGTGTCTTGT

1664/6881
FIGURE 1538

MAEKFDHLEEHLEKFVENIRQLGIIVSDFQPSSQAGLNQKLNFIIVTGLQDIDKCRQQLHDITVPLEVFEYIDQGR
NPQLYTKECLERALAKNEQVKGKIDTMKKFKSLLIQELSKVFPEDMAKYRSIRGEDHPPS

1665/6881
FIGURE 1539

GGGATTTGTTATTGCGAATGATGTGGACAACAAGCGCTGCTACCTGCTCGTCCATCAAGCCAAGAGGCTGAGCAG
CCCCTGCATCATGGTGGTCAACCATGATGCCTCCAGCATACCCAGGCTCCAGATAGATGTGGACGGCAGGAAAGA
GATCCTCTTCTATGATCGAATTTTATGTGATGTCCCTTGCACTGGAGACGGCACTATGAGAAAAAACATTGATGT
TTGGAAAAAGTGGACCACCTTAAATAGCTTGCAGCTACATGGCTTACAGCTGCGGATTGCAACACGCGGGGCTGA
ACAGCTGGCTGAAGGTGGAAGGATGGTGTATTCCACGTGTTCACTAAACCCTATTGAGGATGAAGCAGTCATAGC
ATCTTTACTGGAAAAAGTGAAGGTGCTTTGGAGCTTGCTGATGTGTCTAATGAACTGCCAGGGCTGAAGTGGAT
GCCTGGAATCACACAGTGGAAAGTAATGACGAAAGATGGGCAGTGGTTTACAGACTGGGACGCTGTTCCCTCACAG
CAGACACACCCAGATCCGACCTACCATGTTCCCTCCGAAGGACCCAGAAAAGCTGCAGGCCATGCACCTGGAGCG
ATGCCTTAGGATATTACCCCATCATCAGAATACTGGAGGGTTTTTTGTGGCAGTATTGGTGAAAAATCTTCAAT
GCCGTGGAATAAACGTCAGCCAAAGCTTCAGGGTAAATCTGCAGAGACCAGAGAAAGCACACAGCTGAGCCCTGC
AGATCTCACAGAAGGGAACCCACAGATCCCTCTAAGCTGGAAAGTCCGTCATTACAGGAACTGGTGACACAGA
AATAGCTCATGCAACTGAGGATTTAGAGAATAATGGCAGTAAGAAAGATGGCGTGTGTGGTCTCTCCATCAAA
GAAAAATGAAGTTATTTGGATTTAAAGAAGATCCATTTGTATTTATTCCTGAAGATGACCCATTATTTCCACCTAT
TGAGAAATTTTATGCTTTGGATCCTTCATTCCCAAGGATGAATTTGTTAACTCGGACTACAGAAGGGAAGAAAAG
GCAGCTCTACATGGTTTCTAAGGAGTTGCGGAATGTGCTGCTGAATAACAGTGAGAAGATGAAGGTTATTAACAC
GGGGATCAAAGTCTGGTGTAGAAATAACAGCGGTGAAGAGTTTGACTGTGCTTTCCGGCTGGCACAGGAGGGAAT
ATATACATTGTATCCATTTATTAACCTCAAGAATTATTACTGTATCAATGGAAGATGTTAAGATACTGTTGACCCA
GGAAAATCCCTTTTTTTAGAAAACCTCAGCAGTGAGACCTACAGTCAAGCAAAGGACCTGGCAAAGGGAAGCATCGT
GCTGAAGTATGAACCAGATTCTGCGAATCCAGACGCTCTGCAGTGTCCCATCGTCTTATGCGGATGGCGGGGAAA
GGCCTCCATTGAACTTTTGTGCCCAAGAATGAACGGCTTCATTATCTCAGGATGATGGGGCTGGAGGTATTGGG
AGAAAAGAAGAAGGAAGGGGTATCCTCACAAATGAGAGTGCAGCCAGCACCGGACAGCCAGACAATGACGTGAC
TGAGGGACAGAGAGCAGGAGAGCCCAACAGCCCAGATGCAGAAGAGGCCAACAGTCCAGACGTGACAGCAGGCTG
TGACCCGGCGGGGGTCCATCCACCCCGGTGAGCAGGCCCAAGGCAGCGGGGGCCACACCCCTCACACGCAAAAC
TGGCTTCTTCTGGTCACTGGTGTCTGAAACCAAATCCAGAGCAGCCTGTGGCCTGTAAAGCATATATTTCTAATG
ACTGCAGACTGGTGGGATCATAGGAGCCTTCTGAATGACCAGGACTGCTTTCTTTGGAGCTGATGAAAATGTACT
CTTTTAGCGTGTAGAAATCACTTGTTTTATTTGTTTCTTTGGCCAAGCTGGGTCTAGTGTTTCTTTTGCTGGG
AATAGACTTTCAAAGTTGTACTTCTATCAAGAAACAAAACCTGCCCTTGAGAAATTCAGGTCTTTTGTTAAGC
CTGTATTGGTCTTAAGGTGCAGTATTTTTTAAATTATTATTTATAGAAAGAATCTATAAATCTTGGGGAAGTGT
GTTATAAGCTTTAATAATTACATTGAGCTGCACCTCAGTGGTGTGTTCATTAAACATGCAGTGGGGTTAATATCTGA
GGCCTCAGATGACTTTGTGCCTTTTGGAAATAAAGGGTAAATAAACTCTCCAGAGTAAGA'CTGTATCGTGAAT
TGTCATACTAATTATTGAGGGGGACTTATGTGCTTTTATTGAATGGAGTGCTTTACAATTTTTATTTTTTAAATGG
GGTTGGGATCCTTGGAATATTTCAATAAAATTGATAAAATAT

1666/6881
FIGURE 1540

TCCTGCTTCGCCCTCCAGCGCCTAGAAGCCTGCAGCTCCGGAGCAGTGGCCGCGCCACGCCGGCCCCAGCGCGC
AGAACCCTGCAGGCCCCGCCGTCGCCCCGGGCGCGCCGCCATGTCCTACCCGCAGTTTGGATACCCCTACT
CCTCGGCTCCCCAGTTCTTGATGGCCACCAACTCCCTGAGCACGTGCTGCGAGTCCGGAGGCCGCACGCTGGCGG
ACTCCGGGCCCCCGCCTCGGCCAGGCGCCGGTCTACTGCCCGGTCTACGAGAGCCGGCTGCTGGCCACCGCGC
GCCACGAGCTCAACTCGGCCCGGGCGCTGGGCGTCTATGGGGTTCCTATGGCGGATCGCAGGGCTATGGCAACT
ACGTGACCTACGGCTCGGAGGCGTCCGCCTTCTACTCGCTGAACAGCTTTGATTCCAAGGATGGTTTCGGGATCTG
CGCATGGGGGCTGGCACCAGCCGCTGCGCCTACTACCCCTACGAGCCAGCTCTGGGCCAGTACCCCTATGACA
GGTATGGAACCATGGACAGCGGCACGCGGCGCAAGAAGCCACGCGCGAGACCACCAGCACGCTCAAGGCCTGGC
TGCAGGAGCACCGCAAGAACCCCTACCCACCAAGGGCGAGAAGATCATGCTGGCCATCATCACCAAGATGACCC
TCACACAGGTCTCCACCTGGTTTCGCCAACGCGCGCCGGCGCTCAAGAAGGAGAACAAGATGACGTGGCCGCCGC
GGAACAAGTGGCAGACGAGAAGCGGCCCTACGCGGAGGGCGAGGAGGAGGAGGGGGCGAGGAGGAGGCGCGGG
AGGAGCCCCCTCAAGAGCTCCAAGAAGCAGAGCCCGTGGGCAAAGAGGAGAAGGAGCTGGAGCTTAGTGACTTGG
ACGACTTCGACCCGCTGGAAGCAGAGCCCGCGGCGTGCGAGCTGAAGCCGCCCTTCCACTCCCTGGACGGCGGTCT
TGGAGCGCGTCCCCGCCGCGCCGACGGCCCGGTCAAGGAGGCCCTCAGGCGCGCTCCGGATGTCTCTGGCCGCGG
GTGGCGGAGCTGCTCTGGACGAGGACCTGGAGAGGGCCCGGAGCTGTCTCCGCAGCGCGGCGGGCCGGGCGGAGC
CACTGCCGGGCGCAGAGGGCGGCCCTCAGGTCTGCGAGGCCAAGCTGGGGTTTGTGCGGGCGGGGGCGTTCGGCAG
GCCTGGAGGCTAAGCCGCGCATCTGGTCCCTGGCCACACAGCCACCGCCGCGCGCGCCGCCACCTCCCTGA
GCCAGACTGAGTTTCCGTCTGTCATGCTCAAGCGCCAAGGTCCCGCGGCCCTGCGGCTGTGTCTCCGCGCCCG
CCACGTCCCCGTCTGTGGCCCTTCCCCACTCTGGCGCCCTGGACAGGCACCAGGACTCCCCGGTAACCAAGTCTCA
GAAACTGGGTGGACGGGGTCTTCCACGACCCCATCTCAGGCACAGCACTTTGAACCAGGCCTGGGCCACCGCCA
AGGGCGCCCCCTCTGGACCCCGGGCCTCTGGGACGCTCGCTGGGGGCGGGCGGAACGTGCTGACTGCACCCCTGG
CCC CGCCCTTTCGCGCTGCCGTGCCCCAGGACGCCCCAGCTGCAGGCGCCGCCAGGGAGCTGCTCGCCCTGCCCCA
AGGCCGGCGGCAAACCTTCTGCGCCTGAGGCGGGCGGGTCCCAGGCCAGGAGGGAACCCGCGCTCAGGCGGAC
GGCGCCGACTCTTTTCACTGAGTTTCCAGAGGAAGACTAGCGCGGCCACCGCGAAGCCGCCAACCCACCGGAGAG
GGGGCTTCTGAACTTGACTCCTGGGAACATGGACAAGCCCGGCGCTGCCACGCCGGGGCCTCCACCGCCTGGGC
CTGAGCCTGACCGGGCCATTCCCAAATTTGGGACGCGGAAGGAGAGGCTCTCGGAGCAGAAGAGGCCAGATACCC
TGAAGCATAAAGTTTACGTCAAAGTTTACATGGAGAAGGCGGTTCCGTTCTGAAGCGTGGTCTGCTGTCCCCTG
GGCGTGAGGCCTCCTGGGCCTGTGCGGCCTCCGATTTTCATCCTCAGCACGTAATGCTCACCAACAGCACTTGAC
TGAGTTGACTCTTGACACTCTTGACTCCATAATATGATGCTTTTTAAGATGTATGTTACACCAATAATTGCCT
GCTTCAGAGGCTAATATAACAAAACCAATAAAACCGAG

1667/6881
FIGURE 1541

GACTGCGCGGCGGCAACAGCAGACATGTCGGGGGTCCGGGGCCTGTCGCGGCTGCTGAGCGCTCGGCGCCTGGCG
CTGGCCAAGGCGTGCCAACAGTGTTGCAAACAGGAACCCGAGGTTTTCACTTCACTGTTGATGGGAACAAGAGG
GCATCTGCTAAAGTTTCAGATTCCATTTCTGCTCAGTATCCAGTAGTGGATCATGAATTTGATGCAGTGGTGGTA
GGCGCTGGAGGGGAGGCTTGCGAGCTGCATTTGGCCTTTCTGAGGCAGGGTTAATACAGCATGTGTTACCAAG
CTGTTTCCTACCAGGTCACACACTGTTGCAGCACAGGGAGGAATCAATGCTGCTCTGGGGAACATGGAGGAGGAC
AACTGGAGGTGGCATTCTACGACACCGTGAAGGGCTCCGACTGGCTGGGGGACCAGGATGCCATCCACTACATG
ACGGAGCAGGCCCCCGCCCGTGGTCGAGCTAGAAAATTATGGCATGCCGTTTAGCAGAACTGAAGATGGGAAG
ATTTATCAGCGTCATTGTTGGTGACAGAGCCTCAAGTTTGAAAGGGCGGGCAGGCCATCGGTGCTGCTGTGTG
GCTGATCGGACTGGCCACTCGCTATTGCACACCTTATATGGAAGGTCTCTGCGATATGATACCAGCTATTTTGTG
GAGTATTTTGCCTTGGATCTCCTGATGGAGAATGGGGAGTGCCGTGGTGTCTCGCACTGTGCATAGAGGACGGG
TCCATCCATCGCATAAGAGCAAAGAACACTGTTGTTGCCACAGGAGGCTACGGGCGCACCTACTTCAGCTGCACG
TCTGCCCACACCAGCACTGGCGACGGCACGGCCATGATCACCAGGGCAGGCCTTCCTTGCCAGGACCTAGAGTTT
GTTTCAGTTCCACCCTACAGGCATATATGGTGCTGGTTGTCTCATTACGGAAGGATGTCGTGGAGAGGGAGGCATT
CTCATTAACAGTCAAGGCGAAAGGTTTATGGAGCGATACGCCCCGTGTCGCAAGGACCTGGCGTCTAGAGATGTG
GTGTCTCGGTCCATGACTCTGGAGATCCGAGAAGGAAGAGGCTGTGGCCCTGAGAAAGATCACGTCTACCTGCAG
CTGCACCACCTACCTCCAGAGCAGCTGGCCACGCGCCTGCCTGGCATTTCAGAGACAGCCATGATCTTCGTGGC
GTGGACGTACGAAGGAGCCGATCCCTGTCTCCCCACCGTGCATTATAACATGGGCGGCATTCCCACCAACTAC
AAGGGGCAGGTCTTGAGGCACGTGAATGGCCAGGATCAGATTGTGCCCCGCCCTGTACGCCTGTGGGGAGGCCGCC
TGTGCCTCGGTACATGGTGCCAACCGCCTCGGGGCAAACTCGCTCTTGACCTGGTTGTCTTTGGTCGGGCATGT
GCCCTGAGCATCGAAGAGTCATGCAGGCCTGGAGATAAAGTCCCTCCAATTAAACCAAACGCTGGGGGAAGAATCT
GTCATGAATCTTGACAAATTGAGATTTGCTGATGGAAGCATAAGAACATCGGAAGTGCAGCTCAGCATGCAGAAG
TCAATGCAAAATCATGCTGCCGTGTTCCGTGTGGGAAGCGTGTGCAAGAAGGTTGTGGGAAAATCAGCAAGCTC
TATGGAGACCTAAAGCACCTGAAGACGTTCCGACCGGGGAATGGTCTGGAACACGGACCTGGTGGAGACCCTGGAG
CTGCAGAACCTGATGCTGTGTGCGCTGCAGACCATCTACGGAGCAGAGGCACGGAAGGAGTCACGGGGCGCGCAT
GCCAGGGAAGACTACAAGGTGCGGATTGATGAGTACGATTACTCCAAGCCCATCCAGGGGCAACAGAAGAAGCCC
TTTGAGGAGCACTGGAGGAAGCACACCCTGTCTATGTGGACGTTGGCACTGGGAAGGTCACTCTGGAATATAGA
CCCGTGATCGACAAAACCTTTGAACGAGGCTGACTGTGCCACCGTCCCGCCAGCCATTGCTCCTACTTGATGAGAC
AAGATGTGGTGATGACAGAATCAGCTTTTGTAATTATGTATAATAGCTCATGCATGTGTCCATGTCATAACTGTC
TTCATACGCTTCTGCACTCTGGGGAAGAAGGAGTACATTGAAGGGAGATTGGCACCTAGTGGCTGGGAGCTTGCC
AGGAACCCAGTGGCCAGGGAGCGTGGCACTTACCTTTGTCCCTTGCTTCATTCTTGTGAGATGATAAACTGGGC
ACAGCTCTTAAATAAAATATAAATGA

1668/6881
FIGURE 1542

MSGVRGLSRLLSARRLALAKAWPTVLQTGTRGFHFTVDGNKRASAKVSDSISAQYPVVDHEFDVAVVGAGGAGLR
AAFGLSEAGFNTACVTKLFPTRSHTVAAQGGINAALGNMEEDNWRWHFYDTVKGSDWLGDDAIHYMTEQAPAAV
VELENYGMPFSRTEDGKIYQRAFGGQSLKFGKGGQAHRCVVADRTGHSLHTLYGRSLRYDTSYFVEYFALDLL
MENGEGRGVIALCIEDGSIHRIRAKNTVVATGGYGRTYFSCSAHTSTGDGTAMITRAGLPCQDLEFVQFHPTGI
YGAGCLITEGCRGEGGILINSQGERFMERYAPVAKDLASRDVVSRSMTLEIREGRGCGPEKDHVYLQLHHLPPPEQ
LATRLPGISETAMIFAGVDVTKEPIPVLPVHYNMGGIPTNYKGQVLRHVNGDQIVPGLYACGEAACASVHGAN
RLGANSLLDLVVFGRACALSIEESCRPGDKVPPIKPNAGEESVMNLDKLRFADGSIRTSELRLSMQKSMQNHAAV
FRVGSVLQEGCGKISKLYGDLKHLKTFDRGMVWNTDLVETLELQNLMLCALQTIYGAEARKESRGAHAREDYKVR
IDEYDYSKPIQGQKKPFEEHWRKHTLSYVDVGTGKVTLEYRVIDKTLNEADCATVPPAIRSY

1669/6881
FIGURE 1543

CTGGAGCTGCAGAACCTGATGCTGTGTGCGCTGCAGACCATCTACGGAGCAGAGGCACGGAAGGAGTCACGGGGC
GCGCATGCCAGGGAAGACTACAAGGTGGGCCTTCTCACCACGCCCACCTGCACCTGCCTTTTCCTGCCACCTGGT
GGGACTCAGCCCCACCCCTGCATTTTCTCTGCATTTTCTTTTCGTTGCCCCAAAAGTAAATCCAAAAAATGCCTTT
TTCCCCCCTGGTAACCTTTGATCCCTGGGTTCTCGCCATCTTCTGGATCACTGTGACCTTTTCCTTGCTTTGGGTC
GGCATCCACTGATGCCAGCAGTGGCATCTCCAAGCCAATGTGCTTTGCTGTTAGAAGGCCAAGGTTAGAAGTGCA
GCTAGAGTGGCAAGACCAGGAAATAAATGCCAGTTTATTAAATAACGAGTAAGCCACCGTTTCAAACCTGCCCTG
TGGAGGAAATGCCAGTTTATTAAATAACGAGTAAGCCACCGTTTCAAACCTGCCCTGTGGAGGAAATGCCAGTTT
ATTAAATAACGAGTAAGCCACCGTTTCAAGCCTGCCCTGTGGAGGAAATGCCAGTTTATTAAATAACGAGTAAGC
C

1670/6881
FIGURE 1544

TTTACGATATCCAAATAAACTGGACACCATCACATGGACGTGGCAAGGACCTGGAGCGCTGGAAATCCTGTGGCT
CACGCTGTGTCACTTTTACAACCAAGTGGAAATCGAGTTCCTTCCTGTGTACAGCCCTTCTGAGGAGGAGAAGAG
GAACCCCGCGCTGTATGCCAGCAACGTGCGGCGAGTCATGGCCGAGGCCTTGGGTGTCTCCGTGACTGACTACAC
GTTTCGAGGACTGCCAGCTGGCCCTGGCGGAAGGACAGCTCCGTCTCCCCGCTGACACTTGCCTTTTAGAATTTGC
CAGGCTCGTGCGGGGCCTCGGGCTAAAACCAGAAAAGCTTGAAAAAGATCTGGACAGATACTCAGAAAGAGCCAG
GATGAAGGGAGGAGAGAAGATAGGTATTGCGGAGTTTGCCGCTCCCTGGAAGTCCCCGTTTCTGACTTGCTGGA
AGACATGTTTTCTACTGTTTCGACGAGAGCGGCAGCGCGAGGTGGACCTGCGAGAGTGTGTGGTTGCCCTGTCTGT
CGTCTGCCGGCCGGCCCGGACCCTGGACACCATCCAGCTGGCTTTCAAGATGTACGGAGCGCAAGAGGACGGCAG
CGTCGGCGAAGGTGACCTGTCTGCATCCTCAAGACGGCCCTGGGGGTGGCAGAGCTACCCGTGACCGACCTATT
CCGAGCCATTGACCAAGAGGAGAAGGGGAAGATCACATTTCGCTGACTTCCACAGGTTTGCAGAAATGTACCCCTGC
CTTCGCAGAGGAATACCTGTACCCGGATCAGACACATTTTCGAAAGCTGTGCAGAGACCTCACCTGCGCCAATCCC
AAACGGCTTCTGTGCCGATTTTCAGCCCGGAAAACCTCAGACGCTGGGCGGAAGCCTGTTTCGCAAGAAGCTGGATTA
GGACCCAGGGTTGCGGAGAGACGCGGCCCTCCCGCGTGGACATCACCGCCATGAGCCTCTTTGCGAGTGACCTC
TGGGCTCCGCTCCTCACTCCTGCTGTACAGGCACTGTCTTCAGCCCGAGTTCAGGGGCCTCGGGGGCTGTTTGT
ATCTTGTTCTCTTTGTGAAGTGTGTTGCAGAACCAGCGCTTACTGTGCGAGAATCGGAGGGCGCGCACGCGGATCC
CCCGCTGGCCTGGACCCCGTGGGGTCAAGTTCCCTGCCGGGCGGGGGGCACCGGTGCCGCCCGCTGTTCTCCCA
CGGGGCCCTGGTTTTCGAGTCTCTGTACAGCCTCTTCCGGCGGCAGCGTGCACCGGGCGGGCCTCCGTGCACACT
CAGCACACGCCTGCCACACAGCGTGCCTTGCCTGTACTCTGGCAGCAAACCTGTCTGCCTCTGTGGATCCACA
GCCTGGCAGAGCCGAGCCGTACCTGATTTTTTCACTGTTTCTACCTGTGTGCTGGAGCTCATGAGTATTTTATAA
ACTCCATTTAGGTACTTTCAGGAAACATGCAGCATTTTTTAAAAAATGAAAATTGTTTTTCTACTTCATTTTTCTCT
TTTAGAGTCAAAGGATATTTATTTATAGGCCTTTTTTTTTTTTAAATATAGAATCTGAGGCTGTTTGGGCTTTGACT
TAAATTTCCATCAGGCCTCTCTCCAGCAGGTAATCCCTCTCCTTCCGCTGGGTCCCCTGGGGAGGTGTGAACCTCA
AGGGCCTAGCCCCAAAACACTTTTTCTGCTTTTCTTAATCCTTTTCCAGTCCCCTCTTTTTTTTATAAACGTTGGC
AGTTTGATGTTTCTGTTTTCGGCATAACGTAATCCATTTCACTGTAGCCTAAACTCCAGTCCGAGGTTGGATATTG
TTCAAATGAGCAGGGCCCCGAGCTGGAAGCGCAAGGCAGCCGCCGCGTGCCGCTCCTCCCTTGCCCTCAGGCCAG
GTCCCTGCTGGAAGCGGCTGCATCTTCTGTGACCCCTGGTTTTCCATGGTGACTGGCGTCACGCTGCCACCCGAG
TATGGCTGACCTTCTGTCAGAGAGAGGAGCCGAGTCTTTTGCTTGTGGAAGGAGACGCTGGGCTGTGCGGTGCG
GAGGGTGATGAGGATGTCTGGTGACAGCCGTGCGGACACCACTCCTCTCTGCAGCACTGCCTCCAGCGCCAGGG
TCGCGGGCACATCCCACTGAGAGCGGGGGTCCCTGCCCCATCTTAGAGTCAAAGGCAGAGGGGCTTCCAGGCCCTG
GATGGGGTATTTTGGTGTACCTGAAGTCCCTCTGACATCACCTTGTTTTCATCATTTTTTATGACAGAATTAGAA
ACCATCCTTCAAGCACAATAATCATCACAGACTTGAGTTTGCTTCTTAAAGCAAAGGCTCCGGGTTTGTGTTGGA
AAATTTTTTTGATTTCTGAAATGAATTGATTTTTATATTGGGGCATCTCTATAGAAAAGTGACCACCAAGGCCAG
TAAGTACGGGAAAAAATGTTTACTAACTTCCTCAGAGATTGCTGATACGCGTTTCTCCACTGACAGACATTTAAA
AACAACCTTCAGTCCGTTTCAATCAATCACCTCGACTTGTTTTTTAGCATGGACACTGCCAGCAGGACAGACAG
GGATGGAGTAAACCGAAGTCAATTTTCAGGGCTCTTGGCGTGTGGACACAGAAGAAATCCTAGTGCAGCCTTTGG
TAGCTAACAGTCACTGATTTTATAATTGGAGAATGCGTAAAGATTCATTTTTCAAGGAGAAGAGCCTGCAAATGG
CCAATGAAGGAGGTAAATAAACTAAGATATTCCGAGGGAAGGGACCCAGGCCACCTCCCTTCCGCAGGTCTGCAG
ATGAAGGGTTTTTTGAAATGAAATGCCACTGTGCATTTTTCAGAAAAAAAATCTCTGATAAACAGACTTTGAATGG
ATGTTTGTCTCCTGATTCTCTTTTCTCTTCGTGGCGACTTAGAGTTGGCGGATATTCGGAAGTGTGAATGTAC
ATAGCGTTGAGTTAAACCCCTTGTGTGTGAGACAGGACGCGAGCGGGCCCTGGTGCCCTGGGGGCCAGACCCGTG
GGCAGGTGGGGCATGGGCCCTGGCCTGCGGGGACCTGCTGGGGTGTGAGGGCAGAGGGAGGGTTGCCATGAAGGA
ACTTGGGATTTTCAATGGAATAAGTAAACATAAAGTCTATACCTTGGG

1671/6881
FIGURE 1545

GGCGGCTGAGAGGCGGGCGGGCCGGGGGCGCCGGGCGCGGGGCCGCCATGTGGAGCGGCCGCAGCTCCTTCACCA
GCTTGGTGGTGGGCGTGTTTCGTGGTCTACGTGGTGCACACCTGCTGGGTCATGTACGGCATCGTCTACACCCGCC
CGTGCTCCGGGCGACGCCAACTGCATCCAGCCCTACCTGGCGCGGGCGGCCAAGCTGCAGCTGAGCGTGACACCA
CGACGAGGTCCACCTGGGTGCTGAGAACAAACATCGACCTGGTCTTGAATGTGGAAGACTTTGATGTGGAGTCCA
AATTTGAAAGGACAGTTAATGTTTCTGTACCAAAGAAAACGAGAAACAATGGGACGCTGTATGCCTACATCTTCC
TCCATCACGCTGGGGTCCCTGCCGTGGCACGACGGGAAGCAGGTGCACCTGGTCAGTCCTCTGACCACCTACATGG
TCCCCAAGCCAGAAGAAATCAACCTGCTCACC GGAGTCTGATACACAGCAGATCGAGGCGGAGAAGAAGCCGA
CGAGTGCCCTGGATGAGCCAGTGTCCCACTGGCGACCGCGGCTGGCGCTGAACGTGATGGCGGACAACCTTTGTCT
TTGACGGGTCTCCCTGCCCTGCCGATGTGCATCGGTACATGAAGATGATCCAGCTGGGGAAAACCGTGCATTACC
TGCCCCATCTGTTCATCGACCAGCTCAGCAACCGCGTGAAGGACCTGATGGTCATAAACCGCTCCACCACCGAGC
TGCCCCCTCACCGTGTCTACGACAAGGTCTCACTGGGGCGGCTGCGCTTCTGGATCCACATGCAGGACGCCGTGT
ACTCCCTGCAGCAGTTCCGGGTTTTTCAGAGAAAGATGCTGATGAGGTGAAAGGAATTTTTGTAGATACCAACTTAT
ACTTCCTGGCGCTGACCTTCTTTGTGCGAGCGTTCCATCTTCTCTTTGATTTCTGGCCTTTAAAAATGACATCA
GTTTCTGGAAGAAGAAGAAGAGCATGATCGGCATGTCCACCAAGGCAGTGCTCTGGCGCTGCTTCAGCACCGTGG
TCATCTTTCTGTTCCTGCTGGACGAGCAGACGAGCCTGCTGGTGCTGGTCCCGGCGGGTGTGGAGCCGCCATTG
AGCTGTGGAAAGTGAAGAAGGCATTGAAGATGACTATTTTTTGGAGAGGCCTGATGCCCCGAATTTAGTTTGGCA
CTTACAGCGAATCTGAGAGGAAAACCGAGGAGTACGATACTCAGGCCATGAAGTACTTGTACATACCTGCTGTACC
CTCTCTGTGTCGGGGGTGCTGTCTATTCACTCCTGAATATCAAATATAAGAGCTGGTACTCCTGGTTAATCAACA
GCTTCGTCAACGGGGTCTATGCCTTTGGTTTCTCTCATGCTGCCCCAGCTCTTTGTGAACCTACAAGTTGAAGT
CAGTGGCACATCTGCCCTGGAAGGCCTTCACCTACAAGGCTTTCAACACCTTCATTGATGACGTCTTTGCCTTCA
TCATCACCATGCCACGTCTCACCGGCTGGCCTGCTTCCGGGACGACGTGGTGTCTTCTGGTCTACCTGTACCAGC
GGTGGCTTTATCCTGTGGATAAACGCAGAGTGAACGAGTTTGGGGAGTCTACGAGGAGAAGGCCACGCGGGCGC
CCCACACGGACTGAAGGCCGCCCCGGGCTGCCGCCAGCCAAGTGCAACTTGAATTGTCAATGAGTATTTTTGGAAG
CATTTGGAGGAATTCCTAGACATTGCGTTTTCTGTGTTGCCAAAATCCCTTCGGACATTTCTCAGACATCTCCCA
AGTTCCCATCACGTCAGATTTGGAGCTGGTAGCGCTTACGATGCCCCACGTGTGAACATCTGTCTTGGTCACAG
AGCTGGGTGCTGCCGGTCACCTTGAGCTGTGGTGGCTCCCGGCACACGAGTGTCCGGGGTTCGGCCATGTCCTCA
CGCGGGCAGGGGTGGGAGCCCTCACAGGCAAGGGGGCTGTTGGATTTCCATTTAGGTGGTTTTCTAAGTGCTCC
TTATGTGAATTTCAAACACGTATGGAATTCATTCGCATGGACTCTGGGATCAAAGGCTCTTCTCTTTTGT
GAGAGTTGGTTGTTTTAAAGCTTAATGTATGTTTCTATTTTAAATAAAAAAAAAAAAAAAAAAAAAA

1672/6881
FIGURE 1546

MWSGRSSFTSLVVGVFVVYVVHTCWVMYGIVYTRPCSGDANCIQPYLARRPKLQLSVYTTTRSHLGAENNIDLVL
NVEDFDVESKFERTVNVSVPPKTRNNGTLYAYIFLHHAGVLPWHDGKQVHLVSPLTTYMVPKPEEINLLTGESDT
QQIEAEKKPTSALDEPVSHWRPRLALNVMADNFVFDGSSLPADVHRMVKMIQLGKTVHYLPILFIDQLSNRVKDL
MVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQFGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLF
DFLAFKNDISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLEQTSLLVLVPAGVGAAIELWKVKKALKMTIFWR
GLMPEFQFGTYSESERKTEEYDTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGVYAFGFLFMLP
QLFVNYKLKSV AHL PWKAFTYKAFNTFIDDVFAFIITMPTSHRLACFRDDVVFVLYLYQRWLYPVDKRRVNEFGE
SYEEKATRAPHTD

1673/6881
FIGURE 1547

CTTCCCTTTTGCGGCTATCACCGAAGCAGGAGTGGCCAAAATGAAGTTTAATCCCTTTGTGACTTCCGACCGAAG
CAAGAATCGCAAAAGGCATTTCAATGCACCTTCCCACATTGGAAGGAAGACTATGTCTTCCCCTCTTTCCAAAGA
GCTGAGACAGAAGTACAACGTGTGATCCATGCCCATCCGAAAGGATGATGAAGTTCAGGTTGTACGTGGACACTA
TAAAGGTCAGCAAAATTGGCAAAGTAGTCCAGGTTTACAGGAAGAAATATGTTATCTACATTGAACGGGTGCAGCG
GGAAAAGGCTAATGGCACAACGTCCACGTAGGCATTACCCCCAGCAAGGTGGTTATCACTAGGCTAAAACCTGGA
CAAAGACTGTGAAAAGATCCTTGAACGGAAAGCCAAATCTTGCCAAGTAGGAAAGGAAAAGGGCAAATACAAGGA
AGAAACAATTGAGAAGATGCAGGAATAAAGTAATCTTATATACAAGCTTCGATTAAAACCTGAAACAAAGAAAAA

1674/6881
FIGURE 1548

CCAGAACACAGGTGTCATGAAAAC TACCCCTAAAAGCCAAAATGGGAAAGGAAAAGACTCATATCAACATTGTCTG
TCATTGGACACGTAGATTTCGGCAGGATGTCTACAAAATTGGTGGTATTGGTAGTGTTCTGTGGCCGAGTGGAG
ACTGGTATTCTCAAACCCGGTATGGTGGTCACCTTTGCTCCAGTCAACGTTACAACAGAAGTAAAATCTGTCGAA
ATGCACCATGAAGCTTTGGGTGAAGCTCTTCCTGGGGACAGTGTGGGCTTCCATGTCAAGAATGTGTCTGTCAAG
GATGTTTCGTCTGGCAACGTTGCTGGTGACAGCAAAAATGACCCACCAATGGAAGCAGCTGGCTTCACTGCTCAG
GTGATTATCCTGAACCATCCAGGCCAAATAAGCGCTGGCTATGCCCCTGTATTGGATTGCCACACGGCTCATATT
GCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCGTTCTGGTAAAAGCTGGAAGATGGCCCTAAATTC
TTGAAGTCCGGTGATGCTGCCATTGTTGATATGGTTCCTGGCAAGCCCATGTGTGCTGAGAGCTTCTCAGACTAT
CCACCTTTGGGTCGCTTTGCTGTTTCGTGATATGAGACACACAGTTGCGGTGGGTGTCATCAAAGCAGTGGACAAG
AAGGCTGCTGGAGCTGGCAAGGTCACCAACTCTGCCCAGAAAGCTCAGATGGCTAAATGAATATTATCCCTAATA
C

1675/6881
FIGURE 1549

CGACACAGTAGCATTCTGTGCCAATTTCTGGTTGGAATGGTAACAACATGCTGGAGCCAAGTGCTAACATGCCTTG
GTTCAAGGGATGGAAAGTCACCCGTAAGGATGGCAATGCCAGTGAACCATGCTGCTTGAGGCTCTGGACTGCAT
CCTACCACCAACTCGTCCAAGTACAAGCCCTTGCGCCTGCCTCTCCAGGATGTCTACAAAATTGGTGGTATTGG
TAGTGTTTCTGTTGGCCGAGTGGAGACTGGTATTCTCAAACCCGGTATGGTGGTCACCTTTGCTCCAGTCAACGT
TACAACAGAAGTAAAAATCTGTCGAAATGCACCATGAAGCTTTGGGTGAAGCTCTTCCTGGGGACAGTGTGGGCTT
CCATGTCAAGAATGTGTCTGTCAAGGATGTTTCGTCTGGCAACGTTGCTGGTGACAGCAAAAATGACCCACCAAT
GGAAGCAGCTGGCTTCACTGCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCTGGCTATGCCCCTGT
ATTGGATTGCCACACGGCTCATATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCGTTCTGGTAA
TATGGTTTCTGGCAAGCCCATGTGTGCTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTGCTGTTTCGTGA
TATGAGACACACAGTTGCGGTGGGTGTCATCAAAGC

1676/6881
FIGURE 1550

GCCAAAATGGGAAAGGAAAAGACTCATATCAACATTGTCGTCATTGGACACGTAGATTTCGGGCAAGTCCACCACT
ACTGGCCATCTGATCTATAAATGCAGTAGCATCGACAAAAGAACCATTGAAAAATTTGAGAAGGAGACTGCTGAG
ATGGGAAAGGGCTCTTTCAAGTATGGCTGGGTCTTGGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATT
GATATCTCCTTGTGGAAATTTGAGACCAGCAAGTACTATGTGACTATCACTGATGCTCCAGGACACAGAGACTTC
ATCAAAAACATGATTACAGGGACATCTCAGGCTGACTGTGCTGTCCCGATTGTTGCTGCTGGTGTGGTGAATTT
GAAGCTGGTATCTCTAAGAATGGGCAGACCCGAGAGCATGCCCTTCTGGCTTACACACTGGGTGTGAAACAATA
ATTGTTGGTGTTAACAAAATGGATTCCACTGAGCCACCCTACAGCCAGAAGAGATATGAGGAAATTGTTAAGGAA
GTCAGCACTTACATTAAGAAAATTGGCTACAACCCCGACACAGTAGCATTGTGCCAAATTCCTGAAGTCCGGTG
ATGCTGCCATTGTTGATATGGTTCCTGGCAAGCCCATGTGTGCTGAGAGCTTCTCAGACTATCCACCTTTGGGTC
GCTTTGCTGTTCGTGATATGAGACACACAGTTGCGGTGGGTGTC

1677/6881
FIGURE 1551

AAATTGTTAAGGAAGTCAGCACTTACATTAAGAAAATTGGCTACAACCCGACACAGTAGCATTGTGCCAATTT
CTGGTTGGAATGGTAACAACATGCTGGAGCCAAGTGCTAACATGCCTTGGTTCAAGGGATGGAAAAGTCACCCGTA
AGGATGGCAATGCCAGTGGAACCATGCTGCTTGAGGCTCTGGACTGCATCCTACCACCAACTCGTCCAACGACA
AGCCCTTGCGCCTGCCTCTCCAGGATGTCTACAAAATTGGTGGTATTGGTAGTGTTCTGTGGCCGAGTGGAGA
CTGGTATTCTCAAACCCGGTATGGTGGTCACCTTTGCTCCAGTCAACGTTACAACAGAAGTAAAAATCTGTCGAAA
TGCACCATGAAGCTTTGGGTGAAGCTCTTCCTGGGGACAGTGTGGGCTTCCATGTCAAGAATGTGTCTGTCAAGG
ATGTTTCGTCGTGGCAACGTTGCTGGTGACAGCAAAAATGACCCACCAATGGAAGCAGCTGGCTTCACGCTCAGG
TGATTATCCTGAACCATCCAGGCCAAATAAGCGCTGGCTATGCCCTGTATTGGATTGCCACACGGCTCATATTG
CATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCGTTCTGGTAAAAAGCTGGAAGATGGCCCTAACACC
TTTGGGTCGCTTTGCTGTTTCGTGATATGAGACACACAGTTGCGGTGGG

1678/6881
FIGURE 1552

CTTTTTCACAACGGGTTTGCCGCCAGAACACAGGTGTCATGAAAACCTACCCCTAAAAGCCAAAATGGGAAAGGAA
AAGACTCATATCAACATTGTCGTCATTGGACACGTAGATTTCGGGCAAGTCCACCACTACTGGCCATCTGATCTAT
AAATGCAGTAGCATCGACAAAAGAACCATTGAAAAATTTGAGAAGGAGACTGCTGAGATGGGAAAGGGCTCTTTC
AAGTATGGCTGGGTCTTGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTGTGGAAA
TTTGAGACCAGCAAGTACTATGTGACTATCACTGATGCTCCAGGGATGTCTACAAAATTGGTGGTATTGGTAGTG
TTCCTGTTGGCCGAGTGGAGACTGGTATTCTCAAACCCGGTATGGTGGTCACCTTTGCTCCAGTCAACGTTACAA
CAGAAGTAAAATCTGTCGAAATGCACCATGAAGCTTTGGGTGAAGCTCTTCCTGGGGACAGTGTGGGCTTCCATG
TCAAGAATGTGTCTGTCAAGGATGTTTCGTCGTGGCAACGTTGCTGGTGACAGCAAAAATGACCCACCAATGGAAG
CAGCTGGCTTCACTGCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCTGGCTATGCCCCGTATTGG
ATTGCCACACGGCTCATATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCGTTCTGGTAAAAAGC
TGGAAGATGGCCCTAAATTCTTGAAGTCCGGTGATGCTGCCATTGTTGATATGGTTTCCTGGCAAGCCCATGTGTG

1679/6881
FIGURE 1553

CTTTTTCACAACGGGTTTGCCGCCAGAACACAGGTGTCATGAAAACCTACCCCTAAAAGCCAAAATGGGAAAGGAA
AAGACTCATATCAACATTGTCGTCATTGGACACGTAGATTTCGGGCAAGTCCACCACTACTGGCCATCTGATCTAT
AAATGCAGTAGCATCGACAAAAGAACCATTGAAAAATTTGAGAAGGAGACTGCTGAGATGGGAAAGGGCTCTTTC
AAGTATGGCTGGGTCTTGGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTGTGGAAA
TTTGAGACCAGCAAGTACTATGTGACTATCACTGATGCTCCAGGACACAGAGACTTCATCAAAAACATGATTACA
GGGACATCTCAGGCTGACTGTGCTGTCCCGATTGTTGCTGCTGGTGTCTTCTCAAACCCGGTATGGTGGTCACCT
TTGCTCCAGTCAACGTTACAACAGAAGTAAAATCTGTGCAAATGCACCATGAAGCTTTGGGTGAAGCTCTTCCTG
GGGACAGTGTGGGCTTCCATGTCAAGAATGTGTCTGTCAAGGATGTTTCGTCGTGGCAACGTTGCTGGTGACAGCA
AAAATGACCCACCAATGGAAGCAGCTGGCTTCACTGCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGCG
CTGGCTATGCCCCGTGATTGGATTGCCACACGGCTCATATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTG
ATCGCCGTTCTGGTAAAAAGCTGGAAGATGGCCCTAAATTCTTGAAGTCCGGTGATGCTGCCATTGTTGATATGG
TTCCTGGCAAGCCC

1680/6881
FIGURE 1554

CTTTTTCACAACGGGTTTGCCGCCAGAACACAGGTGTCATGAAAACTACCCCTAAAAGCCAAAATGGGAAAGGAA
AAGACTCATATCAACATTGTCGTCATTGGACACGTAGATTGGGGCAAGTCCACCACTACTGGCCATCTGATCTAT
AAATGCAGTAGCATCGACAAAAGAACCATTGATATCTCCTTGTTGGAAATTTGAGACCAGCAAGTACTATGTGACT
ATCACTGATGCTCCAGGACACAGAGACTTCATCAAAAACATGATTACAGGGACATCTCAGGCTGACTGTGCTGTC
CCGATTGTTGCTGCTGGTGTGGTGAATTTGAAGCTGGTATCTCTAAGAATGGGCAGACCCGAGAGCATGCCCTT
CTGGCTTACACACTGGGTGTGAAACAATAATTGTTGGTGTTAACAAAATGGATTCCACTGAGCCACCCTACAGC
CAGAAGAGATATGAGGAAATTGTTAAGGAAGTCAGCACTTACATTAAGAAAATTGGCTACAACCCCGACACAGTA
GCATTTGTGCCAATTTCTGGTTGGAATGGTAACAACATGCTGGAGCCAAGTGCTAACATGCCTTGTTCAAGGGA
TGGAAAGTCACCCGTAAGGATGGCAATGCCAGTGAACCATGCTGCTTGAGGCTCTGGACTGCATCCTACCACCA
ACTCGTCCAAGTACAAGCCCTTGCGCCTGCCTCTCCAGGATGTCTACAAAATTGGTGGTATTGGTAGTGTTCCT
GTTGGCCGAGTGGAGACTGGTATTCTCAAACCCGGTATGGTGGTCACCTTTGCTCCAGTCAACGTTACAACAGAA
GTTGTGGGCTTCCATGTCAAGAATGTGTCTGTCAAGGATGTTTCGTCGTGGCAACGTTGCTGGTGACAGCAAAAAT
GACCCACCAATGGAAGCAGCTGGCTTCACTGCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAA

1681/6881
FIGURE 1555

TATAAATGCAGTAGCATCGACAAAAGAACCATTGAAAAATTTGAGAAGGAGACTGCTGAGATGGGAAAGGGCTCT
TTCAAGTATGGCTGGGTCTTGGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTGTGG
AAATTTGAGACCAGCAAGTACTATGTGACTATCACTGATGCTCCAGGACACAGAGACTTCATCAAAAACATGATT
ACAGGGACATCTCAGGCTGACTGTGCTGTCCCGATTGTTGCTGCTGGTGTTGGTGAATTTGAAGCTGGTAICTCT
AAGAATGGGCAGACCCGAGAGCATGCCCTTCTGGCTTACACACTGGGTGTGAAACAATAATTGTTGGTGTTAAC
AAAATGGATTCCACTGAGCCACCCTACAGCCAGAAGAGATATGAGGAAATTGTTAAGGAAGTCAGCACTTACATT
AAGAAAAATTGGCTACAACCCCGACACAGTAGCATTGTGCCAATTTCTGGTTGGAATGGTAACAACATGCTGGAG
CCAAGTGCTAACATGCCTTGGTTCAAGGGATGGAAAGTCACCCGTAAGGATGGCAATGCCAGTGGAAACCATGCTG
CTTGAGGGCTCCAGTCAACGTTACAACAGAAGTAAAATCTGTCGAAATGCACCATGAAGCTTTGGGTGAAGCTCT
TCCTGGGGACAGTGTGGGCTTCCATGTCAAGAATGTGTCTGTCAAGGATGTTTCGTCGTGGCAACGTTGCTGGTGA
CAGCAAAAATGACCCACCAATGGAAGCAGCTGGCTTCACTGCTCAGG

1682/6881
FIGURE 1556

GTCGGCGTGTCGAGTGGCTCTTCTGGCTGCTGAGGCGGGTTAAGGTCTGAGGGTCTTGTTGGGGCCACGGCGCTG
ATCACCAGGTGTTTGGCTTGGTCGGTTCTTATTTCTCGCCTGGCAATGGCGACGTACACCTGCATAACTTGCCGG
GTGGCGTTCCGCGACGCGGACATGCAGCGGGCCCACTATAAGACGGACTGGCACCGCTACAACCTGCGGCGGAAG
GTGGCCAGCATGGCCCCAGTGACCGCCGAGGGCTTCCAGGAGCGAGTGCGGGGCGCAGCGGGCCGTGCGGGAGGAG
GAGAGCAAGGGCTCGGCCACCTACTGCACCGTTTGCAGTAAGAAGTTTGCCTCTTTCAACGCCTACGAGAACCAC
CTCAAGTCCCGGCGTCACGTTGAGCTGGAGAAGAAGGCCGTGCAGGCAGTGAATCGGAAAGTGAGATGATGAAT
GAAAAGAAGTTGGAGAAAGGACTGGGCGTGGACAGTGTGGACAAGGATGCCATGAACGCGGCCATCCAGCAGGCC
ATCAAGGCCCAGCCGTCCATGTCTCCAAGAAGGCGCCCCAGCGCCTGCAAAGGAGGCCAGGAATGTCGTGGCC
GTGGGTACTGGTGGCCGTGGGACCCACGACCGAGACCCGAGTGAGAAACCACCCCGGCTCCAGTGGTTTGAACAG
CAGGCGAAGAAGTTGGCAAAGCAGCAGGAGGAGGACAGCGAGGAGGAGGAAGAGGACCTGGATGGAGACGATTGG
GAAGATATTGATTCTGATGAAGAATTGGAATGTGAGGATACTGAAGCAATGGACGATGTGGTGGAGCAGGATGCA
GAGGAGGAAGAGGCTGAGGAAGGCCACCCCTTGGTGCCATCCCTATCACGGACTGCTTATTTTGTTCCTCAT
TCCAGCTCGCTGATGAAGAATGTGGCTCACATGACCAAAGACCACAGTTTCTTTATTCCTGATATAGAATATCTT
TCAGATATTAAGGGACTGATTAAATACTTGGGAGAGAAAGTTGGTGTTGGCAAGATTTGCTTGTGGTGCAACGAG
AAAGGGAAGTCCTTCTACTCCACAGAAGCTGTACAGGCACATATGAATGACAAAAGCCACTGTAAGCTCTTCACA
GATGGCGATGCTGCTTTGGAATTTGCAGACTTCTATGATTTTAGGAGTAGCTATCCAGATCACAAGGAAGGGGAG
GACCCCAATAAGGCTGAGGAGTTGCCCTCAGAAAAGAACTTGAATATGATGATGAAACCATGGAATTGATTCTG
CCTTCTGGTGCCAGAGTGGGTCAICGCTCCTTGATGAGATACTACAAACAGCGATTTGGCTTGTCAAGAGCTGTG
GCAGTTGCCAAAAATCGGAAGGCCGTGGGCCGAGTACTTCAGCAGTACAGAGCCCTGGGATGGACTGGCAGCACA
GGAGCGGCTCTTATGCGAGAGCGAGACATGCAGTATGTCCAAAGGATGAAATCAAATGGATGCTGAAGACAGGA
ATGAAGAACAATGCCACCAAGCAGATGCACTTTGGGTCCAAGTGAGATTCTGAGAGTCTGCTGGGATTGAGCAA
TCATCTCCTGCCCAAGTTTCTCCTTGCCCTGAGGACAGTGAAAGACAGATCATAGGAGAGACCCCTTTTGCTGC
TACTTCATTTCGTTCTGACCTAATAATAAAAGTTAGAACCAT

1683/6881
FIGURE 1557

GAACTCCAAG**ATG**GGAGGCAAGCTCAGCAAGAAGAAGAAGGGCTACAATGTGAACGACGAGAAAGCCAAGGAGAA
AGACAAGAAGGCCGAGGGCGCGGCGACGGAAGAGGAGGGGACCCCGAAGGAGAGTGAGCCCCAGGCGGCCGCAGA
GCCCCGCCGAGGCCAAGGAGGGCAAGGAGAAGCCCCGACCAGGACGCCGAGGGCAAGGCCGAGGAGAAGGAGGGCGA
GAAGGACGCGGCGGCTGCCAAGGAGGAGGCCCCGAAAGCGGAGCCCGAGAAGACGGAGGGCGCGGCAGAGGCCAA
GGCTGAGCCCCCGAAGGCGCCCGAGCAGGAGCAGGCGGCCCGGCCCGCTGCGGGCGGCGAGGCCCCCAAAGC
TGCTGAGGCCCGCGCGGCCCGGCCGAGAGCGCGGCCCTGCCGCCGGGAGGAGCCAGCAAGGAGGAAGGGGA
ACCCAAAAAGACTGAGGCGCCCGCAGCTCCTGCCCGCCAGGAGACCAAAGTGACGGGGCCCCAGCTTCAGACTC
AAAACCCGGCAGCTCGGAGGCTGCCCCCTCTTCCAAGGAGACCCCGCAGCCACGGAAGCGCCTAGTTCCACACC
CAAGGCCCAGGGCCCCGCGAGCCTCTGCAGAAGAGCCCAAGCCGGTGGAGGCCCCGGCAGCTAATTCGACCAAAC
CGTAACCGTGAAAGAG**TGACA**AGGACAGCCTATAGGAAAAACAATACCACTTAAAACAATCTCCTCTCTCTCT
CTCTCTCTCTCTATCTCTCTCTCTATCTCCTCTCTCTCTCTCCTCTCCTATCTCTCCTCTCTCTCTCTCTCT
ACTAACTTGTTTCAAATTGGAAGTAATGATATGTATTGCCCAAGGAAAAATACAGGATGTTGTCCCATCAAGGGA
GGGAGGGGGTGGGAGAATCCAAATAGTATTTTTGTGGGGAAATATCTAATATACCTTCAGTCAACTTTACCAAGA
AGTCCTGGATTTCGAAGATCCGCGTCTGAAAGTGCAGTACATCGTTTGTACCTGAAACTGCCGCCACATGCACTC
CTCCACCGCTGAGAGTTGAATAGCTTTTCTTCTGCAATGGGAGTTGGGAGTGATGCGTTTGATTCTGCCACAGG
GCCTGTGCCAAGGCAATCAGATCTTTATGAGAGCAGTATTTTCTGTGTTTTCTTTTAAATTTACAGCCTTTCTTA
TTTTGATATTTTTTTAATGTTGTGGATGAATGCCAGCTTTCAGACAGAGCCCACTTAGCTTGTCCACATGGATCT
CAATGCCAATCCTCCATTCTTCCTCTCCAGATATTTTGGGAGTGACAAACATTCTCTCATCCTACTTAGCCTAC
CTAGATTTCTCATGACGAGTTAATGCATGTCCGTGGTTGGGTGCACCTGTAGTTCTGTTTATTGGTCAGTGGA
TG

1684/6881
FIGURE 1558

MGGKLSKKKKGYNVNDEKAKEKDKKAEGAATEEEGTPKESEFQAAAEPAEAKEGKEKPDQDAEGKAEEKEGEKDA
AAAKEEAPKAPEKTEGAAEAKAEPKAPQEQAAPGPAAGGEAPKAAEAAAAPAESAAPAGEEPSKEEGEPKK
TEAPAAPAAQETKSDGAPASDSKPGSSEAAPSSKETPAATEAPSSTPKAQGPAASAEEPKEVEAPAAANSQITVTV
KE

1685/6881
FIGURE 1559

CGAGAGTCGTCGGGGTTTCCTGCTTCAACAGTGCTTGGACAGAACCTGGCGCTCGTCCCCACACCGGCCGGCTG
CCCATAGCCAGCCCTCCGTCACCTCCTCAGCCGCGCTCTCCTTAGTCGCCGCCATGACGACCGCGTCCAC
CTCACAGGTGCGCCAGGACTACCACCAGGACTAAAGGCCGCCATCAACCGCCAGATCAACCTGGAGCTCTACGCC
TCCTGCGTTTACCTGTCCATGTCTTACTACTTTGACCGCGATGATGTGGCTTTGAAGAACTTTGCCAAATACTTT
CTTCACCAATCTCATGAGGAGAGGGAACATGCTGAGAACTGATGAAGCTGCAGAACCAAGGAGGTGGCCGAATC
TTCCTTCAGGATATCAAGAAACCGGACTGTGATGACTGGGAGAGCGGGCTGAATGCGATGGAGTGTGCATTACAT
TTGGAAAAAATGTGAATCAGTCACTACTGGAAGTGCACAACTGGCCACTGACAAAAATGACCCCCATTTGTGT
GACTTCATTGAGACACATTACCTGAATGAGCAGGTCAAAGCCATCAAAGAATTGGGTGACCACATGACCAACTG
TGCAAGATGGGAGCACCCGAATCTAGCTTGGCGGAATATCTCTTTGACCAGCACACCCTGGGAGACAGTGATAAT
GAAAGCTAAGCCTCAGGCTAATTTCCCATAGCCGTGGGGTGACTTCCCTGGTCACCAAGG

1686/6881
FIGURE 1560

MSYYFDRDDVALKNFAKYFLHQSHEEREHAEKLMKLQNGGGGRIFLQDIKKPCDDWESGLNAMECALHLEKNVN
QSLLELHKLATDKNDPHLCDFIETHYLNEQVKAIKELGDHMTNLCKMGAPESSLAEYLFQHTLGDSDNES

1687/6881
FIGURE 1561

ATGCCCCAAAACGATCAGTGTGCGTGTGACCACCATGGACGCAGAGCTGGAGTTTACCATCCAGCCCCAACACCACC
GGGAAGCAGCTATTTGACCAGAAGGTGACTGCCCAGGAAGTGCAGGAAGGAAAGCCCCCTGCTCTTTAAGTTCAGT
GCCAAGTTCTACCCCTGAGGATGTGTCCGACCGAGGAATTGATTTCAGGACACCACTCAGCGTCTGTTCCCTTCTGCA
ATGAAAGAGGGCATTCTCAGTGATGATATTTACTGCCGGCCTGAGACTGCTGTGCTGCTGGCCTCCCATGCTGTC
CAGTCTAAGTATGGGAACCTTCAGTAAGGAGGTGCATAAGTCTGGCTACCTGGCCGGAGACGAGTTGCTCCACAG
AGAGTCCTGGAACAGCACAACTCAGCAAGGACCAGTGGGAGGAGCGGATCCAGGTGTGGCATGAGGAACACCGT
GGCATGCTCAGGGAGGATGCTGTCCTGGAGTATCTGAAGATTGCTCAAGATCTGGAGATGTATGGTGTAACACTAC
TTCAGCATCAAGAAAAAGAAAGGCTCAGAGCTGTGGCTGGGGGTGGATGCACTGGGTCTCAACATCTATGAGCAG
CATGACAGACTAACTCCCAAGATAGGCTTTCCCTTGGAGTGAAATCAGGAGCATTTCCTTCAATGATAAGAACTTT
GTCATCAAGCCCATTGACAAAAGAGCCCCGGACTTTGTCTTCTATGCTCCCTGGCTGCAGATTAACAAGCGGATC
TTGGCCTTGTGCATGGGGAACCGTGAACATATACATGCGCCGTCGCAAGCCTGACACCATTGAGGTGCAGCAGATG
AAGGCACGGGCCCCGGGAGGAGAAGCACCAGAAGCAGATGGAGCGTGCTATGCTGGAAAATGAGAAGAAGCGTGAA
ATGGCAGAAAAGCAGAAAGAGAAGATTGAACGGGAGAAGGAGCTGATGGGGAGGCTGAAGCAGATCGAGGAACAG
ACTAAGAAGGCTCAGCAAGAACTGGAAGAACAGACCCGTAGGGCTCTGGAACCTGGGAAGGAACGGAAGCATGCC
CAGAGCGAGGCTGAAAAGCTGGCCAAGGAGCTTCAAGAAGCTGAAGAGGCCAAGGAAAAGAAAGAGAGTGAGGCT
ATGGAGTGGCAGCAGAAGGCCCAGATGGTACAGGAAGACTTGGAGAAGACCCGTGCTGAGCTGAAGACTGCCATG
AGTACATCTCATGTGGCAGAGCCTGCTGAGAATGAGCAGGATGAGCAGGATGAGAATGGGGCAGAGGCTAGTGCT
GACCTACGGGCTGATGCTATGGCCAAGGACCGCAGTGAGGAGGAATGTACCACTGAGGCAGAGAAGAATGAGCGT
GTGCAGAAGCACCTGAAGGCCCTCACTTCGGAGCTGGCCAGTGCCCGAGATGAGTCCAAGAAGACTGCCAATGAC
ATGATCCATGCTGAGAACATGTGA

1688/6881
FIGURE 1562

ATGCCGCCCTCGCCTGCGTCCTGCGGCCGTCCCGAGGTGTCACGCTGTCAACAACACAAAGTCGTAGTTGACGTC
GACCATGAGCACTTAGCAGGAGGGCACGCACAGGGACTTGTGCCCGGCGGGGTCCAGCTCCTGCACCTTCAGCTG
CCACTCCATCCTCTGCACAGCGTTTCAGGGCCGCAGCCTCGTGCTGCTGCCGCATGAGGAGGAAGAAGCTAGATGAA
CTTATGAGTGAAGAAGCCTATGAGAAATACATAAAATCTATTGAGGAGTGA

1689/6881
FIGURE 1563

MPPSPASCGRPEVSRQQHKVVVDVDHEHLAGGHAQGLVPGGVQLLHLQLPLHPLHSVQGRSLVLLPHEEEELDE
LMSEEAYEKYIKSIEE

1690/6881
FIGURE 1564

GCCGAGCGATGGGCATCTCTCGGGACAACCTGGCACCAGCGCCGCAAAACCGGGGGCAAGAGAAAGCCCTACCACA
AGAAGCGGAAGTATGAGTTGGAGCGCCCAGCTGCCAACACCAAGATTGGCCCCCGCCGCATCCACACAGTCCGTG
TGCAGGGAATGTTGTACTCGTAAACAAGGATCATCGATGTTGTCTACAATGCATCTAATAATGAGCTGGTTCGT
ACCAAGACCCCTGGTGAAGAATTGCATCGTGCTCATCGACAGCACACCGTGCCGACAGTGGTAAGATGTCCCACTA
CGTGCTGCCCCCTGGGCCGCAAGAAGGGAGCCAAGCTGACTCCTGAGGAAGAAGAGATTTTAAACAAAAAACGATT
TAAACAAATTCAGAAGAAATATGATGAAAGGAAAAAGAATGCCAAAATCAGCAGTCTCCTGGAAGAGCAGTTCCA
GCAGGGCAAGCTTCTTGATGCATCGCTTCAAGGCCGGGACAGTGTGGCCGAGCAGATGGCTATGTGCTAGAGGG
CAAAGGGTTGGAGTTCATCTTAGGAAAATCAAGGCCCGGAAAGGCAAATAAATCCTTGTTTTGTCTTCACCCAT
GTAATAAAGGTGTTTATTGTTTTGTTC

1691/6881
FIGURE 1565

CCGAGGCCAAGTCCCGGGCGCTAGCCACCTCCCACCCGCTCTTGGCTCCTCTCCTCTAGGCCGTCGCTTTTCGG
GTTCTCTCATCGCTTCGTCTGTCGCCAATGTTTGGAGAGAAGGCCAGCAGTCCTTCAGGGAAGATGGGAGGCGAG
GAGAAGCCGATTGGTGCTGGTGAAGAGAAGCAAAAGGAAGGAGGCCAAAAAGAAGAACAAGAAGGATCTGGAGAT
GGAGGTCGAGCTGAGTTGAATCCTTGGCCTGAATATATTTACACACGTCCTTGAGATGTATAATATACTAAAAAGCA
GAACATGATTCCATTCTGGCAGAAAAGGCAGAAAAAGATAGCAAGCCAATTAAAGTCACCTTGCCTGATGGTAAA
CAGGTTGATGCGGAATCTTGGAAAACTACACCATATCAAATTGCCTGTGGAATTAGTCAAGGCCTGGCCGACAAC
ACCGTTATTGCTAAAGTAAATAATGTTGTGTGGGACCTGGACCGCCCTCTGGAAGAAGATTGTACCTTGGAGCTT
CTCAAGTTTGAGGATGAGGAAGCTCAGGCAGTGTATTGGCACTCTAGTGCTCACATAATGGGTGAAGCCATGGAA
AGAGTCTATGGTGGATGTTTATGCTACGGTCCGCCAATAGAAAATGGATTCTATTATGACATGTACCTCGAAGAA
GGGGGTGTGTCTAGCAATGATTTCTCTCTCTGGAGGCTTTGTGTAAGAAAATCATTAAAGAAAAACAAGCTTTT
GAAAGACTGGAAGTTAAGAAAGAACTTTACTGGCAATGTTTAAGTACAACAAGTTCAAATGCCGGATATTGAAT
GAAAAGGTGAATACTCCAACACCACAGTCTATAGATGTGGCCCTTGATAGATCTCTGCCGGGGTCTCATGTT
AGACACACGGGCAAAATTAAGGCTTTAAAAATACACAAAAATTCCTCCACGTAAGGGAAGGCAAAGCAGATATG
GAGACTCTCCAGAGAATTTATGGCATTTCATTCCCAGATCCTAAAATGTTGAAAGAGTGGGAGAAGTTCCAAGAG
GAAGCTAAAAACCGAGATCATAGGAAAATTGGCAGGGACCAAGAACTATATTTCTTTCATGAACTCAGCCCTGGA
AGTTGCTTTTTTCTGCCAAAAGGAGCCTACATTTATAATGCACTTATTGAATTCATTAGGAGCGAATATAGGAAA
AGAGGATTCCAGGAGGTAGTCACCCCAAACATCTTCAACAGCCGACTCTGGATGACCTCGGGCCACTGGCAGCAC
TACAGCGAGAACATGTTCTCCTTTGAGGTGGAGAAGGAGCTGTTTGCCCTGAAACCCATGAACTGCCCAGGACAC
TGCCTTATGTTTGATCATCGGCCAAGGTCCTGGCGAGAACTGCCTCTGCGGCTAGCTGATTTTGGGGTACTTCAT
AGGAACGAGCTGTCTGGAGCACTCACAGGACTCACCCGGGTACGAAGATTCCAACAGGATGATGCTCACATATTC
TGTGCCATGGAGCAGATTGAAGATGAAATAAAAGGTTGTTTGGATTTTCTACGTACGGTATATAGCGTATTTGGA
TTTTCTTTTAACTAAACCTTTCTACTCGCCCGGAAAAATTCCTTGGAGATATCGAAGTATGGGATCAAGCTGAG
AAACAACCTGAAAACAGTCTGAATGAATTTGGTGAAAAGTGGGAGTTAACTCTGGAGATGGAGCTTTCTATGGC
CCAAAGATTGACATACAGATTAAAGATGCGATTGGGCGGTACCACCAGTGTGCAACCATCCAGCTGGATTTCCAG
TTGCCCATCAGATTTAATCTTACTTATGIAAGCCATGATGGTGATGATAAGAAAAGGCCAGTGATTGTTTCATCGA
GCCATCTTGGGATCAGTGGAAAAGATGATTGCTATCCTCACAGAAAACCTATGGGGGCAAATGGCCCTTTTGGCTG
TCCCCTCGCCAGGTAATGGTAGTTCCAGTGGGACCAACCTGTGATGAATATGCCCAAAGGTACGACAACAATTC
CACGATGCCAAATTCATGGCAGACATTGATCTGGATCCAGGCTGTACATTGAATAAAAAGATTGGAATGCACAG
TTAGCACAGTATAACTTCATTTTAGTTGTTGGTGAAAAGAGAAAATCAGTGGCACTGTTAATATCCGCACAAGA
GACAATAAGGTCCACGGGGAACGCACCATTTCTGAACTATCGAGCGGCTACAGCAGCTCAAAGAGTTCCGCAGC
AAACAGGCAGAAGAAGAATTTTAATGAAAAAATTACCCAGATTGGCTCCATGGAAAAGGAGGAACAGCGTTTCCG
TAAAATTGACTTTGTACTCTGAAAACGTCAATTTATATTGAACTTGGAGGAGTTTGGCAAAGTCTGAATAGGTCA
ACCTGCAGGCGTAACATTTTTGACCTAGTCAGTTTTTAAACAATGTGCATTTGAAGGAGTTAATTTAAAGAGAG
CCAATAAAATGATTTTACTCATTCAATCTGAGTACTGGAAGTGAAACATGAGGAATGCTTTAGTGTAATGTGG
GAGAACTTTTTTGTAATTTAATGCAATTGAAAAAGTTTTCAAATTCAATTAAGATAACTAGAATTGGATTATGG
TGTAAT

1692/6881
FIGURE 1566

MFEEKASSPSGKMGEEKPIGAGEEKQKEGGKKKNKEGSGDGGRAELNPWPEYIYTRLEMYNILKAEHDSILA EK
AEKDSKPIKVTLPD GKQVDAESWKTPYQIACGISQGLADNTVIAKVNNVVWDLDRPLEEDCTLELLKFEDEEAQ
AVYWHSSAHIMGEAMERVYGGCLCYGPP IENGFFYDMYLEEGGVSSNDFSSLEALCKKIIKEKQAFERLEVKKET
LLAMFKYNKFKCRILNEKVNTPTTTVYRCGPLIDLRCRGPVHRHTGKIKALKIHKNSSTYWEGKADMETLQRIYGI
SFPDPKMLKEWEKFQEEAKNRDHRKIGRDQELYFFHELSPGSCFFLPKGAYIYNALIEFIRSEYRKRGFQEVVTP
NIFNSRLWMTSGHWQHYSENMF SFEVEKELFALKPMNCPGHCLMFDHRPRSWRELPLRLADFGVLHRNELSGALT
GLTRVRRFQQDDAHIFCAMEQIEDEIKGCLDFLRTVYSVFGFSFKLNLSTRPEKFLGDI EVWDQAEKQLENSLNE
FGEKWELNSGDGAFYGP KIDIQIKDAIGRYHQCATIQLDFQLPIRFNLTYVSHDGD DKRPVIVHRAILGSVERM
IAILTENYGGKWPFWLSPRQVMVVPVGPTCDEYAQKVRQQFHDAKFMADIDLDPGCTLNKKIRNAQLAQYNFILV
VGEKEKISGTVNIRTRDNKVGERTISETIERLQQLKEFRSKQAE EEF

1693/6881
FIGURE 1567

GAGCATGGATGATTGGCCAGAAATGAAGAAGAAGTTTGCAGATGTATTTGCAAAGAAGACGAAGGCAGAGTGGTG
TCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTTGAGGAGGTTGTTTCATCATGATCACAA
CAAGGAACGGGGCTCGTTTATCACCAGTGAGGAGCAGGACGTGAGCCCCGCCCTGCACCTCTGCTGTTAAACAC
CCCAGCCATCCCTTCTTTCAAAGGGATCCTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAATTTGGATT
CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAATAAGGCTGGTAGCAAGTTCTGGAT
CTTATACCCAACACACAGCAACATCCAGAAATAAAGATCTCAGGACCCCCCAGCAAGTCGTTTTGTGTCTCCTTG
GACTGAGTTAAGTTACAAGCCTTTCTTATACCTGTCTTTGACAAAGAAGACGGGATTGTCTTTACATAAAACCAG
CCTGCTCCTGGAGCTTCCCTGGACTCAACTTCCTAAAGGCATGTGAGGAAGGGGTAGATTCCACAATCTAATCCG
GGTGCCATCAGAGTAGAGGGAGTAGAGAATGGATGTTGGGTAGGCCATCAATAAGGTCCATTCTGCGCAGTATCT
CAACTGCCGTTCAACAATCGCAAGAGGAAGGTGGAGCAGGTTTCTTCATCTTACAGTTGAGAAAACAGAGACTCA
GAAGGGCTTCTTAGTTTCGTGTTTCCCTTAGCGCCTCAGTGATTTTTTCATGGTGGCTTAGGCCAAAAGAAATATC
TAACCATTCAATTTATAAATAATTAGGTCCCCAACGAATTAAATATTATGTCCTACCAACTTATTAGCTGCTTGA
AAAATATAATACACATAAATAAAAAAA

1694/6881
FIGURE 1568

GGCGCCGGGGATTGGGAGGGCTTCTTGACGGCTGCTGGGCTGGGGCTAAGGGCTGCTCAGTTTCCTTCAGCGGGG
CACTGGGAAGCGCC**ATGG**CACTGCAGGGCATCTCGGTCGTGGAGCTGTCCGGCCTGGCCCCGGGCCCCGTTCTGTG
CTATGGTCCTGGCTGACTTCGGGGCGCGTGTGGTACGCGTGGACCGGCCCGGCTCCCGCTACGACGTGAGCCGCT
TGGGCCGGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCGCGGGGAGCCGCCGTGCTGCGGCGTCTGTGCA
AGCGGTTCGGATGTGCTGCTGGAGCCCTTCCGCCGCGGTGTCATGGAGAACTCCAGCTGGGCCCAGAGATTCTGC
AGCGGGAAAAATCCAAGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTG
GCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATTGGCAGAAGTGGTGAGAATCCGTATGCC
CGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCTTATGTGTGCACTGGGCATTATAATGGCTCTTTTTGACC
GCACACGCACTGGCAAGGGTCAGGTCATTGATGCAAAATAGGTGGAAGGAACAGCATATTTAAGTCTTTTTCTGT
GGAAAACCTCAGAAATCAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTATA
CGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCAAGTTCTACGAGCTGCTGATCA
AAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGCATGGATGATTGGCCAGAAATGAAGAAGAAGT
TTGCAGATGTATTTGCAAAGAAGACGAAGGCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTC
CGGTTCTGACTTTTGAGGAGGTTGTTTCATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAGC
AGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCCAGCCATCCCTTCTTTCAAAAGGGATCCCTTCA
TAGGAGAACACACTGAGGAGATACTTGAAGAATTTGGATTTCAGCCGCGAAGAGATTTATCAGCTTAACTCAGATA
AAATCATTGAAAGTAATAAGGTAAAAGCTAGTCTCT**TAA**CTTCCAGGCCACGGCTCAAGTGAATTTGAATACTGC
ATTTACAGTGTAGAGTAACACATAACATTGTATGCATGGAAACATGGAGGAACAGTATTACAGTGTCTTACCCT
CTAATCAAGAAAAGAATTACAGACTCTGATTCTACAGTGATGATTGAATTTCTAAAAATGGTTATCATTAGGGCTT
TTGATTTATAAAACTTTGGGTACTTATACTAAATTATGGTAGTTATTCTGCCTTCCAGTTTGCTTGATATATTIG
TTGATATTAAGATTCTTGACTTATATTTTGAATGGGTTCTAGTGAAAAAGGAATGATATATTCTTGAAGACATCG
ATATACATTTATTTTACACTCTTGATTCTACAATGTAGAAAATGAGGAAATGCCACAAATTGTATGGTGATAAAAG
TCACGTGAAACAGAGTGATTGTTGCATCCAGGCCTTTTGTCTTGGTGTTCATGATCTCCCTCTAAGCACATTCC
AACTTTTAGCAACAGTTATCACACTTGTGAATTTGCAAAGAAAAGTTTCACCTGTATTGAATCAGAATGCCTTCA
ACTGAAAAAACATATCCAAAATAATGAGGAAATGTGTTGGCTCACTACGTAGAGTCCAGAGGGACAGTCAGTTT
TAGGGTTGCCTGTATCCAGTAACTCGGGGCCTGTTTCCCCGTGGGTCTCTGGGCTGTCAGCTTTCCTTTCTCCAT
GTGTTTGATTTCTCCTCAGGCTGGTAGCAAGTTCTGGATCTTATACCCAACACACAGCAACATCCAGAAATAAG
ATCTCAGGACCCCC

1695/6881
FIGURE 1569

MALQGISVVELSGLAPGPF CAMVLADFGARVVRVDRPGSRYDVSRLGRGKRSLVLDLKQPRGA AVLRR LCKRSDV
LLEPFRRGVMEKLQLGPEILQRENPR LIYARLSGFGQSGSFCRLAGHDINYLALSGVLSKIGRSGENPYAPLNLL
ADFAGGGLMCALGIIMALFDRTRTGKGQVIDANMVEGTAYLSSFLWKTQKSSLWEAPRGQNMLDGGAPFYTTYRT
ADGEFMAVGAIEPQFYELLIKGLGLKSDEL PNQMSMDDWPEMKKKFADVFAKKTAEWCQIFDGTDACVTPVLT
EEVVHHDHNKERGSFITSEEQDVSPRPAPLLLNTPAIP SFKRDPFIGEHTEEILEEFGFSREEIYQLNSDKIIES
NKVKASL

1696/6881

FIGURE 1570

TCTTTCTGGTCTCGGCCGCAGAAGCGAGATGACGAAGGGAACGTCATCGTTTGGAAGCGTCGCAATAAGACGCA
CACGTTGTGCCGCCGCTGTGGCTCTAAGGCCTACCACCTTCAGAAGTCGACCTGTGGCAAATGTGGCTACCCTGC
CAAGCGCAAGAGAAAGTATAACTGGAGTGCCAAGGCTAAAAGACGAAATACCACCGGAACTGGTCGAATGAGGCA
CCTAAAAATTGTATACCGCAGATTCAGGCATGGATTCCGTGAAGGAACAACACCTAAACCCAAGAGGGCAGCTGT
TGCAGCATCCAGTTCATCTTAAGAATGTCAACGATTAGTCATGCAATAAATGTTCTGGTTTTAAAAAATAC

1697/6881
FIGURE 1571

MTKGTSSFGKRRNKTHTLCRRCGSKAYHLQKSTCGKCGYPAKRKRKYNWSAKAKRRNTTGTGMRHLKIVYRRFR
HGFREGTTPKPKRAAVAASSSS

1698/6881
FIGURE 1572

GTGTCTGTGGGAGGTTATGTTTATTTGAGACTTCTCCATCGGGATCGCCTGGTGTACCAAGTGTCCACTGGTAC
TGAGGTTTGTGCTGCCTGCCTTCTTGCCATGTCTAACGAAGTAGAAACAAGTGCAACCAATGGTCAGCCCGACCAAC
AGGCCGCACCAAAAAGCACCCTCAAAGAAGGAAAAAAGAAAGGCCCTGAAAAGACAGATGAATATCTCTTAGCAA
GGTTCAAAGGCGATGGTGTAAATATAAGGCCAAGCTGATTGGCATTGATGATGTGCCAGATGCAAGAGGGGATA
AAATGAGCCAAGACTCTATGATGAACTAAAGGGAATGGCGGCAGCTGGTCGGTCTCAGGGACAACACAAACAAA
GGATCTGGGTCAACATTTCCCTTTCTGGGATAAAAAATAATTGATGAGAAAAGTGGGGTAATAGAGCATGAACATC
CAGTAAATAAGATTTCTTTTCATTGCCCGTGATGTGACAGACAACCGGGCATTGGTTACGTGTGTGGAGGAGAAG
GCCAGCATCAGTTTTTTTGCCATAAAAACCGGGCAACAGGCTGAACCATTAGTTGTTGATCTTAAAGACCTTTTTTC
AAGTTATCTATAATGTAAAGAAAAAGGAAGAAGAAAAAGATAGAGGAAGCCAGCAAAGCAGTTGAGAATG
GGAGTGAGGCCCTAATGATTCTAGATGACCAAACCTAACAACTGAAATCGGGTGTGACCAGATGGATTTGTTTG
GGGACATGTCTACACCTCCTGACCTAAATAGTCCAACAGAAAGCAAAGATATCCTGTTAGTGGATCTAAACTCTG
AAATCGACACCAATCAGAATTTCTTAAAGAGAAAATCCATTCTTAAACAAACGGCATCACCTCCTGTTCTCTTCCTC
GACCAACGCCTCAGGCATCCTTCTTGCCCTGAAAATGCCTTTTCTGCCAATCTCAACTTCTTTCCACCCCTAATC
CTGATCCTTTCCGTGACGATCCTTTCACACAGCCAGACCAATCGACACCTTCTTCGTTTGATTCTCTCAAATCTC
CAGATCAGAAGAAAGAGAATTCGAGTAGCTCGTCTACTCCGCTGAGTAATGGGCCCCCTGAATGGTGATGTTGACT
ACTTTGGTCAGCAATTTGACCAGATCTCTAACCGGACTGGCAAACAGGAAGCTCAGGCAGGCCCATGGCCCTTTT
CAAGTTCGCAAACCCAGCCAGCAGTGAGAACTCAAAATGGGGTATCTGAAAGAGAACAGAACGGCTTCTCTGTCA
AATCCTCCCCGAACCTTTTGTGGGAAGCCCTCCCAAAGGACTGTCCATACAGAATGGCGTAAAGCAGGACTTGG
AAAGCTCTGTCCAGTCCCTACCCACATGACTCCATAGCCATTATCCACCTCCACAAAGTACCAAACAGGAAGAG
GCAGAAGGACTGCTAAGTCTTCAGCCAAAGACTTGCTTGATCAGACATCTTTGCTCCTCCCGTCTCAGAACCTT
CAGGCCAGGCGTCAACCCACAGGACAACCTACAGCCCTGCAGCCCAACCTCTGGATCTCTTCAAACAAGTGCTC
CTGCCCCAGTGGGGCCCCCTGGTGGGTCTAGGTAGGTGTAAGTGTACACTCCCTCAGGCAGGACCATGGAACACA
GCATCTTTGGTCTTCAATCAGTCCCCCTTCAATGGCTCCGGGAGCCATGATGGGTGGTCAACCTTCAGGTTTTAGT
CAGCCCGTCATTTTTTGGTACAAGTCCAGCTGTTTCAGGTTGGAACAGCCTTCACCTTTGCAGCCTCAACTCCC
CCTCCAGTGCCTGTTGTCTGGGGCCCCCTTCTGCATCTGTGGCACCCAATGCTTGGTCAACAACAAGCCCTTTGGGG
AATCCTTTTTCAGAGCAATATTTTTCCAGCTCCTGCTGTGTCCACTCAGCCCCCATCCATGCACTCCTCTCTCCTG
GTCATCCTCCTCAGCCACCTCCCAGAGCTGGCCCTCCCAAGGACATCTCCAGTGATGCCTTCACTGCCTTAGAC
CCACTTGGGGATAAAGAGATCAAGGATGTGAAAGAAATGTTTAAAGGATTTCCAAGTGCAGGCAGCCACCTGCTGTG
CCCGCGCGGAAGGGAGAGCAGACTTCTTCTGGGACTTTGAGTGCCTTTGCCAGTTATTTCAACAGCAAGGTTGGC
ATTCTCAGGAGAATGCAGACCATGATGACTTTGATGCTAATCAACTATTGAACAAGATCAATGAACCACCAAAG
CCAGCTCCCAGACAAGTTTCCCTGCCAGTTACCAAATCTACTGACAATGCATTTGAGAACCCTTTCTTTAAAGAT
TCTTTTGGTTCATCACAAGCCTCTGTGGCTTCTTCTCAACCTGTATCTTCTGAGATGTATAGGGATCCATTTGGA
AATCCTTTTGCCTAAATTTCTGAACTTGGTCTGCAGACCATCCAGAGGAATAAAAAGGTTGGCCTTAGTAGTCAA
AACAAAGCTGATAGCCAGACACGTTCTGATTTCTGCCCTTGTTCCAGCTTTGACGTATTATCTGTTGCCTTATTT
CTCATTGCCCTCTTCTACTTGTAAAATGCTTTTCACTTTCTGTCTAGGTTAAAGCTAAACTGAATCTATGGCTTTA
AATAAATTAAGATCCTAAACTCTCTAGCTTAAAGTGTAATGAAGTACAGTAGTTTCCCTACTGAACCCTGCCTCT
TGTGTCCCTGGAACCTTCTAGAACACCTGCCTTCTACCCTCTGGTTGGGAGATGCAGCCACCACATCCCTTCATA
TCATACTGTTTTGAATAAATTTTCAAATCCTTATTGTTTCAGAGTTGTTTGGGGGTTCTGTTTCAGAGCATAAAAC
CTAAAGGTTATAGTAGAACAAGGCACCTTCTTAAAAAGAAATCTTGCTTCAGACCATCAGTTACAGAGAATTTCTA
AAGTAAAATTAAGCAACTACAACCTTCTCCTTAGACACTTTGGAATCTAACCCTTAAGGACCTTTTAAAGAGA
TAGCTTCTCTTCTTCTGAAGATCAATTTCTCCCAAGGCCAAGATTGTCCTTTTCTCCCATTTCTTGCTAGCTAT
TGCAAATGAGGGGAAGAACATTATTCATCTCTCCTCCCCCTTTTTTTCTGATTCTTTTTTTCAGTCAGTTTGTCTCC
TGGGTTCAAGTAGTATTACCACCTTTTACAAGCAACAGACTCTCACAGGGC

1699/6881
FIGURE 1573

TAGGATGGAAAAGGCAGATGTAAAGTCCCTCATGGCGAAATATAACACGGGGGGCAACCCGACAGAGGATGTCTCA
GTCAATAGCCGACCCTTCAGAGTACAGGGCCAAACTCATCTTCAGGAATACAAGCAAGAAAGAACTTATTCAAC
AACCAAGGAAATGCCAGCCCTCCTGCAGGACCCAGCAATGTACCTAAGTTTGGGTCCCCAAAGCCACCTGTGGCA
GTCAAACCTTCTTCTGAGGAAAAGCCTGACAAGGAACCCAAGCCCCGTTTCTAAAGCCCCTGGAGCAGGCCAA
AGATTGGAACACCAGCCAGCTTGACCACCAGAGACCCCGAGGCGAAAGTGGGATTTCTGAAACCTGTAGGCCCC
AAGCCCATCAACTTGCCCAAAGAAGATTCCAAACCTACATTTCCCTGGCCTCCTGGAAACAAGCCATCTCTTCAC
AGTGTAACCAAGACCATGACTTAAAGCCACTAGGCCCCGAAATCTGGGCCTACTCCTCCAACCTCAGAAAATGAA
CAGAAGCAAGCGTTTCCCAAATTGACTGGGGTTAAAGGGAAATTTATGTCAGCATCACAAAGATCTTGAACCCAAG
CCCCCTCTTCCCCAAACCCGCCTTTGGCCAGAAGCCGCCCTTAAGTACCGAGAACTCCCATGAAGACGAAAGCCCC
ATGAAGAATGTGTCTTCATCAAAAGGTCCCCAGCTCCCCTGGGAGTCAGGTCCAAAAGCGGCCCTTTAAACCA
GCAAGGGAAGACTCAGAAAATAAAGACCATGCAGGGGAGATTTCAAGTTTGCCCTTTCTGGAGTGGTTTTGAAA
CCTGCTGCGAGCAGGGGAGGCCTAGGTCTCTCCAAAATGGTGAAGAAAAAAGGAAGATAGGAAGATAGATGCT
GCTAAGAACACCTTCCAGAGCAAAATAAATCAGGAAGAGTTGGCCTCAGGGACTCCTCCTGCCAGGTTCCCTAAG
GCCCCCTTCTAAGCTGACAGTGGGGGGGCCATGGGGCCAAAGTCAGGAAAAGGAAAAGGGAGACAAGAATTCAGCC
ACCCCGAAACAGAAAGCCATTGCCTCCCTTGTTTTACCTTGGGTCCACCTCCACCAAACCCAACAGACCACCAAAAT
GTTGACCTGACGAAATTCACAAAACCTCTTCTGGAAACAGTACTAGCAAAGGCCAGACGTCTTACTCAACAACCT
TCCCTGCCACCACCTCCACCATCCCATCCGGCCAGCCAACCACCATTGCCAGCATCTCACCCATCACAACCACCA
GTCCCAAGCCTACCTCCCAGAAACATTAAACCTCCGTTTGACCTAAAAAGCCCTGTCAATGAAGACAATCAAGAT
GGTGTACGCACTCTGATGGTGCTGGAATCTAGATGAGGAACAAGACAGTGAAGGAGAAACATATGAAGACATA
GAAGCATCCAAAGAAAAGAGAGAAGAAAAGGGAAGGAAGAAAAGAGAGTTAGAGCTGGAGAAAAAGGAACAG
AAAGAGAAAGAAAAGAAAAGAAACAAGAAATAAAGAAGAAATTTAAACTAACAGGCCCTATTCAAGTCATCCATCTT
GCAAAAGCTTGTTGTGATGTCAAAGGAGGAAAGAATGAAGTGAAGTCAAGCAAGGAGAGCAAATTGAAATCATC
CGCATCACAGACAACCCAGAAGGAAATGGTTGGGCAGAACAGCAAGGGGTTTATATGGCTATATTTAAACAACCT
GCTGTAGAGATTGACTATGATTCTTTGAACTGAAAAAGACTCTCTTGGTGCCCTTCAAGACCTATTGAAGAT
GACCAAGAAGTATATGATGATGTTGCAGAGCAGGATGATATTAGCAGCCACAGTCAGAGTGGAAGTGGAGGGATA
TTCCCTCCACCACAGATGATGACATTTATGATGGGATTGAAGAGGAAGATGCTGATGATGGTTTCCCTGCTCCT
CCTAAACAATTGGACATGGGAGATGAAGTTTACGATGATGTGGATACCTCTGATTTCCCTGTTTCATCAGCAGAG
ATGAGTCAAGGAACATAATTTTGAAAAGCTAAGACAGAAGAAAAGGACCTTAAGAAGCTAAAAAAGCAGGAAAAA
GAAGAAAAAGACTTCAGGAAAAAATTTAAATATGATGGTGAAATTAGAGTCCTATATTCAACTAAAGTTACAACCT
TCCATAACTTCTAAAAAGTGGGGAACCAGAGATCTACAGGTAAACCTGGTGAATCTCTAGAAGTTATACAAACC
ACAGATGACACAAAAGTTCTCTGCAGAAATGAAGAAGGGAATATGGTTATGTCCTTCGGAGTTACCTAGCGGAC
AATGATGGAGAGATCTATGATGATATTGCTGATGGCTGCATCTATGACAATGACTAGCACTCAACTTTGGTCATT

1700/6881
FIGURE 1574

MAKYNTGGNPTEDEVSVNSRPFRTGPNSSSGIQARKNLFNNQGNASPPAGPSNVPKFGSPKPPVAVKPSSEEKPD
KEPKPPFLKPTGAGQRFGTPASLTTRDPEAKVGFLKPVGPKPINLPKEDSKPTFPWPPGNKPSLHSVNQDHDLP
LGPKSGPTPPTSENEQQAFFPKLTGVKGKFMASQDLEPKPLFPKPAFGQKPPLSTENSHEDESPMKNVSSSKGS
PAPLGVRSSKSGPLKPARESENKDHAGEISSLPFGVVLKPAASRGGLGLSKNGEEKKEDRKIDAAKNTFQSKIN
QEELASGTPPARFPKAPSKLTVGGPWGQSQEKEKGDKNSATPKQKPLPPLFTLGPPPPKPNRPPNVDLTKFHKTS
SGNSTSKGQTSYSTSLPPPPPSHPASQPPLPASHPSQPPVPSLPPRNIKPPFDLKSPVNEDNQDGVTHSDGAGN
LDEEQDSEGETYEDIEASKEREKKREKEEKKRLELEKKEQKEKEKKEQEIKKKFKLTGPIQVIHLAKACCDVKGG
KNELSFQGEQIEIIRITDNPEGKWLGRRTARGSYGYIKTTAVEIDYDSLKLKDSLGLAPSRIEDDQEVYDDVAE
QDDISSHSQSGSGGIFPPPPDDDIYDGIEEDADDGFFAPPKQLDMGDEVYDDVDTSDFPVSSAEMSQGTNFGKA
KTEEKDLKKLKKQEKEEKDFRKKFKYDGEIRVLYSTKVTTSTSKKWGTRDLQVKPGESLEVIQTTDDTKVLCRN
EEGKYGYVLRSYLADNDGEIYDDIADGCIYDND

[illegible]

1702/6881
FIGURE 1576

MERSGPSEVTGSDASGDPQLAVTMGFTGFGKKARTFDLEAMFEQTRRTAVERSRTLEAREKEEEMNREKELRR
QNEDIEPTSSRSNVVRDCSKSSSRDTSSSESEQSSDSSDELIGPPLPPKMVGKPVNFMEEDILGPLPPPLNEEE
EEAEEEEEEEEEEENPVHKIPDSHEITLKHGKTKTVSALGLDPSGARLVTGGYDYDVKFWDFAGM DASFKAFRSLQ
PCECHQIKSLQYSNTGDMILVVSGSSQAKVIDRDGFVMECIKGDQYIVDMANTKGHTAMLHTGSWHPKIKGEFM
TCSNDATVRTWEVENPKKQKSVFKPRTMQGKKVIPTTCTYSRDGNLIAAACQNGSIQIWDRNLTVHPKFHYKQAH
DSGTDITSCVTF SYDGNVLASRGDDSLKLWDIRQFNKPLFSASGLPTMFPMTDCCFSPDDKLIVTGTSIQRGCGS
GKL VFFERRTFQRVYEIDITDASVVRCLWHPKLNQIMVGTGNGLAKVYYDPNKSQRGAKLCVVKTQRKAKQAETL
TQDYIITPHALPMFREPRQRSTRKQLEKDRLDPLKSHKPEPPVAGPGRGGRVGTGGTLSSYIVKNIALDKTDDS
NPREAILRHAKAAEDSPYWVSPAYSKTQPKTMFAQVESDDEEAKNEPEWKRRKI

1703/6881
FIGURE 1577

CGGGCTGTAGAGCCTTGCGCGCGCAGTGGGGATGGAACGTTGCTAGGCTTAGCGGGTCTGGCTGCTGGGGGCCCCG
AGCAGCACGCTCGGAGCCGCCGCGCGCCAAAGCGGAATCTGGGAGGCGAGCAGCTCTGCAGTTAATGCACGTAT
TTTAAACTCCCGGGCCTGCGGACGCT**ATG**CACAGGAAGCACCTCCAGGAGATTCCAGACCTGAGTAGCAACGTTG
CCACCAGCTTCACGTGGGGATGGGATTCCAGCAAGACTTCTGAACTGCTGTCAGGCATGGGGGTCTCCGCCCTGG
AGAAAGAGGAGCCCCGACAGTGAGAACATCCCCCAGGAAGTCTCTCAAACCTGGGCCACCCGGAGAGCCCCCAC
GGAAACGGCTGAAGAGCAAAGGGAGTGACAAAGACTTTGTGATTGTCCGCAGGCCTAAGCTAAATCGAGAGAACT
TTCCAGGTGTTTCATGGGACTCCCTTCCGGATGAGCTGCTCTTGGGAATCTTTTCCTGTCTGTGCCTCCCTGAGC
TGCTAAAGGTCTCTGGTGTTTGTAAGAGGTGGTATCGCCTAGCGTCTGATGAGTCTCTATGGCAGACCTTAGACC
TCACAGGTAAAAATCTGCACCCGGATGTGACTGGTCCGGTTGCTGTCTCAAGGGGTGATTGCCTTCCGCTGCCAC
GATCATTTATGGACCAACCATTGGCTGAACATTTTCAGCCCTTTTCGTGTACAGCACATGGACCTATCGAACTCAG
TTATAGAAGTGTCCACCCTCCACGGCATACTGTCTCAGTGTTCCAAGTTGCAGAATCTAAGCCTGGAAGGCCTGC
GGCTTTTCGGATCCCATTGTCAATACTCTCGCAAAAAACTCAAAATTTAGTGCAGCTTAACCTTTCTGGGTGTTCTG
GATTCTCTGAATTTGCCCTGCAGACTTTGCTAAGCAGCTGTTCCAGACTGGATGAGCTGAACCTCTCCTGGTGT
TTGATTTCACTGAAAAGCATGTACAGGTGGCTGTTGCGCATGTGTGACAGACCATCACCCAGCTGAATCTTAGCG
GCTACAGAAAGAATCTCCAGAAATCAGATCTCTCTACTTTAGTTAGAAGATGCCCAATCTTGTCCATCTAGACT
TAAGTGATAGTGTGATGCTAAAGAATGACTGCTTTTCAGGAATTTTTCCAGCTCAACTACCTCCAACACCTATCAC
TCAGTCGGTGCTATGATATAATACCTGAACTTTACTATTAGTGACAAGAGCTGGGGTTAGGATCCGGTTGGACT
CTGACATCGGATGCCCTCAAACATACAGAACTTCCAAACTCAAGTCCAGCCATAAGCTATTTTGCCAACATGTCA
GAGTAATCTGTATTTTTGTATGTGATTTCTACTTTTATAGACTTGTTTTAAACAAT**TAA**AACACATTTTTATAAA
AATGAGTGCTTAAACTAAAAAAAAAAAAAAAAAAAAA

1704/6881
FIGURE 1578

MHRKHLQEIPDLSSNVATSFTWGWDSSTSELLSGMGVSALEKEEPPDSENIPQELLSNLGHPESPFRKRLKSKGS
DKDFVIVRRPKLNRENFPGVSWDSLPEDELLLGIFSCLCPELLKVSGVCKRWYRLASDESLWQTLDDLTKGNLHPD
VTGRLLSQGVIAFRCPRSFMDQPLAEHFSFPRVQHMDLSNSVIEVSTLHGILSQCSKLQNLSEGLRLSDPIVNT
LAKNSNLVRLNLSGCSGFSEFALQTLSSCSRLELNLSWCFDFTEKHVQVAVAHVSETITQLNLSGYRKNLQKS
DLSTLVRRCPNLVHLDLSDSVMLKNDCFQEFFQLNYLQHLSSLRCYDIIPETLLLVTRAGVRIRLDSDIGCPQTY
RTSKLKSSHKLFCQHVRVICIFVCDFFYFRLVLKQ

1705/6881
FIGURE 1579

GAATTCCGGGCTGTAGAGCCTTGCGCGCGCAGTGGGGATGGAACGTTGCTAGGCTTAGCGGGTCTGGCTGCTGGG
GGCCCGAGCAGCACGCTCGGAGCCGCCGCGCCAAAGCGGGAATCTGGGAGGCGAGCAGCTCTGCAGTTAATGC
ACGTATTTTAACTCCCGGGCCTGCGGACGCTATGCACAGGAAGCACCTCCAGGAGATTCCAGACCTGAGTAGCA
ACGTTGCCACCAGCTTCACGTGGGGATGGGATTCCAGCAAGACTTCTGAACTGCTGTCAGGCATGGGGGTCTCCG
CCCTGGAGAAAAGAGGAGCCCGACAGTGAGAACATCCCCAGGAAGTCTCTCAAACCTGGGCCACCCGGAGAGCC
CCCCACGGAAACGGCTGAAGAGCAAAGGGAGTGACAAAGACTTTGTGATTGTCCGCAGGCCTAAGCTAAATCGAG
AGAACTTTCCAGGTGTTTCATGGGACTCCCTTCCGGATGAGCTGCTCTTGGGAATCTTTTCCTGTCTGTGCCTCC
CTGAGCTGCTAAAGGTCTCTGGTGTGTGTAAGAGGTGGTATCGCCTAGCGTCTGATGAGTCTCTATGGCAGACCT
TAGACCTCACAGGTAAAAATCTGCACCCGGATGTGACTGGTCGGTTGCTGTCTCAAGGGGTGATTGCCTTCCGCT
GCCCACGATCATTTATGGACCAACCATTTGGCTGAACATTTTCAGCCCTTTTCGTGTACAGCACATGGACCTATCGA
ACTCAGTTATAGAAGTGTCCACCCTCCACGGCATACTGTCTCAGTGTTCCAAGTTGCAGAATCTAAGCCTGGAAG
GCCTGCGGCTTTCGGATCCCATTGTCAATACTCTCGCAAAAACTCAAATTTAGTGCGACTTAACCTTTCTGGGT
GTTCTGGATTCTCTGAATTTGCCCTGCAGACTTTGCTAAGCAGCTGTTCCAGACTGGATGAGCTGAACCTCTCCT
GGTGTTTTGATTTCACTGAAAAGCATGTACAGGTGGCTGTTGCGCATGTGTCAGAGACCATCACCCAGCTGAATC
TTAGCGGCTACAGAAAGAATCTCCAGAAATCAGATCTCTCTACTTTAGTTAGAAGATGCCCCAATCTTGTCCATC
TAGACTTAAGTGATAGTGTGTCATGCTAAAGAATGACTGCTTTCAGGAATTTTTCCAGCTCAACTACCTCCAACACC
TATCACTCAGTCGGTGCTATGATATAATACCTGAACTTTACTTGAAGTTGGAGAAAATCCCACACTAAAAACAC
TACAAGTTTTTGAATCGTGCCAGATGGTACCCTTCAACTGTTAAAGGAAGCCCTTCCTCATCTACAGATTAATT
GCTCCCATTTACCACCATTGCCAGGCCAACTATTGGCAACAAAAGAACCAGGAGATATGGGGCATCAAATGCC
GACTGACACTGCAAAAGCCCAGTTGTCTATGAAGTATTTATTGCAGGATGGTGTCTCTTCTTTAGAACAGGGAAA
ATAGGCAGGAAGCCCAATTGCTGGAGTACTTAGCTAGTTTTATTCTTGGTTTTCCCTTTGCCTTCATTCTGCAAG
TATACTAGGGAGCCATTTGAGAGGG

1706/6881
FIGURE 1580

MHRKHLQEIPDLSSNVATSFTWGWDSSTSELLSGMGVSALEKEEPDSENIPQELLSNLGHPESP
PRKRLKSKGS
DKDFVIVRRPKLNRENFP
GVSWD
SLPDELLLGIF
SCLCLPELLK
VSGVCKRWY
RLASDESLWQ
TLDLTGKNL
HPD
VTGRLLSQGVIA
FRCPRSFMDQ
PLAEHFSPF
RVQHMDLSN
SVIEVSTLH
GILSQCSKLQ
NLSLEGLRL
SDPIVNT
LAKNSNLVRLN
LSGCSGFSE
FALQTLSSC
SRLDELNL
SWCFDFTEK
HVQVAVAHV
SETITQLNL
SGYRKNLQKS
DLSTLVRRCP
NLVHLDLSD
SVMLKNDC
FQEFFQLN
YLQHL
SLSRCYDI
IPETLLEL
GEIPTLKT
LQVFGIV
PDGT
LQLLKEAL
PHLQINCS
HFTTIAR
PTIGNKKN
QEIWGIK
CRLTLQK
PSCL

1707/6881
FIGURE 1581A

ATTCTTCTAAGGAGCCTAAATTCACCAAGTGCCGTTACCTGAGCGAGAGACTTTTTTCATGCCACTGGACAGATG
AGGTTTCATCATGGTACAAAGAACCTAGGACCCATACAGCTGTTCTATACCAGAAGGAACACTCAAGAATGGACTC
AAGAATGGAAAAGATGCCCTGATTATGTTTCTGCTGGGGAAAACAGCTGTTACTTTAATTCATCGTTTACCTCCA
TCTGGATACCTTATTGTATCAAGCTAACTAGCAATGGTGGTACAGTGGATGAAAAGTGTCTCTGTTGATGAAA
TAGTGCAACCAGATCCACCCATTGCCCTCAACTGGACTTTACTGAACGTCAGTTTAACTGGGATTCATGCAGATA
TCCAAGTGAGATGGGAAGCACCGCAATGCAGATATTCAGAAAGGATGGATGGTCTGGAGTATGAACTTCAAT
ACAAAGAAGTAAATGAACTAAATGGAAAATGATGGACCCTATATTGACAACATCAGTTCAGTGTACTCATTGA
AAGTGGATAAGGAATATGAAGTGCGTGTGAGATCCAAACAACGAAACTCTGGAAATTATGGCGAGTTCAGTGAGG
TGCTCTATGTAACACTTCCTCAGATGAGCCAATTTACATGTGAAGAAGATTTCTACTTTCCATGGCTCTTAATTA
TTATCTTTGGAATATTTGGGCTAACAGTGATGCTATTTGTATTCTTATTTTCTAAACAGCAAAGGATTAAAATGC
TGATTCTGCCCCCAGTTCAGTTCCAAAGATTAAAGGAATCGATCCAGATCTCCTCAAGGAAGGAAAATTAGAGG
AGGTGAACACAATCTTAGCCATTTCATGATAGCTATAAACCCGAATTCCACAGTGATGACTCTTGGGTTGAATTTA
TTGAGCTAGATATTGATGAGCCAGATGAAAAGACTGAGGAATCAGACACAGACAGACTTCTAAGCAGTGACCATG
AGAAATCACATAGTAACCTAGGGGTGAAGGATGGCGACTCTGGACGTACCAGCTGTTGTGAACCTGACATTCTGG
AGACTGATTTCAATGCCAATGACATACATGAGGGTACCTCAGAGGTTGCTCAGCCACAGAGGTTAAAAGGGGAAG
CAGATCTCTTATGCCTTGACCAGAAGAATCAAAATAACTCACCTTATCATGATGCTTGCCCTGCTACTCAGCAGC
CCAGTGTTATCCAAGCAGAGAAAAACAAACCACAACCACTTCTACTGAAGGAGCTGAGTCAACTCACCAAGCTG
CCCATATTTCAGCTAAGCAATCCAAGTTCACTGTCAAACATCGACTTTTATGCCCAGGTGAGCGACATTACACCAG
CAGGTAGTGTGGTTCCTTTCCCGGGGCCAAAAGAATAAGGCAGGGATGTCCCAATGTGACATGCACCCGGAAATGG
TCTCACTCTGCCAAGAAAACCTTCCTTATGGACAATGCCTACTTCTGTGAGGCAGATGCCAAAAAGTGCTCCCTG
TGGCTCCTCACATCAAGGTTGAATCACACATACAGCCAAGCTTAAACCAAGAGGACATTTACATCACCACAGAAA
GCCTTACCAGTCTGCTGCTGGGAGGCCTGGGACAGGAGAACATGTTCCAGGTTCTGAGATGCCTGTCCCAGACTATA
CCTCCATTTCATATAGTACAGTCCCCACAGGGCCTCATACTCAATGCGACTGCCTTGCCCTTGCCCTGACAAAAGAGT
TTCTCTCATCATGTGGCTATGTGAGCACAGACCAACTGAACAAAATCATGCCTTAGCCTTTCTTTGGTTTCCCAA
GAGCTACGTATTTAATAGCAAAGAATTGACTGGGGCAATAACGTTTAAAGCCAAAACAATGTTTAAACCTTTTTTG
GGGGAGTGACAGGATGGGGTATGGATTCTAAAATGCCTTTTCCCAAATGTTGAAATATGATGTTAAAAAATAA
GAAGAATGCTTAATCAGATAGATATTCCATTGTGCAATGTAAATATTTTAAAGAATTGTGTCAGACTGTTTAGT
AGCAGTGATTGTCTTAATATTGTGGGTGTTAATTTTTGATACTAAGCATTGAATGACTATGTTTTTAATGTATAG
TAAATCACGCTTTTTGAAAAAGCGAAAAAATCAGGTGGCTTTTGCAGTTTCAGGAAAATTGAATGCAAACCATAGC
ACAGGCTAATTTTTTGTGTTTCTTAAATAAGAACTTTTTTATTTAAAAAACTAAAACTAGAGGTGAGAAATT
TAACTATAAGCAAGAAGGCAAAAATAGTTTGATATGTAAAACATTTATTTTGACATAAAGTTGATAAAGATAT
TTTTAATAATTTAGACTTCAAGCATGGCTATTTTATATTACACTACACACTGTGTACTGCAGTTGGTATGACCCC
TCTAAGGAGTGTAGCAACTACAGTCTAAAGCTGGTTTAAATGTTTGGCCAATGCACCTAAAGAAAAACAACTCG
TTTTTTACAAAGCCCTTTTATACCTCCECCAGACTCCTTCAACAATTCTAAAATGATTGTAGTAATCTGCATTATT
GGAATATAATTGTTTTATCTGAATTTTTTAAACAAGTATTTGTTAATTTAGAAAACTTTAAAGCGTTTGCACAGAT
CAACTTACCAGGCACCAAAAGAAGTAAAAGCAAAAAAGAAAACCTTTCTTACCAAATCTTGGTTGATGCCAAAA
AAAAATACATGCTAAGAGAAGTAGAAATCATAGCTGGTTTACACTGACCAAGATACTTAAGTGCTGCAATTGCAC
GCGGAGTGAGTTTTTTAGTGCGTGAGATGGTGAGAGATAAGATCTATAGCCTCTGCAGCGGAATCTGTTTACAC
CCAATTGGTTTTTGCTACATAATTATCCAGGAAGGGAATAAGGTACAAGAAGCATTTTGTAAAGTTGAAGCAAATC
GAATGAAATTAAGTGGTAAATGAAACAAAGAGTTCAAGAAATAAGTTTTTGTTCACAGCCTATAACCAGACACA
TACTCATTTTTTCATGATAATGAACAGAACATAGACAGAAGAAACAAGGTTTTTCAAGTCCCCACAGATAACTGAAAA
TTATTTAAACCGCTAAAAGAACTTTCTTTCTCACTAAATCTTTTATAGGATTTATTTAAAATAGCAAAAGAAGA
AGTTTTCATCATTTTTTACTTCTCTCTGAGTGGACTGGCCTCAAAGCAAGCATTTCAGAAGAAAAAGAAGCAACCT
CAGTAATTTAGAAATCATTTTGCATCCCTTAATATCCTAAACATCATTCAATTTTGTGTTGTTGTTGTTGTTGAGA
CAGAGTCTCGCTCTGTGCGCAGGCTAGAGTGCAGTGGCGCGATCTTGACTCACTGCAATCTCCACCTCCCACAGG
TTCAGGCGATTCCCGTGCTCAGCCTCCTGAGTAGCTGGGACTACAGGCACGCACCACCATGCCAGGCTAATTTT
TTTGTATTTTAGCAGAGACGGGGTTTACCATGTTGGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCACCC
GACTCGGCCTCCCAAAGTGCTGGGATTACAGGTGTAAGCCACCGTGCCAGCCCTAAACATCATTCTTGAGAGCA

1708/6881
FIGURE 1581B

TTGGGATATCTCCTGAAAAGGTTTATGAAAAGAAGAATCTCATCTCAGTGAAGAATACTTCTCATTTTTTAAAA
AAGCTTAAACCTTTGAAGTTAGCTTTAACTTAAATAGTATTTCCCATTTATCGCAGACCTTTTTTAGGAAGCAAG
CTTAATGGCTGATAATTTTAAATTCTCTCTCTTGCAGGAAGGACTATGAAAAGCTAGAATTGAGTGTTTAAAGTT
CAACATGTTATTTGTAATAGATGTTTGATAGATTTTCTGCTACTTTGCTGCTATGGTTTTCTCCAAGAGCTACAT
AATTTAGTTTCATATAAAGTATCATCAGTGTAGAACCTAATTCAATTCAAAGCTGTGTGTTTGGAAGACTATCTT
ACTATTTACAACAGCCTGACAACATTTCTATAGCCAAAAATAGCTAAATACCTCAATCAGTCTCAGAAATGTCAT
TTTGGTACTTTGGTGGCCACATAAGCCATTATTCAGTAGTATGACTAGTTGTGTCTGGCAGTTTATATTTAACTC
TCTTTATGTCTGTGGATTTTTTCCTTCAAAGTTTAAATAAATTTATTTTCTTGGATTCCTGATAGTGTGCTTCTGT
TATCAAACACCAACATAAAAAATGATCTAAACC

1709/6881
FIGURE 1582

CCTTCACACAGCTCTTTACCCATGCCTGGATCACTTCCTTTGAATGCAGAAGCTTGCTGGCCAAAAGATGTTGGG
ATTGTTGCCCTTGAGATCTATTTTCCTTCTCAATATGTTGATCAAGCAGAGTTGGAAAAATATGATGGTGTAGAT
GCTGGGAAGTATACCATTGGCTTGGGCCAGGCCAAGATGGGCTTCTGCACAGATAGAGAAGATATTAACCTCTCTT
TGCATGACTGTGGTTCAGAATCTTATGGAGAGAAAATAACCTTTCTATGATTGCATTGGGCGGCTGGAAGTTGGA
ACAGAGACAATCATCGACAAATCAAAGTCTGTGAAGACTAATTTGATGCAGCTGTTTGAAGAGTCTGGGAATACA
GATATAGAAGGAATCGACACAATAATGCATGCTATGGAGGCACAGCTGCTGTCTTCAATGCTGTAACTGGATT
GAGTCCAGCTCTTGGGATGGACGGTATGCCCTGGTAGTTGCAGGAGATATTGCTGTATATGCCACAGGAAATGCT
AGACCTACAGGTGGAGTTGGAGCAGTAGCTCTGCTAATTGGGCCAAATGCTCCTTTAATTTTTGAACGAGGGCTT
CGTGGGACACATATGCAACATGCCTATGATTTTTACAAGCCTGATATGCTATCTGAATATCCTATAGTAGATGGG
AAACTCTCCATACAGTGCTACCTCAGTGCATTAGACCGCTGCTATTCTGTCTACTGCAAAAAGATCCATGCCAG
TGGCAGAAAAGAGGGAATGATAAAGATTTTACCTTGAATGATTTTGGCTTCATGATCTTTCACTCACCATATTGT
AAACTGGTTCAGAAATCTCTAGCTCGGATGTTGCTGAATGACTTCCTTAATGACCAGAATAGAGATAAAAATAGT
ATCTATAGTGGCCTGGAAGCCTTTGGGGATGTTAAATTAGAAGACACCTACTTTGATAGAGATGTGGAGAAGGCA
TTTATGAAGGCTAGCTCTGAACTCTTCAGTCAGAAAAACAAAGGCATCTTTACTTGTATCAAATCAAATGGAAAT
ATGTACACATCTTCAGTATATGGTTCCCTTGCTATCTGTTCTAGCACAGTACTCACCTCAGCAATTAGCAGGGAAG
AGAATTGGAGTGTTCCTTATGGTTCTGGTTTGGCTGCCACTCTGTACTCTCTTAAAGTCACACAAGATGCTACA
CCGGGGTCTGCTCTTGATAAAATAACAGCAAGTTTATGTGATCTTAAATCAAGGCTTGATTCAAGAAGTGGTGTG
GCACCAGATGTCTTCGCTGAAAACATGAAGCTCAGAGAGGACACCCATCATTGTTGGTCAACTATATTCCCCAGGGT
TCAATAGATTCACTCTTTGAAGGAACGTGGTACTTAGTTAGGGTGGATGAAAAGCACAGAAGAACTTACGCTCGG
CGTCCCCTCCAAATGATGACACTTTGGATGAAGGAGTAGGACTTGTGCATTCAAACATAGCAACTGAGCATATT
CCAAGCCCTGCCAAGAAAGTACCAAGACTCCCTGCCACAGCAGCAGAACCTGAAGCAGCTGTCATTAGTAATGGG
GAACATTAAGATACTCTGTGAGGTGCAAGACTTCAGGGTGGGGTGGGCATGGGGTGGGGGTATGGGAACAGTTGG

1710/6881
FIGURE 1583

MPGSLPLNAEACWPKDVGIVALEIYFPSQYVDQAELEKYDGVDAKYTIIGLGQAKMGFCTDREDINSLCMTVVQN
LMERNNLSYDCIGRLEVGTETIIDKSKSVKTNLMQLFEESGNTDIEGIDTTNACYGGTAAVFNAVNWIESSWDG
RYALVVAGDIAVYATGNARPTGGVGAVALLIGPNAPLIFERGLRGTHMQHAYDFYKPDMLSEYPIVDGKLSIQCY
LSALDRCYSVYCKKIHAQWQKEGNDKDFTLNDFGFMIFHSPYCKLVQKSLARMLLNDFLNDQNRDKNISIYSGLEA
FGDVKLEDITYFDRDVEKAFMKASSELF SQTKASLLVSNQNGNMYTSSVYGSLASVLAQYSPQQLAGKRIGVFSY
GSGLAATLYSLKVTQDATPGSALDKITASLCDLKSRLDSRTGVAPDVFAENMKLREDTHHLVNYIPQGSIDSLFE
GTWYLVVRVDEKHRRTYARRPTPNDDTLDEGVGLVHSNIATEHIPSPAKKVPRLPATAAEPEAAVISNGEH

1711/6881
FIGURE 1584

CAATGGGTTTGCCACCAGAACACAGGTGTTGTGAAAACTACCCCTAAAAGCCAAAATGGGAAAGGAAAAAGACTCA
TATCAACATTGTCGTCAATTGGACACGTAAATTCGGGCAAGTCCACCCTACTGGCCATCTGACCTACAAATGTGG
TGGCATCGACAAAAGAACCATTGAAAAATTTGAGAAGGAGGCTGCTGAGATGGGAAAGGACTCCTTCAAGTATGC
CTGGGTCTTGCCATAAAGCTGAAAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTGTGGAAATTTGAGAC
CAGCAAGTACTATGTGACTATCATTGATGCCCCAGGACTCAGAGACTTCATCAAAAACATGATTACAGGGACATC
TCAGGCTGTGCTGTCTGATGGTTGCTGCTGCTGCTGGTGGCGAATTTGAAACTGGTATCTCCAAGAATGGGCAGACC
TGAGAGCATGCCCTTCTGGCTTACACACTGGGTGTGAAACAATAATTGTTGGTGTAAACAAAATGGATTCCACT
GAGCCACCCTACAGCCAGAAGAGAGAAGAGGAAATTGTTAAGGAAGTCAGCACTTACATTAAAGAAAATTTGGTTAC
AACCCTGACACAGTAGCATTTGTGCCAATTTCTGGTTGGAATGGTGACAACATGCTGGAGCCGAGTGCTAACATG
CCTTGGCTCAAGGGATGGAAAGCCACCCGTAAGGATGGCAGTGCCAGCGGCACCATGCTGCTTGAGGCTCTGGAC
TGCATCCTACCACCAACTCATCCAAGTGAAGCCCTTGCCTGCTGCTCCTCAGGATGTCTACAAAATTTGGTGGT
ATTGGTACTGTTCTGTTGGCCGAGTGGAGACTGGTGTCTCAAACCTGGTGTGGTGGTACCTTTGCTCCAGTC
AACATTACAACAGAAAGTAAAATCTGTGCAATGCACCATGAAGCTTTGAGTGAAGCTCTTCTGGGGACAATGTG
GGCTTCAATGTCAAGAATGTGTCTGTCAAGGATGTTCTGTCGTGGCAACGTTGCTGGTGACAGCAAAAATGACCCA
CCAATGGAAACAGCTGACTTCATTGCTCAGGTAATTATCCTGAACCATCCAGGCCAAATAAGCGCTGGCTATGCC
CCTATATTGGATTGCCACGCGGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCGGTTCT
GGTAAAAAGCTGGAAAGATGGCCCTAAATTCTTGAAGTCTGGTGTGCTGCCATTGTTGATATGGTTCTTGGCAAG
CCCATTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCATTTTGCTGTTCTGATATGAGACAGACAGTTGCG
GTGGGTGTGATCAAAAGCAGTGGACAAGAAGGCTGCTGGAGGTGGCAAGGTCACGAAGTCTGCCCAGACAGCTCAG
AAGGCTAAATGAATATTATCCCTAATACCTGCCACCCAACTCTTAAATCAGTGGTGGGAAGAATGGTCTCAGAACTG
TTTGTTCATTAATTGGCCATTTAAGTTTAGTAGTGAAAGACTGGTTAATGATAACAATGCATCGTAAAACCTTCAGA
AGGAAAGGAGAATGTTTTGTGGACCACTTTGGTTTTCTTTTTTGATGTGGTAGTTTTAAGTTATTAGTTTTTAA
AATCAGTACTTTTTAATGGAAACAACCTTGACCAAAAATTTGTCACAGAATTTTGAGACC

1712/6881
FIGURE 1585

MDSTEPYPYSQKREEEIVKEVSTYIKKIGYNPDTVAFVPISGWNGDNMLEPSANMPWLKGWKATRKGDSASGTMLL
EALDCILPPTHPTDKPLRLPLQDVYKIGGIGTVPVGRVETGVLKPGVVVTFAPVNITTEVKSVEMHHEALSEALP
GDNVGFNVKNVSVKDVRRGNVAGDSKNDPPMETADFIAQVIILNHPGQISAGYAPILDCHAAHIACKFAELKEKI
DRSGGKKLEDGPKFLKSGDAAIVDMVPGKPIVESFSYDYPPLGHFAVRDMRQTVAVGVKAVDKKAAGGGKVTKSA
QTAQKAK

1713/6881
FIGURE 1586

CACAGGTGTTGTGAAAACCTACCCCTAAAAGCCAAAATGGGAAAGGAAAAGACTCATATCAACATTGTCGTCATTG
GACACGTAAATTCGGGCAAGTCCACCACTACTGGCCATCTGACCTACAAATGTGGTGGCATCGACAAAAGAACCA
TTGAAAAATTTGAGAAGGAGGCTGCTGAGATGGGAAAGGACTCCTTCAAGTATGCCTGGGTCTTGCCATAAACTGA
AAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTGTGGAAATTTGAGACCAGCAAGTACTATGTGACTA
TCATTATGCCCTTCTGGCTTACACACTGGGTGTGAAACAATAATTGTTGGTGTAAACAAAATGGATTCCACTGA
GCCACCCTACAGCCAGAAGAGAGAAGAGGAAATTGTTAAGGAAGTCAGCACTTACATTAAGGGTGACAACATGCT
GGAGCCGAGTGCTAACATGCCTTGGCTCAAGGGATGGAAAGCCACCCGTAAGGATGGCAGTGCCAGCGGCACCAT
GCTGCTTGAGGCTCTGGACTGCATCCTACCACCAACTCATCCAAGTGAAGCCCTTGCGCCTGCCTCTCCAGGA
TGTCTACAAAATTGGTGGTATTGGTACTGTTCTGTTGGCCGAGTGGAGACTGGTGTCTCAAACCTGGTGTGGT
GGTCACCTTTGCTCCAGTCAACATTACAACAGAAGTAAAATCTGTCGAAATGCACCATGAAGCTTTGAGTGAAGC
TCTTCCTGGGGACAATGTGGGCTTCAATGTCAAGAATGTGCTGTCAAGGATGTTTCGTCGTGGCAACGTTGCTGG
TGACAACCATCCAGGCCAAATAAGCGCTGGCTATGCCCTATATTGGATTGCCACGCGGCTCAC

1714/6881
FIGURE 1587

AAATTGTTAAGGAAGTCAGCACTTACATTAAGAAAATTGGTTACAACCCTGACACAGTAGCATTGTGCCAATTT
CTGGTTGGAATGGTGACAACATGCTGGAGCCGAGTGCTAACATGCCTTGGCTCAAGGGATGGAAAGCCACCCGTA
AGGATGGCAGTGCCAGCGGCACCATGCTGCTTGAGGCTCTGGACTGCATCCTACCACCAACTCATCCAAGTACA
AGCCCTTGCGCCTGCCTCTCCAGGATGTCTACAAAATTGGTGGTATTGGTACTGTTCTGTGGCCGAGTGGAGA
CTGGTGTCTCAAACCTGGTGTGGTGGTCACCTTTGCTCCAGTCAACATTACAACAGAAGTAAAATCTGTCGAAA
TGCACCATGAAGCTTTGAGTGAAGCTCTTCCTGGGGACAATGTGGGCTTCAATGTCAAGAATGTGTCTGTCAAGG
ATGTTTCGTCTGGCAACGTTGCTGGTGACAGCAAAAATGACCCACCAATGGAAACAGCTGACTTCATTGCTCAGG
TAATTATCCTGAACCATCCAGGCCAAATAAGCGCTGGCTATGCCCCTATATTGGATTGCCACGCGGCTCACATTG
CATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCGGTTCTGGTAAAAAGCTGGAAGATGGCCCTACCACCT
TTGGGTCATTTTGCTGTTCGTGATATGAGACAGACAGTTGCGGTGGGTGTCATCAAAGCAGTGGACAAGAAGGCT
GCTGGAGGTGGCAAGGTCACGAAGTCTGCCCAGACAGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCC
ACCCAACCTCTTAATCAGTGGTGGAAAGATGGTCTCAGAACTGTTTGTTTCAATTGGCCATTTAAGTTTAGTAGTG
AAAGACTGGTACTTTTTTAATGGAAACAACCTTGACCAAAAATTTGTCACAGAATTTGAGACCTGTAAAAAAGTT
TAATGAG

1715/6881

FIGURE 1588A

TTTGTCCATGTCTCGGACAGAGCCTGGGAAGCTGCCAGTGAGATTTTCAGAGACCAAGAGCGCGAAGGGGCGGGCG
ATGTGGCAATCCGTCTGGGATGTGAAAAGCGTGGAGCGCATTTAGAGGAATTCGACGAAAACACAGGAAATCACT
CCTCTCCCGCTCCTGGGCGCCGCTGCCACTGGGGCAGAGGACTGGGAACCGCGGCAGCGGGATAAGTGGCCAGC
CAGAGAGCGCAGCTCCCGCGCCCGGTCTGCCCTGCGAACCAGCGCGGCCCTGGCGCTGAGGCTGCTCCGGCC
ATGGGCCCTCGGCCCCGCGCCCGCCAGGGGTGCTGTGCGCTGCTGTGGCTCCTCACTGTTGTTCTACGCTGC
TGCCTATCATTCAATGTTGATGTGAAAATTCAATGACTTTCAGCGGCCCGGTGGAAGACATGTTTGGATATACT
GTTCAACAATATGAAAATGAAGAAGGAAAATGGGTGCTTATTGGTTCTCCGTTAGTTGGCCAACCCAAAAACAGA
ACTGGAGATGTCTATAAGTGTCCAGTTGGGAGAGGTGAATCATTACCTTGTGTAAAGTTGGATCTACCAGTTAAT
ACATCAATTCCCAATGTCACAGAAGTAAAGGAGAACATGACATTTGGATCAACTTTAGTCACCAACCCAAATGGA
GGATTTCTGGCTTGTGGGCCCTTATATGCCTATAGATGTGGACATTTGCATTACACAACCTGGAATCTGTTCTGAC
GTCAGCCCCACATTTCAAGTCGTGAATTCATTGCCCCGTGTACAAGAATGCAGCACTCAACTGGACATAGTCATA
GTGCTGGATGGTTCCAACAGTATTTACCCATGGGACAGTGTACAGCTTTTTTAAATGACCTTCTTGAAAGAATG
GATATTGGTCTTAAACAGACACAGGTTGGAATTGTACAGTATGGAGAAAACGTGACCCATGAGTTCAACCTCAAT
AAGTATTCTTCCACCGAAGAGGTACTTGTTCAGCAAAGAAAATAGTCCAGAGAGGTGGCCGCCAGACTATGACA
GCTCTTGGAATAGACACAGCAAGAAAGGAGGCATTACGGAAGCCCGGGTGCCCGAAGAGGAGTTAAAAAAGTC
ATGGTTATTGTGACAGATGGAGAGTCTCATGACAATCATCGACTGAAGAAGGTCATCCAAGACTGTGAAGATGAA
AACATTCAACGGTTTTCCATAGCTATTCTTGGCAGCTATAACCGAGGAAATTTAAGCACTGAAAAATTTGTGGAG
GAAATAAAATCAATTGCAAGTGAACCCACTGAAAAGCATTTCTTCAATGTCTCTGATGAATTGGCTCTAGTCACC
ATTGTTAAAACTCTGGGAGAAAGAATATTTGCCCTGGAAGCCACAGCTGACCAGTCAGCAGCTTCATTTGAAATG
GAAATGTCTCAGACTGGCTTCAGTGCTCATTATTCACAGGACTGGGTCTATGCTTGGAGCAGTAGGAGCCTATGAT
TGGAATGGAACAGTTGTCTATGCAGAAGGCTAGTCAAATCATAATCCCTCGAAACACAACCTTTAATGTTGAGTCT
ACCAAAAAGAATGAACCGCTTGCTTCTTATTTAGGTTACACTGTAAACTCTGCTACTGCTTCTTCTGGAGATGTG
CTCTATATTGCTGGACAGCCTCGGTACAATCATACAGGCCAGGTCATTATCTACAGGATGGAAGATGGAAACATC
AAAATTCTCCAGACGCTCAGTGGAGAACAGATTGGTTCCCTACTTTGGCAGTATTTTAAACAACAACCTGACATTGAC
AAGGATTCTAATACTGACATTCTTCTAGTCGGAGCCCTATGTACATGGGAACAGAGAAGGAGGAGCAAGGAAAA
GTGTATGTGTATGCTCTCAATCAGACAAGGTTTGAATATCAAATGAGCCTGGAACCTATTAAGCAGACGTGCTGT
TCATCTCGGCAGCACAAATTCATGCACAACAGAAAACAAAATGAGCCATGCGGGGCTCGTTTTTGGAACTGCAATT
GCTGCTGTAAAAGACCTCAATCTTGATGGATTTAATGACATCGTGATAGGAGCTCCGCTGGAAGATGATCACGGG
GGAGCTGTGTACATTTATCATGGAAGTGGCAAGACTATAAGGAAAGAGTATGCACAACGTATTCCATCAGGTGGG
GATGGTAAGACACTGAAATTTTTTGGCCAGTCTATCCACGGAGAAAATGGATTTAAATGGTGACGGTCTGACAGAT
GTGACTATTGGGGGCCTTGGTGGTGTGCTGCCCTCTTCTGGTCCCGAGATGTGGCCGTAGTTAAAGTGACCATGAAT
TTTGAGCCAAATAAAGTGAATATTCAAAGAAAACTGCCATATGGAGGGAAAGGAAACAGTATGCATAAATGCT
ACAGTGTGTTTTGATGTGAAATTAAGTCTAAAGAAGACACGATTTATGAAGCTGATTTGCAGTACCGTGTCAAC
CTAGATTCACTAAGACAAATATCACGAAGTTTTTCTCTGGAACCTCAAGAGAGAAAGGTTCAAAGGAACATCACA
GTTCGAAAATCAGAATGCACTAAGCACTCCTTCTACATGTTGACAAGCATGACTTTCAGGACTCTG**TG**AGAATAA
CGTTGGACTTTAATCTTACCGATCCAGAAAATGGGCCTGTTCTTGATGATTCTCTACCAAACCTCAGTACATGAAT
ATATTCCTTTTGCCAAAGATTGTGGAATAAGGAAAAATGTATCTCAGACCTCAGCCTGCATGTGCCACCACTG
AAAAGGACCTGCTGATTGTCCGATCCAGAATGATAAGTTCAACGTTAGCCTCACAGTCAAAAATACAAAGGACA
GTGCCTATAACACCAGGACAATAGTGCAATTATTCTCAAATCTAGTTTTTTTCAGGAATTGAGGCTATCCAAAAAG
ACAGTTGTGAATCTAATCATAATATCACATGTAAAGTTGGATATCCCTTCCTGAGAAGAGGAGAGATGGTAACTT
TCAAAATATTGTTTCAGTTTAAACACATCCTATCTCATGAAAATGTGACCATTTATTTAAGTGCAACAAGTGACA
GCGAAGAACCTCCTGAAACCTTTCTGATAATGTAGTAAACATTTCTATCCCGGTAAAATATGAAGTTGGACTAC
AGTTTTACAGCTCTGCAAGTGAATACCACATTTCAATTGCTGCCAATGAGACAGTCCCTGAAGTTATTAATTCTA
CTGAGGACATTGGAAATGAAATTAATATCTTCTACTTTGATTAGAAAAAGTGATCTTTTCCAATGCCAGAGCTTA
AGCTGTCAATTTCAATCCCCAATATGACATCAAATGGTTACCCTGTGCTGTACCCAACCTGGATTGTCTCTCTG
AGAATGCAAACTGCAGACCCCATATCTTTGAGGATCCTTTCAGTATCAACTCTGGAAAGAAAATGACTACATCAA
CTGACCATCTCAAACGAGGCACAATTCTGGACTGCAATACATGTAAATTTGCTACCATCACATGTAATCTCACTT
CTTCTGACATCAGCCAAGTCAATGTTTCGCTTATCTTGTGGAAACCAACTTTTATAAAATCATATTTTCCAGCT

1716/6881
FIGURE 1588B

TAAATCTTACTATAAGGGGAGAACTTCGGAGTGAAAATGCATCTCTGGTTTTAAGTAGCAGCAATCAAAAAAGAG
AGCTTGCTATTCAAATATCCAAAGATGGGCTACCGGGCAGAGTGCCATTATGGGTCATCCTGCTGAGTGCTTTTG
CCGGATTGTTGCTGTTAATGCTGCTCATTTTAGCACTGTGGAAGATTGGATTCTTCAAAAGACCACTGAAAAAGA
AAATGGAGAAATGAAATATTTTATGAAAGAAAAATAACAATTATTCAATAATCTATCCTCAGGTTTGCCTCAA
ATATGTGACAAGAAATGTATAATTCATGACATAGTCATGTAACATATGTAATCCATCAGGGATTCACTACTTGGA
AATGACAGGTCATGCATTATCCAAAAACAATACCAAAAAAGACATATTTTATAAAATGACAAAAAATATTTTACAT
AATTACTCATTTTTGTTGAGTAAGCAAAATTACAAAGTGTTTTTAAAAAACCTGTACAAATATGTTTATGTATT
AAATCACCATCCAAATATTTAAGGAATATATAAAAAAGATTTTTATGATCATAGAAACATCTATTTTCAAAACAA
TATAAATTAAGCTTTTCCCCTTGATTCTGTTGGATATCCATGTTTCAGCATGACAGTCAGCACTCGTAAATGCCA
AGAAAAGAATTACCTGAAAAAGATCATTTCTCCCTATTCAAATGAGAATATTTTCCCTTGGTAGAATCCATATAC
AATATGGATTGAAAATTAAGTCACCAAGAATACATTTAGCATCTTTGTGTTGGGTTCTATACCTAAAAATTTTCC
CTCCCTGCCCCAAGGTGATTGGAAAGTACTGCAATTGAGCTAAAATTTTATCTAGGATGGAAAATCAGGATAGACT
CGTTTTAAAAACAAGTATATTAAATGGGTAAATTAAGCTTTTACAGAACATGCTTAATTTTGATATTGAGCTCTA
AATGCAAACTCTTTTATACTGAAAAAACACTTAAAGTAGTTTTGTGTGGCATCACAGTGATTTGTCTATGAAAAG
CCATATATGGGGGACATGCTAAAATGGCTTCTGAATGAAATACGACAGCAGAGAAAGATGCCACTGAAATGCTGA
AATTATCTTTGCTGAGCAGCTTTTGAATGCTAAGGGTTCCAGTATGTGACCCAAAGAAAGAGTTGTCTCAACTCC
TTGGTACAGGGTTCATTCAAACCCCCAAGCTGTGAGAGTGTGTTATTTTTAATTTTTTAAAAGGTATTTAATTT
CCAACCACACTTCTTATTTTTTTGAAAAGACAATTTTCCATTTCAGTATTACATTTTACCAAGAAGTCACTGCTT
TTTAGGTGTGTTGCATCAATATTTAAATAAAATCCCAGAAATGTATTTTAAAGAATTTTCAAGTTTGAAAACTCAA
ACCAACAGGAAGATATCACACCTTTGTATGTGCTTCTTTGTTCTTGAAGTAGTCATTATGGTTTCATTGGAATCTA
CTGTAGCATAAGCTCCTAGGTTGCTCCATTTCTTAGGAAAAATAGCAATGAATGAATGTATAGTAGCTGCATGTGT
GAACTACTGCTGTAAAGTTTGCTGACATTTCTGCAACAACATTTCTCCATCTGATTTACCAGAACCTGTAACAAG
ACCAGAACATGTATTATCCAGAACTCCTGGGCTCTGCTTTGTTCAAAGAGGAGCAAATCCACATAGAAATTAA
ATGTTATAAATTTATTTTTTTAACTAATTTCCAAAGAATTTAGCTGAAGACTCAGAGTCAGCCTACCTCTTGAC
TCTCCACATCCGCATCTAAGATCCTGAAGGCCAAAGGAATGCGCCTGTGGGATGCCAAAGCCATCAGTAGCTGGA
AGAAAGAATACCTCTTTCTAGAGGTTTGGTGTCTCTTGCTGGCCTGTCATTATTTGGAATACGCGCTTTTGGA
ATTTCTTTCATTTTCGCTATTTCCAGGTTTCAGAAATCATACCTACCCTTGTTCTTTCTTTGCCAGTAAACTC
AGGGTTTCTCTTATTCAGAGTTACCATGTTGCACACCCCCAGTGCTCAGCCTGCCAGAAAGCCCTTCTCTGATCT
CAGCAAGATCTTAGTAGTAAAGCTAACGGATCCATTGAAATTCATACTCAGCATCTGTGACTACTAGACAAAGCC
CATTTACTGAACCATAAGTGTGCACTTTTAACTAAATTGTTAACTGAAAGGGAAAAAATAGAAATGAGGGCATT
TTGAAGTTTTTGAAGAAAGAGAGGAAGAGCTGTTGGCCAGATCAAAGAGATACTTATAAGCCCGGCACAATTTTA
ACATAAGTCATTCCCTGGCTATTAAGTAAATATTTTCATGAACCAGAAGTCCTGTTTCTCTAATATTATAATTTGT
TGAGGTTTGTGTGTGTGTGTGTGTGTCATGTGCAGACACATGTACACATATAAATTGAATACAAAAATAGCTCTAT
AACACCAAAAAACAGAGTTTACAGAAAATAAACACAAAAGCTATATCTGCAAGACAAGTTTGATTCATCTAGTTT
CATATAGTTTTCATATAGTTTCATTTTTATTAATATTTAGGTTTAACTTATAGTTCTGCAATTATTTAAAAACAA
GTACAGAGCGTTTGATTAAAAAAGTCAACAAATGTTTCAAAACAGCTTTGTACAAATGTTATAAACATATTTA
ATGATTAAGAAATGTACTAGACTCTATCATTTACTTTTTAAAACATTTAATTAGAAAAACAGGTGATATTTAAGAC
TATTTATAAACTTATTGGCCAAATTGCCAAAAA

1717/6881
FIGURE 1589

MAPRPRARPGVAVACCWLLTVVLRCCVSFNVDVKNSMTFSGPVEDMFGYTVQQYENEEGKWVLIGSPLVGQPKNR
TGDVYKCPVGRGESLPCVKLDLPVNTSIPNVTEVKENMTFGSTLVNPNNGGFLACGPLYAYRCGHLHYTTGICSD
VSPTFQVVNSIAPVQECSTQLDIVIVLDGSNSIYPWDSVTAFLNDLLERMDIGPKQTQVGIVQYGENVTHEFNLN
KYSSTEEVLVAAKKIVQRGGRQTM TALGIDTARKEAFTEARGARRGVKKVMVIVTDGESHDNHRLLKKVIQDCEDE
NIQRFSAIALGSYNRGNLSTEFVVEEIKSIASEPTKHHFFNVSEALVTIVKTLGERIFALEATADQSAASFEM
EMSQTGFSAHYSQDWVMLGAVGAYDWNGTVVMQKASQIIIPRNTTFNVESTKKNEPLASYLG YTVNSATASSGDV
LYIAGQPRYNHTGQVIIYRMEDGNIKILQTLSGEQIGSYFGSILTTTDDIDKDSNTDILLVGAPMYMGTEKEEQGK
VYVYALNQTRFEYQMSLEPIKQTCSSRQHNSCTTENKNEPCGARFGTAIAAVKDLNLDGFNDIVIGAPLEDDHG
GAVYIYHSGSKTIRKEYAQRIPSGGDGKTLKFFGQSIHGEMDLNGDGLTDVTIGGLGGAALFWSRDVAVVKVTMN
FEPNKVNIQKKNCHMEGKETVCINATVCFDVKLKS KEDTIYEADLQYRVTLDSL RQISRSFFSGTQERKVQRNIT
VRKSECTKHSFYMLTSM TFR TL

1718/6881
FIGURE 1590

GTGTAGGGGTAGATTTTCGCTGCAGTGTTCCCCGAGCCTGTTAGACGCAGCGCGCCGGGAGACTGAGAGAGGAAA
GGATAGAGGAAGTGCTGCCCTAGGCTGCATGAGTCGAAGCAAGCGTGTTTCCTTCCCGCCAGGCAAGTGCCCTTA
GAAACCGGGCCCCCGCCCCCTTCCTGGCCTGCATTCCCATCCCCCTCTCCCGGGGCGGAGGTGAGGACCTCCTTGGT
TCCTTTGGTTCTGTGTCAGTGAGCCCCCTTCCTTGCCCATGAAGCTCGTGAGGAAGAACATCGAGAAGGACAATGCGG
GCCAGGTGACCCTGGTCCCCGAGGAGCCTGAGGACATGTGGCACACTTACAACCTCGTGACAGGTGGGCGACAGCC
TGCGCGCCTCCACCATCCGCAAGGTACAGACAGAGTCCTCCACGGGCAGCGTGGGCAGCAACCGGGTCCGCACTA
CCCTCACTCTCTGCGTGGAGGCCATCGACTTCGACTCTCAAGCCTGCCAGCTGCGGGTTAAGGGGACCAACATCC
AAGAGAATGAGTATGTCAAGATGGGGGCTTACCACACCATCGAGCTGGAGCCCAACCGCCAGTTCACCCTGGCCA
AGAAGCAGTGGGATAGTGTGGTACTGGAGCGCATCGAGCAGGCCTGTGACCCAGCCTGGAGCGCTGATGTGGCGG
CTGTGGTTCATGCAGGAAGGCCTCGCCCATATCTGCTTAGTCACTCCCAGCATGACCCCTCACTCGGGCCAAGGTGG
AGGTGAACATCCCTAGGAAAAGGAAAAGGCAATTGCTCTCAGCATGACCGGGCCTTGGAGCGGTTCTATGAACAGG
TGGTCCAGGCTATCCAGCGCCACATACACTTTGATGTTGTAAAGTGTCATCCTGGTGGCCAGCCCAGGATTTGTGA
GGGAGCAGTTCTGCGACTACCTGTTTCAACAAGCAGTGAAGACCGACAACAAACTGCTCCTGGAAAACCGGTCCA
AATTTCTTCAGGTACATGCCTCCTCCGGACACAAGTACTCCCTGAAAGAGGCCCTTTGTGACCCTACTGTGGCTA
GCCGCCTTTTCAGACACTAAAGCTGCTGGGGAAGTCAAAGCCTTGGATGACTTCTATAAAATGTTACAGCATGAAC
CGGATCGAGCTTTCTATGGACTCAAGCAGGTGGAGAAGGCCAATGAAGCCATGGCAATTGACACATTGCTCATCA
GCGATGAGCTCTTCAGGCATCAGGATGTAGCCACACGGAGCCGGTATGTGAGGCTGGTGGACAGTGTGAAAGAGA
ATGCAGGCACCGTTAGGATATTCTCTAGTCTTCACGTTTCTGGGGAACAGCTCAGCCAGTTGACTGGGGTAGCTG
CCATTCTCCGCTTCCTGTTCCCGAACTTTCTGACCAAGAGGGTGATTCCAGTTCTGAAGAGGATTAATGATTGA
AACTTAAAATTGAGACAATCTTGTGTTTCCTAAACTGTTACAGTACATTTCTCAGCATCCTTGTGACAGAAAGCT
GCAAGAATGGCACTTTTTGATTATACAGGGATTTCTTATGTCTTTGGCTACACTAGATATTTTGTGATTGGCAA
GACATGTATTTAAACAATAAACTA

1719/6881
FIGURE 1591

CTTCCCTTTTGC GGCTATCACCGAAGCAGGAGTGGCCAAAATGAAGTTTAATCCCTTTGTGACTTCCGACCGAAG
CAAGAATCGCAAAAGGCATTTCAATGCACCTTCCCACATTGGAAGGAAGACTATGTCTTCCCCTCTTTCCAAAGA
GCTGAGACAGAAGTACAACGTGTGATCCATGCCCATCCGAAAGGATGATGAAGTTCAGGTTGTACATGGACACTA
TAAAGGTCAGCAAATTGGCAAAGTAGTCCAGGTTTACAGGAAGAAATATGTTATCTACATTGAACGGGTGCAGCG
GGAAAAGGCTAATGGCACAACTGTCCACGTAGGCATTACCCCAGCAAGGTGGTTATCACTAGGCTAAACTGGA
CAAAGACTGTGAAAAGATCCTTGAACGGAAAGCCAAATCTTGCCAAGTAGGAAAGGAAAAGGGCAAATACAAGGA
AGAAACAATTGAGAAGATGCAGGAATAAAGTAATCTTATATACAAGCTTCGATTAAAACCTGAAACAAAGAAAAA

1720/6881
FIGURE 1592

GCGCGCGGCTCCGCTGGGAAGCGAGACCCGGGTGGCGGGACAAGACTTGCTTCCCGGCCACGCGCGCTCGGCCGG
CCGTGGGGCGGGGCATAGGCCGTGACGTGATGTCGCGTATCGAGTCTCCGCCCCCTTCCCGCCTCCCGTATATA
AGACTTCGCCGAGCGCTCTCACTCGCACAAAGTGGACCGGGGTGTTGGGTGCTAGTCGGCACCAGAGGCAAGGGTG
CGAGGACCACGGCCGGCTCGGACGTGTGACCGCGCCTAGGGGGTGGCAGCGGGCAGTGCGGGGCGGCAAGGCGAC
CATGGAGCTTTTTCGGGACTATCACCTACCAGCCAGCCGCCAGCACCAAATGTGCGAGCAGGCGCTGGGCAAGGG
TTGCGGAGCGGACTCGAAGAAGAAGCGGCCGCCGAGCCCCCGAGGAATCGCAGCCACCTCAGTCCCAGGCGCA
AGTGCCCCCGGGCGGCCCTCACCACCATCACCACCATTCGCACTCGGGGCCGGAGATCTCGCGGATTATCGTCGA
CCCCACGACTGGGAAGCGCTACTGCCGGGGCAAAGTGCTGGGAAAGGGTGGCTTTGCAAAATGTTACGAGATGAC
AGATTTGACAAATAACAAAGTCTACGCCGCAAAAATTATTCCTCACAGCAGAGTAGCTAAACCTCATCAAAGGGA
AAAGATTGACAAAGAAATAGAGCTTCACAGAATTCTTCATCATAAGCATGTAGTGCAGTTTTTACCCTACTTCGA
GGACAAAGAAAACATTTACATTCTCTTGAATACTGCAGTAGAAGGTCAATGGCTCATATTTTGAAAGCAAGAAA
GGTGTGACAGAGCCAGAAGTTCGATACTACCTCAGGCAGATTGTGTCTGGACTGAAATACCTTCATGAACAAGA
AATCTTGACAGAGATCTCAAAC TAGGGAAC TTTTTATTAATGAAGCCATGGAAC TAAAGTTGGGGACTTCGG
TCTGGCAGCCAGGCTAGAACCCTTGGAACACAGAAGGAGAACGATATGTGGTACCCCAAATTATCTCTCTCTGA
AGTCTCAACAAACAAGGACATGGCTGTGAATCAGACATTTGGGGCCCTGGGCTGTGTAATGTATACAATGTTACT
AGGGAGGCCCCCATTTGAAACTACAAATCTCAAAGAAACTTATAGGTGCATAAGGGAAGCAAGGTATACAATGCC
GTCTCATTTGCTGGCTCCTGCCAAGCACTTAATTGCTAGTATGTTGTCCAAAACCCAGAGGATCGTCCCAGTTT
GGATGACATCAATCGACATGACTTTTTTTTTGCAGGGCTTCACTCCGGACAGACTGTCTTCTAGCTGTTGTCTATAC
AGTTCCAGATTTCCACTTATCAAGCCCAGCTAAGAATTTCTTTAAGAAAGCAGCTGCTGCTCTTTTTTGGTGGCAA
AAAAGACAAAAGCAAGATATATTGACACACATAATAGAGTGTCTAAAGAAGATGAAGACATCTACAAGCTTAGGCA
TGATTTGAAAAAGACTTCAATAACTCAGCAACCCAGCAAAACACAGGACAGATGAGGAGCTCCAGCCACCTACCAC
CACAGTTGCCAGGTCTGGAACACCCGCAGTAGAAAAACAAGCAGCAGATTGGGGATGCTATTCCGGATGATAGTCAG
AGGGACTCTTGGCAGCTGTAGCAGCAGCAGTGAATGCCCTTGAAGACAGTACCATGGGAAGTGTTCAGACACAGT
GGCAAGGGTTCTTCGGGGATGTCTGGAACACATGCCGGAAGCTGATTGCATTCCCAAAGAGCAGCTGAGCACATC
ATTTCACTGGGTCACCAAATGGGTTGATTACTCTAACAAATATGGCTTTGGGTACCAGCTCTCAGACCACACCGT
CGGTGTCCTTTTCAACAATGGTGCTCACATGAGCCTCCTTCCAGACAAAAAACAGTTCACTATTACGCAGAGCT
TGGCCAATGCTCAGTTTTTCCAGCAACAGATGCTCCTGAGCAATTTATTAGTCAAGTGACGGTGCTGAAATACTT
TTCTCATTACATGGAGGAGAACCTCATGGATGGTGGAGATCTGCCTAGTGTACTGATATTGAAGACCTCGGCT
CTACCTCCTTCAGTGGCTAAAATCTGATAAGGCCCTAATGATGCTCTTTAATGATGGCACCTTTCAGGTGAATTT
CTACCATGATCATACAAAAATCATCATCTGTAGCCAAAATGAAGAATACCTTCTCACCTACATCAATGAGGATAG
GATATCTACAAC TTT CAGGCTGACA ACTCTGCTGATGTCTGGCTGTT CATCAGAATTA AAAAATCGAATGGAATA
TGCCCTGAACATGCTCTTACAAAGATGTA ACTGAAAGACTTTTCGAATGGACCCTATGGGACTCCTCTTTTCCAC
TGTGAGATCTACAGGGAACCCAAAAGAATGATCTAGAGTATGTTGAAGAAGATGGACATGTGGTGGTACGAAAAC
AATTCCCCTGTGGCCTGCTGGACTGGGTGGAACCAGAACAGGCTAAGGCATACAGTTCTTGACTTTGGACAATCC
AAGAGTGAACCAGAAATGCAGTTTTCTTGAGATACCTGTTTTAAAGGTTTTTCAGACAATTTTGAGAAAGGTG
CATTGATTCTTAAATCTCTCTGTTGAGAGCATTTT CAGCCAGAGGACTTTGGA ACTGTGAATATACTTCTCTGAAG
GGGAGGGAGAAGGGAGGAAGCTCCCATGTTGTTTAAAGGCTGTAATTGGAGCAGCTTTTGGCTGCGTAACTGTGA
ACTATGGCCATATATAATTTTTTTTTT CATTAATTTTTTGAAGATACTTGTGGCTGGAAAAGTGCATTCTTGTTAAT
AAACTTTTTTATTTATTACAGCCCAAAGAGCAGTATTTATTATCAAAATGTCTTTTTTTTTTATGTTGACCATTTTA
AACCGTTGGCAATAAAGAGTATGAAAACGC

1721/6881
FIGURE 1593

ATGGAAGGCATCACCGCTGTCACGGTCAACCAGAGCCTGCTGAACTCCCTTAACTGGAGATGGACTCCAGCATCC
AGGAGACCACACCCAGGAGAAGAACCAGATCAAGACACTCAACAACAAGTTTGCCTCCTTCATAGACAAGGTACA
GTTCTGAGCAGCAGAACAAGATGCTGGAGACCAACTGGAGCCTCCTGCAGCAGGAGAAGATGGCTCGGAGCAA
CATGGACAACATGAGAAGCTGAAGCTGGAGGCGGAACCTGGCAACATGCAGGGGCTGCTGGAGGACTTCAAGAAC
AAGTATGAGGATGAGATCAATAAGCGTACAGGGATGGAGAATGAATTTTTCCTCATCAAGAAGGATGTGGATAAA
GCTTACATGACAAGGCAGCTGTATGAAGAGGAGATCCAGGAGCTGCAGTCCCAGATCTCGGACACGTCTGTGGTG
CTGTCCATGGACAACAGCCGCTCCCTGGACATACGTGGGGAGCTGGCCGATAAGGATGCCAACGCCAAGCTGTCT
GAGCTGGAGGCCGCCCTGCAGTGGACCAAGCAGGACATGGGCGGCAGCTGCCTGCTGGAGGGCGAGGAGAGCCGG
CTGGAGTCTGGGATGCAGAACATGAGTATCCGTACGAAGACCACCAGCGGCTATGCAGGTGGTCTGAGCTCGACC
TATGGGGGCCTCACAAGCCCCGGCCTCAGCTACGGCCTGGGCTCCAGTTTGGCTCTGGTGCGGGCTCCTGCGCT
TTCAGCCGCACCTGCTCCATCAGGGCCATGATTGTGAAGAAGATTGAGACCCACGATGGGAAGCTGGTGTCCGAG
TCCTCTGACGTCTGCTCAAGTGA

1722/6881
FIGURE 1594

MEGITAVTVNQSLNLSLNWRWTPASRRPHPGEEPQDQTQQQVCLLHRQGTVPGAAEQDAGDQLEPPAAGEDGSEQ
HGQHEKLKLEAELGNMQGLLEDFKNKYEDEINKRTGMENEFFLIKDVDKAYMTRQLYEEEEIQELQSQISDTSVV
LSMDNSRSLDIRGELADKDANAKLSELEAALQWTKQDMGGSCLEGEESRLESGMQNMSIRTKTTSGYAGGLSST
YGGLTSPGLSYGLGSSFGSGAGSCAFSRTCSIRAMIVKKIETHDGKLVSESSDVLLK

1723/6881
FIGURE 1595

GTTGAAGGAGGCATTGTTTTGGGAGGGGGTTTTGCCCTCCTTCGATGCATTCCAGCCTTGGACTCATTGACTCCA
GCTAATGAAGATCAAAAAATTGGTATGGAAATTGTTAAAAGAACACTCAAAATTCAGCAATGACCACTGCTACG
AATGCAGGTGTTGAAGGATCTTTGATAGTTGAGAAAATTATGCAAAATTCCTCAGAAGTTGGTTATGATGCTATG
GTTGGAGATTTTATGAATATGGTAGAAAAAGGAATTATTGACCCAACAAAGCTTGTGAGAACTGCTTTATTGGAT
GCTGCTGGTGTGGCCTCTCTGTAACTACAGCAGAAGTTGTAGTCACAGAAATTCCTAAAGAAGAGAAGGACCCT
GGAATGGGTGCAATGGGTGGAATGGGAGGTGGTATGGGAGGTGGCATGTTCTAACTCCTAGACTAGTGCTTTACC
TTTATTAATGAACTGTGACAGGAAGCCCAAGGCAGTGTTCCTCACCAATAACTTCAGAGAAGTCAGTTGGAGAAA
ATGAAAAATATATAATGGTTTACTGCTGTCATTGTCCATGCCTACAGATAATTTATTTTGTATTTTGAATAAAA
AACATTTGTACATTCTTGATACTGGGTACAAGAGCCATGTACCAATGTACTGCTTT

1724/6881
FIGURE 1596

ACCTGTCTCGCCGCGCGCATGCCCTGCAGCCGCCCCACAGAAATGCTTCGGTTACCCACAGTCTTTCGCCAGATG
AGACCAGTGTCCAGGGTACTGGCTCCTCATCTCACTCGAGCTTATGCCAAAGATGTAAAATTTGGTGCAGATGCC
CGAGCCTTAATGCTTCAAGGTGTAGACCTTTTAGCCGATGCTGTGGCCGTTACAATGGAGCCAAAGGGAAGAACA
GTGATTATTGAGCAGAGCTGGGGAAGTCCCAACGTAACAAAAGATGGTGTGACTGTTGCAAAGTCAATTGACTTG
AAGGATAAATATAAAAAACATTGGAGCTAACTTGTTCAAGATGTTGCCAATAACACAAATTGAAAAACGTATTCA
AGAAATCATTGGGCAGTTAGATGTCACAAGTGAATATGAAAAGGAAAACTGAATGAATGGCTGGCAAACT
TTCAGATGGAGTAGTTGTGCTGAAGTTTGGTGGGACAAGTGATGTTGAAGTGAATGAAAAGAAAGACAGAGTTAC
AGATGCCCTTAATGCTACAAGAGCTGCTGTTGAAGGAGGCATTGTTTTGGGAGGGGGTTTTGCCCTCCTTCGATG
CATTCCAGCAATGACCACTGCTACGAATGCAGGTGTTGAAGGATCTTTGATAGTTGAGAAAATTATGCAAAATTC
CTCAGAAGTTGGTTATGATGCTATGGTTGGAGATTT

1725/6881
FIGURE 1597

CTCTGTCCCTCACTCGCCGCCGACAACCTGTCTCGCCGCGCGCATGCCCTGCAGCCGCCCCACAGAAATGCTTCG
GTTACCCACAGTCTTTTCGCCAGATGAGACCAGTGTCCAGGGTACTGGCTCCTCATCTCACTCGAGCTTATGCCAA
AGATGTAAATTTGGTGCAGATGCCCAGCCTTAATGCTTCAAGGTGTAGACCTTTTAGCCGATGCTGTGGCCGT
TACAATGGAGCCAAAGGGAAGAACAGTGATTATTGAGCAGAGCTGGGGAAGTCCCAACGTAACAAAAGATGGTGT
GACTGTTGCAAAGTCAATTGACTTGAAGGATAAATATAAAAAACATTGGAGCTAAACTTGTTCAAGATGTTGCCAA
TAACACAAATGAAGAATCTGGGGATGGCACTACCACTGCTACTGTACTGGCAGGCTCTATAGCCAAGGAAGGCTT
CCAGAAGATTAGCAAAGGTGCTAATCCAGTGGAATCAGGAGAGGTGTGATGTTAGCTGTTGATGCTGTAATTGC
TGAACCTAAAAAGCAGTCTAAACCTGTGACCACCCCTGAAGAAATTGCACAGGTTGCTATGATTTCTGCAAAATGG
AGACAAAGAAATTGGCAATATCATCTCTGATGCAATGAAAAAGGTTGGAAGAAAGGGTGTATCACAGTAAAGGA
TGAAAAACACTGAATGATGAATTAGAAATTATTGAAGGCATGAAGTTTGATTGAGGGTATATTTCTCCATACTT
TATTAATACATCAAAAAGGTCAGAAATGTGAATTCCAGGATGCCATATGTTCTGTTGAGTGAAAAGAAAATTTCTAG
TGTCAGTCCATTGTACCTGCTCTTGAAATTGCCAATGCTCACCATAAGCCTTTGGTGATAATCGCTGAAGATGT
TGATGGAGAAGCTCTAAGTACACTCATCTTGAATAGGCTAAAGGTTGGTCTTCAGGTTGTGGCAGTCAAGGCTCC
AGGGTTTGGTGACAATAGAAAGAACCAACTTAAAGATATGGCTATTGCTACTGGTGGTGCAGTGTGTTGGAGAAGA
GGGGTTGACCCTGAATCTTGAAGATGTTTCAGCCTCATGACTTAGGAAAAGTTGGAGAGGTCATTGTGACCAAAGA
CGATGCCATGCTCTTAAAAGGAAAAGGTGACAAGGCTCAACTTGAAAAACGTATTCAAGAAATCATTGGGCAGTT
AGATGTCACAACCTAGTGAATATGAAAAGGAAAACTGAATGAATGGCTGGCAAACTTTTCAGATGGAGTAGTTGT
GCTGAAGTTTGGTGGGACAAGTGATGTTGAAGTGAATGAAGGCATTGTTTGGGAGGGGGTTTTGCCCTCCTTCG
ATGCATTCCAGCCTTGGAATCATTGACTCCAGCTAATGAAGAT

1726/6881
FIGURE 1598

ACGAACAGGCCAATAAGGAGGGAGCAGTGCGGGGTTTAAATCTGAGGCTAGGCTGGCTCTTCTCGGCGTGCTGCG
GCGGAACGGCTGTTGGTTTCTGCTGGTTGTAGGTCCTTGGCTGGTCGGGCCTCCGGTGTTCTGCTTCTCCCCGCT
GAGCTGCTGCCTGGTGAAGAGGAAGCCATGGCGCTCCGAGTCACCAGGAACTCGAAAATTAATGCTGAAAAATAAG
GCGAAGATCAACATGGCAGGCGCAAAGCGCGTTTCTACGGCCCCCTGCTGCAACCTCCAAGCCCCGACTGAGGCCA
AGAACAGCTCTTGGGGACATTGGTAACAAAGTCAGTGAACAACCTGCAGGCCAAAATGCCTATGAAGAAGGAAGCA
AAACCTTCAGCTACTGGAAGTCAATTGATAAAAACTACCAAAACCTCTTGAAAAGGTACCTATGCTGGTGCCA
GTGCCAGTGTCTGAGCCAGTGCCAGAGCCAGAACCTGAGCCAGAACCTGAGCCTGTTAAAGAAGAAAACTTTCG
CCTGAGCCTATTTTGGTTGATACTGCCTCTCCAAGCCCCAATGGAAACATCTGGATGTGCCCCCTGCAGAAGAAGAC
CTGTGTCAGGCTTTCTCTGATGTAATTCTTGCAAGTAAATGATGTGGATGCAGAAGATGGAGCTGATCCAAACCTT
TGTAAGTGAATATGTGAAAGATATTTATGCTTATCTGAGACAACTTGAGGAAGAGCAAGCAGTCAGACCAAAATAC
CTACTGGGTTCGGGAAGTCACTGGAAACATGAGAGCCATCCTAATTGACTGGCTAGTACAGGTTCAAATGAAATTC
AGGTTGTTGCAGGAGACCATGTACATGACTGTCTCCATTATTGATCGGTTTCATGCAGAATAATTGTGTGCCCAAG
AAGATGCTGCAGCTGGTTGGTGTCACTGCCATGTTTATTGCAAGCAAATATGAAGAAATGTACCCTCCAGAAATT
GGTGACTTTGCTTTTGTGACTGACAACACTTATACTAAGCACCAAAATCAGACAGATGGAAATGAAGATTCTAAGA
GCTTTAAACTTTGGTCTGGGTTCGGCCTCTACCTTTGCACTTCCTTCGGAGAGCATCTAAGATTGGAGAGGTTGAT
GTCGAGCAACATACTTTGGCCAAATACCTGATGGAACCTAACTATGTTGGACTATGACATGGTGCACCTTCTCCT
TCTCAAATTGCAGCAGGAGCTTTTTGCTTAGCACTGAAAATTCTGGATAATGGTGAATGGACACCAACTCTACAA
CATTACCTGTATATACTGAAGAATCTCTTCTTCCAGTTATGCAGCACCTGGCTAAGAATGTAGTCATGGTAAAT
CAAGGACTTACAAAGCACATGACTGTCAAGAACAAGTATGCCACATCGAAGCATGCTAAGATCAGCACTCTACCA
CAGCTGAATTCTGCACTAGTTCAAGATTTAGCCAAGGCTGTGGCAAAGGTGTAACTTGTAAACTTGAGTTGGAGT
ACTATATTTACAAATAAAATTGGCACCATGTGCCATCTGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

1727/6881
FIGURE 1599

MALRVTRNSKINAENKAKINMAGAKRVPTAPAATSKPGLRPTALGDIGNKVSEQLQAKMPMKKEAKPSATGKVI
DKKLPKPLEKVPMLVPVPVSEPVPEPEPEPEPEPEPVKEEKLSPILVDTASPSMETSGCAPAEEDLCQAFSDVI
LAVNDVDAEDGADPNLCSEYVKDIYAYLRQLEEEQAVRPKYLLGREVTGNMRAILIDWLQVQMKFRLQETMYM
TVSIIIDRFMQNNCVPKKMLQLVGVTAMFIASKYEEMYPPEIGDFAFVTDNTYTKHQIRQMEMKILRALNFGLGRP
LPLHFLRRASKIGEVDVEQHTLAKYLMELTMLDYDMVHFPPSQIAAGAFCLALKILDNGEWTPTLQHYLSYTEES
LLPVMQHLAKNVVMVNQGLTKHMTVKKNKYATSKHAKISTLPQLNSALVQDLAKAVAKV

1728/6881
FIGURE 1600

GCTGGCAAGCGCTTCCTGCGCAGCGCCTAGGCGACCTGGAGTTTGTGACGCTGTGATGGTCTAGAGGCTGGAGAT
TCAAGATCTGGGTGCCATCATTTTCTGGTTCTGTTGATGACCCTCTTCCAGGTTACATACAGCTTACATCTTGCA
TCCTCAAGCGTTTTTCTTATAAGGCTAAAAATTCACAAAGCATATATCAATGAATCAGGAGGATCTAGATCCGGA
TAGTACTACAGATGTGGGAGATGTTACAAATACTGAAGAAGAAGCTTATTAGAGAATGTGAAGAAATGTGGAAAGA
TATGGAAGAATGTCAGAATAAATTATCACTTATTGGAACCTGAAACACTCACCGATTCAAATGCTCAGCTATCATT
GTTAATTATGCAAGTAAAATGTTTAACCGCTGAACTCAGTCAATGGCAGAAAAAACACCTGAAACAATTCCTT
GACTGAAGACGTTCTCATAACATTAGGAAAAGAAGAGTTCCAAAAGCTGAGACAAGATCTTGAAATGGTACTGTC
CACTAAGGAGTCAAAGAATGAAAAGTTAAAGGAAGACTTAGAAAGGGAACAACGGTGGTTGGATGAACAGCAACA
GATAATGGAATCTCTTAATGTACTACACAGTGAATTGAAAAATAAGGTTGAAACATTTTCTGAATCAAGAATCTT
TAATGAACTGAAAACATAAATGCTTAATATAAAAGAATATAAGGAGAAACTCTTGAGTACCTTGGGCGAGTTTCT
AGAAGACCATTTTCTCTGCCTGATAGAAGTGTTAAAAAGAAAAAGAAAAACATTCAAGAATCATCTGTAAACCT
GATAACACTGCATGAAATGTTAGAGATTCTTATAAATAGATTATTTGATGTTCCACATGATCCATATGTCAAAT
TAGTGATTCCTTTTGGCCACCTTATGTTGAGCTGCTGCTGCGTAATGGAATTGCCTTGAGACATCCAGAAGATCC
AACCCGAATAAGATTAGAAGCTTTCATCAGTAAAGGATGTTTTCTTTTTTACACAGTAAAAATCTTATCAT
TCAAGGATATTGGAACCACAGGACTATTTGGATAAAAAACATTATTTGCAAATTAATGCGCATAGGCCATCTTAC
TTTTATTGCAAAATGGCATGTGCTGCCATCTATTATTCATTTTTAAATGGTCATTTCTTATTCACTGAGTGCTTT
AGTGTTTTAACTATATGGATAAGAATGCAGGTAGATAATATTCTAGGCATAAAACATTTAATGTACCTTACCTC
ATGCAATATTCTTTGGATTCTTTGTTGATTTATGATATTGCTAATATAATATTTTCTTAAAAATATATAACAATAT
CTTTTATGCATTTTGAGTTCCAGCTGGTGCTTCTTTATATTTAGAAATTATAATGGGAAGGTCATTTAATTTACA
GATGGTTTTAAATTTGAGGTAATATCTGAGGTGGCATAATTTAAAAATATTTAGCAAATTTGTTTCATATATACT
GTCTTATTTCTAGATTTGTTTAAATTTGGAATATGAAAACTAATGGATAAAGCTAGCATAAAAATTGATATTTTA
GTTTGTATTATTAATATATCATGTTACCTTATATATTAATCTACTCTTGATTCTGCTAATTATTACCAACAAAAT
TGTATTCATGACATTTTATTAATCCTCTGTGAATTTCTGTAAATAAAATTATTTCTGAAAATCTCT

1729/6881
FIGURE 1601

MNQEDLDPDSTTDVGDVTNTEELIRECEEMWKDMEECONKLSLIGTETLTDSNAQLSLLIMQVKCLTAELSQWQ
KKTPETIPLTEDVLITLGKEEFQKLRODLEMVLSTKESKNEKLKEDLEREQRWLDEQQQIMESLNVLHSELKNKV
ETFSESRIFFNELKTKMLNIKEYKEKLLSTLGEFLEDHFPLPDRSVKKKKKNIQESSVNLITLHEMLEILINRLFD
VPHDPYVKISDSFWPPYVELLLRNGIALRHPEDPTRIRLEAFHQ

1730/6881
FIGURE 1602

GCAGGAAGATGGCGGCGGTAGCGGAGGTGTGAGTGACGCGGGACTCAGCGGCCGGATTTTCTCTTCCCTTCTTT
TCCCTTTTCCCTTCCCTATTTGAAATTGGCATCGAGGGGGCTAAGTTCGGGTGGCAGCGCCGGGCGCAACGCAGGG
GTCACGGCGACGGCGGCGGCGGCTGACGGCTGGAAGGGTAGGCTTCATTACCGCTCGTCCTCCTTCCTCGCTCC
GCTCGGTGTCAGGCGCGGCGGCGGCGGCGGGCGGACTTCGTCCCTCCTCCTGCTCCCCCCCACACGGGAGCGG
GCACTCTTCGCTTCGCCATCCCCGACCCTTCACCCCGAGGACTGGGCGCCTCCTCCGGCGCAGCTGAGGGAGCG
GGGGCCGGTCTCCTGCTCGGTTGTGCGAGCCTCC**ATG**TCGGATAATCAGAGCTGGAACCTCGTCGGGCTCGGAGGAG
GATCCAGAGACGGAGTCTGGGCCGCCTGTGGAGCGCTGCGGGGTCTCAGTAAGTGGACAACTACATTCATGGG
TGGCAGGATCGTTGGGTAGTTTTGAAAAATAATGCTCTGAGTTACTACAAATCTGAAGATGAAACAGAGTATGGC
TGCAGAGGATCCATCTGTCTTAGCAAGGCTGTCATCACACCTCACGATTTTGATGAATGTCGATTTGATATTAGT
GTAAATGATAGTGTGTTGGTATCTTCGTGCTCAGGATCCAGATCATAGACAGCAATGGATAGATGCCATTGAACAG
CACAAGACTGAATCTGGATATGGATCTGAATCCAGCTTGCGTCGACATGGCTCAATGGTGTCCCTGGTGTCTGGA
GCAAGTGGCTACTCTGCAACATCCACCTCTTCATTCAAGAAAGGCCACAGTTTACGTGAGAAGTTGGCTGAAATG
GAAACATTTAGAGACATCTTATGTAGACAAGTTGACACGCTACAGAAGTACTTTGATGCCTGTGCTGATGCTGTC
TCTAAGGATGAACTTCAAAGGGATAAAGTGGTAGAAGATGATGAAGATGACTTTCCTACAACGCTTCTGATGGT
GACTTCTTGTCATAGTACCAACGGCAATAAAGAAAAGTTATTTCCACATGTGACACCAAAAGGAATTAATGGTATA
GACTTTAAAGGGGAAGCGATAACTTTTAAAGCAACTACTGCTGGAATCCTTGCAACACTTTCTCATTGTATTGAA
CTAATGGTTAAACGTGAGGACAGCTGGCAGAAGAGACTGGATAAGGAAACTGAGAAGAAAAGAAGAACAGAGGAA
GCATATAAAAATGCAATGACAGAACTTAAGAAAAAATCCCACTTTGGAGGACCAGATTATGAAGAAGGCCCTAAC
AGTCTGATTAATGAAGAAGAGTTCTTTGATGCTGTTGAAGCTGCTCTTGACAGACAAGATAAAATAGAAGAACAG
TCACAGAGTGAAAAGGTGAGATTACATTGGCCTACATCCTTGCCCTCTGGAGATGCCTTTTTCTTCTGTGGGGACA
CATAGATTTGTCCAAAAGCCCTATAGTCGCTCTTCCCTCCATGTCTTCCATTGATCTAGTCAGTGCCTCTGATGAT
GTTACAGATTACAGCTCCCAGGTTGAAGAGATGGTGCAGAACCACATGACTTACTCATTACAGGATGTAGGCGGA
GATGCCAATTGGCAGTTGGTTGTAGAAGAAGGAGAAATGAAGGTATACAGAAGAGAAGTAGAAGAAAATGGGATT
GTTCTGGATCCTTTAAAGCTACCCATGCAGTTAAAGGCGTACAGGACATGAAGTCTGCAATTATTTCTGGAAT
GTTGACGTTGCAATGACTGGGAAACAACCTATAGAAAACCTTTCATGTGGTGGAAACATTAGCTGATAATGCAATC
ATCATTTATCAAACACACAAGAGGGTGTGGCCTGCTTCTCAGCGAGACGTATTATATCTTTCTGTCATTGAAAG
ATACCAGCCTTGACTGAAAATGACCCTGAAACTTGGATAGTTTGTAAATTTTCTGTGGATCATGACAGTGCTCCT
CTAAACAACCGATGTGTCCGTGCCAAAATAAATGTTGCTATGATTTGTCAAACCTTGGTAAGCCCACCAGAGGGA
AACCAGGAAATTAGCAGGGACAACATTCTATGCAAGATTACATATGTAGCTAATGTGAACCCTGGAGGATGGGCA
CCAGCCTCAGTGTTAAGGGCAGTGGCAAAGCGAGAGTATCCTAAATTTCTAAAACGTTTTACTTCTTACGTCCAA
GAAAAAACTGCAGGAAAGCCTATTTTGTTC**TAG**TATTAACAGGTACTAGAAGATATGTTTTATCTTTTTTAACT
TTATTTGACTAATATGACTGTCAATACTAAAATTTAGTTGTTGAAAGTATTTACTATGTTTTTT

1731/6881
FIGURE 1603

MSDNQSWNSSGSEEDPETESGPPVERCGVLSKWTNYIHGWQDRWVVLKNNALSYKSEDETEYGCRGSICLSKAV
ITPHDFDECRFDISVND SVWYLRAQDPDHRQQWIDAIEQHKTESGYGSESSLRRHGSMVSLVSGASGYSATSTSS
FKKGHSLREKLAEMETFRDILCRQVDTLQKYFDACADAVSKDELQDKVVEDDEDDFPTRSDGDFLHSTNGNKE
KLFPHVTPKGINGIDFKGEAITFKATTAGILATLSHCIELMVKREDSWQKRLDKETEKRRRTEEAYKNAMTELKK
KSHFGGPDYEEGPNSLINEEEFFDAVEAALDRQDKIEEQSQSEKVRHLHWPTSLPSGDAFSSVGTHRFBVQKPYRS
SSMSSIDLVSASDDVHRFSSQVEEMVQNHMTYSLQDVGGDANWQLVVEEGEMKVYRREVEENGIVLDPLKATHAV
KGV TGHEVCNYFWNVDRNDWETTIENTFHVETLADNAIIYQTHKRVWPASQRDVLYLSVIRKIPALTENDPET
WIVCNFSVDHDSAPLNNRCVRKINVAMICQTLVSPPEGNQEISRDNILCKITYVANVNPGGWAPASVLRVAKR
EYPKFLKRETSYVQEKTAGKPILF

1732/6881
FIGURE 1604

AGTACAATCTGCTGCCAGGACCTGGACATTGACAGATAAAAATGAAGTGGGTGAGTTAACTACAGAGGGAAGAAT
ATGAAGAAGCTGCTTCATTATGCTATAGTGACTCCAAATATTGAACCCTGTGCTTCACAGTCATCTCATCCTAAGG
GAGAATTGGTGCCAGATGTCAGAATTTCTACAATTCATGATATTCTTCATAGTCAAGGAAATAACTCTGAAGTAA
GAGAACTGCAATAGAAGTTGGAAAAGGATGTGATTTCATATTTCAAGTCATTCAAAGACAGATGCTACAACCTT
TTCTTTTATTCAGAGTCATCACCAGTGTTATCGCCAAGGAAGCCTTCTCACCCAGTCATGGATTTTTTTCAGTTCA
CATCTTTTAGCTGACTCTTCCTCACCAGCAACAAATTCTAGTCATACAGATGCCATGAAATACTTGTGAGCGAT
TTTCTTGTTTCTGATGAAAACCTTCAGAAGATGGAAAATGTGCTTGATCTTTGGAGTTCAGGTCTTAAGACAAAC
ATCATATCTGAACTAAGTAAATGGAGACTTAATTTTATTGACTGGCACC GAATGGAAATGAGAAAAGAGAAAGAA
AAACATGCAGCACATTTAAAACAACCTGTGTAATCAGATCAATGAATTGAAGGAGCTGCAAAAAACCTTTGAAATC
TCCATTGGGAGAAAAGATGAGGTGATTTCTAGCTTGTCTCATGCCATAGGCAAGCAAAAGGAAAAGATAGAGTTG
ATGAGAACATTCTTCCACTGGCGAATCGGCCATGTCAGAGCCAGACAGGATGTTTATGAAGGTAACTAGCTGAC
CAGTACTACCAGAGAACTTTACTGAAGAAAGTCTGGAAAGTCTGGCGTTCCGTAGTGCAAAAGCAGTGGAAGAT
GTGGTAGAAAAGAGCTTGTCAAGCAAGAGCTGAAGAAGTTTGTATCCAGATTTCCAATGATTATGAAGCCAAAGTT
GCTATGTTATCTGGAGCTTTGGAAAATGCAAAAGCTGAGATTCAAAGAATGCAACATGAAAAAGAGCACTTTGAA
GATTCCATGAAAAAGCTTTTCATGAGGGGTGTATGTGCATTAAATCTTGAAGCCATGACTATATTTCAAACAGA
AATGATGCAGCTCCTCCGATGCCCTTACCAGTTACATCACCCTGCTGCCATCCCCACCAGCCGCCGTCCGAGGA
GCCAGCGGACTGCCGTTCCCTCAGCTGCTTCGATGACTTCTACCAGGGCTGCTTCCGCATCTTCTGTTACGTT
CCTGTTTCTGCTCTTGGTGCAGGATCTGCAGCTACTGCTGCATCAGAAGAAATGTATGTGCCAAGAGTTGTAACC
TCTGCACAACAGAAAGCAGGAAGAACTATTACAGCCCGGATCACAGGAAGATGTGATTTTGCTTCAAAAAATAGA
ATTAGCAGCAGTTTAGCTATAATGGGAGTTTCTCCTCCCATGAGCTCAGTTGTTGTGGAAAAACATCATCCAGTC
ACAGTGCAAACCATTCCTCAAGCAACTGCAGCAAAATATCCCCGGACCATTCATCCTGAAAAGTAGTACCTCAGCT
TCCAGATCACTTGGAACCAGATCAGCTCACACCCAGTCTCTCACAAGTGTTTATTCCATAAAAGTGGTTGACTAA
AGTGAATATGTCCATAGTGGGGTCTTTTAATCCCTCTGGTCTTACCAAGGGTTAGAAGTCTTTTGGTTTTAACTT
TTCCATATTGTTAGAACATCATGGAGACATCATGTTTCTGTTCAAAATTACAAGAGGCTTTTTCAAGCTCTAC
CATGCTTTGTAACATATGTAGAAATTATTTTAATGTTATTTTTTTATTTAAGCAATTAAGTAAAACTTTTTTAA
TT

1733/6881
FIGURE 1605

MSSDEEKYSLPVVQNDSSRGSSVSSNLQEEYEELLHYAIVTPNIEPCASQSSHPKGELVPDVRISTIHDLHSQG
NNSEVRETAIEVGKGCDFHISHSKTDESSVLSPRKPSHPVMDFFSSHLLADSSSPATNSSHTDAHEILVSDFL
VSDENLQKMENVLDLWSSGLKTNIISELSKWRLNFI DWHRMEMRKEKEKHAAHLKQLCNQINELKELQKTFEISI
GRKDEVISLSHAIGKQKEKIELMRTFFHWRIGHVRARQDVYEGKLADQYYQRTLLKKVWKVWRSVVQKQWKDVV
ERACQARAEVCIQISNDYEAKVAMLSGALENAKAEIQRMQHEKEHFEDSMKKAFMRGVCALNLEAMTIFQNRND
AGIDSTNNKKEEYGPVGQKEHSAHLDPSAPPMPLPVTSPLLPSPPAAVGGASATAVPSAASMTSTRAASASSVH
VPVSALGAGSAATAASEEMYVPRVVTSAQQKAGRTITARITGRCDFASKNRISSSLAIMGVSPPMSSVVVEKHP
VTVQTIPQATAAKYPRTIHPESSTSASRSLGTRSAHTQSLTSVHSIKVVD

1734/6881
FIGURE 1606

ATGGAGGGTTCGTGGCTATGCCAAGGAGGGACTAAAAGATCTGGCCACCAGGACACCCAGAACTCCTAAGAAGAAA
TTAACATCTTGTGAGCAGCCCTTTGGCTGTGAAAATGCAAATGACTCAGACTGGCTGCCAAGAGTCACCTGTGAA
GCTCAACTGGCACAGGACTCAGGGCTGAGCTCCATTCTTAACCTCTCCATCCCATACAGCCAAACAAGCAGAACAC
AGGTTGCGCCCAAGGGTTCTGAACCCAGGATGTATAAAGAAGATGGGCCAGCGAGAGCTCACCGGATGCCGCCAG
AACCGCGACGCTTTCCAAGGCACGGGGCCCTCTCTCGGGGCGAACCATTCCAGGGCGCCCTGCCCTTCACAAAG
AAAAGAGAACTCTCCCCGGGGCTCCCGCCGGCTTCTCCGGGATCGGTACGTTTCCCAGAATTAAACAGAAAAAG
CCTGGGAGTGGGCAAGTTGGCAAAAGGAAGAGAGGCCTGTTTGGCTGTGACATGTGGGTGGAGGGTCATAAAGGC
CAGGTGGGGAATGGCAGTGTCCGGCTGAGGGAGGGAGCTGCCACACTGCCTGATCATTTCGCGTGGCAGCAGCGGG
GAGGAGATCGGCAGCACCTTTGGCCACAGAGCTGCGCCTCTGTCAAAACAGGCAGCGCTGCAGGCGGCCAGAGA
TCCACTTCCACAGATTCTCGTGGCCAGGGCAGGGGTGTGTTGTGGTGGGCAGACTGGCCAGGCGACCTTGGCCCA
CCATCACCCCTCTCTTCACAGCCAGATGCGTTCTCGGGGCCCCAGGCCTGCACCCGTTTCTTCTCCCGCATCACG
AAGGCCAATGTGGACCTGCTC¹CCGAGGGGGGCTCCCGAGCGACAGCGGCTGCTGCCTGCGGCTCTGGCCTGCTGG
GGGCTGGGGCCAGCGCGGGGCGGAGAGGGCTCGGCAGTTCACAAAAGCGCTGAGGCCAGCCTCTCTGCAGGGTGTG
CGGGGGTCTCTGCTGAGCGAGGCTGATGTGCGGGCTCTGGGAGGCCTGGCTTGCGACCTGCCTGGGCGCTTTGTG
GCCGAGTCGGCCGAAGTGCTGCTACCCCGGCTGAGGACTGCCATCAGGCTACAAGGCCACTTTGCCACAACAGGC
AGAAAACAAGGAACACTTGGGAATTTACATCTCCTTGTTTGGCCCTTAGACAATGATCAACTTGTATTGGAATAT
GAAACCCAGCTCCCTGGCCTGAGTCTGATCAAACTCTCAGGATTTTTAAAAACCCTCAGTGGACAAAAGTCTACT
CACGCTGCTTTGGTAGAATTGGACATAGCCAAGGAGCTCATCAGAAAAGGAGCTGCTAGTCACAGGCAGCAACAA
ACCCACCTCCACACAGGGATCCACTGTGGGGCTGCAATAACTGCTCCTTCTCTGAGTGATACAGGACATTCTGAG
GAAAAGTGGCTGGTGGATGGGCAGTATGTAATGACACAAGCTCATGAGTACAAGCTGAGACATGATGGGAGTCTA
CGGGTCCCATCTACACAGCTTGATGCAGCTCTTCCAATTAATGGCCAGTGTCTGGCTGAAC TATTATAG

1735/6881
FIGURE 1607

MEGRGYAKEGLKDLATRTPTPKKKLTSCEQPFGCENANDSDWLPRVTCEAQLAQDSGLSSILNSPSHTAKQAEH
RLRPRVLNPGCIKKMGQRELTGCRQNRDAFQGTGPSLGANPFQGALPFTKKRELSPGLPPASPGSVTFPRIKQKK
PGSGQVGKRKRGLFGCDMWVEGHKGQVGNGSVRLREGAATLPDHSRGSSGEEIGSTFGHRAAPLSQTRTAIRLQG
HFATTGRKQGTGNLHLLVWPLDNDQLVLEYETQLPGLSLIKLSGFLKTLGQKSTHAALVELDIAKELIRKGAA
SHRQQQTHLHTGIHCGAAITAPSLSDTGHSEEKWLVDGQYVMTQAHEYKLRHDGSLRVPSTQLDAALPINGQCLA
ELL

1736/6881
FIGURE 1608

GGGGCGCACAGAGCCAGAGGGGCTTGCGAGCGGCGGCTGAGGGACCGGGGAGGGGGCGCCGAGCGGCTCCAGC
GCAGAGACTCTCACTGCACGCCGAGGGGCGCCCTTCCTCGCTCGCGCCCGCGCGACCGCGCGCCCCAGTCCC GCC
CCGCCCCGCTAACCGCCCCAGACACAGCGCTCGCCGAGGGTCGCTTGGACCCTGATCTTACCCGTGGGCACCCTG
CGCTCTGCCTGCCGCGAAGACCGGCTCCCCGACCCGAGAGTCAAGGAGAGAGGGTGAAGCGGAGCAGCCCGAGG
CGGGGAGCCTCCCGGAGCAGCGCCGCGCAGAGCCCGGGACAATGGGGCCGCGGCGGCTGCTGCTGGTGGCCGCC
TGCTTCAGTCTGTGCGGCCGCTGTTGTCTGCCCCGACCCGGGCCGCGAGGCCAGAATCAAAAGCAACAAATGCC
ACCTTAGATCCCCGGTCATTTCTTCTCAGGAACCCCAATGATAAATATGAACATTTTGGGAGGATGAGGAGAAA
AATGAAAGTGGGTAACTGAATACAGATTAGTCTCCATCAATAAAAGCAGTCCTCTTCAAAAACAACCTTCTGCA
TTCATCTCAGAAGATGCCTCCGATATTTGACCAGCTCCTGGCTGACACTCTTTGTCCCATCTGTGTACACCGGA
GTGTTTGTAGTCAGCCTCCCACTAAACATCATGGCCATCGTTGTGTTTCATCCTGAAAATGAAGGTCAAGAAGCCG
GCGGTGGTGTACATGCTGCACCTGGCCACGGCAGATGTGCTGTTTGTGTCTGTGCTCCCCCTTAAGATCAGCTAT
TACTTTTCCGGCAGTGATTGGCAGTTTGGGTCTGAATTGTGTGCTTCGTCACTGCAGCATTTTACTGTAACATG
TACGCCTCTATCTTGCTCATGACAGTCATAAGCATTGACCGTTTCTGGCTGTGGTGTATCCCATGCAGTCCCTC
TCCTGGCGTACTCTGGGAAGGGCTTCCTTCACTTGTCTGGCCATCTGGGCTTTGGCCATCGCAGGGGTAGTGCCT
CTGCTCCTCAAGGAGCAAACCATCCAGGTGCCCCGGGCTCAACATCACTACCTGTCTATGATGTGCTCAATGAAACC
CTGCTCGAAGGCTACTATGCCTACTACTTCTCAGCCTTCTCTGCTGTCTTCTTTTTTGTGCCGCTGATCATTTCC
ACGGTCTGTTATGTGTCTATCATTCGATGTCTTAGCTCTTCCGCAGTTGCCAACCGCAGCAAGAAGTCCC GGCT
TTGTTCTGTGCTGCTGTTTTCTGCATCTTCATCATTTGCTTCGGACCCACAAACGTCTCTCTGATTGCGCAT
TACTCATTCCTTTCTCACACTTCCACCACAGAGGCTGCCTACTTTGCCTACCTCCTCTGTGTCTGTGTGCTCAGCAGC
ATAAGCTGCTGCATCGACCCCTAATTTACTATTACGCTTCCTCTGAGTGCCAGAGGTACGTCTACAGTATCTTA
TGCTGCAAAGAAAGTTCGGATCCCAGCAGTTATAACAGCAGTGGGCAGTTGATGGCAAGTAAAATGGATACCTGC
TCTAGTAACCTGAATAACAGCATATACAAAAGCTGTTAACTTAGGAAAAGGGACTGCTGGGAGGTTAAAAAGAA
AAGTTTATAAAAGTGAATAACCTGAGGATTCTATTAGTCCCCACCCAACTTTATTGATTACCTCCTAAAACAA
CAGATGTACGACTTGCATACCTGCTTTTTATGGGAGCTGTCAAGCATGTATTTTTGTCAATTACCAGAAAGATAA
CAGGACGAGATGACGGTGTATTCCAAGGGAATATTGCCAATGCTACAGTAATAAATGAATGTCACTTCTGGATA
TAGCTAGGTGACATATACATACTTACATGTGTGTATATGTAGATGTATGCACACACATATATTATTTGCAGTGCA
GTATAGAATAGGCACTTTAAACACTCTTTCCCCGACCCAGCAATTATGAAAATAATCTCTGATTCCCTGATT
TAATATGCAAAGTCTAGGTTGGTAGAGTTTAGCCCTGAACATTTTCATGGTGTTCATCAACAGTGAGAGACTCCAT
AGTTTGGGCTTGTACCACTTTTGCAAATAAGTGTATTTTGAAATTGTTTGACGGCAAGGTTTAAAGTTATTAAGAG
GTAAGACTTAGTACTATCTGTGCGTAGAAGTTCTAGTGTTTTTCAATTTTAAACATATCCAAGTTTGAATTCCTAA
AATTATGGAAACAGATGAAAAGCCTCTGTTTTGATATGGGTAGTATTTTTTACATTTTACACACTGTACACATAA
GCCAAAACCTGAGCATAAGTCTCTAGTGAATGTAGGCTGGCTTTCAGAGTAGGCTATTCTGAGAGCTGCATGTG
TCCGCCCCCGATGGAGGACTCCAGGCAGCAGACACATGCCAGGGCCATGTGAGACACAGATTGGCCAGAAACCTT
CCTGCTGAGCCTCACAGCAGTGAGACTGGGGCCACTACATTTGCTCCATCCTCCTGGGATTGGCTGTGAAGTGT
CATGTTTATGAGAACTGGCAAAGCAGAATGTGATATCCTAGGAGGTAATGACCATGAAAGACTTCTCTACCCAT
CTTAAAAACAACGAAAGAAGGCATGGACTTCTGGATGCCCATCCACTGGGTGTAAACACATCTAGTAGTTGTTCT
GAAATGTCAGTTCTGATATGGAAGCACCCATTATGCGCTGTGGCCACTCCAATAGGTGCTGAGTGTACAGAGTGG
AATAAGACAGAGACCTGCCCTCAAGAGCAAAGTAGATCATGCATAGAGTGTGATGTATGTGTAATAAATATGTTT
CACACAAAACAAGGCCTGTGAGCTAAAGAAGTTTGAACATTTGGGTTACTATTTCTTGTTGTTATAACTTAATGAA
AACAAATGCAGTACAGGACATATATTTTTTAAATAAGTCTGATTTAATTGGGCACTATTTATTTACAAATGTTTT
GCTCAATAGATTGCTCAAATCAGGTTTTCTTTTAAAGAAATCAATCATGTGCTGCTTAGAAAATAACAGAAGAAA
ATAGAATTGACATTGAAATCTAGGAAAATTATTCTATAATTTCCATTTACTTAAGACTTAATGAGACTTTTAAAG
CATTTTTTAAACCTCCTAAGTATCAAGTATAGAAAATCTTCATGGAATTCACAAAGTAATTTGGAAATTAGGTTGA
AACATATCTCTTATCTTACGAAAAAATGGTAGCATTTTAAACAAAATAGAAAGTTGCAAGGCAATGTTTATTTA
AAAGAGCAGGCCAGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCGGGTGGATCACGAG
GTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAACCCGTCTCTACTAAAAATGCAAAAAAATTAGCCGGG
CGTGGTGGCAGGCACCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGACTGGCGTGAACCCAGGAGGCGGA
CCTTGTAGTGAGCCGAGATCGCGCCACTGTGCTCCAGCCTGGGCAACAGAGCAAGACTCCATCTC

1737/6881
FIGURE 1609

GAAGAGGCGAGAACGACCCCCGGTCCGACCAAAGCCCGCGCGCCGCTGCGTCCCGCGTCCAGCACCTATGTCCCG
CTGCCGTCGCTGCCGCCACCATGCCCAAGAGAAAGGCTGAAGGGGATGCTAAGGGAGATAAAGCCAAGGTGAAGG
ACGAACCACAGAGAAGATCCGCGAGGTTGTCTGCTAAACCTGCTCCTCCAAAGCCAGAGCCCACGCCTAAAAGGC
CCCTGCAAAGAAGGGAGAGAAGGTACCCAAAGGGAAAAAGGGAAAAGCTGATGCTGGCAAGGAGGGAAATAACCC
TGCAGGAAATGGAGATGCCAAAACAGACCAGGCGCAGAAAGCTGAAGGTGCTGGAGATGCCAAGTGAAGTGTGTG
CATTTTGTATAACTGTGTACTTCTGGTGACTGTACAGTTTGAATACTATTTTTTATCAAGTTTTATAAAAATGC
AGAATTTTGTGTTTATTTTATTTTATTTTATTTTAAAGCTATGTTGTTAGCACATAGAACACTTCATTGTTGTTTT
GGGGGAAGGGGCATATGTCGCTAATAGAATGTCTCAAAGCTGGATTGATGTGGAGGATTCCCTGACTTTGACAC
ACATGGCCACCTTGGCACAAAAGCCTTGTGGTATAGAAAAACAAATT

1738/6881
FIGURE 1610

GGCGAGAACGACCCCCGGTCCGACCAAAGCCCGCGCGCCGCTGCGTCCCGCGTCCAGCACCTATGTCCCGCTGCC
GTCGCTGCCGCCACCATGCCCAAGAGAAAGGCTGAAGGGGATGCTAAGGGAGATAAAGCCAAGGTGAAGGACGAA
CCACAGAGAAGATCCGCGAGGTTGTCTGCTAAACCTGCTCCTCCAAAGCCAGAGCCCACGCCTAAAAGGCCCTG
CAAAGAAGGGAGAGAAGGTACCCAAAGGGAAAAAGGGAAAAGCTGATGCTGGCGAGGAGGGATTCCCTGACTTTG
ACACACATGGCCACCTTGGCACAAAAGCCTTGTGGTATAGAAAAACAAATTTGTTTTTATGTCCTCGTCTCCCTT
TCCCTCTTTCAGCATAGACTTAACTCCCTTAAGCCCAGACATCTGTTGGGACCTGACCCCTAGTCATTGGTTACC
AGTGTGTTAGGCAATCTGGACTTTCCAGTGATGCCACTGAGATGGCACCTGTCAAAGAGCAGTGGTTCTGTTTC
TAGATTATGGATCTTCAGATAAATTCTGCCATTTTCATTTAACTTCCTGAAAGTCAGGGTCGGCTTGTGAAAAGT
TGTTAAACAACATGCTAAATGTGAAATGTCAACCCTCACTCTAAACTTTCCCTGTTTCAGAGCATCAGATGAAGAC
TTCATTGGGTTTTATAGTGGCTTTCTGATTTTTGGTAGTCCATTGAAGAAGGGAGTTTGAAAGTTGTTGTATACT
GTTAACGATTGTCTGCCCATGTCCTGCCTGAAATACCA

1739/6881
FIGURE 1611

GGGAGATAAAGCCAAGGTGAAGGACGAACCACAGAGAAGATCCGCGAGGTTGTCTGCTAAACCTGCTCCTCCAAA
GCCAGAGCCCACGCCTAAAAGGCCCTGCAAAGAAGGGAGAGAAGGTACCCAAAGGGAAAAAGGGAAAAGCTGAT
GCTGGCAAGGAGGGAAATAACCCTGCAGGAAATGGAGATGCCAAAACAGACCAGGCGCAGAAAGCTGAAGGTGCT
GGAGATGCCAAGTGAAGTGTGTGCATTTTTGATAACTGTGTACTTCTGGTGACTGTACAGTTTGAAATACTATTT
TTTATCAAGTTTTATAAAAATGCAGAATTTTGTGTTATTTATTTATTTTTTTTAAAGCTATGTTGTTAGCACA
TAGAACACTTCATTGTTGTTTTTGGGGGAAGGGGCATATGTCGCTAATAGAATGTCTCCAAAGCTGGATTGATGT
GGAGAAAACACCTTTCCTTCTAGTTTTGAGAGACTTCCTCTTGGCTTCCAGGAGGAGGGATTCCCTGACTTTGA
CACACATGGCCACCTTGGCACAAAAGCCTTGTGGTATAGAAAAAACTCCCTTAAGCCCAGACATCTGTTGGGACC
TGACCCCTAGTCATTGGTTACCAGTGTGTTAGGCAATCTGGACTTTCAGTGATGCCACTGAGATGGCACCT

1740/6881
FIGURE 1612

AAACCTCGCCCAGATTTCAGGCGTGTAACCAGCCGGAGCGGCGCGGCAGCGGCAGGACCGCCGTGGCGCCTAGAG
TAGCGACCCGCGGGGAGCACGGGGCGACGCTGGCTGCAGAGACCCGGTGACAGCTGTATGCTTGAAATCTTGGAT
ACTGCAGGAACGGAGCAATTTACAGCAATGAGGGATTTATACATGAAAAATGGACAAGGGTTTGCATTAGTTTAT
TCCATCACAGCACAGTCCACATTTAACGATTTACAAGACCTGAGAGAACAGATTCTTCGAGTTAAAGACACTGAT
GATGTTCCAATGATTCTTGTGGTAATAAGTGTGACTTGGAAGATGAAAGAGTTGTAGGGAAGGAACAAGGTCAA
AATCTAGCAAGACAATGGAACAACCTGTGCATTCTTAGAATCTTCTGCAAAATCAAAAATAAATGTTAATGAGATC
TTTTATGACCTAGTGCGGCAAATTAACAGAAAACTCCAGTGCCTGGGAAGGCTCGCAAAAAGTCATCATGTCAG
CTGCTTTAATATACTAAATGCATTGTAGCTCTGAGCCAGGTCTGAAGAACTGTTGCCCAATTCAACAGTGCCAGC
ATTCCAACCTTTGTTAAACCTACCAACATCTTAAATGGACTTTCCTGTGGTGGTACCCTTTAAGAGGCGGATGAAA
GCTACTATATCAGTTTGCACATTCTAATCACTTTCCAGTATCACAAGAGAGATTTTTACTTATATAATAGTCCTA
GAGTATGCAGCTGGTAAAACCAGAGGCTACATCCAGTATTACTGCTAAGAGACATTCTTCATCCACCAATGTTGT
ACATGTATGAAAAATGGTGTACTGTATACTTTAACATGCCCCATACTTTGTATTGGAGAGTACAATAATGTAAATC
CTAAAAGCACCCTATTTTAGCATAATAAAAGAAAGTCCAAAGAGCTCCTATATAGACTACTCCAGATAACTTCG
CTTCTTTGATACTTGTAGCTTATTGTAATTTTTTTTAAAGAAATTCAGGTCATTATTATTGTACAAAATAAGCGC
TTTGATTAACACAGCTATATAGTTTTTTTTTAATTTTTTAATGTCCTTAGATTAAAGACGTTGCCTTTAATATCTGTTG
GGAAGGAAATGTCCAGACTTTTCAAATCTCTTATTATATGTTTCCTTTTTTTTGTTTACATAGGGAACAATGTTTA
TAGTCGTGTGTACAGTGGGGTCTACAACAAGAAGTGATATT

1741/6881
FIGURE 1613

MREYKLVVLGSRGVGKSALTQFVQGIFVEKYDPTIEDSYREQVEVDAQQCMLEILD
TAGTEQFTAMRDLYMKNQ
QGFALVYSITAQSTFNDLQDLREQILRVKDTDDIFYDLVRQINRKTPVPGKARKKSSCQLL

1742/6881
FIGURE 1614

TTGGAGCAGGCCTGCTGCCTTCATGTCCACTCTCCTCATCAATCAGCCCCAGTATGCATGGCTGAAAGAGGTGGG
GCTCCGAGAGGAAAAATGAGGGCGTGATAATGGAAGCTGGGGAGGCCGGGGAGAGGTTATTATGACCTGTTGCTC
TGCTAACAACTAGCCAATAGCAAGAGTCCGACAGGCCAGTGTGGCAGACTATGAAGAACTGTAAAGAAAAGCAAC
AGAAGCATGGAAAAATCTGGGCAGATATTCTGCTCCAAAACGAGGAGAAATAGTAAGACAGATTGACGATGCCTT
GTGGGAGAAGATCCAAGTACTAGGAAGCTTGGTGTCTTTGGAGATGGGGAAAATCTTAGTGGAAGGTGTGGGTGA
AGTTTCAGGAGTATGTGGATATCTGTGACTATGCTGTTGGTTTATCAAGGATGATTGGAGGACCTATCTTGCTTC
TGAAAGACCTGGCCATGCACTGATTGAGCAGTGGAATCCTGTAGGCCTGGTTGGAATCATCACGGCATTCAATTT
CCCTGTGGCAGTGTATGGTTGGAACAACGCCATTGTTCATGATCTGTGGAAATGTCTGCCTCTGGAAAGGAGCTCC
AACCACCTCCCTCATTAGTGTGGCTGTCAAAAGATAATAGCCAAGGTTCTGGAGGACAACAAGCTGCTTGGTGC
AATTTGTTCCCTTGACTTGTGGTGGAGCAGATACCGGCACAGCAATGGCCAAAGATGAACGAGTGAACCTGCTGTC
CTTCACCGGGAGCACTCAGGTGGGAAAACAGATGGCCCTGATGGTGCAGGAGAGGTTTGGGAGAAGTTTGTGGA
ACTTGGAGGAAACAGTACCATTATTGCCTTTGAAGATGCAGACCTCAGCTTAGTTGTTCCATCAGCTCTCTTCAC
TGCTGTGGGAATAGCTGGCCAGAGGTGTACCACTGCGAGGCGACTGTTTGTACATGAAAGCATCCATCATGAGGT
TGTAACAGACTTAAAAAGGCCTACGCACAGATCCGAGTTGGGAACCCATGGGACCCTAATGTTCTCTATGGGCC
ACTCCACACCAAGCAGGCAGTGAGCATGTTTCTTGGAGCAGCGGAAGAAGCAAAGAAAGAAGGTAGCACAGTGGT
CTATGGGGGCAAGGTTATGGATCGCCCTGGAAATTATGTAGAACCGACAATTGTGACAGGTCTTGCCCACGATGC
ATCCATTGCACACACAGAGACTTTTGCTCCGATTCTGTATGTCTTTAAATTCAAGAATGAAGAAGAGGTCTTTGC
ATGGAATACTGAAGTAAACAGAGACTTTCAAGTAGCAACTTTACCAAAGATCTGGGCAGAATCTTTCGCTGGCT
TGGACCTAAAGGATCAGACTGTGGCACTGTAAATGTCAACATTCCAACAAGTGGGGCTGAGATTGGAGGTGCCTT
TGGAGGAGAAAAGCACACTGGTGGTGGCAGGGAATCTGGCAGTGATGCCTGGAAACAGTACATGAGAAGGTCTAC
TTGTACTATCAACTACAGTAAAGACTTTCTCTGGCCCAAGGAATCAAGTTTCAGTAAAGGTGTTTTAGATGAAC
ATCCCTTAATTTGAGGTGTTTCGGCAGCTGTTTTTGAAGAAGACAAAGAAAATTAAAGTTTTCTTGAATAAATGC
ATTATTATGACTGTGACAGTGACTAATCCCCCTATGACCCCCAAAGCCCTGATTAAATCAAAGACTCCTTTTTTA
AAAATCAAAATAAAATTGTTACAACAT

1743/6881
FIGURE 1615

CCTCTTTTTCCGGCTGGAACCATGGAGGGTGTAGAAGAGAAGAAGAAGGAGGTTCCCTGCTGTGCCAGAAACCCTT
AAGAAAAAGCGAAGGAATTTCTAGAGCTGAAGATCAAGCGCCTGAGAAAGAAGTTTGCCCAAAGATGCTTCGA
AAGGCAAGGAGGAAGCTTATCTATGAAAAAGCAAAGCACTATCACAAGGAATATAGGCAAATGTACAGAACTGAA
ATTTCGAGTGGCGAGGATGGCAAGAAAAGCTGGCAACTTCTATGTACCTGCAGAACCCAAATTGGCGTTTGTTCATC
AGAATCAGAGGTATCAGTGCTGTGAGCCCAAAGGTCCGAAAGGTGTTGCAGCTTCTTCGCCTTCGTCAAATCTTC
AATGGAACCTTTGTGAAGCTCAACAAGGCTTCGATTAAACATGCTGAGGATTGTAGAGCCATATATAGCATGGGGG
TACCCCAATCTGAAGTCAGTAAATGAACTAATCTACAAGCGTGGTTATGGCAAAATCAATAAGAAGCGAATTGCT
TTGACAGATAACGCTTTGATTGCTCGATCTCTTGGTAAATACGGCATTATCTGCATGGAGGATTTGATTCATGAG
ATCTATACTGTTGGAAAACGCTTCAAAGAGGCAAATAACTTCCTGTGGCCCTTCAAATTGTCTTCTCCACGAGGT
GGAATGAAGAAAAAGACCACCCATTTTGTAGAAGGTAGAGATGCTGGCAACAGGGAGGACCAGATCAACAGGCTT
ACTAGAAGAATGAACTAAAGGTGTCTACCATGATTATTTTTCTAAGCTGGTTGGTTAATAAACAGTACCTGCTCTC
AAATTGA

1744/6881
FIGURE 1616

MEGVEEKKKEVPAVPETLKKKRRNFVELKIKRLRKKFAQKMLRKARRKLIYEKAKHYHKEYRQMYRTEIRVARMA
RKAGNFYVPAEPKLAFFVIRIRGISAVSPKVRKVLQLLRRLRQIFNGTFVKLNKASINMLRIVEPYIAWGYPNLKSV
NELIYKRGYGKINKKRIALTDNALIARSLGKYGIICMEDLIHEIYTVGKRFEANNFLWPFKLSSPRGGMKKKTT
HFVEGRDAGNREDQINRLTRRMN

1745/6881
FIGURE 1617

GCACCATGGCGGTTGGCAAGAACAAGCACCTTACGAAAGGCAGCAAAAAGGGGGCCAAGAAGAAAGTGTTGATC
CATTTTCTAAGAAAGATTGGTATGATGTGAAAGCACCTGCTATGTTCAATATAAGAAATATTGGAAAGATGCTCA
TCACCAGGACCCAAGGAACCAAAATTGCATCTGATGGTCTCAAGGGTCGTGTGTTTGAAGTGAGTCTTGCTGATT
TGCAGAATGATGAAGTTGCACTTAGAAAATTCAAGCTGATTACTGAAGATGTTCAGGGTAAAACTGCCTAACTT
CCATGGCATGGATCTTACCTGTGACAAAATGTGTTCCATGGTCAAAAAATGGCAGACAATGATTGAAGCTCACGT
TGACGTCAGGACTATTGATGGTTACTTGCTTCGTCTGTTCTGTGTTGGTTTTACTAAAAACGCAACAATCAGAT
ACAGAAGACCTCTTATGCCCAGCACCAACGGGTCCGCCAAATCCGGAAGAAGATGATGGAAATCATGACCCGAGA
GGATTCCAGACAGCATTGGAAAAGACATAGAAAAGGCTTGCCAATCTATCCTCTCCATGATGTCTTCGTTAGAAA
AGTAAAAATGCTGAAGAAGCCCAAGTTTGAATTGGGAAAGCTCATGGAGCTTCATGGTGAAGGCAGTAGTTCTGG
AAAAGCCACTGGGGACGAGAGAGGTGCTAAAGTTGAACGAGCTGATGGTTTTGAACCACCAGTCCAAGAATCTGT
TTAAAGTTCAGACTTCAAATAGTGGCAAATAAAAAGTGCTATTTGTGA

1746/6881
FIGURE 1618

MDLTCDKMCSMVKKWQTMIEAHVDVRTIDGYLLRLFCVGFTKKRNNQIQKTSYAQHQRVRQIRKKMMEIMTREDS
RQHWKRHRKGLPIYPLHDVFVRKVKMLKKPKFELGKLMELHGEGSSSGKATGDERGAKVERADGFEPPVQESV

1747/6881
FIGURE 1619

TTTCTGCCCATGGACACCGCCGAAGAAGCATTGTTAAAGTCTCTCTTCACCCTGCCGTGTCATGTCTAAGTCAGAGT
CTCCTGAAGAGCCCCGAACAGCTGAGGAAGCTCTTCATTGGAGGGCTGAGCTTTGAAACAACGATGAGAGCCTTG
AGGAGCCATTTTGAGCAATGGGGAATGCTCACGGACTGTGTGGTCATGAGAGATCCAAACACCAAGCACCCCAGG
GGCTTTGGGTTTGTGCACATATGCTACTGTGGAGGAGGTGGATGCAGCCATGAATGCAAGGCCACACAAGGTGGAT
GGAAGAGTTGTGGAACCAAAGAGAGCTGTCTCGAGAGAAGATTCTGAAAGACCAGGTGCCCACTTAAGTGTGAAA
AAGATATTTGTTGGTGGCATTAAAGAAGACACTGAAGAACATCACCTAAGAGATGATTTTGAACAGTATGGAAAA
ATTGAAGTGATTGAAATCATGACTGACCGAGGCAGTGGCAAGAAAAGGGCTTTGCCTTTGTAAATTTTGACGAC
CATGACTCCATGGATAAGATTGTCATTTCAGAAATACCATACTGTGAATGGCCACAAGTGTGAAGTTAGGAAAGCC
CCGTACAGCAAGAGATGGATAGTGCTTCATCCAGCCAAAGAGGTCGAAGTGGTTCTGGAAACTTTGGTGGTGGT
CGTGGAGGTGGTTTCGGTGGGAATGACAACTTTGGTCATGGAGGAACTTCAGTGGTTGTGGTGGCTTTGGTGGC
AGTCATGGTGGTGGTGGATATGGTGGCAGTGGGGATGGCTATAATGGATTGTGTAATGATGGAAGCGATTTTGA
GGTGGTGGGAAGCTACAATGATTTTGGCAATTACAACAATCAGTCTTCAAATTTTGACCCATGAAGGGAGGAAAT
TTTGGAGGCAGAAGCTCTGGCCCTTATGGTGGTGGAGGCCAATACCTTTGCAAAACCACAAAACCAAGGTGGCTAT
GGCGGTTCCAGTAGCAGCGGTAGCTATGGCAGTGGCAGAAGATTTTAATTAGGAAACAAAGCTTAGCAGGAGCGG
AGAGCCAGAGAAGTGACAGGGAAGCTACAGGTTACAACAGATTTGTGAACTCAGCCAAGCACAGTGGTGGCAGGG
CCTAGCTGCTACAAAGAAGACATGTTTTAGACAAATACTCATGTGTATGGGCAAAAAACTCGAGGACTGTATTTG
TGACTAATTGTATAACAGGTTATTTTAGTTTCTGTTCTGTGGAAAGTGTAAGCATTCCAACAAAGGGTTTTAAT
GTAGATTTTTTTTTTGCACCTATGCTGTTGATTGCTAATGTAATAGTCTGATCGTGATGCTGAATAAATGTCTTT
TCTTTTTAATGTGCTGTGTAAAGTTAGTCTACTCTGAAGCCATCTTGGTAAATTTCCCCAACAGTGTGAAGTTAG
AATTCCTTCAGGGTGATGCCAGGTTCTATTTGGAATTTATATACAACCTGCTTGGAGGGAGAAGCCATTGTCTTC
AGAAACCTTGGTGTAGTIGAAGTATAGTTACCGTTGTGACCTGAAGTTCACCATTAAAAGGGATTACCCAAGCA
AAATCATGGAATTATTGGTTATAAAAGTGATTGTTGGCACATCCTATGCAATATATCTAAATTGAATAATGGTAC
TAGATAAAATTATAGATGGGAATGAAGCTTGTGTATCATCCATTATCATGTGTAATCAATAAATGATTTAATTCT
CTTGAA

1748/6881
FIGURE 1620

MRALRSHFEQWGLTDCVVMRDPNTKHPRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPKRAVSREDSERPGAH
LTVKKIFVGGIKEDTEEHHLRDDFEQYGKIEVIEIMTDRGSGKKRGFAFVNFDDHDSMDKIVIQKYHTVNGHNCE
VRKAPSQQEMDSASSSQGRSGSGNFGGGRGGGFGGNDNFHGNGNFSGCGGFGGSHGGGGYGGSGDGYNGFGNDG
SDFGGGGSYNDFGNYNQSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPQNQGGYGGSSSSGSYGSGRRF

1749/6881
FIGURE 1621

CCGCCGAAGAAGCATTGTTAAAGTCTCTCTTCACCCTGCCGTCATGTCTAAGTCAGAGTCTCCTGAAGAGCCCGA
ACAGCTGAGGAAGCTCTTCATTGGAGGGCTGAGCTTTGAAACAACCTGATGAGAGCCTTGAGGAGCCATTTTGAGC
AATGGGGAATGCTCACGGACTGTGTGATTCTGAAAGACCAGGTGCCCACTTAAGTGTGAAAAAGATATTTGTTGG
TGGCATTAAAGAAGACACTGAAGAACATCACCTAAGAGATGATTTTGAACAGTATGGAAAAATTGAAGTGATTGA
AATCATGACTGACCGAGGCAGTGGCAAGAAAAGGGGCTTTGCCTTTGTAAATTTTGACGACCATGACTCCATGGA
TAAGATTGTCATTTCAGAAATACCATACTGTGAATGGCCACAACCTGTGAAGTTAGGAAAGCCCCGTCACAGCAAGA
GATGGATAGTGCTTCATCCAGCCAAAGAGGTCGAAGTGGTTCTGGAAACTTTGGTGGTGGTCGTGGAGGTGGTTT
CGGTGGGAATGACAACTTTGGTCATGGAGGAACTTCAGTGGTTGTGGTGGCTTTGGTGGCAGTCATGGTGGTGG
TGGATATGGTGGCAGTGGGGATGGCTATAATGGATTTGGTAATGATGGAAGCGATTTTGGAGGTGGTGGAGCTA
CAATGATTTTGGCAATTACAACAATCAGTCTTCAAATTTTGGACCCATGAAGGGAGGAAATTTTGGAGGCAGAAG
CTCTGGCCCTTATGGTGGTGGAGGCCAATACTTTGCAAAGCAGAAGATTTTAATTAGG

1750/6881
FIGURE 1622

AAGTCTCTCTTCACCCCTGCCGTCATGTCTAAGTCAGAGTCTCCTGAAGAGCCCGAACAGCTGAGGAAGCTCTTCA
TTGGAGGGCTGAGCTTTGAAACAACCTGATGAGAGCCTTGAGGAGCCATTTTGAGCAATGGGGAATGCTCACGGAC
TGTGTGGTCATGAGAGATCCAAACACCAAGCACCCAGGGGCTTTGGGTTTGTACATATGCTACTGTGGAGGAG
GTGGATGCAGCCATGAATGCAAGGCCACACAAGGTGGATGGAAGAGTTGTGGAACCAAGAGAGCTGTCTCGAGA
GAAGATTCTGAAAGACCAGGTGCCCACTTAAGTGTGAAAAAGATATTTGTTGGTGGCATTAAAGAAGACACTGAA
GAACATCACCTAAGAGATGATTTTGAACAGTATGAAAAATTGAAGTGATTGAAATCATGACTGACCGAGGCAGT
GGCAAGAAAAGGGGCTTTGCCTTTGTAAATTTTGACGACCATGACTCCATGGATAAGATTGTCATTTCAGAAATAC
CATACTGTGAATGGCCACAACGTGAAGTTAGGAAAGCCCCGTCACAGCAAGAGATGGATAGTGCTTCATCCAGC
CAAAGAGGTCGAAGTGTTCTGGAAACTTTGGTGGTGGTCGTGGAGGTGGTTTCGGTGGGAATGACAACCTTGGT
CATGGAGGAACTTCAGTGGTTGTGGTGGCTTTGGTGGCAGCTATAATGGATTTGGTAATGATGGAAGCGATTTT
GGAGGTGGTGGAAAGCTACAATGATTTTGGCAATTACAACAATCAGTCTTCAAATTTTGGACCCATGAAGGGAGGA
AATTTTGGAGGCAGAAGCTCTGGCCCTTATGGTGGTGGAGGCCAATACTTTGCAAAACCACAAAACCAAGGTGGC
TATG

1751/6881

FIGURE 1623

ACCCTGCCGTCATGTCTAAGTCAGAGTCTCCTGAAGAGCCCGAACAGCTGAGGAAGCTCTTCATTGGAGGGCTGA
GCTTTGAAACAACCTGATGAGAGCCTTGAGGAGCCATTTTGAGCAATGGGGAATGCTCACGGACTGTGTGGTCATG
AGAGATCCAAACACCAAGCACCCAGGGGCTTTGGGTTTGTACATATGCTACTGTGGAGGAGGTGGATGCAGCC
ATGAATGCAAGGCCACACAAGGTGGATGGAAGAGTTGTGGAACCAAAGAGAGCTGTCTCGAGAGAAGATTCTGAA
AGACCAGGTGCCCACTTAACTGTGAAAAAGATATTTGTTGGTGGCATTAAAGAAGACACTGAAGAACATCACCTA
AGAGATGATTTTGAACAGTATGGAAAAATTGAAGTGATTGAAATCATGACTGACCGAGGCAGTGGCAAGAAAAGG
GGCTTTGCCTTTGTAAATTTTGACGACCATGACTCCGTGGTGGCTTTGGTGGCAGTCATGGTGGTGGTGGATATG
GTGGCAGTGGGGATGGCTATAATGGATTTGGTAATGATGGAAGCGATTTTGGAGGTGGTGGGAAGCTACAATGATT
TTGGCAATTACAACAATCAGTCTTCAAATTTTGGACCCATGAAGG

1752/6881
FIGURE 1624

CAAAGGCTACTAAGTTAATGGTATTTTCTGCACAGAAAATACCATTAACTTAGTAGCCTTTGCTTAAAGGTGGGA
TTAATTCTCCATGAAGTCAGAATGAGACAATAAGCAGCATTAACCTTCATAGGCACACAGAACTAGTGCTCAAAC
GCTACCACCCCTTTTCAATTGCTATCTTTTGAAAGGCACCACTATTTGTTTTGCTGGGGTCTCGGGTGGACCCTTA
TTCGCTCCGACAAGATGAAAGAAACAATCATGAACCAGGAAAAAAGCTCGCCAACTGCAGGCACAAGTGCGCATTG
GTGGGAAAGGAACTGCTCGCAGAAAGAAGAAGGTGGTTCATAGAACAGCCACAGCAGATGACAAAAAAGCTTCAGT
TCTCCTTAAAGAAGTTAGGGGTAAACAATATCTCTGGTATTGAAGAGGTGAATATGTTTACAAACCAAGGAACAG
TGATCCACTTTAACAACCCTAAAGTTCAGGCATCTCTGGCAGCGAACACTTTCACCATTACAGGCCATGCTGAGA
CGAAGCAGCTGACAGAAATGCTACCCAGCATCTTAAACCAGCTTGGTGCGGATAGTCTGACTAGTTTAAGGAGAC
TGGCCGAAGCTCTGCCCAAACAATCTGTGGATGGAAAAGCACCCTTGCTACTGGAGAGGATGATGATGATGAAG
TTCCAGATCTTGTGGAGAATTTTGATGAGGCTTCCAAGAATGAGGCAAACTGAATTGAGTCAACTTCTGAAGATA
AAACCTGAAGAAGTTACTGGGAGCTGCTATTTTATATTATGACTGCTTTTTAAGAAATTCTTGTTTATGGATCTG
ATAAAATCTAGATCTCTAATATTTTTAAGCCCAAGCCCCCTTGGACACTGCAGCTCTTTTTCAGTTTTTGCTTATAC
ACAATTCATTCTTTGCAGCTAATTAAGCCGAAGAAGCCTTAAGTGGGAATTC

1753/6881
FIGURE 1625

MKETIMNQEKLAQLAQVRIGGKGTARRKKKVHRTATADDKKLQFSLKKLGVNNISGIEEVNMFNQTGTVIHFN
NPKVQASLAANTFTITGHAETKQLTEMLPSILNQLGADSLTSLRRLAEALPKQSVGKAPLATGEDDDDEVDPDV
ENFDEASKNEAN

CGCGTGGCGCTGCGGAGACCCGGTCCAGACGCGCTGGCGGCCCGGCACACAAGGCGCTTTCTAGCTCCCTCCCC
CGAGCGCACAGCCCGCTCCTTCCGCGGCGCTGCAGTGGCAGGCTTGCTCTGCCCTACCGTGACGCGCTCCGGA
GACGCTCTGCGGGTCTTGACACCCGGGTCCGCGGCGTGGGGACGACAGACGGAGGCGAACGCCATCGGTAGCCGG
TCCGCGAGCCATCGTTTCGGGGCGCAGTCTCTCCCCGGCTGGCCCTCCTTTCTCCGGGGCATTGCCACCGCTTC
CCTGGGCTGAGACGACCGGTTTCGTGCGCTCCTTGCCCGTGACCGTGCCTAGAACTCAGTTGTGCGTTGCGGCCAG
TCGCCACTGCTGAGTGGAAACAAAATGTCAGTCAGTGTGCATGAGAACCAGCAAGTCCAGGGCCAGCAGCGGCTCC
ATTAACATCTATCTGTTTACAAAGTCTCTACGCTGACAGCGTCTCTACTCACCTGAATCTTTTACGCCAGCAG
CGTCTCTTCACTGACGTCTTCTCCATGCCGGAAATAGGACCTTCCCTTGCCACCGGGCAGTGTGGCTGCATGC
AGTCGCTACTTTGAGGCCATGTTTCAGTGGTGGCCTGAAAGAGAGCCAGGACAGTGAGGTCAACTTTGACAATTCC
ATCCACCCAGAAGTCTTGAGCTGCTGCTTGACTATGCGTACTCCTCCCGGGTCATCATCAATGAAGAAAATGCA
GAATCGCTCCTGGAAGCTGGTGACATGCTGGAGTTTCAAGACATCCGGGATGCATGTGCAGAGTTCTCTGGA
AACCTGCATCCACCAACTGCCTGGGCATGCTGCTGCTGTCTGATGCACACCAGTGCACCAAGCTGTACGAACTA
TCTTGAGAAATGTGTCTCAGCAACTTCCAAACCATCAGGAAGAATGAAGATTTCTCCAGCTGCCCCAGGACATG
GTAGTCAACTCTTTGTCCAGTGAAGAGCTGGAGACAGAGGATGAAAGGCTTGTGTACGAGTCTGCAATTAAGTGG
ATCAGCTATGACCTGAAGAAGCGCTATTGCTACCTCCCAAGCTGTTGCAGACAGTAAGGCTGGCACTTCTGCCA
GCCATCTATCTCATGGAGAATGTGGCCATGGAGGAACTCATCACCAGCAGAGAAAGAGTAAGGAAATTGTGGAA
GAGGCCATCAGGTGCAAACTGAAAATCCTGCAGAAATGACGGTGTGGTAACCAGCCTCTGTGCCCGACCTCGGAAA
ACTGGCCATGCCCTCTTCTTCTGGGAGGACAGACTTTCATGTGTGACAAGTTGTATCTGGTAGACCAGAAAGGCC
AAAGAAATCATTCCCAAGGCTGACATTCCAGCCCCAAGAAAAGAGTTTAGTGCATGTGCGATTGGCTGCAAGTG
TACATTACTGGGGGGCGGGGGTCTGAAAATGGGGTCTCAAAAGATGTCTGGGTTTATGATACCCTGCACGAGGAG
TGGTCCAAGGCTGCCCCCATGCTGGTGGCCAGGTTTGGCCATGGCTCTGCTGAACTGAAGCACTGCCTGTATGTG
GTTGGGGGGCACACGGCCGCAACTGGCTGCCTCCCGGCTCCCCCTCAGTCTCTCTAAAGCAGGTAGAACATTAT
GACCCCACAATCAACAAATGGACCATGGTGGCCCCACTCCGAGAAGGCGTTAGCAACGCCGCAGTAGTGAGTGCC
AAACTTAAGTTATTTGCTTTTCGGAGGTACCAGTGTGAGTGCATGACAAGCTCCCCAAAGTTTCAAGTGTACGATCAG
FGTGAAAACAGGTGGACTGTACCGGCCACCTGTCCCCAGCCCTGGCGTTACACAGCAGCAGCTGTGCTGGGGAAC
CAGATTTTTATTATGGGGGGTGATACAGAAATTTCTGCTGCTCTGCTTTATAAATTCAACAGTGAGACTTACCAG
TGGACCAAGGTGGGAGATGTGACAGCAAAAGCGCATGAGCTGCCATGCTGTGGCCTCTGGAAACAAACTCTACGTG
GTTGGAGGATACTTTGGCATTTCAGCGATGCAAGACTTTGGACTGCTACGATCCAACATTAGACGTGTGGAACAGC
ATCACCAGTGTCCCGTACTCGCTGATTCTTACTGCATTTGTGAGCAGCTGGAAACATCTGCCTTCTTAAATGCAG
TACATTCTAAAGAGAGTGAGCATGAGCTCACTCCATCACTCGATGAGATAATATGAGATTTCTACTTTCGGAGAGG
CCAAGTCTAATGAAGAGAAAAAAGGAAAAAGAGTTGCAAGACTCGAATAAAATCTGCTGCACCTTGTAAATGCT
CTAACTGGACATGAAGGAAAGGGGGCGAGGGAGGGGGGTGGGATTTTTGGTGCAAGTAGCACATGGTTTTAAATATG
AATGAACAAACCTGTGATCTAGTCTTGTCTTGTAAATTGTGGATTAAATGTCAATGTTAATCAGCCCCCTCAAAGGG
AGAGAAAAGCTGGACCTTTTCCCTTGCTGTACCATATTTCAGCATTGATTTCATGGGCCCCACCATTTATGTGT
AGAATTTGAAATGGTTGTACCTCTCTCTGAGGACAGAGCTTGAAGCCTCCACACCAGCTGCTGCTGGAGATTCA
AAGCCCAACTGTGGGTCCGAGAGGGAAGCTGGCTGGGCTGGCTGAAGAATGAAGACCAGTGGACTCTCCGTAAAT
CTCTAAGGGGTCTGCTCCCCAGGAACGTTTCTGAACAATGGGGACTTTGTTGGTAGCCATTTGGTAGATGTTCTT
TTCTATTTTATAAGTGACTTTAAACTTTCCCTTGGCTGTTAAGAAGTTTGTATAGATTTAGCTATTTATTGTTCG
ATGCCTGCATGCTGAAACAATGCCTACAGCTGTCTTCACATGTATGGACGTGTGTGAATGGTTGTACGTTTTCGA
CATTTTGTGGCTGTTGAGATGTGCTTTGCTGCACAAACATGAAAATTTTTGAGTTACAATTTGGAGCATAACTGG
AGGGTGGGTGAGGGAGGGGTGGATTTTTAAATGTCAAGACAGGGAAGGATGACAAAATGAAATTTAAATGACA
TCCTAGAGGTAGAGAAACCGTGGAGATCGCTTTTCTCAGACTACCAACTTTTAAATGGGATTTTCATGGGGTTTG
TTGTGCTGATAGGGTAAGGGGAGGCTGCTTTCTGCCCTTCTCCCCACTCCCATCTGATTTACTTAATTCAGTCTC
AGCTGCTGAAATTTGGAAAGGACCAAATGCTTTACAGTTTTTTTTCTTTGTGTAGTATCTTGAAATCCTGGAAAA
TTCTATGGAATAGTTCTGTATATAGGGCACAAAGTAAAGGCATTGTCCAAAGTTTATTTATTTATTTATTTACCTA
AGAATGCTTTGCCATAACCACATTTAATGGGAAAAACGGCAGTATCACAGATGTAAATTAAGTACCAGATTTAC
TGGGCTGAACTCATTCTCTTCTTGCTATATGATTTAGCAAGTTCTAGAAGGTCTCCAAGACAATAATTACATTG
GCACAATGTATACTTCAGTGCTCACCCGTAGGCAAATCTCTTTTTAAAAAAGTCTTTGGTGCACAAGTAACACAT

1755/6881
FIGURE 1626B

TTGGCCACAAAACACCAAAGAATTGTAGGCAGTGGCCCCATTGAGAAGTTTTCCGGTAGAGTTGGAAATCAGTT
GTGAATACATTCTTTGCTAGTTGGAGTGCTTGTTTACTAAGCATGTGCCGTCGTAGGTATTAGTGCTAGTCTCAG
ATAGGTGCTTCCCCTGAGGTGCAGGGGAAGACCAAAGTTTGCAACTCGAACTGCTTTTCGTCCATGTTTTCTCACAT
TGCTGTATTTTAGAAAATAGGGGTTAAGACTGATAACAACCTTTTACATTGTGACTGTGTTTGCATTGTCTAATG
ACAGATAAATCCTTAACATTTCTCTCCACCTTAGTACTTTAGACTAATTGTGTTTGTCCGTCCATGCCATGAATG
AGTGGGCTGTAGTTGGGCCCTAAATAAATGAGCTGTTGGAAGAAAAGAATCACAGTACTTTCCAGCAGTCAGTCCC
TGGTTCCTAGATGTGTTCTAAGCAATGCAAATGTCTAATTGTCCCCAGTGGGCATAGTCAGTGTCGTTTATATT
GTAGCAGTTACAGCTCTGTAGTTTATGATGCAAATCTGCCAAGAGAGATGTATGTGTCACTGCATGGCTTCTGAA
AGCAGGATGAATTTTCTGCAGCTGTTTCAAAGTTGGGGTCTGTTCTTGAATCCTCTATTAATTACTGTGTGTGAG
CCAGAGGGAGCTGTGGTAAGGGTTGGGCCCCAGCCTGTAGGGAACCTTTCTGGACTCCCCTCTTTGAATCGATA
TAGGCATTTGGTCTCACTACTTGACCATTCTCACCTGTGAAACGTCCCACACTTTGAAGCAAATACAATTCACA
GCACAGTACACACAAAAACCTTGGCATAAGACAGAGAAGGTTCTTCTTATTTTGTGGGCTGGTTGCTGTAGAAAC
ACATAACAAAGGGCAGCCCTCCACTTCTGGTATAATTGTGTAGCCCCCTTTCTTTGGGCTTGACACCTGTCTTGA
ATAAGAGTGATTAGAGCTGCATAATGTCCCTCTCTTGGCTATTGACCATGTGGTTCACGTACAAAACCTCTGTATA
AGTTGAAGGAAAATGTTTCATGTTTCATATGTACTTGTTTGCTATGACTACATTTTGAGGTTTTGTAAAACCTGTTAT
TTTTTTTTTTTTTCACAATGTGAACTGAAGGTCAATAAATTATTAGAGATTTTCTCTTC

1756/6881
FIGURE 1627

CTGATCCGGGCCGGGCGGGGAAGTCGGGTCCCGAGGCTCCGGCTCGGCAGACCGGGCGGAAAGCAGCCGAGCGGGCC
ATGGAGCTGTGCGGGCTGGGGCTGCCCCGGCCGCCCATGCTGCTGGCGCTGCTGTTGGCGACACTGCTGGCGGGCG
ATGTTGGCGCTGCTGACTCAGGTGGCGCTGGTGGTGCAGGTGGCGGAGGCGGCTCGGGCCCCGAGCGTCTCGGCC
AAGCCGGGGCCGGCGCTGTGGCCCCCTGCCGCTCTCGGTGAAGATGACCCCGAACCTGCTGCATCTCGCCCCGGAG
AACTTCTACATCAGCCACAGCCCCAATTCCACGGCGGGCCCCCTCCTGCACCCTGCTGGAGGAAGCGTTTCGACGA
TATCATGGCTATAATTTTGGTTTCTACAAGTGGCATCATGAACCTGCTGAATTCAGGCTAAAACCCAGGTTTCAG
CAACTTCTTGTCTCAATCACCCCTTCAGTCAGAGTGTGATGCTTTCCCCAACATATCTTCAGATGAGTCTTATACT
TTACTTGTGAAAGAACCAGTGGCTGTCCTTAAGGCCAACAGAGTTTGGGGAGCATTACGAGGTTTAGAGACCTTT
AGCCAGTTAGTTTATCAAGATTCTTATGGAACTTTCACCATCAATGAATCCACCATTATTGATTCTCCAAGGTTT
TCTCACAGAGGAATTTTGATTGATACATCCAGACATTATCTGCCAGTTAAGATTATTCTTAAACTCTGGATGCC
ATGGCTTTTAATAAGTTAATGTTCTTCACTGGCACATAGTTGATGACCAGTCTTTCCCATATCAGAGCATCACT
TTTCCTGAGTTAAGCAATAAAGGAAGCTATTCTTTGTCTCATGTTTATACACCAAATGATGTCCGTATGGTGATT
GAATATGCCAGATTACGAGGAATTCGAGTCCTGCCAGAATTTGATACCCCTGGGCATACACTATCTTGGGGAAAA
GGTCAGAAAGACCTCCTGACTCCATGTTACAGTAGACAAAACAAGTTGGACTCTTTTGGACCTATAAACCCCTACT
CTGAATACAACATACAGCTTCCTTACTACATTTTTCAAAGAAATTAGTGAGGTGTTTCCAGATCAATTCATTCAT
TTGGGAGGAGATGAAGTGGAATTTAAATGTTGGGAATCAAATCCAAAAATTCAAGATTTTCATGAGGCAAAAAGGC
TTTGGCACAGATTTTAAGAACTAGAATCTTTCTACATTCAAAGGTTTTTGGATATTATTGCAACCATAAACAAG
GGATCCATTGTCTGGCAGGAGGTTTTTGATGATAAAGCAAAGCTTGCGCCGGGCACAATAGTTGAAGTATGGAAA
GACAGCGCATATCCTGAGGAACTCAGTAGAGTCACAGCATCTGGCTTCCCTGTAATCCTTTCTGCTCCTTGGTAC
TTAGATTTGATTAGCTATGGACAAGATTGGAGGAAATACTATAAAGTGGAACCTCTTGATTTTGGCGGTACTCAG
AAACAGAAACAACCTTTTCATTGGTGGAGAAGCTTGTCTATGGGGAGAATATGTGGATGCAACTAACCTCACTCCA
AGATTATGGCCTCGGGCAAGTGCTGTTGGTGAGAGACTCTGGAGTTCCAAAGATGTCAGAGATATGGATGACGCC
TATGACAGACTGACAAGGCACCGCTGCAGGATGGTGAACGTGGAATAGCTGCACAACCTCTTTATGCTGGATAT
TGTAACCATGAGAACATG**TAAAA**AAATGGAGGGGAAAAAGGCCACAGCAATCTGTACTACAATCACTTTATTTTG
AAATCATGTAAATAAGATATTAGACTTTTTTTGAATAAAATATTTTTATTGATTGAA

1757/6881
FIGURE 1628

MELCGLGLPRPPMLLALLLATLLAAMLALLTQVALVVQVAEAAARAPSVSAKPGPALWPLPLSVKMTPNLLHLAPE
NFYISHSPNSTAGPSCITLLEEAFFRRYHGYIFGFYKWHHEPAEFQAKTQVQQLLVSITLQSECDAFPNISSDESYT
LLVKEPVAVLKANRVW GALRGLETFSQLVYQDSYGTFTINESTIIDSPRFSHRGILIDTSRHYLPVKIILKTLD
MAFNKFENVLHWHIVDDQSFPYQSITFPELSNKGSYSLSHVYTPNDVRMVIEWARLRGIRVLPEFDTPGHTLSWGK
GQKDLLTPCYSRQNKLDSEFGPINPTLNTTYSFLTTFEKEISEVFDPQFIHLGGDEVEFKWESNPKIQDFMRQKG
FGTDFKKLESFYIQKVLDIATINKGSIVWQEVFDDKAKLAPGTIVEVWKDSAYPEELSRVTASGFPVILSAPWY
LDLISYGQDWRKYYKVEPLDFGGTQKQKQLFIGGEACLWGEYVDATNLTPRLWPRASAVGERLWSSKDV RDMDDA
YDRLTRHRCRMVERGIAAQPLYAGYCNHENM

1758/6881

FIGURE 1629

ATGGAAGAAGATGAGTTCATTGGAGAAAAACATTCCAACGTTATTGTGCAGAATTCATTAAACATTCACAACAG
ATAGGTGATAGTTGGGAATGGAGACCATCAAAGGACTGTTCTGATGGCTACATGTGCAAAATACACTTTCAAATT
AAGAATGGGTCTGTGATGTCACATCTAGGAGCATCTACCCATGGACAGACATGTCTTCCCATGGAGGAGGCTTTC
GAGCTACCCTTGGATGATTGTGAAGTGATTGAAACTGCAGCAGCGTCCGAAGTGATTAAATATGAGTATCATGTC
TTATATTCCTGTAGCTACCAAGTGCCTGTACTTTACTTTAGGGCAAGCTTTTTAGATGGGAGACCTTTAACTCTG
AAGGACATATGGGAAGGAGTTCATGAGTGCTATAAGATGCGACTGCTACAGGGACCATGGGACACTATTACGCAA
CAGGAACATCCAATACTTGGGCAACCCTTTTTTGTACTTCATCCCTGCAAGACGAATGAATTCATGACTCCTGTA
TTAAAGAATTCTCAGAAAATCAATAAGAATGTCAACTATATCACATCATGGCTGAGCATTGTAGGGCCAGTTGTT
GGGCTGAATCTACCTCTGAGTTATGCCAAAGCAACGTCTCAGGATGAACGAAATGTCCCTTAA

1759/6881
FIGURE 1630

MEEDFIGEKTFFQRYCAEFIKHSQQIGDSWEWRPSKDCSDGYMCKIHFQIKNGSVMSHLGASTHGQTCLPMEEAF
ELPLDDCEVIETAAASEVIKYEHVLYSCSYQVPVLYFRASFLDGRPLTLKDIWEGVHECYKMRLQLQGPWDTITQ
QEHPILGQPFFVLHPCKTNEFMTPLKNSQKINKNVNYITSWLSIVGPVVGLNLPLSYAKATSQDERNVP

1760/6881
FIGURE 1631

TTTGCAGATGACGCCGCCGAGGAAACTGTGTACTATTAGCCATGGTCAACCCACCGTGTTCTTCGACATTGCC
GTCGATGGCGAGCCCTTGGGCCGCGTCTCCTTTGAGCTGTTAGCTGACAAGGTCCCAAAGACAGCAGAAAATTT
CATGCTCTGAGCACTGGAGAGAAAGGATTTGGTTATAAGGGTTCCTGCTTTCACAGAATTATTCCAGGGTTTATG
TGTCAGGGTGGTGACTTCACACGCCATAATGGCACTAGTGGCAAGTCCATCTATGGGGAGAAATTTGAAGATGAG
AACTTCATCCTAAAGCATAACAGGTCCTGGCATCTTGTCCATGGCAAATGCTGGACCCAACACAAATGGCTCCAG
TTTTTCATCTGCACTGCCAAGACTGAGTGGTTGGATGGCATGCATGTGATCTGTGGCAAAGTGAAAGAAGGCATG
AATATTGTGGAGGTCATGGAGTGCTTTGGGTCCAGGAATGGCAAGACCAGCAAGAAGATCACCATTGCTGACTGT
GGACAACTCGAATAAGTTTGACTTGTGTTTTATCTTAACCACCAGACCATTCTTCTGTAGCTCAGGAGAGCACC
CCTCCATCCCATTGCTCGCAGTATCCTAGAATCTTTGTGCTCTCGCTGCAGTTCCCTTTGGGTTCCATGTTTTTC
CTTGTTCCCTCCCATGCCTAGCTGGATTGCAGAGTTAAGTTTATGATTATGAAATAAAAACTAAATAACAA

1761/6881
FIGURE 1632

CTCTTTTCGCTCAGGCCCGTGGCGCCGACAGG**AT**GGGCAAGTGTCGTGGACTTCGTACTGCTAGGAAGCTCCGTAG
TCACCGACGAGACCAGAAGTGGCATGATAAACAGTATAAGAAAAGCTCATTGGGCACAGCCCTAAAGGCCAACCC
TTTTGGAGGTGCTTCTCATGCAAAAGGAATCGTGCTGGAAAAAGTAGGAGTTGAAGCCAAACAGCCAAATTCTGC
CATTAGGAAGTGTGTAAGGGTCCAGCTGATCAAGAATGGCAAGAAAATCACAGCCTTTGTACCCAATGACGGTTG
CTTGAACTTTATTGAGGAAAAATGATGAAGTTCTGGTTGCTGGATTGGTCGCAAAGGTCATGCTGTTGGTGATAT
TCCTGGAGTCCGCTTTAAGGTTGTCAAAGTAGCCAATGTTTCTCTTTGGCCCTATACAAAGGCAAGAAGGAAAG
ACCAAGATCA**TAA**ATATTAATGGTGAAAACACTGTAGTAATAAATTTTCATATGCC

1762/6881

FIGURE 1633

MGKCRGLRTARKLRSHRRDQKWHDKQYKKAHLGTALKANPFGGASHAKGIVLEKVGVEAKQPNSAIRKCVRVQLI
KNGKKITAFVPNDGCLNFIENDEVLVAGFGRKGHAVGDIPGVRFKVVKVANVSLALYKGKKERPRS

1763/6881
FIGURE 1634

TTTATTTTAATTGCCGTAAAGGAAGTGTATTTTTGTTTTGTTTTTTAAACACAGCACTTTAAATCCAGTTTGTGTT
TTGTCAACTTGAAGTGAATCTCTTTTGTACTTTGGAGGTGATAAATAGTTTTCAAATCTGCTGATTTGTATAC
TGTGGCACAAAGTATCTTTGAAGTGTGATAGTGAAAGGAGACCTTCAACAATTTTTAGTCTAGGCGAGAGGAATAT
TAGGAATGTGACTTCTAAATTTTACAATAGAGCAGTTATTTTAAGGTCATGGTTAACATTTCTTAAGGTTCAACT
AAAATTCAGTTAAAATTTTCAGAGCTACGAGGAAGTAAATCTTAGCTAAAAATTACCTGTTGTAGATAGTATTAA
TTAGATTGTTTGCAGCTATTAATTCATCATAAAGATAAAATGAAGAACTCTCCCTTTTTTTAAACA⁴AAAAAAT
TATTTCTAGATTAATAGGCTAGTAGTTATTTCTGCAGAAACAACGTATGGAAGTGAAGCCACCTATTTTTATTT
TAGACTAATTTAAACCACTTGAATGGATTCTAGGAAACATCTTAAGCTTGTGTGTTGCCTGTGGTGGTTTTTGTG
TTTGGGGGTGTTTTTGGTTTTGGTTTTGATTTTCTGTATTTTGTATCTGGGGATTTTTTGTGTTGTTTGGT
TTTGGTTTTGGTTTTATATTTTTGGCATGTCTATGGCAGTTAAAAGTGGTATATTTTGCTTTAGATAGGGAATCA
GGTTATAATCATTTGTTCTTCTCTAAACTGCCTCTTGGGCTTTACATCAGGTCAAGGATTTTATAGGTTTCTCAA
AAATAGGATTTCTGTGCTAGTGTATGCATGCTGAGTAAGTCACCTTTCTGGCTCTAATTTCTGGGTGGCCATCTGTT
GTCCAGCTCTGCTGCCAACTGGACTTTCCGAAAGCCATGTCAACTAATTTTTTATATGCTAAGACAAATCGAATA
TGAAAAGAGGAAGAATATTCTAGATATTCTAAGACATTTCTTAATTTGGCATCTCAGAGGAGGTAGGTGGAAAGT
AAAGGAAGAGATAATTTTGGGGGAAAATTTGTGGAAACATACAAAACGTTTTGCTTTGTATAGATGCTAAACAGA
GTGGGAGGCAGCATATTTGTAACAACAACCATTTCTGACCTTTTGAAACACAAGCTTTTGAGAAAGTCAGGGAGAG
ACACAGTATGAATAAAAGCAATTAACATTTTCTTTAATGTATATTTTTCAAAGAGGACCACGGAATCCTGTTCTC
TAACCCAAGGGGCAGTGTAGGTGGTTTTTAAGCCCACAGAATATTGAGATATTTCTCTTGTGGTTTTGGTGGGGTG
GTGGGATGCAGAAGGTTATTAAAGATCAATTTAAGCATCAGATAGACTATCCCTTTTATTTTTTTAACTTTTAGG
TTCAGGGGTACATGTGCAGGTTGTTATATAGGTAAACTCATGTCAAGTGGTTTTGTTGTACAGATTATTTTGTCA
CCCAGGTGCTAAGCCTAGTACCCAGTAGTTATTTTCCCTGCTCTTCTCCCTCCTCCCACCTCCACCCTCAAGTA
GGCCCCAGTGTCTGTTGTTCCTTTCTTTTGTGTCCCTGAGTTCTCATCATTTTAGCTCCTACTTCTAAATGAGAACA
TGTATTTGGTTTTCTGTTCTGTGTTAGTTTGCTAAGGATAATGGCCTCCAGCTCAGATGGAATATCTCTATCATA
TAGACCTGTTGTTACAGGGCAGGATCGGATGATGGACACTGAAGTCCTCAGCTTGCTAAGTTTCAAGTTGCTCTCCC
TAGCCTCCTTTTGGCTTCAGAGTCTTTTGATTCCATCTATCCTGGTATTTTTTGTGTGCTGATGTTTAGTTCTGG
ATTGGCTTCAGCTGTGCTAATAGGAAGGGCGTTGTCTTTTCAAGCAATCTTAAAGGTGGTCAATCAAAGGCCA
GAGTCTGAATCCCTTCTGTGGCTTAAATAATTTGAGGATCAAGTCCAGTGTCTTGTTAATCCCTGTTCTACTGTG
CCAGACACTATCTTGAATGCTTTTATATGTTTCAAGTTTCAAAATCGCTCTTTCATACCAGGGGATGATAGTAACGT
GTAACCTGCAATAGATTCTTTCATCTTAGTAATAAGATGATCAGTCTAGTTAGGACAAAATAGAGATTGAATAAA
TTAACTTTTCCAAGTTTACAGAGTAAAAATGAGCAGATCTCTGCCTGGTTTTGTGAAAAAGAGTTAGCACTGGTA
AATAGAATATTTCTACTCCTACACCATTTCTTTCAGTATATCATCACTGAAGACAGGAAGATAGGCACACAGATTC
TTCTCGTAGTAATTCATAGTGCCTAGGTGAAAGAGATGAAGTATGTATTAAGTACAATGTGATGGCATTTA
TTATTCAGATAATCCCAGGATTCTAGAAGAAAAATAAGAAGAGTGACAGTTCAGTTAGGGTGTGAACCTCCAGAG
GAGCACTGCTTAAGCTGAAGTTGAGAGCATTGTGCAAAAGCACAGTAGTCTGTTAAGAACTAGAAATAACCTAGC
TTGTGCCACTTCGGGAGTATTAAGACATAAGCCTAGAAAGGTAGGCAAGGTTAGATCTTAGACTGTCTTGTATT
TTTCTCATTCCTGTTGATTACCTACCTCAAAATTTGAATATGTTTTTCTCTCCTGCCTAACACAAAACCTACTCAAGG
GCAGAAAATTTAAATTTCTCCTTGGTGTATGTGCAAAAGAAGGTTGAATATATTTCATGCCTACCTTATTTTGGACTA
GGAATACAGTAGTATACTTTCCGAAGACTTGCCTGAATAGTATATAAGGTGGAGGCAACTGACTAGTTAGGTCAG
TATTTTTTAGAACTCTTAATAGCTCATACTCTTGATACCAAAAGCAGCCCTGATTGTTAAAGCACACACCTGCAC
AAGAAGCAGTGATGGTTGCATTTACATTTCTGGGTGCACAAAAAAAATTTCTCAAAAAGCAAGGACTTACGCTT
TTTGCAAAAGCCTTTGAGAAGTTACTGGATCATAGGAAGCTTATAACAAGAATGGAAGATTCTTAAATAACTCACT
TTCTTTGGTATCCAGTAACAGTAGATGTTTCAAAATATGTAGCTGATTAATACCAGCATTGTGAACGCTGTACAAC
CTTGTGGTTATTACTAAGCAAGTTACTACTAGCTTCTGAAAAGTAGCTTCATAATTAATGTTATTTATACACTGC
CTTCCATGACTTTTACTTTGCCCTAAGCTAATCTCCAAAATCTGAAATGCTACTCCAATATCAGAAAAAAGGGG
GAGGTGGAATTATATTTCTGTGATTTTAAGAGTACAGAGAATCATGCACATCTCTGATTAGTTCATATATGTCT
AGTGTGTAATAAAAGTCAAGATGAAGTCTC

1764/6881
FIGURE 1635

MASSSDGISLSYRPVVTGQDRMMDTEVLSLLSSVALPSLLLASESFD SIYPGIFCVLMFSSGLASAVLIGRALSF
QAILKGGQSKGQSLNPFCGLNNLRIKSSVLLIPVLLCQTLS

1765/6881
FIGURE 1636

CGGGATTTAGATCACGTCCCGCAGGCCGGCGGAAGTAGCTGATACTCTCATTGGTTGCAAAACCTTGATCTGTGA
AAGCGGGCGTTTTTGGAAGATACCGGAAGTAGAGTCACGGAGAGGTATTAAGAAATGGAGAGAAAAATAAGCAGAA
TCCACCTTGTTTCTGAACCCAGTATAACTCATTTTCTACAAGTATCTTGGGAGAAAAACACTGGAATCTGGTTTTG
TTATTACACTTACTGATGGTCATTTCAGCATGGACTGGGACAGTTTCTGAATCAGAGATTTCCCAAGAAGCTGATG
ACATGGCAATGGAAAAAGGGAAATATGTTGGTGAAGTGAAGAAAGCATTGTTGTCAGGAGCAGGACCAGCTGATG
TATACACGTTTAAATTTTTCTAAAGAGTCTTGTTATTTCTTCTTTGAGAAAAACCTGAAAGATGTCTCATTTCAGAC
TTGGTTTCTTCAACCTAGAGAAAGTTGAAAACCCAGCTGAAGTCATTAGAGAACTTATTTGTTATTGCTTGGACA
CCATTGCAGAAAAATCAAGCCAAAAATGAGCACCTGCAGAAAGAAAATGAAAGGCTTCTGAGAGATTGGAATGATG
TTCAAGGACGATTTGAAAAATGTGTGAGTGCTAAGGAAGCTTTGGAGACTGATCTTTATAAGCGGTTTATTCTGG
TGTTGAATGAGAAGAAAAACAAAAATCAGAAGTTTGCATAATAAATTATTAAATGCAGCTCAAGAACGAGAAAAGG
ACATCAAACAAGAAGGGGAAACTGCAATCTGTTCTGAAATGACTGCTGACCGAGATCCAGTCTATGATGAGAGTA
CTGATGAGGAAAGTGAAGAACAACTGATCTCTCTGGGTTGGCTTCAGCTGCTGTAAGTAAAGATGATTCCATTA
TTTCAAGTCTTGATGTCAGTATGATATTGCACCAAGTAGAAAAAGGAGACAGCGAATGCAAAGAAATCTTGGGACAG
AACCTAAATGGCTCCTCAGGAGAATCAGCTTCAAGAAAAGGAAAAGCCTGATTCTTCACTACCTGAGACGTCGA
AAAAGGAGCACATCTCAGCTGAAAACATGTCTTTAGAACTCTGAGAAACAGCAGCCCAGAAGACCTCTTTGATG
AGATTTAAACAGTCTCAAAAAATACTTTGATGTTCACTAGACTATGTTTTCTATTTCATTTCTTTAAATGAAAAAG
GAGAATTTCAAGTCAGCAGCCGCTATTACCGTATCTTACAATTTAATTACATACACAGTGAATTGAAACCATTGT
GCAAAATGGATTACACATGTATACAAAGATACGATTTGATGATGACACTGGCACATTGAGTTCTAAACTATTTCAT
TCAGCATGCCTATAATTACATAAATTGTATGAGACTTTTTGTTGCAAAGGACACATTTATCATATTCATTCACAC
ATATTATATGTGATAGCTGTCCAACATCCTGTCTGGGAAGATTTTGAAGAACAGGACAAAGAAAACATCATTTTAA
AATGTCTTCAGCTTTTTTTGAATAGACGTATTCAAACATATTCTGAACATTGATGTTTGAACATTTTAAATTTGTG
TGATGATGTAGAAAATATAATTTTAGTTTGTACATAAACATTGTGAAAATCTGATAATAAATTTTGTATACATT
GAAAAAAAAA

1766/6881
FIGURE 1637

MERKISRHLVSEPSITHFLQVSEKTLSESGFVITLTDGHSWTGTVSESEISQEADDMAMEKGKYVGELRKALL
SGAGPADVYTFNFSKESCYFFFEKNLKDVSFRLGSFNLEKVENPAEVIRELICCYCLDTIAENQAKNEHLQKENER
LLRDWNDVQGRFEKCVSAKEALETDLTKRFLVLNEKKTIRSLHNKLLNAAQEREKDIKQEGETAICSEMTADR
DPVYDESTDEESENQTDLSGLASAAVSKDDSIISLSDVTDIAPSRKRRQRMQRNLGTEPKMAPQENQLQEKEKPD
SSLPETSKKEHISAENMSLETLRNSSPEDLFDEI

1767/6881
FIGURE 1638

CGGGATTTAGATCACGTCCCGCAGGCCGCGGAAGTAGCTGATACTCTCATTGGTTGCAAAACCTTGATCTGTGA
AAGCGGGCGTTTTTGAAGATACCGGAAGTAGAGTCACGGAGAGGTAGGATCCGGAAGTGGGGCTGCCTCTTTAAA
TAACAAAAATCTGAGGTATTAAGAAATGGGAGAGAAAAATAAGCAGAATCCACCTTGTTTCTGAACCCAGTATAAC
TCATTTTCTACAAGTATCTTGGGAGAAAAACACTGGAATCTGGTTTTGTTATTACACTTACTGATGGTCATTTCAGC
ATGGACTGGGACAGTTTTCTGAATCAGAGATTTCCCAAGAAGCTGATGACATGGCAATGGAAAAAGGGAAATATGT
TGGTGAAGTGAAGAAAGCATTGTTGTCAGGAGCAGGACCAGCTGATGTATACACGTTTAATTTTCTAAAGAGTC
TTGTTATTTCTTCTTTGAGAAAAACCTGAAAGATGTCTCATTTCAGACTTGGTTCCTTCAACCTAGAGAAAGTTGA
AAACCCAGCTGAAGTCATTAGAGAACTTATTTGTTATTGCTTGGACACCATTGCAGAAAATCAAGCCAAAAATGA
GCACCTGCAGAAAGAAAAATGAAAGGCTTCTGAGAGATTGGAATGATGTTCAAGGACGATTTGAAAAATGTGTGAG
TGCTAAGGAAGCTTTGGGAGACTGATCTTTATAAGCGGTTTATTCTGGTGTGAATGAGAAGAAAAACAAAAATCAG
AAGTTTGCATAATAAATTATTAATGCAGCTCAAGAACGAGAAAAAGGACATCAAACAAGAAGGGGAAACTGCAAT
CTGTTCTGAAATGACTGCTGACCGAGATCCAGTCTATGATGAGAGTACTGATGAGGAAAGTGAAAACCAAATGA
TCTCTCTGGGTTGGCTTCAGCTGCTGTAAGTAAAGATGATTCCATTATTTCAAGTCTTGATGTCACTGATATTGC
ACCAAGTAGAAAAAGGAGACAGCGAATGCAAAGAAATCTTGGGACAGAACCTAAATGGCTCCTCAGGAGAAATCA
GCTTCAAGAAAAGGAAAAGCCTGATTCTTCACTACCTGAGACGTCGAAAAAGGAGCACATCTCAGCTGAAAACAT
GTCTTTAGAACTCTGAGAAACAGCAGCCAGAAGACCTCTTTGATGAGATTTAACAGTCTCAAAAAATACTTTG
ATGTTCACTAGACTATGTTTTCTATTCAATTTCTTTAAATGAAAAAGGAGAATTTCAAGTCAGCAGCCGCTATTA
CCGTATCTTACAATTTAATTACATACACAGTGAATTGAAACCATTGTGCAAAATGGATTACACATGTATACAAAG
ATACGATTTGATGATGACACTGGCACATTGAGTTCTAAACTATTTCATTTCAGCATGCCTATAATTACATAAATTGT
ATGAGACTTTTTTGTGCAAAGGACACATTTATCATATTTCATTTCACACATATTATATGTGATAGCTGTCCAACATC
CTGTCTGGGAAGATTTTGAAAACAGGACAAAGAAAACATCATTTTAAATGTCTTCAGCTTTTTTTGAATAGACG
TATTCAAACATATTCTGAACATTGATGTTTGAACATTTTAATTTGTGTGATGATGTAGAAAATATAATTTTAGTT
TGTACATAAACATTGTGAAAAATCTGATAATAAAATT1TTGATACATTGAAAAA

1768/6881
FIGURE 1639

MERKISRHLVSEPSITHFLQVSEKTLSESGFVITLTDGHSAWTGTVSESEISQEADDMAMEKGKYVGELRKALL
SGAGPADVYTFNFSKESCYFFFEKNLKDVSFRLGSFNLEKVENPAEVIRELICYCLDTIAENQAKNEHLQKENER
LLRDWNDVQGRFEKCVSAKEALETDLYKRFILVLNEKKTIRSLHNKLLNAAQEREKDIKQEGETAICSEMTADR
DPVYDESTDEESENQTDLSGLASAAVSKDDSIISLSDVTDIAPSRKRRQRMQRNLGTPEPKMAPQENQLQEKEKPD
SSLPETSKKEHISAENMSLETLRNSSPEDLFDEI

AGGTTAAACAGAATCTGGTGATTATGGGTAAGAAGACCTGGTTCTCCATTCTCGAGAAGAATCGACCTTTAAAGGCTAGAAATTAATTTAGTTCTCAGCAGAGAACTCAAGGAACCTCCACAAGGAGCTCATTCTTTCCAGAAGTCTAGATGATGCCTTAAAACTTACTGAACAACCAGAATTAGCAAATAAAGTAGACATGGTCTGGATAGTTGGTGGCAGTTCGTTTTATAAGGAAGCCATGAATCACCAGGCCATCTTAACTATTTGTGACAAGGATCATGCAAGACTTTGAAAGTGACACGTTTTTTCCAGAAATTGATTTGGAGAAATATAAACTTCTGCCAGAATACCCAGGTGTTCTCTCTGATGTCCAGGAGGAGAAAAGCATTAAGTACAAATTTGAAGTATATGAGAAGAATGATTAATATGAAGGTGTTTTCTAGTTTAAGTTGTTCCCCCTCCCTCTGAAAAAGGTAAGTATTTTTTACATTAGAAAAGGTTTTTTGTTGACTTTAGATCTATAATTATTTCTAAGCAACTAGTTTTTTATTCCCCACTACTCTTGTCTCTATCAGATACCATTTATGAGACATTCTTGCTATAACTAAGTGCTTCTCCAAGACCCCAACTGAGTCCCAGCACCTGCTACAGTGAGCTGCCATTCCACACCCATCACATGTGGCACTCTTGCCAGTCCCTTGACATTGTGCGGGCTTTTACATGTTGGTAATATTTATTAAAGATGAAGATCCACATACCCTTCAACTGAGCAGTTTCTACTAGTGGAAATACCAAAGCTTCTACGTGTATATCCAGAGGTTGTAGATAAATGTTGCCACCTTGTTGTAAACAGTGAAAAATTGAAAAACAACCTGGAAGTCCAGTGATGGGAAAAATGAGTATGTTTCTGTCTTAGATTGGGGAACCCAAAGCAGATTGCAAGACTGAAATTTCAGTGAAAGCAGTGATTTGCTAGGTCATACCAGAAATCATCAATTGAGGTACGGAGAACTGAACTGAGAAGGTAAGAAAAGCAATTTAAAGTCAGCGAGCAGGTTCTCATTGATAACAAGCTCCATACTGCTGAGATACAGGGAAATGGAGGGGGGAAAGCTGGAGTATTGATCCCGCCCCCTCCTTGTTGTGCACTCCCTGTCTGTGTGTGGGCGGAACATAGTCCAGCTGCTCTATAGCAAGTCTCAGGTGTTTGCAAGTGTGCTGGCATGCACGGGAACAGTGAAATGCCAAACACTTAAAGCAATTCGATGTTTAAAGTATGTAAGTCTTTTTTTTTTTAGACAGCGTTTCGCTCTTGTGCCCAGGCTAGCATGCAATGGTGTGACCTCGGCTTACTGCAACCTCCGCCTTCCCAGATTCAAGCGATTCTCCTGCCTCAGGCTCCCAAGTAGCTAGACCAGGTGCGCGCCACCACGCCCCGGCTAATTTTTGTATTTTGTATTTTGTATTTTAGTAGAGATGGGGTTTACCATGTTGGTCAGGCTAGTCTCGAACTCGTGACCGCAAGCGATTACCCACCTCAGCCTCCCAAAGTGCTGGGATTACCGGCTTGAGCCACCACACCCGGGCACATCTTCATTCTTTTTATGTAGTAAAAAGTATAAGGCCACACATGGTTTTATTTGAGTATTTTATAATTTAAAAAAATACAGAAGCAGGAAAACCAATTATAAGTTCAAGTGAGGGATGATGGTTGCTTGAACCAAAGGGTTGCATGTAGTAAGAAAATTGTGATTTAAGATATATTTTAAAGTTATAAGTAGCAGGATATTCTGTGTGGAGTTTGACTTTGGTTTTGGGGCCAGGGAGTTTCAGATGCCTTTGAGAAATGAATGAAGTAGAGAGAAAAATAAAGAAAAACCAGCCAGGCACAGTGGCTCACACCTGTAATCCCAGCGCTTTGGGAGGCTAAGGCAGGCAGATCACTTGAGACCAGCTTGGGCAACATGGCAAAAGCCCCATCTCTACAAAAACACAAAAATTAGCTGGGCATTGTGGCGCACCTGTATTCCCATCTAGTCAGGAAGCTGAGATGGAAGAATTAATTGAGCCACGAGTTCAAGGCTGCAGTGAGTCGTGATTGTGCCACTGCACTCCAGCCGGGGTGACAGAAGAGACCTTGTCTCGAAAAGGAATCTGAAAACAATGGAACCATGCCTTCATAATTCTAGAAAAGTTATTTTCAACTGATAAATCTATATTACCCAAATAATCAAGGTGAAGGTAAAATAATACATTTTTAGACAAGCAAAGACTCAGGGGTACCTCCATGTGCCCTTTTTAGGGAAGCTGTTGAGAAAATACTCCAGCAAATGAAGGAGTACACAAACCAGAGAATGACATGAATCCAGCAAATAGGATCCAACACAGCAATATTCCAGCTATGGAGCTAGCTTTAAAAAGGAACAGTAAAAATATTAATCGGTAGCTGGGTGGAATGGCCCATGCCTGTAGTCCCAGCTACTCAGGAGGCTCAGCAGCAGGACGACTTGAGCCCAAGAGTTCCAGACCAGCCTGGCCACCTTAGTGAGATCCCTTCTCTTAAAAATAATAACTTATTGCCAGATTGTTGGGGCATTGGAAGAAGTTTATTGAAGATAAAGCAAAAGTAAAAAACAAGGGGAAAGGTTGGTTAGGCAATCATTCTAGGGCAGAAAGAAGTACAGGATAGGAAGAGCATAATACACTGTTTTTCTCAACAAGGAGCAGTATGTACACAGTCATAATGATGTGACTGCTTAGCCCTAAATATGGTAACTACTCTGGGACAATATGGGAGGAAAAGTGAAGATTGTGATGGTGTAAAGAGCTAAATCCTCATCTGTATATCCAGAAATCACTATATAATATATAATAATGAAATGACTAAGTTATGTGAGGAAAAAACAGAAGACATTGCTAAAAGAGTTAAAAGTCATTGCTCTGGAGAATTAGGAGGGATGGGGCAGGGGACTGTTAGGATGCATTATAAACTGAAAAGCCTTTTTTAAAAATTTATGTATTATAATATGCATTCACTTGAAAAACTAAAAAACAATAATTTGGAAAAACCCATGAAGGTAACTAACGGAAAGGAAAAACTAAGAGAATGAAAAGTATTGCTCTGGAAAGAACAACCTGGCAGGACTGTTGTTTTTATTGTAAGACTTTTGGAGCCATTTAATTGTACTTAACCATTTTTCATCTATTTCTTTAATAAGAACAATTCCATCTTAATAAAGAGTTACACTTGTTAATA

1770/6881
FIGURE 1641

TTACCTTCTACTGAAGAGGTTGTGGTCATTCTCTGGAAATATCTGAATTCATTCTGAGCGGTGGCCAGGGCAGG
TCCCCGTTCTTGCCGATGCCCATGTTCTGGGACACAGCGACGATGCAGTTTAGCGAACCAACCATGACAGCAGCG
GGAGGACCTCCGAGCCCGCTCGTTACAGCAGAACGCGCGGTCAAGTTTGGCGCGAAATTGTGGCCGCCCCGCCCC
CTCGTCCCTATTTGTGCAGGCGAGGCCCCGCCCCCGCCCCGGCGCACGCAGGGTCGCGGCGTGCTCGCGCCCG
CAGACGCCTGGGAACTGCGGCCG

1771/6881
FIGURE 1642A

CTCCAATACCGCAGGAGGGCGGTCTTCCCCGGCTCGCCAACTCGGCTGCTCTGGGGGATTTCGTGCGCGGTAAGAA
GCTGCGCGGTAGCGCGGTGAGGTGAGGTTCTCAGCCACCAAAGCTGCAGGGTCTCGTCGTTCGTTCCCTCTGGCC
TGGCGGAAC TTGCGTGGGAAGCTGGGAGGACAGAAGGCTTAGCCGCTGGGTCCCTGAGCTGGCTGGAGCGCGGGC
TGTCTAGGGGCGGCGACCTCAGCTGTTGGGCTCCGGCTGCTGGGGGCTGTGCGTCCAGCCGCCCTGGAATCCGCC
TGTGGGTGGGCCGCTTGGCTCTCCCACTTCACCTCTTGATAACCCAGAGCCTCCCCCTTCCCACGTACGTAGGG
GAAGGATAATCTACTTCCTTTTGAACAGCTTCGGTCCCCACTATGACAGTCGCATAAACTTCAGCGAAGAGTGCG
CTGGTAAAGTGGCATGGAGTTTCTCACACCAATTCATTGGGTCCACCCTTCAGCTTCTGTGGAAGGGGTCTTTCT
GTTACTAGGAGCTGAGACTTGGGGGGTTGCCAGGGATGCTGGTCTTAAAAGGTGATAATTTAGGCCGGGCGCGGT
GGCTCACGCCTGTAATCCCAGCACTTTGGGAGGTCGAGGCGGGCAGATCTCCTGAGCTCAGGAGTTCGAGACCAC
CCTGGGCAACATGGTGAACCCCTTCTCTACTAAAAATACAAAAATTAGCTGGGCGTGGTGGCACGCGCCTGTAA
TCCCAGCTATTCCGGAGGCTGAGGCCCGAGAATCGCTTGAGCCCTGGCGGCAGAGGTTGCAGTGAGCCAAGATCG
CCCCTGCACTCCAGGTTGGGCTACAGAGTGAGACTCCGTCTCAACAACGACCACAACAACAACAAAAAGGTGG
TGGCTTAATACAGCCATGCTCCCCCTTAAGAACTGGTATAGTTATGAGAAATGGTTGGGCCGTTTCGTGGTTGTGT
GAACATCATAGTGTACTTGCACAAACCTACACAGCTGGGCCGTATGGGATAGCCTGTTACTCCTAGTCTACAGAC
CTGTACAGTATACTACTAAATACTGTAGGCAGTTGTAAGGATGGTGTGTATCTAAACACAGAAAAGATACTG
TAAAAATATAGTGTAAAGAAAACATGGTACAGCTGAATAGGGCACTTACGCATGGAGCTTGCAGGGCTGTCCGT
AGCTATTAAAGTGAAGTCAAGTGGTATGTGAGTGTGAAGGCCTACGATATTATTTAGGGTATTACTGTACACTA
CTGTAGACTTTTATAAATGCGGTATGCTTAGTCTAAGTTTATTAAAAATAAGGTAATAACCTTAGCTTACTGTGCT
TTTTTAAC TTTTATAA ACTTTTAAATTAATTTTAACTCCTTGACCTTTTTTTTTTTTTTTTGAGACGGAGTTTATTC
TCTCTGTCTCTCATTTTTTGAGACAGAGTTTTGCTCTTGTCAACCAGGCTGGAGTGCAGTGGCGCAATCTCAGCTC
ACTGCAACGTCCACCTCTTGAGTTCAAGCGATTCTCCTGCCTCAGCTTCCCAGGTGGTGC GCGCCTGTAGCTGGG
ACTACAAGAGTGCGCCACCACGCCCAGCTAATTTTTGTATTTTTTAGTAGAGATGGGGTTTGACCATGTTGGCCAG
GATGGTCTCGATATCCTGACCTTGTGATCCACCTGGCCTTGGCCTCCCAAAGTGTGGGATTACAGGCGTGAGCC
ACCATACCCGGCCCACTCTTTTGTAAATAACACTTAGCTTAAATGCTAATGTGTTGTATAGCTATATAAAAATAT
TTTCTTTATTCCCTTACATTATTCTATAGCTTTTTTCTGTAAAAATTTTTTTTTTGTGTTATAAACTAAGACACAC
ACATTGFGCTACACCGGGTCAGGAGCATCAATATCACTCTTTTCTTCTCCACATCTTGTCTACTGGAAGGTT
TTCAGGGGCAGTAACATGAATGGAGCTGTCTCTCTATAATAACTGCTTTTTTCTGGAATACTTATAATTGTCT
AGTATTATGTACAGTACATCATTGTAAGCATTATGCTTGTATATGACTGGCATCCAGGTTTGTTTACACCAGCA
TTACCACAGACATGAGTAATGTGTTACACTACAAGTTATGAGGGCTACAAAGTCAATAGGAATTTTTTACGCTCCA
TTATAATCATCTGAGACCAGTATCATGTGTGCAGTCGCTGTTGACCTAAATGTTATGTAGCATGTGACTAGCTGA
TGAATCTTTGATTATGGCTGAATGTTCTCATTTCATTGCAGGAAAAAATATCCTCCAAATCACTAGGTAGTATGT
AAGTGACCAAACTTTTTTCCATTTTATGTTGGAGCCAAATCATTAGTGTTAGGATAAAATTACTTCTTTATGTAT
GTGCTCTAAAAATGAAAAGTTATTTCTGAATATTAAAGCATATGTATTAAAGAGTATAAAAAACAAGATACAGATTTT
GGTGTGAAAATATATCTTATGATTCAAGTCATAATTTAAATAGAATTGAAGATGATGTGAAATCACTGGGCTGGAA
GTAGCTTATACCTTGATTAGTAAGAGGAAGCCCGGGATCATCCTGTGATGGTAAACACTTTTATATGTTTTACTT
ATAACTTTGCCAGGAAATTTCAACAAACTTCATATTTAAAGGACATGATTTCTGTATACTTAGTAATCTGCTATGC
AAATTGTTGCATTGAAATGGCAGACGAAGCAAGAAGATTGGGAGAAAGTAGCTGTGGGACTTGGAGATAGGAAAA
TAAACAGCCGGGAAAACCTGCAGAATGTGGGAGGAATAATTGCATTCAATTGTATTACTATCTGATTTATATTTTAT
GAAATAAATTTGGTTTCTTAAGATAGTTTTTCAATTTTAAGCACACCTTTTTTAACTGGTGTGGCAGCTTTTCTGG
TAAGTGGTAGATTTATGTTAGAAGCATGTCTATGCAGCATATTATAGCATTAAATATGTATACAGATATCTAACT
GAAATAAAAAGTGTTTTAATAATTAAAAGTTTAAACATATGGGCATATGTGACATATAGTGATATAGCATGTCTCT
TTAGTTTTGTTGTTTTGTTGTTGATGGCTAACCAACCATGCTTGTCTTAAAAATTGATAAGGTACCACTGATGA
AATTATGACCAAGTGGGCCCGAGTTAGTACCACATATAACAAGAGACCCTTGCCCTGCAACATCATGGGAGGACAT
GAAGAAGGGATCCTTTGAGGGAACAAGCCAAAACCTACCAAAGCGTAAACAACCTTGAAGCCAATAGGCTATCCCT
CAAAAATGATGCACCCCAAGCAAAACATAAAAAGAACA AAAAAGAGTACTTAAATGAAGATGTGAATGG
ATTCATGGAATACCTAAGACAGAATTCACAGATGGTTCACAATGGGCAAATTATAGCAACAGACAGTGAGGAAGT
AAGGGAAGAAATTGCAGTTGCTTTAAAGAAAAGACAGTCGACGGGAAGGAAGAAGATTAAAAAGACAAGCGGCAAA
GAAAAATGCAATGGTGTGTTTCCATTGTAGAAAACCTGGTCATGGAATTGCAGATTGCCCGCGGCCCTTGAAAA

1772/6881
FIGURE 1642B

TCAAGACATGGGCACTGGGATATGTTACAGGTGTGGGTCCACAGAGCACGAAATAACCAAGTGTAAGGCTAAAGT
AGACCCGGCTCTTGGCGAATTTCCTTTTGCAAAATGTTTTGTTTGTGGAGAAATGGGGCACCTGTCTAGATCTTG
TCCTGATAATCCCAAAGGACTCTATGCTGATGGTGGCGGTTGCAAACTTTGTGGCTCTGTGGAACATTTAAAGAA
AGATTGCCCTGAAAGTCAGAATTCAGAGCGAATGGTTCACAGTTGGTCGCTGGGCAAAGGGAATGAGTGCAGACTA
TGAAGAAATTTTGGATGTACCTAAACCGCAAAACCCAAAACAAAAATACCTAAAGTTGTTAATTTT**TGATAACA**
GCTAGCACTATCATGAGTTACTACCTCATTGTTACTTTCTAAACCAGGCCCGCTTCACGAGTTAGAGTTGAGCTC
CCCTGTAGCCAGGACTATGCTGTAGATATCAGTATGATCTGGGTGTGGCCAAAACAATTTCTTTATTCTGTCT
ATCAAATAGTACTTCTACCACTGTTTGGAGAAAATTGAAGAAAAGAATAAGATGATTAAATGAATTCTCTAAAAG
AACATATTTTAAGAGACAGAACTTAGACATAACCAAGTAGTTGTATACCTGATTGTAACAATCATCTTTTATAAA
AGCAAAATTATGCATAAATGTAAAACACCCCTAAACAAAGGGAACAAATGAATTTTGGTTATATTGTTTTCTTG
GCTCAAAGTATCAATTTATTATTATAATAGAAATTTATAAGTTGCTAGAAAGTCTATATTTTAAAGTACGGAAT
AAAAATATGTTTTCTATTAAGCAATAGAAATATTTTTGTGTATAATTTTCTGAATACTTGATTCTCGATTGAAA
TATCCATTGTTGTTAATATCCATGTAACAATCCATTGGAAACAAGATTTTTTTGAATCCTAGATGAGAAATAAA
CAGGGATTTGGTTTTTGTTTTAGTTTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

1773/6881
FIGURE 1643

MTRWARVSTTYNKRPLPATSWEDMKKGSFEGTSQNLPKRKQLEANRLSLKNDAPQAKHKKNNKKKKEYLNEDVNGF
MEYLRQNSQMVHNGQIIATDSEEVREEIAVALKKDSRREGRRLLKRQAAKKNAMVCFHCRKPGHGIADCPAALNQ
DMGTGICYRCGSTEHETKCKAKVDPALGEFFFAKCFVCGEMGHLSRSCPDNPKGLYADGGGCKLCGSVEHLKKD
CPESQNSERMVTVGRWAKGMSADYEEILDVPKPQKPKTKIPKVVNF

1774/6881
FIGURE 1644

GGGGAGGCTGTGATGGGTTGACAGGTGCGTGACAGTGGGAGCTGCTCTCGGCACAAGCATGTACGGCAAAGGCAA
GAGTAACAGCAGCGCCGTCCCGTCCGACAGCCAGGCCCGGGAGAAGTTAGCACTCTACGTATATGAATATCTGCT
CCATGTAGGAGCTCAGAAATCAGCTCAAACATTTTTATCAGAGATAAGATGGGAAAAAACATCACATTGGGGGA
ACCACCAGGATTCTTACATTCTTGGTGGTGTGTATTTTGGGATCTCTACTGTGCAGCTCCAGAGAGACGTGAAAC
ATGTGAACACTCAAGTGAAGCAAAAGCCTTCCATGATTACAGTGTCTGCAGCAGCTCCCAGTCCAGTGTAGGAAA
CATTCCCCCAGGAGATGGCATGCCAGTAGGTCCTGTACCACCAGGGTTCTTTCAGCCTTTTATGTCACCTCGGTA
CCCTGGAGGTCCAAGGCCCCCATTGAGGATACCTAATCAGGCACCTGGAGGTGTCCAGGAAGTCAGCCATTACT
CCCCAGTGGAATGGATCCAACCTCGACAACAAGGACATCCAAATATGGGTGGGCCAATGCAGAGAATGACTCCTCC
AAGAGGAATGGTGCCCTTAGGACCACAGAACTATGGAGGTGCAATGAGACCCCCACTGAATGCTTTAGGTGGCCC
TGGAATGCCTGGAATGAACATGGGTCCAGGTGGTGGTAGACCTTGGCCAAACCAACAAATGCCAATTCAATACC
ATACTCCTCAGCATCTCCTGGGAATTATGTAGGTCCTCCAGGAGGTGGAGGGCCACCAGGAACACCCATCATGCC
TAGTCCAGCAGATTCAACCAACTCTGGTGATAACATGTATACTTTAATGAATGCAGTACCTCCTGGACCTAACAG
ACCTAATTTTCCAATGGGTCCCTGGGTGAGATGGTCCCATGGGTGGATTAGGAGGAATGGAGTCACATCACATGAA
TGGCTCTTTAGGCTCAGGAGATATGGACAGTATTTCCAAGAATTCTCCCAATAATATGAGCCTGAGTAATCAACC
GGGCACTCCAAGGGATGATGGCGAAATGGGGGAAATTTCTTAAATCCTTTTCAGAGTGAGAGTTACTCCCCTAG
CATGACAATGAGCGTGTGATCCATTACCAAGTCTCCTCATGAAAACCAAGTGTGAGTCAGCCCTTCACAGAACTAC
TACGGAAGAAAATTATTCATCACAGTGTACAGTTAAACAAAGGAATCTCAGTCACACCAAACCAACCTTTTTATT
TCCTGCTCTCTCCCCTCTTTTGTGAAGAAAGCGGGTCCAAATGTGATTCAAACAACGTACGGAGTGGCATATTA
GAATTGCCCTAAACTGAACTGCAATAATTATGTGTGTATGTATATGTGTGGGAAAGAGAATGTACTGTATATGT
GTATGTTATACAGACATATACACATACATACATTGACCCACAGGACATTGTAAAATATTATCACATGACATCTTA
AGTAGAAATAAGTAGGGACTTTTATTCCATCCTTTTTTTCACGTTTACATTTTAATTATTACAAGTTGCTCCTGC
CCCCTCCCTGAACTATTTTGTGCTGTGTATATCACTGCTTTATATAAGTTATTTTTTAAGGTGAACTCAGATGTT
ATGGTTTTGTAAATGTCTGCAATCATGGATAGGAATAAAATCGCTTATTTGAGAGCTTTC

1775/6881
FIGURE 1645

MYGKGKSNSSAVPSDSQAREKLALYVYEYLLHVGAQKSAQTFLSEIRWEKNITLGEPPGFLHSWWCVFWDLYCAA
PERRETCEHSSEAKAFHDYSAAAAPSPVLGNIPPGDGMFVGPVPPGFFQPFMSPRYPGGPRPPLRIPNQALGGVP
GSQPLLP SGMDPTRQQGHFNMGGPMQRMTPPRGMVPLGFPQNYGGAMRPPLNALGGPGMPGMNMGPGGGRPWPNPT
NANSIPYSSASPGNYVGPPGGGGPPGTFIMPSPADSTNSGDNMYTLMNAVPPGPNRPNFPMGPGSDGPMGGLGGM
ESHMNGSLGSGDMDSISKNSPNNMSLSNQPGTPRDDGEMGGNFLNPFQSESYSPSMTMSV

1776/6881
FIGURE 1646A

GAATTCCTCAGCTCTCTGCTCGCTCTGCTCGCAGTCACAGACACTTGAGCACACGCGTACACCCAGACATCTTCCG
GCTGCTATTGGATTGACTTTGAAGGTTCTGTGTGGGTCGCCGTGGCTGCATGTTTGAATCAGGTGGAGAAGCACT
TCAACGCTGGACGAAGTAAAGATTATTGTTGTTATTTTTTTTTTCTCTCTCTCTCTCTCTTAAGAAAGGAAAAATA
TCCCAAGGACTAATCTGATCGGGTCTTCCTTCATCAGGAACGAATGCAGGAATTGGGAACTGAGCTGTGCAAGT
GCTGAAGAAGGAGATTTGTTTGGAGGAAACAGGAAAGAGAAAGAAAAGGAAGGAAAAAATACATAATTTTCAGGGA
CGAGAGAGAGAAGAAAAACGGGGACTATGGGGAGAAAAAAGATTTCAGATTACGAGGATTATGGATGAACGTAACA
GACAGGTGACATTTACAAAGAGGAAATTTGGGTTGATGAAGAAGGCTTATGAGCTGAGCGTGCTGTGTGACTGTG
AGATTGCGCTGATCATCTTCAACAGCACCAACAAGCTGTTCCAGTATGCCAGCACCGACATGGACAAAGTGCTTC
TCAAGTACACGGAGTACAACGAGCCGCATGAGAGCCGGACAAACTCAGACATCGTGGAGACGTTGAGAAAGAAGG
GCCTTAATGGCTGTGACAGCCAGACCCCGATGCGGACGATTCCGTAGGTCACAGCCCTGAGTCTGAGGACAAGT
ACAGGAAAATTAACGAAGATATTGATCTAATGATCAGCAGGCAAGATTGTGTGCTGTTCCACCTCCCAACTTCG
AGATGCCAGTCTCCATCCCACTGTCCAGCCACAACAGTTTGGTGTACAGCAACCCTGTCAGCTCACTGGGAAAACC
CCAACCTATTGCCACTGGCTCACCCTTCTCTGCAGAGGAATAGTATGTCTCCTGGTGTAACACATCGACCTCCAA
GTGCAGGTAACACAGGTGGTCTGATGGGTTGGAGACCTCACGTCTGGTGCAGGCACCACTGCAGGGAACGGGTATG
GCAATCCCCGAAACTCACCAGGTCTGCTGGTCTCACCTGGTAACTTGAACAAGAATATGCAAGCAAAATCTCCTC
CCCCAATGAATTTAGGAATGAATAACCGTAAACCAGATCTCCGAGTTCTTATTCCACCAGGCAGCAAGAATACGA
TGCCATCAGTGTCTGAGGATGTGACCTGCTTTTGAATCAAAGGATAAATAAATCCCAGTCGGCTCAGTCATTGG
CTACCCCACTGGTTTCCGTAGCAACTCCTACTTTACCAGGACAAGGAATGGGAGGATATCCATCAGCCATTTCAA
CAACATATGGTACCGAGTACTCTCTGAGTAGTGCAGACCTGTCTCTGTCTGGGTTTAAACACCGCCAGCGCTC
TTCACCTTGGTTTCAGTAACTGGCTGGCAACAGCAACACCTACATAACATGCCACCATCTGCCCTCAGTCAGTTGG
GAGCTTGCCTAGCACTCATTTATCTCAGAGTTCAAATCTCTCCCTGCCTTCTACTCAAAGCCTCAACATCAAGT
CAGAACCTGTTTTCTCTCCTAGAGACCGTACCACCACCCCTTCGAGATACCCACAACACACGCGCCACGAGGCGG
GGAGATCTCCTGTTGACAGCTTGAGCAGCTGTAGCAGTTCTGTACGACGGGAGCGACCGAGAGGATCACCAGGAACG
AATTCACCTCCCCCATTGGACTCACCAGACCTTCGCCGGACGAAAGGGAAAGTCCCTCAGTCAAGCGCATGCGAC
TTTCTGAAGGATGGGCAACATGATCAGATTATTACTTACTAGTTTTTTTTTTTTTCTTGCAGTGTGTGTGTGTC
TATACCTTAATGGGGAAGGGGGTTCGATATGCATTATATGTGCCGTGTGTGGAAAAAAAAAAGTCAGGTACTCT
GTTTTGTAAAAGTACTTTTAAATTGCCTCAGTGATACAGTATAAAGATAAACAGAAATGCTGAGATAAGCTTAGC
ACTTGAGTTGTACAACAGAACACTTGTACAAAATAGATTTTAAAGGCTAACTTCTTTTCACTGTTGTGCTCCTTTG
CAAAATGTATGTTACAATAGATAGTGTCTGTTGTCAGGTTCAACGTTATTTACATGTAAATAGACAAAAGGAAAC
ATTTGCCAAAAGCGGCAGATCTTTACTGAAAGAGAGAGCAGCTGTTATGCAACATATAGAAAAATGTATAGATGC
TTGGACAGACCCGGTAATGGGTGGCCATTGGTAAATGTTAGGAACACACCAGGTCACCTGACATCCCAAGAATGC
TCACAAACCTGCAGGCATATCATTGGCGTATGGCACTCATTAAAAAGGATCAGAGACCATTAAAAGAGGACCATA
CCTATTAAAAAAAATGTGGAGTTGGAGGGCTAACATATTTAATTAAATAAAATAAAATCTGGGTCTGCATCT
CTTATTAAATAAAAATATAAAAATATGTACATTACATTTTGCTTATTTTCATATAAAAAGGTAAGACAGAGTTTGC
AAAGCATTTGTGGCTTTTTGTAGTTTACTTAAAGCCAAAATGTGTTTTTTTCCCTTGATAGCTTCGCTAATATTT
TAAACAGTCCTGTAAAAAACCAAAAAGGACTTTTTGTATAGAAAGCACTACCCTAAGCCATGAAGAACTCCATGC
TTTGCTAACCAGATAACTGTTTTCTCTTTGTAGAAGTTTTGTTTTTTGAAATGTGTATTTCTAATTATATAAAAT
ATTAAGAATCTTTTTAAAAAATCTGTGAAATTAACATGCTTGTGTATAGCTTTCTAATATATATAATATTATGGT
AATAGCAGAAGTTTTGTTATCTTAATAGCGGGAGGGGGGTATATTTGTGCAGTTGCACATTTGAGTAACTATTTT
CTTTCTGTTTTCTTTTACTCTGCTTACATTTTATAAGTTTAAAGGTCAGCTGTCAAAGGATAACCTGTGGGGTTA
GAACATATCACATTGCAACACCCTAAATTGTTTTTAATACATTAGCAATCTATTGGGTCAACTGACATCCATTGT
ATATACTAGTTTCTTTTCATGCTATTTTTATTTTGTTTTTTGCATTTTTATCAAATGCAGGGCCCTTTCTGATCT
CACCATTTACCATGCATCTTGAATTCAGTAAGTGCATATCCTAACTTGCCCATATTCTAAATCATCTGGTTGG
TTTTACGCTAGAAATTTGATACGCTTTTTAGAAATATGCCCAGAATAGAAAAGCTATGTTGGGGCACATGTCCTG
CAAATATGGCCCTAGAAACAAGTATATGGAATTTACTTGGTGAATAAGTTATAAATTTCCACAGAGAAAAATG
TGAAAGACTGGGTGCTAGACAAGAAGGAAGCAGGTAAAGGGATAGTTGCTTTGTCTATCCGTTTTTAATTATTTTA
ACTGACCCCTGACAATCTTGTGACCAATATAGGACTGTTGAACAATCCCGGTGTGTGACAGACCCCAATGTCAC
TTCTGCATAAAGCATGTATGTCTATTTTTTTCTTCAATAAAGAGATTTAATAGCCATTTCAAGAAATCCCAT

1777/6881
FIGURE 1646B

AAGAACCTCTCTATGTCCCTTTTTTTAATTTAAAAAAATGACTCTTGTCTAATATTCGTCTATAAGGGATTAATT
TTCAGACCCCTTTAATAAGTGAGTGCCATAAGAAAAGTCAATATATATTGTTTAAAAGATATTTTCAGTCTAGGAAAG
ATTTTCCTTCTCTTGGAATGTGAAGATCTGTGATTTCATCTCCAATCATATGCATTGACATACACAGCAAAGAAG
ATATAGGCAGTAATATCAACACTGCTATATCATGTGTAGGACATTTCTTATCCATTTTTTCTCTTTTACTTGCTAT
AGTTGCTATGTGTTTCTCATTGTAAAAGGCTGCCGCTGGGTGGCAGAAGCCAAGAGACCTTATTAAGTAGGCTAT
ATTTTCTTAACTTGATCTGAAATCCACAATTAGACCACAATGCACCTTTGGTTGTATCCATAAAGGATGCTAGC
CTGCCTTGTAATAATGTTTTATATATT

1778/6881
FIGURE 1647

MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSTNKLQYASTDMDKVLLKYTEYNEP
HESRTNSDIVETLRKKGLNGCDSPDPDADDSVGHSPESDKYRKINEDIDLMISRQRLCAVPPPNFEMPVSIPVS
SHNSLVYSNPVSSLGNPNLLPLAHPQLQRNSMSPGVTHRPPSAGNTGGLMGGDLTSGAGTSAGNGYGNPRNSPGL
LVSPGNLNKNMQAKSPPPMNLGMNNRKPDLRVLIIPPGSKNTMPVSEDVDLLLNQRINNSQSAQSLATPVVSVAT
PTLPGQGMGGYPSAISTTYGTEYSLSSADLSSLSGFNTASALHLGSGVTGWQQQHLHNMPPSALSQLGACTSTHLS
QSSNLSLPSTQSLNIKSEPVSPPRDRTTTPSRYPQHTRHEAGRSPVDSLSSCSSSYDGSREDHRNEFHSPIGLT
RSPDERESPSVKRMRLSEGWAT

1779/6881
FIGURE 1648

ATGCAGGCCCGACAAGTAATGCTAGCAGTGGCACTTTATAGCCACGGCTGCACAGAAATCAGAACATTTTCTTTA
GATTTTTTTGAAGAAGCGCATCTTTCAGATTACACAAGCAGGATGACGCTGGCTGATGATGTAACCCTGGACGAC
CTGATCATGGCTAAAGATGACCTCTCTGGTGCTGACATCAAGGCAATCTGTACAGAAGCTGGTCTGATGGCCTTA
AGAGAACGTAGAATGAAAGTAACAAATGAAGACTACATTGACTTTTCTAAAATAGAAATCAGGGAAGGT**TAA**

1780/6881
FIGURE 1649

MQARQVMLAVALYSHGCTEIRTFSLDFLKKRIFQIHTSRMTLADDVTLDDLIMAKDDL
SGADIKAICTEAGLMAL
RERRMKVTNEDYIDFSKIEIREG

1781/6881
FIGURE 1650

TTTCCTCTTTCTCTAAGAGTCTCTCTCTCCCTTTCCCTCTCTCTCCCCCAATCTGTCTTTCTAGCATGTTGCC
TTTTTCAACCACATTTGTGTTTCAGGTGTAGAGAGGAGAGAGAGTGAACAGGGAGCGGGGCTTTTGTCTGTTGGT
CTCCCTGGACTGAAGAGAGGGAGAATAGAAGCCCCAAGACTAAGATTCTCAAAATGTTTATTACCCAGAACTCTT
TGTCTGGGTCAGTCAAGAACCATTTCCAAACAAGGACATGGAGGGAAGGCTTCCTAAGGGAAGACTTCCTGTCCC
AAAGGAAGTGAACCGCAAGAAGAACGATGAGACAAACGCTGCCTCCCTGACTCCACTGGGCAGCAGTGAACTCCG
CTCCCCAAGAATCAGTTACCTCCACTTTTTTTTAAATCGTAACACCTCCATTTGTATTACATATGGTGTATGGGTAT
TGATGAGGTCATGGTATCATATATGGGATTTTTTCTGTGTAAATCATCAAGTATAAGAAGAACTATGGGACTC
TGAGCCTTGCTTTAGAGAATTTACAGTGGACAAATAGGTGTCTCAAAACCAGTTTTTAATCATTCTGACTCAAGT
GAAAACGCTCAGAATTTACACTGTGAATCCACGTTTACAACCCTTACAGGTGGGCCTTCAGGCCTGGTTCGCTA
CAACAATGTCTTCCACAACCTCAAACCTCCACCGCGCTCACACAACCGGTCCACTCCTGCCTTTTCACTCACACAG
CTCCCGACTGCTTCTTGCAGAGGCTGAGAGTCCCCCCCCCACCCTTTTTTTTTTCAATTTAGATGTAACAAACCTAG
TAGTTTATGTTTCATCAATTGTCTGTATATCTCTATATTTTATCCATGTACTCTTTTGATGTATAGAAGTAGTTTG
AAACTCATTGTTTCCCTTGTGGTAAGTGACCGAGATGCTGCCACAGGACCTGAGACACTGATGAATGGTGCTATTT
TGGACTTTCAACATGCTCCTTGGCGAGGTAGCTCTGATGGAGTTATTTTTTTATTTCCATGTTCTAAGAAGGTGTT
GGTACTCTGTTTCCCTGAATGTTGTTCTCTAGACTGGATTGACTTGTTTTTCTTGTGTTCTCAGTGTGGCTTTCT
TCCTCAGTGTTGTAGGTTGAGCGAATGCTACCAGAGTGTGAGAGACCATTGTCTCGTTGGCTGGCGCTCACGGAC
ATGCAGTCACGGTAGCGGGAGCAATCACAAAACCTGTAATTTACTTACCAAATCTCTTCCCTTCCGTAGCCTCGCC
TGCTTGACTTAGAGAAAAGAAAAGCAATAATTTTACAGGCATTTTGAGGTGTCTCTTTGGGTTCCTTCTGTTTGAA
AGGATATTTGTGCGAAAAAAGAGCAAAACCGTTTTTAAATAAACTCCCCCTGGAAAAAAACCCAAAACACTGGCAT
CTGAGTAGGAATATGAAAATGACACCTTTTCCAAATATTTAAATTGGAAAACAAGGTCTACAAAATCATGATACTT
TTTTAAAAGGCAGAGCATTCTTTTTTTCGGCAATTTTGATAAGCAAGGTGTAGATTTACATTTTTGTCTTGTCTC
CAACGAAATGGATAAAACAAAATAAATTACCATCTACTCATGGAATGTTGTTGTGTTAGCCAGTCTGAAAGCCCCA
CCTTAATTTTTATATACTGTCTTTAGCTCTTCTTTTGACAGGGCAGGCCTTGTTCTGAACTGTTTCGCTTCTGA
CTGTTAAACACCGATGACGCATGCACTGCACTTCTTCGTTTTCTTCTTGCTCCCCCATTGGCCTGAGTTTCTTGT
GCATTACTCCTCTCCCTCCTTCGTTAGAATAGGTATATCAGCTGTGTAAATAGAGCAAGAAAACAGTATTCTGCA
TCTGTGGCATTATGTAGAGTTGCAGTTGTGTACTGCTGAAAATGCAGGCTTTTGTAACAGTGTGATCTTTACTG
ATGCACTCATGACAAGTACCCAATGTATTTTAGCTATTTTAGTAGTATTTGTTCAATAAATACGCAAGCTGTAAG
GTAACGTCTG

1782/6881
FIGURE 1651

MVYYPELFVWVSQEPFPNKDMEGRLPKGRLPVPKEVNRKKNDETNAASLTPLGSSELRSPRISYLHFF

1783/6881
FIGURE 1652

TTTTGGCTCTCTGACCAGCACCATGGCAGTTGGCAAGAACAAGTGCCTTACGAAAGGCGGCAAAAAGGGAGCCAA
GAAGAAAGTGGTTGATCAATTTTCTAAGAAAGATTGGTATGATGTGAAAGCATCTGCTATGTTTCAGTATAAGAAA
TATTGGAAAGACGCTCGTCCAGGACCCAAGGAACCAAAATTGCATCTGATGGTCTCAAGGGTCGTGTGTTTGA
AGTGAGTCTTGCTGATTTGCAGAATGATGAAGTTGCATTTAGAAAATTCAAGCTGATTACTGAAGATGTTTCAGGG
CAAAAAGTGCCTGAGCAACTTCCATGGCATGGATCTTACCCGTGATAAAATGTGTTCCATGGTCAAAAAATGGCA
GACAATGATTGAAGCTCATGTTGATGTCAGGACTACCGATGGTTACTTGCTTCATCTGTTCTGTGTTGGTTTTAC
TAAAAACGCAACAATCAGATACGGAAGACCTCTTATGCTCAGCACCAACAGGTCCGCCAAATCCGGAAGAAGAT
GATGGAAATCATGACCCCAGAGGTGCAGACAAATGACTTGAAAGACCCAGAGGTGCAGACAAATTACAGTGGTCA
ATAAATTGATTCCAGACAGCATTGGAAAAGACATAGAAAAGGCTTGCCAACCTATTTATCCTCTCCATGATGTCT
TCGTTAGAAAAGTAAAAATGCTGAAGAAGCCCAAGTTTGAATTGGGAAAGCTCATGGAGCTTCATGGTGAAGGCA
GTAGTTCTGGAAGAGCCACTGGGGATGAGACAAGTGCTAAAGTTGAACGAGCTGATGGATATGAACCACCAGTCC
AAGAATCTGTTTAAAGTTCAGACTTCAAATAGTGGCAAATAAAAAGTGCTATTTG

1784/6881
FIGURE 1653

MAVGKNKCLTKGGKKGAKKKVVDQFSKKDWYDVKASAMFSIRNIGKTLVTRTQGTKIASDGLKGRVFEVSLADLQ
NDEVAFRKFKLITEDVQGKNCLSNFHGMDLTRDKMCSMVKKWQTMIEAHVDVRTTDGYLLHLFCVGFTKKRNNQI
RKTSYAQHQQVRQIRKKMMEIMTPEVQTNDLKDPEVQTNYSQ

1785/6881
FIGURE 1654

GCAGCCAGAAAGCTCTGGAGCATCAGGGAGACTCCAACCTTAAGGCAACAGCATGGGTGAATAAGGGCTTCCTGTG
GACTGGCAATGAGAGGCAAAACCTGGTGCTTGAGCACTGGCCCCCTAAGGCAGGCCTTACAGATCTCTTACACTCG
TGGTGGGAAGAGTTTAGTGTGAAACTGGGGTGGAATTGGGTGTCCACGTATGTTCCCTTTTGCCTTACTATATGT
TCTGTCAGTTTCTTTCAGGAAAATCTTCACTTACAACCTTGTAGGGCTGGTGTAACTTACGACTTCACTAACTG
TGACTTTGAGAAGATTAAAGCAGCCTATCTCAGTACTATTTCTAAAGACCTGATTACATATATGAGTGGGACCAA
AAGTACCGAGTTCAACAACACCGTCTCTTGTAGCAATCGGCCACATTGCCTTACTGAAATCCAGAGCCTAACCTT
CAATCCCACCGCCGGCTGCGCGTCGCTCGCCAAAGAAATGTTGCCATGAAAATAAGGCTGCCTTAGCTATCTG
GTGCCCAGGCTATTCGGAAACTCAGATAAATGCTACTCAGGCAATGAAGAAGAGGAGAAAAGGAAAGTCACAAC
CAATAAATGTCTGGAACAAGTGTACAATTACAAGGATTGTGGCGTCGCTTCAATCGACCTTTACTGAAACAACA
GTAAACCATCTTTATTATGGTCATATTTACAGCACCAAAATAAATCATCTTTATTAAGT

1786/6881
FIGURE 1655

CCGCAGCCCATCGGCATGGCTCAAGAGTTTGTGAACTGCAAAATCCAGCCTGGGAAGGTGGTTGTGTTTCATCAAG
CCCACCTGCCCCGTACTGCAGGAGGGCCCAAGAGATCCTCAGTCAATTGCCCATCAAACAAGGGCTTCTGGAATTT
GTCGATATCACAGCCACCAACCACACTAACGAGATTCAAGATTATTTGCAACAGCTCACGGGAGCAAGAACGGTG
CCTCGAGTCTTTATTGGTAAAGATTGTATAGGCGGATGCAGTGATCTAGTCTCTTTGCAACAGAGTGGGGAAGTG
CTGACGCGGCTAAAGCAGATTGGAGCTCTGCAGTAACCACAGAACAGGCCCCATGCTGACGTCCCTCCTCAAGAG
CTGGATGGCATTGCAAATGATGACAGCACTTCTGGTGGATGAATTTGGGGGCACAAACAGCTTTTTTCCTCTTTT
GGCTCAGTATTTAAAAGTGGACCAACTTGCTCTTAATCACAGGGCCAAGAAGGTTGACGGGCCATCTTGGTTTTT
TTCTGGATGTGCTCTTTGGTTTTTCAGAAGACTGTGACAAGTTCTGGCCCAGGATTCGCTCACTGACCCTCAATTG
TCCTCTTTGGCATGCGTTTCTTACTGTTCTCCATGTGTGCGCATGTCTCTACCTCTAAGCCAGTGTTTTTCAACT
ATGTTTATCCAGACTCCTTCTCCACAATGATGAATCCACAGTTGGTTATCTGCTACTGCCCATTAGCTAAAATCA
TTTTGCTGCTTGACTTTATGGAGTTTGTATTATGAAATCAGTGGGTATTTTGAATGTGTTCTTTCTAACTACATG
CATCTCTCCACTCAACTCCACCCCATCCCATCCACCTTGAAAATCACTGCTCTGAACCAGTGTTCTCCACCTTG
TCCTCCACAGATCTCATAGGAAATGTTCAACAATTCTGTGAAAGGTCACAGGACCCAATTGGAGAAATCATATGA
AAAGCATAGTTGGTCTTGGTGTCTATGGATCAGAGGCACAAGTGCAGAGGCTGTGGTCATGCGGAACACTCTGT
TATTTAAGATGGCTATCCAGATAATCCTGAACACTGTGTATTTATTTTATTTAGACTACCAGCAAAGATTAAAGC
ATGAAATGTAAACATCTGATAAACTTACAGCCCCCTACACCAAGAGTGTATCTGTGAAAGAGCTCCTACACTT
TGAAAACTTAAGAATCCCTTATCATGAAGTTTGCCTGTTCTAGAATTGTAAGATTGTTAATTTCTTCAATCTCT
AGTGACAACACTTAATTTCTTTTCTAATAAAAAAACCTATAGATGATTCAGTG

1787/6881
FIGURE 1656

ATCTTGGCGAGGCTGCGGTGTCTGCTGCTACTCTCCGAGCTTCGCAATGCCGCCAAGGACGACGAGAAGAAGGA
CGCTGGAAAGTCAGCCAAGAAAGACAAAGACCCAGTGAACAAATCCGGGGGCAAGGCCAAAAAGAAGAAGTGGTC
CAAAGGCAAAGTTCGGGACAAGCTCAATAACTTAGTCTTGTTTGACAAAGCTACCTATGACAAACTCTGTAAGGA
AGTTCCCAACTATAAACTTATAACCCCAGCTGTGGTCTCTGAGAGACTGAAGATTCGAGGCTCCCTGGCCAGGGC
AGCCCTTCAGGCAAAGCACAGAGCTCAAGTAATTTACACCAGAAATACCAAGGGTGGAGATGCTCCAGCTGCTGG
TGAAGATGCATGAATAGGTCCAACCAGCTGTACATTTGGAAAAATAAACTTTATTAAATC

1788/6881
FIGURE 1657

MPPKDDEKKDAGKSAKKDKDPVNKSGGKAKKKKWSKGKVRDKLNNLVLFDKATYDKLCKEVPNYKLITPAVVSER
LKIRGSLARAALQAKHRAQVIYTRNTKGGDAPAAGEDA

1789/6881
FIGURE 1658

GACTGTACAATTTGTTCAAGGAATTTTTGTAGAAAAATACGATCCTACGATAGAAGATTCTTATAGAAAAGCAAGT
TGAAGTAGATGCACAACAGTGTATGCCTTGAAATCTTGGATACTGCAGGAACGGAGCAATTTACAGCAATGAGGGA
TTTATACATGAAAAATGGACAAGGATTTGCATTAGTTTATTCATCACAGCACAGTCCACATTTAACGATTTACA
AGACCTGAGAGAACAGATTCTTCGAGTTAAAGACACTGATGATGTTCCAATGATTCTTGTTGGTAATAAGTGTGA
CTTGGAAGATGAAAGAGTTGTAGGGAAGGAACAAGGTCAAAATCTAGCAAGACAATGGAACAACCTGTGCATTCTT
AGAATCTTCTGCAAAATCAAAAATAAATGTTAATGAGATCTTTTATGACCTAGTGCGGCAAATTAACAGAAAAAC
TCCAGTGCCCTGGGAAGGCTCGCAAAAAGTCATCATGTCAGCTGCTTTAATATACTAAATGCATTGTAGCTCTGAG
CCAGGTCTGAAGAACTGTTGCCCAATTCAACAGTGCCAGCATTTCCAACCTTGTAAACCTACCAACATCTTAAAT
GGACTTTCTGTGGTGGTACCCTTTAAGAGGCGGATGAAAGCTACTATATCAGTTTGCACATTCTAATCACTTTC
CAGTATCACAAAGAGAGATTTTTACTTTATATAATAGTCCTAGAGTTTGCAGCTGGTAAAACCAGAGGCTACATCCA
GTATTACTGCTAAGAGACATTCTTCATCCACCAATGTTGTACATGTATGAAAATGGTGTACTGTATACTTTAACA
TGCCCCATACTTTGTATTGGAGAGTACAATAATGTAAATCCTAAAAGCACCCTATTTTAGCATAATAAAAGAAA
GTCCAAAGAGCTCCTATATAGACTACTCCAGATAACTTCGCTTCTTTGATACTTGTAGCTTATTGTAATTTTTTT
TAAGAAATTCAGGTCAATTATTATTGTACAAAAATAAGCGCTTTGATTAACACAGCTATATAGTTTTTTTAATTTT
TAAAAAACCTGTGGAGACGGTGATCTTGTCTTTAAAACATGATAGTCCTTTCAGTATAATGTCTTAGATTAAAGA
CGTTGCCCTTAATATCTGTTGGGAAGGAAATGTCCAGACTTTTCAAATCTCTTATTATATGTTTCCTTTTTTTGT
TTACATAGGGAACAATGTTTATAGTCGTGTGTACAGTGGGGTCTACAACAAGAAGTGTATATTTCAAACAATT
TTTTAATGATTTAACAATTTTTGTAAATCATTTTCAGGCTTCTGCAGCTGTAGATTCTCACTGTGAATCCCTTGC
TTGCTCATGCATAAGTGTATTTGCAATACCAAATATACAGGTTTAGTATTTTTGCCTGTTAGTGATTGTTTCACA
TGTGTAACGTTTTGGTTGAGATGTTAAATGGTGGACGAGTACTGTGGATGTGAATGTGGGAAGTAATTTTAATCA
TATGTAATTGGTCACAAGGCCTAATTTGCAGTAACTATTGCTGTTTTATTTAACAATGCCTTGTGTCTTTGTAIG
CATTAATGTTTGGATGTAAAGATTGTGTGTCTATCCAACAGGGAGCCACAGTATTTAAATTGACCAACCTAATGT
TACAACTACTTTGAGGTGGCCAAATGTAAACTAAAAGCCTTAATTAAAGTGGTGCAATTTTGT

1790/6881
FIGURE 1659

MLEILDTAGTEQFTAMRDLYMKNQGQFALVYSITAQSTFNDLQDLREQILRVKDTDDVPMILVGKCDLEDERVV
GKEQGQNLARQWNNCAFLESSAKSKINVNEIFYDLVRQINRKTPVPGKARKKSSCQLL

1791/6881
FIGURE 1660

GCTCCTTCTAGGATCTCTGCCTGGTTTCGGCCCCGCTGCCTCCACTCCTGCCTCCACCATGTCCATTAGGGGACCC
AGAAGTCCTACAAGGTGTCCACCTCTGGCCCCGGGCCTTCAGCAGCCACTCCTACACAAGTGGGCCCCGGTGCCC
ACATCAGCTCCTCAAGCTTCTCCCAAGTGGGCAGCAGCTGCTTTCGGGGTGGCCTGGGCGGCGGCTGTGGTGGGG
CCAGCGGCATGGGAGGCATCACCGCGGTACAGTCAACCAGAGCCTGCTGAGCCCCCTTGTCTGGAGGTGGACC
CCGACATCCAGGCTGTGTGCACCCAGGAGAAGGAGCAGATCAAGACCCTCAACAACAAGTTTGCCTCCTTCATAG
ACAAGGTACGGTTCTTGGAGCAGCAGAACAAGATGCTGGAGACCAAGTGGAGCCTCCTGCAGCAGCAGAAGACGG
CCGGGAGCAACATGGACAACATGTTCAAGAGCTACATCAACAACCTTAGGCGGCAGCTGGAGACTCTGGGCTAGG
AGAACTGAAGCTGGAGGCGGAGCTTGGCAACATGTAGGGGCTGGTGGAGGACTTCAAGAACAAGTATGAGGATG
AGATCAATAAGCGTGCAGAGATGGAGAATGAATTTGTCTCATCAAGAAGGATTGTGGATGAAGCTTACATTAAC
AAGGTAGAGCTGGAGTCTCGCCTGGAAGGGCTGACTGATGAGATCAACTTCCTCAGGCAGCTGTATGAAGAGGAG
ATCCGGGAGCTGCAGTCTGGATCTCAGACACATCTGTGGTGTCTGTCATGGACAACAGCCGCTCCCTGGACATG
AACAGCGTCATCGCTGAGGTCAAGGCACAGTACGAGGAGATCGCCAACCGCAGCCAGGCCGAGGCTGAGAGCATG
TACCAGATCAAGGATGAGGAGCTGCAGAGTCTGGCTGGGAAGCATGGGGATAACCTGCGGTGCACAAAGACTAAG
ATCTCCGAGATGAACCGGAACATCAGCCGGCTCCAGGCTGAGAATGAGGGCCTCAAAGGCCAGAGGGCTTTCTCTG
GAGGCCGCCATTGCAGATGCCGAGCAGTGTGGAGAGCTGGCCATTAAGGATGCTAACGCCAAGTTGTCTGAGCTGG
AGGCCGCCCTGCAGCGGGCCAAGCAGGACATGGCGTGGCAGCTGCGTGAGTACCAGGAGCTTGATGAACGTCAGGC
TGGCCCTGGACATCGAGATCGCCACCTACAAGAAGCTGCTGGAGGGCGAGGAGAGCCGGCTGGAGTCTGGGATGC
AGAACATGAGTATTCATACGAAGACCACCAGCGGTATGCAAGTGGTCTGAGCTCGGCCTGTGGGGGCCTCACAA
GCCCCGGCCTCAGCTACGGCCTGGGCGCCAGCTCCTTCAGCCGCACCAGCTACTCCAGGGCCGTGGTTGTGAAGA
TCGAGACACGTGATGGGAAGCTGGTGTCCGAGTCTCTGACGTCTGCCCAAGTGAACAGCTGTGGCAGCCCCCTC
CCAGCCTACCCCTCCTGCGCTGCCCCAGAGCCTGGGAGGGAGGTCACTATGCAGGGTAGCACTGGGAACAGGAGA
CCCACCTGAGGCTCAGCCCTAGGCCTCAGTCCACCCGCGGGGAGTTTACTGCCTGGGGACCCCCCTTTGCCCA
TGCTCCAGCTACAAAACAATTCAGTTGCTTTTTTTTTTTTTTTTTTGGTCCAAAATAAAACCTCAGCTAGCTCTGC

1792/6881
FIGURE 1661

MRMRSISVQRWRMNLSSRRIVDEAYINKVELESRLLEGLTDEINFLRQLYEEEIRELQSWISDTSVVLSDNSRS
LDMNSVIAEVKAQYEEIANRSQAEAESMYQIKDEELQSLAGKHGDNLRCTKTKISEMNRNISRQAENEGLKGQR
AFLEAAIADAEQCGELA IKDANAKLSSWRPPCSGPSRTWRGSCVSTRS

1793/6881
FIGURE 1662

AGTGGGCAGCAGCTGCTTTCGGGGTGGCCTGGGCGGCGGCTGTGGTGGGGCCAGCGGCATGGGAGGCATCACCGC
GGTCACAGTCAACCAGAGCCTGCTGAGCCCCCTTGTCTGGAGGTGGACCCGACATCCAGGCTGTGTGCACCCA
GGAGAAGGAGCAGATCAAGACCCTCAACAACAAGTTTGCCTCCTTCATAGACAAGGTACGGTTCCTGGAGCAGCA
GAACAAGATGCTGGAGACCAAGTGGAGCCTCCTGCAGCAGCAGAAGACGGCCGGGAGCAACATGGACAACATGTT
CAAGAGCTACATCAACAACCTTAGGCGGCAGCTGGAGACTCTGGGCTAGGAGAACTGAAGCTGGAGGCGGAGCT
TGGCAACATGTAGGGGCTGGTGGCTGGGATGCAGAACATGAGTATTCATACGAAGACCACCAGCGGCTATGCAAG
TGGTCTGAGCTCGGCCTGTGGGGGCCTCACAAGCCCCGGCCTCAGCTACGGCCTGGGCGCCAGCTCCTTCAGCCG
CACCAGCTACTCCAGGGCCGTGGTTGTGAAGATCGAGACACGTGATGGGAAGCTGGTGTCCGAGTCCTCTGACGT
CCTGCCCAAGTGAACAGCTG

1794/6881
FIGURE 1663

CTGGGCGGCGGCTGTGGTGGGGCCAGCGGCATGGGAGGCATCACC GCGGTCACAGTCAACCAGAGCCTGCTGAGC
CCCCTTGTCCTGGAGGTGGACCCCGACATCCAGGCTGTGTGCACCCAGGAGAAGGAGCAGATCAAGACCCTCAAC
AACAAGTTTGCCTCCTTCATAGACAAGGTACGGTTCCCTGGAGCAGCAGAACAAGATGCTGGAGACCAAGTGGAGC
CTCCTGCAGCAGCAGAAGACGGCCGGGAGCAACATGGACAACATGTTCAAGAGCTACATCAACAACCTTAGGCGG
CAGCTGGAGACTCTGGGCTAGGAGAACTGAAGCTGGAGGCGGAGCTTGGCAACATGTAGGGGCTGGTGGAGGAC
TTCAAGAACAAGTATGAGGATGAGATCAATAAGCGTGCAGAGATGGAGAATGAATTTGTCCTCATCAAGAAGGAT
TG TGGATGAAGCTTACATTAACAAGGTAGAGCTGGAGTCTCGCCTGGAAGGGCTGACTGATGAGATCAACTTCCT
CAGGCAGCTGTATGAAGAGGAGATCCGGGAGCTGCAGTCCTGGATCTCAGACACATCATCGCTGAGGTCAAGGCA
CAGTACGAGGAGATCGCCAACCGCAGCCAGGCCGAGGCTGAGAGCATGTACCAGATCAAGGATGAGGAGCTGCAG
AGTCTGGCTGGGAAGCATGGGGAT

1795/6881
FIGURE 1664

GCGGCCGCGGCCGTGAGCCTGCCCCCAACTCGCCCTCAGCCGGCTGGCCGGCGCGGCCATGGAGGTCTACATCCC
GTCCTTTTCGCTATGAAGAGAGCGACCTGGAGCGGGGATACACGGTGTTTAAGATAGAAGTGCTAATGAATGGAAG
AAAACATTTTGTGAAAAGAGATACAGCGAATTTTCATGCTTTGCACAAAAAGCTTAAGAAATGTATAAAAACTCC
AGAAATCCCTTCTAAACATGTTAGGAAGTGGGTCCCCAAAGTCTTGGAACAGCGACGACAAGGCTTGGAAACATA
CTTACAGGCTGTCATTTTAGAAAATGAAGAACTTCCCAAAGTGTTCCTTGAATTTCTAAATGTGCGACACTTGCC
CTCTCTACCAAAGGCAGAAAGTTGTGGATCTTTTGATGAAACAGAGTCTGAAGAGTCAAGCAAAGTGTCCACCA
GCCTGTGCTGCTGTTCCCTCAGGGATCCATATGTCTTGCTGCAGCCAGCGATTTTCCAAATGTGGTTATTGAAGG
AGTCCTCCATGGGATATTTTACCCTCATCTACAGCCAGGTAGAAATCCTACATGGCTAAAAGAAGCAGAAGCAA
GTTTCGAAGTCACAGTCAAGGAAATCAATACCTACCAATTTAACCTAAACGCTATGATATATAACAGCTCTAGCT
AGTGGTAAAGTGCACAGTCCCAGCTTAATTCAGGGCAGGGACATTTCCATTAGAATGGTGCTCTTAAAAATAGAA
ACTGAACCGGGGCGGTGGTCAGGCTAAGGCCAAGTGTTAAGAAGTAGAGTGTAGCTGCCAGCGTAGAAACCCAT
GAAAAGGAGGCCACAGGAGATTCCTGGGAGCACTGGGTGTAGCAAAACAAAGCCACTCTCTGCTTCAGTCGCACC
ATTTGCTAATTGAAAATCATATCCTGAATCATACTGAGACTGATCAACTTTGGTAGCTTTTTTGTTCAGATCTTA
TGACACACTACTCTTCTCACCCTGAGATTTTCTCAGCCAGTGATAGTACATTCTGAAATGCTGGCACCAGGAGAC
GGCCACAGACACACACTGCTAAATGTGAAGATGGAAGTAACTGGAATTAATTTATACTGACAATATTATGGCA
TTTTTAAGATCATGGCATTTTAATTTACATTAGAGTGGAGTTGCATCATACTCAGGGGTTAGCTTCCAAGGTCAG
TACATAGGTAAAAATGGGCTATTAGGATGATCCTTGAAAGCCCTTTAGAAGGGTGCCATGTTGGAAACCTGTACAT
CACAACAAGTAGCTTTTCTCTCTATGTTGGAAAAAAGACTGTTTCTTTGTTTGAAGACCAAGTGAAGTTGTTGG
TGTTTGTGTTAGGGGCCATTTTGTAAAAAAGACACATAACTTTTAACTAGAAATCAGCCCGCAAGATGCT
TGCCCCGCTAGTGGCAGATGTGAAGTGAAGGAGTGAAGCGCCACCCAGCGGATGGACAGCACCCACCTGGGT
TTACTCAAGGTGTGCATTCAATTTAGGTGGGATCGCCACAGGATTTTCATGTTATTTTCTTACGGCTTCCTTTT
CACTGACCTCATTTGTTGAGTTAATGTAAGTTAAATGTGTCTATGATATAACTCCACTGTACATCATCCTTTGAG
TAGTAAAGGATAAAAGCATATATACTACCTATATGTATGTGCTGTATGTGGGCATTTTCATTGAGATCTAATTAAT
AGCTAGCCTATTTATGGTTATTCGTTTTAGTAAGTTCTGTGGGAGCAAGGTATTTAAAATCAAACTAATAACTA
CATCATGGTTTTTTGATTAGGATCTAAATATTCAGGTTTTAAGCCTGCTGCAAAGTTTTAAAATATTATGATAGAT
TCTGTACTACATGTGGGAAACAAGCAAGAACTAAATAATCAAATGTTGTCAACCAAAGTAATAGTTGGGTATTG
GAGATTTTTTTAAAATGTTTTTATGTTATTAGCTATTTGGAGTTAAATAAAAACAGAACAAGGAAAAAAAAAAAA
AAAAAAAAAAAAAA

1796/6881
FIGURE 1665

MEVYIPSFYEESDLERGYTVFKIEVLMNGRKHFVEKRYSEFHALHKKLKKCIKTPEIPSKHVRNWVPKVLEQRR
QGLETYLQAVILENEELPKLFLDFLNVRHLPSLPKAESCGSFDETESEESSKL SHQPVLLFLRDPYVLP AASDFP
NVVIEGVLHGIFYPHLQPR

1797/6881
FIGURE 1666

AGCTCGCGCAGTCGTTTCGGGTGAGCGAAGATGGCGGCCGAGAGGGAACCTCCTCCGCTGGGGGACGGGAAGCCCA
CCGACTTTGAGGATCTGGAGGACGGAGAGGACCTGTTACCCAGCACTGTCTCCACCCTAGAGTCAAGTCCATCAT
CTCCAGAACCAGCTAGTCTTCCCTGCAGAAGATATTAGTGCAAACCTCCAATGGCCCAAACCCACAGAAGTTGTAT
TAGATGATGACAGAGAAGATCTTTTTGCAGAAGCCACAGAAGAAGTTTCTTTGGACAGCCCTGAAAGGGAACCTA
TCCTATCCTCGGAACCTTCTCCTGCAGTCACACCTGTCACTCCTACTACACTCATTGCTCCTAGAATTGAATCAA
AGAGTATGTCTGCTCCCGTGATCTTTGATAGATCCAGGGAAGAGATTGAAGAAGAAGCAAATGGAGACATTTTTG
ACATAGAAATTGGTGTATCAGATCCAGAAAAAGTTGGTGATGGCATGAATGCCTATATGGCATATAGAGTAACAA
CAAAGACATCTCTTTCCATGTTTCAGTAAGAGTGAATTTTCAGTGAAAAGAAGATTTCAGCGACTTTCTTGGTTTGC
ACAGCAAATTAGCAAGCAAATATTTACATGTTGGTTATATTGTGCCACCAGCTCCAGAAAAGAGTATAGTAGGGA
TGACCAAGGTCAAAGTGGGTAAAGAAGACTCATCATCCACTGAGTTTGTAGAAAACGGGAGAGCAGCTCTTGAAA
GGTATCTTCAAAGAACAGTAAACATCCAACCTTTACTACAGGATCCTGATTTAAGGCAGTTCTTGAAAAGTTCAG
AGCTGCCTAGAGCAGTTAATACACAGGCTCTGAGTGGAGCAGGAATATTGAGGATGGTGAACAAGGCTGCCGACG
CTGTCAACAAAATGACAATCAAGATGAATGAATCGGATGCATGGTTTGAAGAAAAGCAGCAGCAATTTGAGAATC
TGGATCAGCAACTTAGGAACTTCATGTCAAGTGTGAAGCCTTGGTCTGTCATAGAAAAGAACCTTTAGCCAACA
CAGCTGCCTTTGCTAAAAGTGCTGCCATGTTAGGTAATTCTGAGGATCATACTGCTTTATCTAGAGCTTTGTCTC
AGCTTGCAAGAGTTGAGGAGAAGATAGACCAGTTACATCAAGAACAAGCTTTTGCTGACTTTTATATGTTTTTCAG
AACTACTTAGTGACTACATTCGTCCTTATTGCTGCAGTGAAAGGTGTGTTTGACCATCGAATGAAGTGCTGGCAGA
AATGGGAAGATGCTCAAAATTACTTTGCTCAAAAAACGTGAAGCTGAAGCAAAAATGATGGTTGCTAACAAACCAG
ATAAAATACAGCAAGCTAAAAATGAAATAAGAGAGTGGGAGGCCGAAAGTGCAACAAGGGGAAAGAGATTTTGAAC
AGATATCTAAAACGATTTCGAAAAGAAGTGGGAAGATTTGAGAAAAGACGAGTGAAGGATTTTAAAACCGTTATCA
TCAAGTACTTAGAATCACTAGTTCAAACACAACAACAGCTGATAAAATACTGGGAAGCATTCTACCTGAAGCCA
AAGCCATTGCCTAGCAATAAGATTGTTGCCGTTAAGAAGACCTTGGATGTTGTTCCAGTTATGCTGGATTCCACA
GTGAAATCATTATAAACCATCTAAATAAACCACTATATATTTTATGAATTACATGTGGTTTTATATACACACACA
CACACACACACACACACACACACACTCTGACATTTTATTACAAGCTGCATGTCCTGACCCTCTTTGAATTAAG
TGGACTGTGGCATGACATTCTGCAATACTTTGCTGAATTGAACACTATTGTGTCTTAAATACTTGCACTAAATAG
TGCACTGCAAGACCAGAAAAATTTACAATATTTTTCTTTACAATATGTTCTGTAGTATGTTTACCCTCTTTATG
AAGTGAATTACCAATGCTTTGAATAATGTTCACTTATACATTCTGTACAGAAATTACGATTTTGTGATTACAGT
AATAAAATGATATTCTTGTG

1798/6881
FIGURE 1667

MAAEREPPPLGDGKPTDFEDLEDGEDLFTSTVSTLESSPSSPEPASLPAEDISANSNGPKPTEVVLDDDDREDLFA
EATEEVSLDSPEREPILSSEPSPAVTPVTPPTTLIAPRIESKSMSAPVIFDRSREEIEEEEANGDIFDIEIGVSDPE
KVGDMNAYMAYRVTTKTSLSMFSKSEFSVKRRFSDFLGLHSLKASKYLHVGYIVPPAPEKSIVGMTKVKGKED
SSSTEFVEKRRAALERYLQRTVKHPTLLQDPDLRQFLESSELPRAVNTQALSGAGILRMVNKAADAVNKMTIKMN
ESDAWFEEKQQQFENLDQQLRKLHVSVEALVCHRKELSANTAFAKSAAMLGNSDHTALSRALSQLAEEVEEKID
QLHQEQAFADFYMFSELLSDYIRLIAAVKGVFDHRMKCWQKWEDAQITLLKKREAEAKMMVANKPDKIQQAKNEI
REWEAKVQQGERDFEQISKIRKEVGRFEKERVKDFKTVI IKYLESIVQTQQQLIKYWEAFLPEAKAIA

1799/6881
FIGURE 1668

AGCTCTCTGGACCTTGGAGCAGGCCTGCCGCCTTCATGTCCACTCTCCTCATCAATCAGCCCCAGTATGCGTGGC
TGAAAGAGCTGGGGCTCCGCGAGGAAAACGAGGGCGTGTATAATGGAAGCTGGGGAGGCCGGGGAGAGGTTATTA
CGACCTATTGCCCTGCTAACAACGAGCCAATAGCAAGAGTCCGACAGGCCAGTGTGGCAGACTATGAAGAACTG
TAAAGAAAGCAAGAGAAGCATGGAAAATCTGGGCAGATATTCTTGCTCCAAAACGAGGAGAAATAGTAAGACAGA
TTGGCGATGCCTTGCGGGAGAAGATCCAAGTACTAGGAAGCTTGGTGTCTTTGGAGATGGGGAAAATCTTAGTGG
AAGGTGTGGGTGAAGTTCAGGAGTATGTGGATATCTGTGACTATGCTGTTGGTTTATCAAGGATGATTGGAGGAC
CTATCTTGCCCTTCTGAAAGATCTGGCCATGCACTGATTGAGCAGTGGAATCCCGTAGGCCTGGTTGGAATCATCA
CGGCATTCAATTTCCCTGTGGCAGTGTATGGTTGGAACAACGCCATCGCCATGATCTGTGGAAATGTCTGCCTCT
GGAAAGGAGCTCCAACCACTTCCCTCATTAGTGTGGCTGTACAAAAGATAATAGCCAAGGTTCTGGAGGACAACA
AGCTGCCTGGTGCAATTTGTTCCCTTGACTTGTGGTGGAGCAGATATTGGCACAGCAATGGCCAAAGATGAACGAG
TGAACCTGCTGTCTTCACTGGGAGCACTCAGGTGGGAAAACAGGTGGGCCTGATGGTGCAGGAGAGGTTTGGGA
GAAGTCTGTTGGAACCTGGAGGAAACAATGCCATTATTGCCCTTTGAAGATGCAGACCTCAGCTTAGTTGTTCCAT
CAGCTCTCTTCGCTGCTGTGGGAACAGCTGGCCAGAGGTGTACCACTGCGAGGCGACTGTTTATACATGAAAGCA
TCCATGATGAGGTTGTAAACAGACTTAAAAAGGCCTATGCACAGATCCGAGTTGGGAACCCATGGGACCCTAATG
TTCTCTATGGGCCACTCCACACCAAGCAGGCAGTGAGCATGTTTCTTGGAGCAGTGGAAGAAGCAAAGAAAGAAG
GTGGCACAGTGGTCTATGGGGGCAAGGTTATGGATCGCCCTGGAAATTATGTAGAACCACCAATTGTGACAGGTC
TTGGCCACGATGCGTCCATTGCACACACAGAGACTTTTGCTCCGATTCTCTATGTCTTTAAATTCAAGAATGAAG
AAGAGGTCTTTGCATGGAATAATGAAGTAAAACAGGGACTTTCAAGTAGCATCTTTACCAAGATCTGGGCAGAA
TCTTTCGCTGGCTTGGACCTAAAGGATCAGACTGTGGCATTGTAAATGTCAACATTCCAACAAGTGGGGCTGAGA
TTGGAGGTGCCTTTGGAGGAGAAAAGCACACTGGTGGTGGCAGGGAGTCTGGCAGTGATGCCTGGAAACAGTACA
TGAGAAGGTCTACTTGTACTATCAACTACAGTAAAGACCTTCTCTGGCCCAAGGAATCAAGTTTCAGTAAAGGT
GTTTTAGATGAACATCCCTTAATTTGAGGTGTTCCAGCAGCTGTTTTTGGAGAAGACAAAGAAAATTAAAGTTTT
CCCTGAATAAATGCATTATTATGACTGTGACAGTACTAATCCCCCTATGACCCCAAAGCCCTGATTAAATCAAG
AGATTCCTTTTTTAAAAATCAAAATAAAATTGTTACAACATAGCCATAGTTACT

1800/6881
FIGURE 1669

ACTGGCTGCTCTGAAAAGCCATCTTTGCATTGTTCCCTCGTCCGCCTCCTTGCTCGCGGCACCGCCTCCGCCACGC
GCCTCCTCCGCCGCCGCGGACTCCGGCAGCTTTATCGCCAGAGTCCCTGAACTCTCGCTTTCTTTTTTAATCGCCT
GCATCGGATCACCGGCGTGCCCCACCATGTCAGACGCAGCCGTAGACACCAGCTCCGAAATCACCACCAAGGACT
TACAGGAGAAGAAGGAAGTTGTGGAAGAGGCAGAAAATGGAAGAGACGCCCTGCTAACGGGAATGCTAATGAGG
AAAATGGGGAGCAGGAGGCTGACAATGAGGTAGATGAAGAAGAGGAAGAAGGTGGGGAGGAAGAGGAGGAGGAAG
AAGGTGATGGTGAGGAAGAGGATGGAGATGAAGATGAGGAAGCTGAGACAGCTACGGGCAAGCGGGCAGCTGAAG
ATGATGAGGATGACACGCGCTCTCCACCACCAACCAACCATGAGAATTTGCAACAGGGGAGGAAAAAAGAAC
CAAAACTTCCAAGGCCCTGCTTTTTTTCTTAAAAGTACTTTAAAAGGAAATTTGTTTGTATTTTT

1801/6881
FIGURE 1670

GGGGGAACATGGCGGCTGCGGAGCCGGCGGTCTTTCGCTCCCCAACAGCGGCGCCGGGGGCGCGGGGGCGCCGT
CGGGCACAGTCCCGGTGCTCTTCTGTTTCTCAGTCTTCGCGCGACCCCTCGTCGGTGCCACACGGGGCGGGCTACG
AGCTGCTCATCCAGAAGTTCCTCAGCCTGTACGGCGACCAGATCGACATGCACCGCAAATTCGTGGTGCAGCTGT
TCGCCGAGGAGTGGGGCCAGTACGTGGACTTGCCCAAGGGCTTCGCGGTGAGCGAGCGCTGCAAGGTGCGCCTCG
TGCCGTTGCAGATCCAGCTCACTACCCTGGGAAATCTTACACCTTCAAGCACTGTGTTTTCTGCTGTGATATGC
AGGAAAGGTTTCAGACCAGCCATCAAGTATTTTGGGGATATTATTAGCGTGGGACAGAGATTGTTGCAAGGGGGCC
GGATTTTAGGAATTCCTGTTATTGTAAACAGAACAAATACCCTAAAGGTCTTGGGAGCACGGTTCAAGAAATTGATT
TAACAGGTGTAAACTGGTACTTCCAAAGACCAAGTTTCAATGGTATTACCAGAAGTAGAAGCGGCATTAGCAG
AGATTCCCGGAGTCAGGAGTGTGTATTATTTGGAGTAGAACTCATGTGTGCATCCAACAACTGCCCTGGAGC
TAGTTGGCCGAGGAGTCGAGGTTACATTGTTGCTGATGCCACCTCATCAAGAAGCATGATGGACAGGATGTTTG
CCCTCGAGCGTCTCGCTCGAACCGGGATCATAGTGACCACGAGTGAGGCTGTTCTGCTTCAGCTGGTAGCTGATA
AGGACCATCCAAAATTCAAGGAAATTCAGAATCTAATTAAGGCGAGTGCTCCAGAGTCGGGTCTGCTTTCCAAAG
TATAGGACATTTGAAGAAGTGGTATGCTACTCACTGGTGAAGGACAGTCAGGTGAAGGACTGTAAGCCACACAA
GCTCTTCTTATCTCTACTAGAAATTAATGTTAAGTCAAAAACGGCTCCTTTTTTGCGCCTCCTAGTGAACTTA
ACCAGCTAGACCATTTGAGTACCAGCATTTAGTTACAAACGTCAAAGGCTTCCGGTGCTGCTTACCTTCCTTTTT
TGTTAATGTGCTTTTATTTATTAATAAATAATTACAATGAAGATGCCTGTTTTGTCTCTACTGTGTACTCTGATCG
TATCTTTCCAAAGTGCAGACTCTTGTAAGTTTTCTTAAATTGTTCACTTTAAAGAAAATGACGTACCAACAATG
ATTTGGCTTTTATATTACTGTAAGATGTTATAATGTTAATGTGGATGTAGTGCTTTTACTTTACAGATTGATTGG
AATAAGATTATTGCATATGAATTTACCCACAGGACTCTGAATCATGTTACCCACTCCCCTCACAATGTTGTCCAC
TTAGTGAGTTGCATTGATCTATCCGTACCAAATGATGTTGAATAATTACATATCTTTCTTGACTATACTGATTTT
TTATTTTGGTCACTATTACTAAATCTCTGTTAATATTCTCTCTTTTAACTGAAAAGGGATGGGATAGAAGGGTTT
GCAATGCCATATTATTGGTGGAGGGCTGTTTTAACATCTTTGAAGTATGGCTTGCTGAATATCTTTACCAACATC
TTGAATATATATTCTAGTGTCCACAAGATTTAGCAAAAAGATAAAGCTTGGGTGGAATATCATTTTAAATGTTT
ATGTTCTGTTCTATATTTTCTTCACCTACTCTCCAAATATTGTAATGCAAAAAGTCTCAGTAATGATTTGGTAGT
ATTAATTTTGTGGTCATTGTTTCTCTTCGATAAATTTATTTTCATTAAATACTTGTTAGAGGGTTTTGAAATGTT
TTTCAAATATGTGAAATGTGAAACTGCTGTCTTTTATATTAAAGTAATTAAAGAAAA

1802/6881
FIGURE 1671

GCTTGCCCGTCGGTCGCTAGCTCGCTCGGTGCGCGTCGTCCCGCTCC**ATG**GCGCTCTTCGTGCGGCTGCTGGCTC
TCGCCCTGGCTCTGGCCCTGGGCCCCGCCGCGACCCCTGGCGGGTCCCGCCAAGTCGCCCTACCAGCTGGTGCTGC
AGCACAGCAGGCTCCGGGGCCGCCAGCACGGCCCCAACGTGTGTGTGTGTGCAGAAGGTTATTGGCACTAATAGGA
AGTACTTCACCAACTGCAAGCAGTGGTACCAAAGGAAAAATCTGTGGCAAATCAACAGTCATCAGCTACGAGTGCT
GTCCTGGATATGAAAAGGTCCCTGGGGAGAAGGGCTGTCCAGCAGCCCTACCACTCTCAAACCTTTACGAGACCC
TGGGAGTCGTTGGATCCACCACCACTCAGCTGTACACGGACCGCACGGAGAAGCTGAGGCCTGAGATGGAGGGGC
CCGGCAGCTTCACCATCTTCGCCCTAGCAACGAGGCCTGGGCCCTCCTTGCCAGCTGAAGTGCTGGACTCCCTGG
TCAGCAATGTCAACATTGAGCTGCTCAATGCCCTCCGCTACCATATGGTGGGCAGGCGAGTCTTGACTGATGAGC
TGAAACACGGCATGACCCTCACCTCTATGTACCAGAATTCCAACATCCAGATCCACCCTATCCTAATGGGATTG
TAACTGTGAACTGTGCCCGGCTCCTGAAAGCCGACCACCATGCAACCAACGGGGTGGTGCACCTCATCGATAAGG
TCATCTCCACCATCACCAACAACATCCAGCAGATCATTGAGATCGAGGACACCTTTGAGACCCTTCGGGCTGCTG
TGGCTGCATCAGGGCTCAACACGATGCTTGAAGGTAACGGCCAGTACACGCTTTTGGCCCCGACCAATGAGGCCT
TCGAGAAGATCCCTAGTGAGACTTTGAACCGTATCCTGGGCGACCCAGAAGCCCTGAGAGACCTGCTGAACAACC
ACATCTTGAAGTCAGCTATGTGTGCTGAAGCCATCGTTGCGGGGCTGTCTGTAGAGACCCTGGAGGGCAGCAC
TGGAGGTGGGCTGCAGCGGGGACATGCTCACTATCAACGGGAAGGCGATCATCTCCAATAAAGACATCCTAGCCA
CCAACGGGGTGATCCACTACATTGATGAGCTACTCATCCCAGACTCAGCCAAGACACTATTTGAATTGGCTGCAG
AGTCTGATGTGTCCACAGCCATTGACCTTTTCAGACAAGCCGGCCTCGGCAATCATCTCTCTGGAAGTGAGCGGT
TGACCCTCCTGGCTCCCTGAATTCTGTATTCAAAGATGGAACCCCTCCAATTGATGCCCATACAAGGAATTTGC
TTCCGAACCACATAATTAAGACCAGCTGGCCTCTAAGTATCTGTACCATGGACAGACCCTGGAACTCTGGGCG
GCAAAAACTGAGAGTTTTTGTATCGTAATAGCCTCTGCATTGAGAACAGCTGCATCGCGGGCCACGACAAGA
GGGGGAGGTACGGGACCCTGTTACGATGGACCGGGTGCTGACCCCCCAATGGGGACTGTGATGGATGTCCTGA
AGGGAGACAATCGCTTTAGCATGCTGGTAGCTGCCATCCAGTCTGCAGGACTGACGGAGACCCTCAACCGGGAAG
GAGTCTACACAGTCTTTGCTCCCAAAATGAAGCCTTCCGAGCCCTGCCACCAAGAGAACGGAGCAGACTCTTGG
GAGATGCCAAGGAACCTGCCAACATCCTGAAATACCACATTGGTGATGAAATCCTGGTTAGCGGAGGCATCGGGG
CCCTGGTGCGGCTAAAGTCTCTCCAAGGTGACAAGCTGGAAGTCAGCTTGAAAAACAATGTGGTGAGTGTCAACA
AGGAGCCTGTTGCCGAGCCTGACATCATGGCCACAAATGGCGTGGTCCATGTGATCACCATGTTCTGCAGCCTC
CAGCCAACAGACCTCAGGAAAGAGGGGATGAACTGCAGACTCTGCGCTTGAGATCTTCAAACAAGCATCAGCGT
TTTCCAGGGCTTCCAGAGGTCTGTGCGACTAGCCCCTGTCTATCAAAAGTTATTAGAGAGGATGAAGCAT**TAGC**
TTGAAGCACTACAGGAGGAATGCACCACGGCAGCTCTCCGCCAATTTCTCTCAGATTTCCACAGAGACTGTTTGA
ATGTTTTTCAAAACCAAGTATCACACTTTAATGTACATGGGCCGACCATAATGAGATGTGAGCCTTGTGCATGTG
GGGGAGGAGGGAGAGAGATGTACTTTTTTAAATCATGTTCCCCCTAAACATGGCTGTTAACCCACTGCATGCAGAA
ACTTGGATGTCACTGCCTGACATTCACTTCCAGAGAGGACCTATCCCAAATGTGGAATTGACTGCCTATGCCAAG
TCCCTGGAAAAGGAGCTTCAGTATTGTGGGGCTCATAAAACATGAATCAAGCAATCCAGCCTCATGGGAAGTCCT
GGCACAGTTTTTTGTAAAGCCCTTGACAGCTGGAGAAATGGCATCATTATAAGCTATGAGTTGAAATGTTCTGTC
AAATGTGTCTCACATCTACACGTGGCTTGGAGGCTTTTATGGGGCCCTGTCCAGGTAGAAAAAGAAATGGTATGTA
GAGCTTAGATTTCCCTATTGTGACAGAGCCATGGTGTGTTTGTAAATAATAAAACCAAAGAAACATA

1803/6881
FIGURE 1672

MALFVRLALALALALGPAATLAGPAKSPYQLVLQHSRLRGRQHGPNVCAVQKVIGTNRKYFTNCKQWYQRKICG
KSTVISYECCPGYEKVPGEKGC PAALPLSNLYETLG VVGSTTTQLYTD RTEKL RPEMEGPGSFTTIFAPSNEAWAS
LPAEVLDSLVS NVNIELLNALRYH MVGRRVLTDELKHGMTLTS MYQNSNIQIHHYPNGI VTVNCARLLKADHHAT
NGVVHLIDKVISTITNNIQQII EIEDTFETLRAAVAASGLNTMLEGNGQYTLLAPTNEAF EKIPSETLNRI LGDP
EALRDLLNNHILKSAMCAEAI VAGLSVETLE GTTLEVGCSGDM LTINGKAIISNKDILATNGVIHYIDELLIPDS
AKTLFELAAESDVSTAIDLFRQAGLGNHLSG SERLTLLAPLNSVFKDGT PPIDAHTRNLLRNHI IKDQLASKYLY
HGQTLET LGGKKLRV FVYRNSLCIENS CIAAHDKRGRYGT LFTMDRVLT PPMGTVM DV LKGDNRFSMLVAAIQSA
GLTETLNREGVYTVFAPTNEAFRALPPRERSRL LGDAKELANILKYHIGDEILVSGGIGALVRLKSLQGDKLEVS
LKNNVSVNKEPVAEPDIMATNGVVHVITNVLQPPANRPQERGDELADSALEIFKQASAFSRASQRSVRLAPVYQ
KLLERMKH

1804/6881
FIGURE 1673

TCAGAGTCCGGCTCAGGCTCCGGCTGCGGCTCCAGCCCGCGATGCCCCATTCCGTGACCCTGCGCGGGCCCTTCGC
CCTGGGGCTTCCGCCTGGTGGGCGGGCCGGGACTTCAGCGCGCCCCCTACCATCTCACGGGTCCATGCTGGCAGCA
AGGCTGCATTGGCTGCCCTGTGCCCAGGAGACCTGATCCAGGCCATCAATGGTGAGAGCACAGAGCTCATGACAC
ACCTGGAGGCACAGAACCGCATCAAGGGCTGCCACGATCACCTCACACTGTCTGTGAGCAGGCCTGAGGGCAGGA
GCTGGCCCAGTGCCCCTGATGACAGCAAGGCTCAGGCACACAGGATCCACATCGATCCTGAGATCCAGGACGGCA
GCCAACAACCAGCAGGCGGCCCTCAGGCACCGGGACTGGGCCAGAAGATGGCAGACCAAGCCTGGGATCTCCAT
ATGGACAACCCCCCTCGCTTTCAGTCCCTCACAATGGCAGCAGCGAGGCCACCCTGCCAGCCCAGATGAGCACCC
TGATGTGTCTCCACCCCCCAGCGCTGACCCAGCCAGAGGCCTCCCGCGGAGCCGGGACTGCAGAGTCGACCTGG
GCTCCGAGGTGTACAGGATGCTGCGGGAGCCAGCCGAGCCCGTGGCCGCGGAGCCCAAGCAGTCAGGCTCCTTCC
GCTACTTGCAGGGCATGCTAGAGGCCGCGCAGGGCGGGGATTGGCCCCGGGCCCTGGCGGGCCCCCGGAACCTCAAGC
CCACGGCCAGCAAGCTGGGCGCTCCGCTGAGCGGCCTGCAGGGGCTGCCCGAGTGCACGCGCTGCGGCCACGGCA
TCGTGGGCACCATCGTCAAGGCACGGGACAAGCTCTACCATCCCGAGTGCTTCATGTGCAGTGACTGCGGCCCTGA
ACCTCAAGCAGCGTGGTTACTTCTTTCTGGACGAGCGGCTCTACTGTGAGAGCCACGCCAAGGCGCGCGTGAAGC
CGCCCGAGGGCTACGACGTGGTGGCGGTGTACCCCAATGCCAAGGTGGAACCTCGTCTTGAGCTGGGACCCCTGCTCC
CACGCCTGCTTCTTAAGGTCCCTGCTCGGCCGGTGTAATATGTTTCACCCTGTCCCTCTAATAAAGCTCCTCTG
CTCCACCTTGAACCTGTACCTGGCCTGCCACCCTCCTGCGCAGGCCATGCATGGCTCCCGAGTACAGTAGTATC
TGCTTAGGTGCCAGGCATGTCTAGGCTCTGGGTGCAGTAGTGAGCAGGACGGGTACCATGCTGCCCTGAAGGGG
CCACAGCCTGGGTGGAAGGCAGACCTGAATCACAACGGGCCAGCTCTAGTAATACGAAGGTGAGGTCTGGGATGC
TGCGTGCGGCGCGACGACAGGAGGTATGACCTGGGTGGGGTCAGGGAAAGTCTTAGCTGAGAACTAAGAGATGAG
GGAGGCACAACTCTGCACGGGGGAACTGTGTGTGCAAAGGTGAGCTGGGGGCGAGAAAGGCCTCTGTGGCCGTC
ATCGGCACTAGCGGGTTGGGGGTGGTGGTGGGGTGCTGGCAGCCTCAGGAGCGATCGCTCCCCTGGAGAGGGTGA
TTGAGTGTGGAGATCACCGGGGCCGCGCGGGCCGTCTGCACTTCTGTTCCAGGTTTTTCTGGCATTCTCTGTTT
CAGGTTTCTTCCACCCACGAGCACTTTATTCTCCTCCGAGACCCCTTTTCTTCCCCTTCCCTCTCTCCACCAGG
GGGCGCGCTTAAATTTCCAGACAGAGACCAGAAGGAAGGTTTAGAAAAGAAAAGAACACTTGCCAGGGCAGCTTT
GCCCTCCAAGAGGCTCCCTCCTGTCTCTAAGTCAATTCCACCCCTCCTCGAAGTCCCGGCTTCCACCCCTCTCCT
CAGAGTCCCGGCGTTTACCTCGTGGTGTGTTTGCCCTTGGGCCTTTCATGCCCCGGCTGCACACATCGTCTGTGAA
TTGTGGCTGTTCACTCCCGAGGATGTGTCCTAGACTCCGGGTCGCGTGGATCTACCCTCTAGTTTACTTGCTCGG
GAGAAGAACTGACTCGTTTTATTTAGTGCCTATTTAGCGAGCCCAGAGTAACGTACATTTGTGCTGTTTTCAAT
TTTGTGCTATCGCAAATCACAAAAAACTGTTATCAATTCACATTCATCATCAGCACGAGACCCATTTCTTGTG
CTCCTGCCAGCTCAGGATATTATGTTTCTTTTTTTCATTTTGGCAGTCTGTTAAGTAAATGTCATATGCGTTTG
TTTTAA

1805/6881
FIGURE 1674

MPHSVTLRGPSPWGFRVLVGGGRDFSAPLTISR VHAGSKAALAALCPGDLIQAINGESTELMTHLEAQNRIKGCHDH
LTLSVSRPEGRSWPSAPDDSKAQAHRIHIDPEIQDGSPTTSRRPSGTGTGPEdGRPSLGSPYGQPPRFPVPHNGS
SEATLPAQMSTLHVSPPPSADPARGLP RSRDCRVDLGSEVYRMLREPAEPVAAEPKQSGSFRYLQGMLEAGEGGD
WFGPGGPRNLKPTASKLGAPLSGLQGLPECTRCGHGIVGTIVKARDKLYHPECFCMCSDCGLNLKQRGYFFLDERL
YCESHAKARVKPPEGYDVVAVYPNAKVELV

1806/6881
FIGURE 1675

CGAGCCCCCGCCGAACCGAGGCCACCCGGAGCCGTGCCCAGTCCACGCCGGCCGTGCCCGGCGGCCTTAAGAACC
CGGCAACCTCTGCCTTCTTCCCTCTTCCACTCGGAGTCGCGCTCCGCGCGCCCTCACTGCAGCCCCCTGCGTCGCC
GGGACCCCTCGCGCGCGACCGCCGAATCGCTCCTGCAGCAGAGCCAACATGCCATCACTCGGATGCGCATGAGAC
CCTGGCTAGAGATGCAGATTAATTCCAACCAAATCCCGGGGCTCATCTGGATTAATAAAGAGGAGATGATCTTCC
AGATCCCATGGAAGCATGCTGCCAAGCATGGCTGGGACATCAACAAGGATGCCTGTTTGTTCGGAGCTGGGCCA
TTCACACAGGCCGATACAAAGCAGGGGAAAAGGAGCCAGATCCCAAGACGTGGAAGGCCAACTTTCGCTGTGCCA
TGAATCCCTGCCAGATATCGAGGAGGTGAAAGACCAGAGCAGGAACAAGGGCAGCTCAGCTGTGCGAGTGTAAC
GGATGCTTCCACCTCTCACCAAGAACCAGAGAAAAGAAAAGTTCGAAGTCCAGCCGAGATGCTAAGAGCAAGG
CCAAGAGGAAGTCATGTGGGGATTCCAGCCCTGATACCTTCTCTGATGGACTCAGCAGCTCCACTCTGCCTGATG
ACCACAGCAGCTACACAGTTCCAGGCTACATGCAGGACTTGGAGGTGGAGCAGGCCCTGACTCCAGCACTGTTCGC
CATGTGCTGTCAGCAGCACTCTCCCGACTGGCACATCCCAGTGGAAGTTGTGCCGGACAGCACCAGTGATCTGT
ACAATTTCCAGGTGTCACCCATGCCCTCCACCTCTGAAGCTACAACAGATGAGGATGAGGAAGGGAAATTACCTG
AGGACATCATGAAGCTCTTGGAGCAGTCGGAGTGGCAGCCAACAACTGGATGGGAAGGGGTACCTACTCAATG
AACCTGGAGTCCAGCCCACCTCTGTCTATGGAGACTTTAGCTGTAAGGAGGAGCCAGAAAATTGACAGCCCAGGGG
GGGATATTGGGCTGAGTCTACAGCGTGTCTTCACAGATCTGAAGAACATGGATGCCACCTGGCTGGACAGCCTGC
TGACCCCACTCCGGTTGCCCTCCATCCAGGCCATTCCCTGTGCACCGTAGCAGGGCCCCCTGGGCCCCCTCTTATTC
CTCTAGGCAAGCAGGACCTGGCATCATGGTGGATATGGTGCAGAGAAGCTGGACTTCTGTGGGGCCCCCTCAACAGC
CAAGTGTGACCCCACTGCCAAGTGGGGATGGGGCCTCCCTCCTTGGGTTCATTGACCTCTCAGGGCCTGGCAGGCC
AGTGTCTGGGTTTTTCTTGTGGTGTAAGCTGGCCCTGCCTCCTGGGAAGATGAGGTTCTGAGACCAGTGATCA
GGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTTCTCTGAGCCCAGCTGCCTGGAGAGGGTCTCGCTGTC
ACTGGCTGGCTCCTAGGGGAACAGACCAGTGACCCCAAGAAAGCATAACACCAATCCCAGGGCTGGCTCTGCACT
AAGAGAAAATTGCACTAAATGAATCTCGTTCCCAAGAACTACCCCTTTTCAGCTGAGCCCTGGGGACTGTTCC
AAAGCCAGTGAAATGTGAAGGAAAGTGGGGTCTTCGGGGCGATGCTCCCTCAGCCTCAGAGGAGCTCTACCCTG
CTCCCTGCTTTGGCTGAGGGGCTTGGGAAAAAACTTGGCACTTTTTCTGTGTGGATCTTGCCACATTTCTGATCA
GAGGTGTACACTAACATTTCCCCCGAGCTCTTGGCCTTTGCATTTATTTATACAGTGCCTTGCTCGGCGCCCACC
ACCCCTCAAGCCCCAGCAGCCCTCAACAGGCCCAGGGAGGGAAGTGTGAGCGCCTTGGTATGACTTAAAATTGG
AAATGTATCTAACCATTAAAGTCATGTGTGAACACATAAGGACGTGTGTAAATATGTACATTTGTCTTTTTTATAA
AAAGTAAATTGTT

1807/6881
FIGURE 1676

MPITRMRMRPWLEMQINSNQIPGLIWINKEEMIFQIPWKHAAKHGWDINKDACLFERSWAIHTGRYKAGEKEPDPK
TWKANFRFCAMNSLPDIEEVKDQSRNKGSSAVRVYRMLPPLTKNQRKERKSKSSRDAKSKAKRKSCGDSSPDTFSD
GLSSSTLPDDHSSYTVPGYMQDLEVEQALTPALSPCAVSSTLPDWHIPVEVVPDSTSDLYNFQVSPMPSTSEATT
DEDEEGKLPEDIMKLLEQSEWQPTNVDGKGYLLNEPGVQPTSVYGDFSCKEEPEIDSPGGDIGLSLQRVFTDLKN
MDATWLDSLTPVRLPSIQAIPCAP

1808/6881
FIGURE 1677

GCCGCTCGCTCGGCTCCGCTCCCTGGCTCGGCTCCCTGCCTCCGCGTCGCAGCCCCCGCGTAGCCGCCTCCGAG
CCCCGCCGCACATCCTCTGAGAAGATGGCTGTGCCACCCACGTATGCCGATCTTGGCAAATCTGCCAGGGATGTC
TTCACCAAGGGCTATGGATTGGCTTAATAAAGCTTGATTGAAAACAAAATCTGAGAATGGATTGGAATTTACA
AGCTCAGGCTCAGCCAACACTGAGACCACCAAAGTGACGGGCAGTCTGGAAACCAAGTACAGATGGACTGAGTAC
GGCCTGACGTTTACAGAGAAATGGAATACCGACAATACACTAGGCACCGAGATTACTGTGGAAGATCAGCTTGCA
CGTGGACTGAAGCTGACCTTCGATTATCCTTCTCACCTAACACTGGGAAAAAAAAATGCTAAAATCAAGACAGGG
TACAAGCGGGAGCACATTAACCTGGGCTGCGACATGGATTTCGACATTGCTGGGCCTTCCATCCGGGGTGCTCTG
GTGCTAGGTTACGAGGGCTGGCTGGCCGGCTACCAGATGAATTTTGAGACTGCAAAATCCCGAGTGACCCAGAGC
AACTTTGCAGTTGGCTACAAGACTGATGAATTCAGCTTCACACTAATGTGAATGACGGGACAGAGTTTGGCGGC
TCCATTTACCAGAAAGTGAACAAGAAGTTGGAGACCGCTGTCAATCTTGCCTGGACAGCAGGAAACAGTAACACG
CGCTTCGGAATAGCAGCCAAGTATCAGATTGACCCTGACGCCTGCTTCTCGGCTAAAGTGAACAACCTCCAGCCTG
ATAGGTTTAGGATACACTCAGACTCTAAAGCCAGGTATTAAACTGACACTGTCAGCTCTTCTGGATGGCAAGAAC
GTCAATGCTGGTGGCCACAAGCTTGGTCTAGGACTGGAATTTCAAGCATAAATGAATACTGTACAATTGTTAAT
TTTAAACTATTTTGCAGCATAGCTACCTTCAGAAATTTAGTGTATCTTTTAATGTTGTATGTCTGGGATGCAAGTA
TTGCTAAATATGTTAGCCCTCCAGGTTAAAGTTGATTCAGCTTTAAGATGTTACCCTTCCAGAGGTACAGAAGAA
ACCTATTTCCAAAAAAGGTCCTTTTCAGTGGTAGACTCGGGGAGAACTTGGTGGCCCCCTTTGAGATGCCAGGTTTC
TTTTTTATCTAGAAATGGCTGCAAGTGGAAGCGGATAATATGTAGGCACTTTGTAAATTCATATTGAGTAAATGA
ATGAAATTGTGATTTCTGAGAATCGAACCTTGGTTCCCTAACCCTAATTGATGAGAGGCTCGCTGCTTGATGGT
GTGTACAAACTCACCTGAATGGGACTTTTTTTAGACAGATCTTCATGACCTGTTCCACCCCAGTTCATCATCATC
TCTTTTACACCAAAAAGGTCTGCAGGGTGTGGTAACTGTTTCTTTTGTGCCATTTTGGGGTGGAGAAGGTGGATGT
GATGAAGCCAATAATTCAGGACTTATTCCTTCTTGTGTTGTGTTTTTTTTTGGCCCTTGACCAGAGTATGAAAT
AGCTTCCAGGAGCTCCAGCTATAAGCTTGAAGTGTCTGTGTGATTGTAATCACATGGTGACAACACTCAGAATC
TAAATTGGACTTCTGTTGTATTCTCACCCTCAATTTGTTTTTTAGCAGTTAATGGGTACATTTTAGAGTCTTC
CATTTTGTGGAATTAGATCCTCCCTTCAATGCTGTAATTAACAACACTTAAAAAAGTTGAATAAAATATTGA
AACCTC

1809/6881
FIGURE 1678

MAVPPTYADLGKSARDVFTKGYGFGLIKLDLKTSENGLEFTSSGSANTETTKVTGSLETKYRWTEYGLTFTEKW
NTDNTLGTEITVEDQLARGLKLTFDSSFSPNTGKKNAKIKTGYKREHINLGCDMDFDIAGPSIRGALVLGYEGWL
AGYQMNFFETAKSRVTQSNFAVGKTDDEFQLHTNVNDGTEFGGSIIYQVNNKKLETAVNLAWTAGNSNTRFGIAAKY
QIDPDACFSKVNNSSLIGLGYTQTLKPGIKLTLALLDGKNVNAGGHKLGLGLEFQA

1810/6881
FIGURE 1679

CTCTTCCTTCGCTAACGCCTCCCGGCTCTCGTCAGCCTCCCGCCGGCCGTCTCCTTAACACCGAACACCATGCCT
TCAATTAAGTTGCAGAGTTCTGATGGAGAGATATTTGAAGTTGATGTGGAAATTGCCAAACAATCTGTGACTATT
AAGACCATGTTGGAAGATTTGGGAATGGATGATGAAGGAGATGATGACCCAGTTCCTCTACCAAATGTGAATGCA
GCAATATTAAAAAAGGTCATTCAGTGGTGCACCCACCACAAGGATGACCCTCCTCCTCCTGAAGATGATGAGAAC
AAAGAAAAGCGAACAGATGATATCCCTGTTTGGGACCAAGAATTCCTGAAAGTTGACCAAGGAACACTTTTTGAA
CTCATTCTGGCTGCAAACTACTTAGACATCAAAGGTTTGCTTGATGTTACATGCAAGACTGTTGCCAATATGATC
AAGGGGAAAACCTCTGAGGAGATTCGCAAGACCTTCAATATCAAAAATGACTTTACTGAAGAGGAGGAAGCCCAG
GTACGCAAAGAGAACCAGTGGTGTGAAGAGAAGTGAAATGTTGTGCCTGACACTGTAACACTGTAAGGAT

1811/6881
FIGURE 1680

MPSIQLQSFIDGEIFAVDVEIAKQSVTIKTTLEDLGMDDEGDDPVPLPNVNAAVLKKVIQWCTHHKDDPPPPEDDE
NKEKQTDDIPVWDQEFLLKVAQGTLFELIRAANYLDIKGLLDVTCKTVANMIKGKTPEEIRKTFNIKNDFTEEEEAA
QVRKENQWCEEK

1812/6881
FIGURE 1681A

CGCTGGGATGGCCGCCACAGCTGTAGGTGCTGCTAGTGTTTTAGCGCTGGTCTTTGCCGGGCGTTGAGGGCAGCTC
AGCCTCCTTGTTTTGTCCGGTTTCGCCTGTGCGTGTTACTCAAGGGCACCAGTATTCCCGCGGTCGGCAGC**ATGGGT**
CGGGAGTCACGCCACTATCGAAAACGATCGGCATCCCGGGGTCGCTCTGGAAGTCGGTCTAGAAGTCGCTCACCC
TCAGACAAAAGAAGTAAACGTGGAGATGACAGACGGTCTAGAAGTAGAGATAGAGATAGGAGGAGAGAGAGGTCT
CGTAGCAGGGATAAAAGAAGATCTCGGTCAAGGGACAGGAAGCGTCTGAGACGTTCCAGAAGTAGAGAGAGAGAC
AGAAGCCGAGAGCGAAGAAGATCTCGAAGTAGAGACAGGAGACGCTCAAGGAGTAGAAGCCGGGGCCGGCGATCC
CGATCCTCCAGTCTTGAAATAAAAGCAAGAAAAGTGAAGTAGATCTAGGTCCAAAGAGAAAAGTATGGTGGG
GAAAGTTCTAAAGAGAAGAAAAAGACAAAGATGACAAGGAGGATGAAAAAGAAAAGATGCTGGCACTTTGAC
CAGAATAAGCTGGAAGAAGAAATGAGAAAGCGAAAAGAAAGAGTAGAAAAATGGCGAGAAGAGCAACGTAAAAAG
GCTATGGAAACATAGGAGAACTGAAAAAGGAAATCGAAGAGATGAAACAAGGGAAAAAGTGGAGTTTAGAGGAC
GATGATGATGACGAAGATGATCCTGCAGAAGCTGAAAAGGAGGGAAATGAAATGGAGGGTGAGGAGTTAGATCCA
TTAGATGCTTACATGGAAGAAGTGAAGAGGGAAGTAAAAAATTTAACATGAGAAGTGTAAGGTGGTGGGGGA
AATGAAAAGAAGTCTGGGCCAACGGTCACAAAAGTTGTCACTGTTGTGACAACCAAAAAAGCAGTTGTGGATTCT
GATAAGAAGAAAGGTGAGCTGATGGAGAATGACCAGGATGCCATGGAGTATTCTTCAGAGGAGGAAGAAGTTGAT
CTTCAGACAGCCCTTACAGGGTATCAAACAAAACAGCGAAAGCTTCTAGAACCAGTTGATCATGGAAAAATTGAG
TATGAGCCATTTAGGAAAACTTCTATGTTGAAGTTCAGAAGTAGCAAAAATGTCTCAAGAAGAGGTAAATGTG
TTTCGATTGGAAATGGAGGGCATTACAGTTAAAGGAAAAGGTTGCCCAAACCAATTAATCCTGGGTCCAGTGT
GGAATTTCCATGAAGATCTTAAATTCCCTCAAGAAGCATGGCTATGAAAAGCCACGCCCATCCAAACCAAGCT
ATTCTGCTATAATGTCTGGACGAGATTTGATTGGCATTGCCAAAACAGGAAGTGGAAGACCATTGCTTTTCTG
TTGCCCATGTTTAGACACATCATGGATCAGAGGTCATTAGAGGAAGGAGAGGGGCCAATAGCTGTCATCATGACT
CCAACTCGAGAAGCTGGCTTTACAGATTACTAAAGAGTGTAAGAAGTTTTCCAAGACTTTGGGACTTAGAGTGGTC
TGTGTTTACGGAGGAACAGGAATCAGTGAGCAGATTGCTGAGCTGAAAAGAGGTGCTGAAATTATTGTTTGCACA
CCTGGTCGAATGATTGACATGTTAGCCGCTAACAGTGGTCGGGTACAAAATCTTCGAAGAGTGACATATGTTGTT
TTAGATGAAGCAGACAGAATGTTTGACATGGGTTTTGAACCCAGGTCATGCGCATCGTGATAATGTTTCGTCT
GATCGACAGACGGTTATGTTTTACGCTACTTTCCCGAGAGCTATGGAGGCTTTGGCTCGCAGGATCCTCAGTAAA
CCTATTGAAGTACAAGTTGGAGGCAGGAGTGTGGTTTTGCTCAGATGTGGAGCAACAAGTGATTGTGATTGAAGAA
GAAAAGAAATTTGAAGTTACTTGAGCTTCTAGGCCATTATCAAGAGTCAGGATCTGTCATTATATTTGTGGAT
AAGCAGGAACATGCTGATGGTCTTCTTAAGGATTTAATGAGAGCATCTTATCCTTGCATGTCTCTTCATGGAGGC
ATTGATCAATATGACAGAGATAGCATCATAAATGACTTTAAGAATGGGACCTGCAAACTTCTTGTGGCTACCTCT
GTTGCTGCCCGAGGTCTAGATGTGAAACATCTGATTCTTGTAGTAAATTATAGCTGCCCCAACCATTTAGAGGAT
TATGTACACAGAGCAGGGCGGACTGGAAGAGCAGGAACAAGGGTTATGCTTATACTTTTATCACAGAGGATCAA
GCTCGCTATGCTGGTGACATAATTAAAGCTCTTGAATTGTCAGGGACTGCAGTACCTCCTGATTTAGAGAACTG
TGGAGTGATTTCAAAGATCAGCAGAAAGCTGAGGGGAAAATAATTAAAAAGAGTAGTGGGTCTCTGGTAAGGGA
TTCAAGTTTGATGAAACAGAACAAGCTTTGGCTAATGAGAGGAAGAAGTTACAAAAAGCAGCTCTTGGTCTACAA
GATTCAGATGATGAGGATGCTGCAGTTGATATTGATGAGCAAATTGAAAGCATGTTTAATTCAAAGAAGAGAGTA
AAGGATATGGCTGCTCCTGGAACATCAAGTGTTCCCTGCTCCAAGTGCAGGAAATGCTGAGAAATTAGAAATTGCT
AAGAGATTGGCTCTTAGAATCAATGCCCAGAAGAATTTGGGCATCGAGTCTCAGGTAGATGTGATGCAGCAGGCC
ACCAATGCAATTCTTAGGGGTGGCACCATTCTGGCTCCCACTGTTTCTGCAAAAACCATTTGCAGAACAACCTTGCT
GAAAAGATCAATGCCAAGCTCAATTATGTGCCGTTAGAGAAACAAGAAGAAGAGAGACAGGATGGTGGACAGAAT
GAATCTTTTAAAGAGATATGAAGAAGAATTAGAGATCAATGACTTCCCACAGACTGCTAGGTGGAAAGTTACCTCT
AAGGAAGCTCTGCAGAGAATCAGTGAATACTCTGAAGCCGAATTACAATCAGAGGAACCTACTTCCCTCCTGGC
AAAGAACCCAAGGAAGGCGAGCGGAAGATTTACTTGGCAATTGAAAGTGCCAAATGAAGTGGCTGTGCAGAAAGCA
AAGGCAGAAATCACCAGGCTCATAAAAGAAGAGCTGATCCGGCTGCAAAATTCATACCAACCAACAAATAAAGGA
AGATACAAAGTCTTATAGACATCCGGAAAAAAGATTTTTACCTGTGCTGGTCTATGATGTATGTGGCAGTTGCTG
TCTGCAGTTTACAATGTATTGTAATGAAGATTTTTTAAATTCTATCTTGCTGATTTTTTTTTTAAATATAAGAAAC
TGGTACTTGGTAAAGAAATCTGTCCGTAAGTACCCCAACAATCAGTCAAATATATTTAAAGCCAGCTGTTTTTC
AGAGTATGATGTCCTTTAATGTAAACTCAAATATCAATATTTTAAATGTCCGATAATATTCTAGAGGTTTAAAA
AATGGAAATATTTGAACTTTCTATTGAAGACAATAAAGTACACAAGTCGTTAAGGGGCTATTCACTTTATCCTGT

1813/6881
FIGURE 1681B

ACTTTCAATGAAATTGTGATCATTTCTAAGAAAAGGTAAAATTCATATCATATTTTGTGTCCCCACCTTGATG
TTACATGACTCTGGAACAATATGAACTGGATTTAAGAATGTTATAATAGAAGTCTTACAAAATGG

1814/6881
FIGURE 1682

MGRESRHYRKRSASRGRSGSRSRSRSPSDKRSKRGDDRRSRSRDRDRRRERSRSRDKRRSRSRDRKRLRRSRRE
RDRSRERRRRSRSRDRRRSRSRSRGRRSRSSSPGNKSKKTENRSRSKEKTDGGESSKEKKDKDDKEDEKEKDAGN
FDQNKLEEEEMRKRKERVEKWREEQRKKAMENIGELKKEIEEMKQGKKWSLEDDDDDEDDPAEAEKEGNEMEGEEL
DPLDAYMEEVKEEVKKFNMRSVKGGGGNEKKS GPTVTKVVTVVTTKAVVDSKDKKGELMENDQDAMEYSSEEEE
VDLQTALTGYQTKQRKLLPVDHGKIEYEPFRKNFYVEVPELAKMSQEEVNVFRLEMEGITVKGKGC PKPIKSWV
QCGISMKILNSLKKHGYEKPTPIQTQAIPAIMSGRDLIGIAKTGSGKTIAFLLPMFRHIMDQRSLEE GEGPIAVI
MTPTRELA LQITKECKKFSKTLGLRVVCVYGGTGISEQIAELKRGAEIIVCTPGRMIDMLAANSGRVTNLRRVTY
VVLDEADRMFDMGFEPQVMRIVDNVRPDRQTVMF SATFPRAMEALARRILSKPIEVQVGGRSVVCSDVEQQVIVI
EEEKKFLKLELLGHYQESGSV IIFVDKQEHADGLLKDLMRASYPCMSLHGGIDQYDRDSIINDFKNGTCKLLVA
TSVAARGLDVKHLILVVNYSCPNHYEDYVHRAGRTGRAGNKGYAYTFITEDQARYAGDI IKALELSGTAVPPDLE
KLWSDFKDQQAEGKI IKKSSGFSGKGFKFDETEQALANERKKLQKAALGLQDSDDEDA AVDIDEQIESMFNSKK
RVKDMAAPGTSSVPAPTAGNAEKLEIAKRLALRINAQKNLGIESQVDVMQQATNAILRGGITLAPT VSAKTIAEQ
LAEKINAKLNYVPLEKQEEERQDGGQNESFKRYEEELEINDFPQTARWKVTSKEALQRISEYSEAAITIRGT YFP
PGKEPKEGERKIYLAIESANELAVQKAKAEITRLIKEELIRLQNSYQPTNKG RYKVL

1815/6881
FIGURE 1683A

GCTGCGGCTCCGCTCTCGTCGCAACGAGATCTTTTCGAGATCTTCTCCGCCCCCGCTACCGGCGCCTCCTCTGCGG
CCACTGAGCCGGAGCCGGCCTGAGCAGCGCTCTCGGTTGCAGTACCCACTGGAAGGACTTAGGCGCTCGCGTGGA
CACCGCAAGCCCCTCAGTAGCCTCGGCCCAAGAGGCCTGCTTTCCACTCGCTAGCCCCGCCGGGGTCCGTGTCC
TGTCTCGGTGGCCGGACCCGGGCCCCGAGCCCCGAGCAGTAGCCGGCGCCATGTCGGTGGTGGGCATAGACCTGGGC
TTCCAGAGCTGCTACGTCGCTGTGGCCCCGCGCCGGCGGCATCGAGACTATCGCTAATGAGTATAGCGACCGCTGC
ACGCCGGCTTGCATTTCTTTTGGTCCTAAGAATCGTTCAATTGGAGCAGCAGCTAAAAGCCAGGTAATTTCTAAT
GCAAAGAACACAGTCCAAGGATTTAAAGATTCCATGGCCGAGCATTCTCTGATCCATTTGTGGAGGCAGAAAAA
TCTAACCTTGCATATGATATTGTGCAGTTGCCATACAGGATTAACAGGTATAAAGGTGACATATATGGAGGAAGAG
CGAAATTTTACCACTGAGCAAGTGAAGTGCCTACAGGATTAACAGGTATAAAGGTGACATATATGGAGGAAGAG
AAGCCTGTAGTTGACTGTGTTGTTTCGGTTCCTTGTTTCTATACTGATGCAGAAAGACGATCAGTGATGGATGCA
ACACAGATTGCTGGTCTTAATTGCTTGCGATTAATGAATGAAACCACTGCAGTTGCTCTTGCAATGGAATCTAT
AAGCAGGATCTTCTGCCTTAGAAGAGAAAACCAAGAAATGTAGTTTTTGTAGACATGGGCCACTCTGCTTATCAA
GTTTCTGTATGTGCATTTAATAGAGGAAAACCTGAAAGTTCTGGCCACTGCATTTGACACGACATTGGGAGGTAGA
AAATTTGATGAAGTGTTAGTAAATCACTTCTGTGAAGAATTTGGGAAGAAATACAAGCTAGACATTAAGTCCAAA
ATCCGTGCATTATTACGACTCTCTCAGGAGTGTGAGAACTCAAGAAATTGATGAGTGCAAATGCTTCAGATCTC
CCTTTGAGCATTGAATGTTTTATGAATGATGTTGATGTATCTGGAACCTATGAATAGAGGCCAAATTTCTGGAGATG
TGCAATGATCTCTTAGCTAGAGTGGAGCCACCACCTTCGTAGTGTTTTGGAACAAACCAAGTTAAAGAAAGAAGAT
ATTTATGCAGTGGAGATAGTTGGTGGTGCTACACGAATCCCTGCGGTAAGAGAAAGATCAGCAAATTTTTCGGT
AAAGAACTTAGTACAACATTAAATGCTGATGAAGCTGTCACCTCGAGGCTGTGCATTGCAGTGTGCCATCTTATCG
CCTGCTTTCAAAGTCAGAGAATTTCTATCACTGATGTAGTACCATATCCAATATCTCTGAGATGGAATTTCTCCA
GCTGAAGAAGGGTCAAGTGAAGTCTTTTCCAAAATCATGCTGCTCCTTTCTCTAAAGTTCTTACATTT
TATAGAAAGGAACCTTTCACTCTTGAGGCCTACTACAGCTCTCCTCAGGATTTGCCCTATCCAGATCCTGTCTATA
GCTCAGTTTTCACTTCAGAAAGTCACTCCTCAGTCTGATGGCTCCAGTTCAAAGTGAAAGTCAAAGTTTCAGTA
AATGTCCATGGCATTTCAGTGTGTCCAGTGCATCTTTAGTGGAGGTTTACAAGTCTGAGGAAAATGAGGAGCCA
ATGGAACAGATCAGAATGCAAAGGAGGAAGAGAAGATGCAAGTGGACCAGGAGGAACCACATGTTGAAGAGCAA
CAGCAGCAGACACCAGCAGAAAATAAGGCAGAGTCTGAAGAAATGGAGACCTCTCAAGCTGGATCCAAGGATAAA
AAGATGGACCAACCACCCCAAGCCAAGAGGCAAAAGTGAAGACCAGTACTGTGGACCTGCCAATCGAGAATCAG
CTATTATGGCAGATAGACAGAGAGATGCTCAACTTGTACATTGAAAATGAGGGTAAGATGATCATGCAGGATAAA
CTGGAGAAGGAGCGGAATGATGCTAAGAACGCAGTGGAGGAATATGTGTATGAAATGAGAGACAAGCTTAGTGGT
GAATATGAGAAGTTTGTGAGTGAAGATGATCGTAACAGTTTTACTTTGAACTGGAAGATACTGAAAATTGGTTG
TATGAGGATGGAGAAGACCAGCCAAAGCAAGTTTATGTTGATAAGTTGGCTGAATTAAGAAATCTAGGTCAACCT
ATTAAGATACGTTTCCAGGAATCTGAAGAACGACCAAAATTATTTGAAGAACTAGGGAAACAGATCCAACAGTAT
ATGAAAATAATCAGCTCTTTCAAAAACAAGGAGGACCAGTATGATCATTTGGATGCTGCTGACATGACAAAGGTA
GAAAAAAGCACAAATGAAGCAATGGAGTGGATGAATAACAAGCTAAATCTGCAGAACAAGCAGAGTTTGACCATG
GATCCAGTTGTCAAGTCAAAAAGAGATTGAAGCTAAAATTAAGGAGCTGACAAGTACTTGTAGCCCTATAATTTCA
AAGCCCAAACCCAAAGTGGAACCTCCAAAAGAGGAACAAAAAATGCAGAGCAGAATGGACCAGTGGATGGACAA
GGAGACAACCCAGGCCCCAGGCTGCTGAGCAGGGTACAGACACAGCTGTGCCTTCGGATTACAGACAAGAAGCTT
CCTGAAATGGACATTGATTGATTCCAACACTTGTTTCTATTAAACAGACTATTATAAGCTTTAAGTTGTCAAC
TTTGTCTAAATATCAACTAGCGCAAGTGAATACTGAAGATTTCTTAGTCAGTTTTTAGGGGATTTTCGGGGAGG
GGAAATAGGTAATGTATGGAGCATTTTCACTTCTAAATAGTTAGATACAGAAATTAAGTGCATTGTATCTTTTC
ATAATGGTACTATTTAGAAGCCAGTTAGTCTTACTGAGCTTATGCTTCACTCCTTTATGTTTAACCATGTGTCT
ACAAGAATAAGTTTGTTTTGAAAGTTGAGCTATAGCTACAGCTCTAGCTATCCAGCAGACTTTTCATTATGACT
TACATGGCAGGAGCTCTAATTATGCTTTAAAAATCTGTTGTGGAGATTGCTTTAAATGCTCCCTGCCTGGTGTGG
GGATGGGGTCCCCCTCTTTGTGAGGGCTGGAGCATGGCACGGCATGGATTAAACACGGCAGAGGAACAAAGGTGTG
CTCTGAGCTTCTTCATATTTACCTTCACCTCACCTGTGTTCTCTTCCCTCTCTCCCAATAAAAGGGCTCCCAT
TATAAATGCCATGTACTTCTCTTGGGAAAATAGACCCCTTGCTAGAGTAAGTTGTTAACTGAGGGCTTTAAAC
CTGGAGGCTCTTCTGAAAGTATGTTTCATGAATACCCCAAGCATCAAGGTCTAAATAATTTTCAGAAGATTAGAA
TTGGGTAGATATACTGTTGGATATAGCCATGGTAAATTTAACTGAGGAATTAATCCTTGTTAATTTTGGTGTAA

1816/6881
FIGURE 1683B

AGATTTGTATCCTGGCCTGTTTATTTCAGGTGGGAGATGTTCTGTATAATTTTGAGGTATAGCTTGAACTCCTAGA
ACAAGAGTTAAAAGTTCTTTTTAGCTCATTACAAATCACTTGTGTGTTAAGTGTTAATATCTGTCATGAACCTGC
CAATTTGTACGTGTTAAGCAGCTGACAGATGATGCAAAAAAACTAAGATACACTGGATTGTACTGGATGAGTCT
GAAATTAGTGTTAAAGAAGTGTTGGTGCCTGATGTTATAACAACACCTCATTCTTAAGTGTGTGGCCAATGTCAGG
TATACCAAAGCATTCTCTGACTGCTTTTTGGGGCAGTGTTGACAGGAGTGAGGCATTTTGAAAACCTCCAAGGGA
AGCCTGTGTTTGAGGCCAGAGTTGGTACCTGCTTTAAGAACTGTTACAGGGCTTGTTGGTAATGTTTTGAATCT
TTGTAAAAATTGATATTCTGTATAACAGAGTGCCCTCTCTGTTACTTTTGGCCTATGTTGTTAGAAATAAGATGCT
ATCTTGTCATAGTTAGAATTAAGCGTTTGTCCATCTCTAGATAACATTGAAAAGTTTGAGTGTTACAGGCTCTAAA
GTGCAATGGAGAACAATTGCTTAGGAGGAGGAAGGGGAAAGTATACTTATGTTGGTGTGTAAGCATGCATGGAGG
CCTCGAGGCACCACAACAAGGCCAGGTTCTTAGCACATCCTCTGTTCTCTACCTGTCATGCTTCAAGAGTTCCAG
CTGGCCTGCTGTGAAGCCAGTAGCTATTTTAAAAAGTGCTGGCTGCAGGATTAAGCCAACCCCTTTACAACTGGCCC
AGACCGTAATGGCCATTTCTTCTTAAAAAAAAAAAAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
GGTGTGTGTGTGTGTGTGTGTGGGGAAGGGTGTGGGTGCTGGGATGGGGGTGAATTTCAAGTTGAAACACGATGA
TGTTGGTCTGCTTGCTCTCTGCTTAGACAGGCTTTAAGACCAATTGGATTTTCATGGAGGCCAGGACAGAGAGTGG
TAATTGATGGCTTGTTGTACAGACAAGCATTTATCCAGGTTGCGTTATCCAACTGATTTGTTAAAGCTCCAGGTC
ACGTTCTTACACTAAGAAAATCATTTCAGTAAACATGAGACAAGTTTAGGAAAACTAATAAAATAAACCTGTCTT
AAACTTG

1817/6881
FIGURE 1684

MSVVGIDLGFQSCYVAVARAGGIETIANEYSDRCTPACISFGPKNRSIGAAKSQVISNAKNTVQGFKRFGRAF
SDPFFVEAEKSNLAYDIVQLPTGLTGIVTYMEEERNFTTEQVTAMLLSKLKETAESVLKKPVVDCVVSVPFCFYTD
AERRSVMDATQIAGLNCLRLMNETTAVALAYGIYKQDLPALEEKPRNVFVDMGHSAYQVSVCAFNRGKLKVLAT
AFDTTLGGRKFDEVLVNHFC EEFGKKYKLDIKSKIRALLRLSQECEKLKKLMSANASDLPLSIECFMNDVDVSGT
MNRGKFLEMCNDLLARVEPPLRSVLEQTKLKKEDIYAVEIVGGATRIPAVKEKISKFFGKELSTTLNADEAVTRG
CALQCAILSPAFAKVRFSITDVVPYPISLRWNSPAEEGSSDCEVFSKNHAAPFSKVLTFYRKEPFTLEAYYSSPQ
DLPYPDPAIAQFSVQKVTPQSDGSSSKVKVKVRVNVHGIFSVSSASLVEVHKSEENEEMETDQNAKEEEKMQVD
QEEPHVEEQQQQTPAENKAESEEMETSQAGSKDKKMDQPPQAKKAKVKTSTVDLP IENQLLWQIDREMLNLYIEN
EGKMIMQDKLEKERNDAKNAVEEYVYEMRDKLSGEYEKFSVEDDRNSFTLKLEDTENWLYEDGEDQPKQVYVDKL
AELKNLGQPIKIRFQESEERPKLFEELGKQIQQYMKIISSEFKNKEDQYDHLDAADMTKVEKSTNEAMEWMNNKLN
LQNKQSLTMDPVVKSKEIEAKIKELTSTCSP IISKPKPKVEPPKEEQKNAEQNGPVDGQGDNPGPQAEEQGTDTA
VPSDSDDKKLPEMDID

1818/6881
FIGURE 1685

GACTGTCTACATTAGTAATTCCCAACTTGGGTCCGAAAGTGAACTTTTGCTGAAGCGAAGTAGCTAACCGCTTCC
ATGTGCAAGGCAGGTTCCAGACTTCGGGGTGAGGAGGATTAAGTGAAGGACCCAGGGGAACCGGTGTGCTCACT
GATCCGCCTCCAGGGCCACCGCCATGTCGAGCCGCGGTGGGAAGAAGAAGTCCACCAAGACGTCCAGGTCTGCCA
AAGCAGGAGTCATCTTTCCCGTGGGGCGGATGCTGCGGTACATCAAGAAAGGCCACCCCAAGTACAGGATTGGAG
TGGGGGCACCCGTGTACATGGCCGCCGTCTTGAATACCTGACAGCGGAGATTCTGGAGCTGGCTGGCAATGCAG
CGAGAGACAACAAGAAGGGACGGGTCACACCCCGGCACATCCTGCTGGCTGTGGCCAATGATGAAGAGCTGAATC
AGCTGCTAAAAGGAGTCACCATAGCCAGTGGGGGTGTGTTACCCAACATCCACCCGAGTTGCTAGCGAAGAAGC
GGGGATCCAAAGGAAAGTTGGAAGCCATCATCACACCACCCAGCCAAAAAGGCCAAGTCTCCATCCCAGAAGA
AGCCTGTATCTAAAAAAGCAGGAGGCAAGAAAGGGGGCCCGGAAATCCAAGAAGCAGGGTGAAAGTCAGTAAGGCAG
CCAGCGCCGACAGCACAAACCGAGGGCACACCTGCCGACGGCTTCACAGTCCTCTCCACCAAGAGCCTCTTCTTG
GCCAGAAGCTGAACCTTATTCACAGTGAAATCAGTAATTTAGCCGGCTTTGAGGTGGAGGCCATAATCAATCCTA
CCAATGCTGACATTGACCTTAAAGATGACCTAGGAAACACGCTGGAGAAGAAAGGTGGCAAGGAGTTTGTGGAAG
CTGTCTTGGAAGTCCGAAAAAGAACGGGCCCTTGGAAGTAGCTGGAGCTGCTGTCAGCGCAGGCCATGGCCTGC
CTGCCAAGTTTGTGATCCACTGTAATAGTCCAGTTTGGGGTGCAGACAAGTGTGAAGAAGTCTTGAAAAAGACAG
TGAAAAAGTGTGCTGGCCCTGGCTGATGATAAGAAAGCTGAAATCCATTGCATTTCCATCCATCGGCAGCGGCAGGA
ACGGTTTTTCCAAAGCAGACAGCAGCTCAGCTGATTCTGAAGGCCATCTCCAGTTACTTCGTGTCTACAATGTCTT
CTTCCATCAAAACGGTGTACTTTCGTGCTTTTTGACAGCGAGAGTATAGGCATCTATGTGCAGGAAATGGCCAAGC
TGGACGCCAACTAGGCTGAGCAATGACAGAACCAGCTGCACCATGTACCCACCTTCAGTTTAAAAGAAAAAAA
AATCCCTTCACTCCTACTGGGAGGTGGGACCCCTTCATTTTCAGTTTTGCTCATCTAGGGAAAATAAGGCTTT
GGTTTCCAGTTTAATTGTTTTTGACCTTCTAAATGTTTTTATGTTAGCACTGATAGTTGGCATTACTGTTGTTA
AGCACTGTGTTCCAGACCGTGTCTGACTTAGTGTAACTAGGAGATTTTATAGTTTTATTTAATGAAACCTGA
TTGACGCACAGCAGTGGGGAGAACAGCGTCTTTTACCTGTCACCGAAGCCAGGAAGCCCCGTTTGTAAAGCGTGTG
TTGTGGTGCTTTATTGTACATCCTCCAGTGGCGTTCTTTTTACTCTAATGTTCTTTTGGTTTCCCCCTCAGAAG
AATCATGAATTTGCAACAGACCTAATTTTTGGTTACTTTTTGTCTTATTGATGGATTTGAAAATGAAAGATTTAA
TAAGGCAAAGCAGAATCTGTTGTCCTTAATTATTTGCAATTTGGAATTTGTGTGAGTTGATTTAGTAAATGT
TAAACCGTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

1819/6881
FIGURE 1686

MSSRGGKKKSTKTSRSKAGVIFPVGRMLRYIKKGHPKYRIGVGAPVYMAAVLEYLTAEILELAGNAARDNKKGR
VTPRHILLAVANDEELNQLLKGVTIASGGVLPNIHPELLAKKRGSKGKLEAIIITPPAKKAKSPSQKKPVSKKAG
GKKGARKSKKQGEVSKAASADSTTEGTPADGFTVLSTKSLFLGQKLNLIHSEISNLAGFEVEAIINPTNADIDLK
DDLGNLLEKKGGKEFVEAVLELRKKNGPLEVAGAAVSAGHGLPAKFVIHCNSPVWGADKCEELLEKTVKNCLALA
DDKKLKSIAFP SIGSGRNGFPKQTAAQLILKAISSYFVSTMSSSIKTVYFVLFDS SIGIYVQEMAKLDAN

1820/6881
FIGURE 1687

GGACGAGGGGGGAGCGGAGGTGGCGGGCGGGCGGTAGCGGTGGCCTTGTTGTCTTCCAGTCTCCTCGGCTCGC
CCTTTAGCCGGCACCCTCCCTTCCCTCCCCCTTCCCTCTCTTCCCTTCCCTTCCCTCCCCCTTTTCCCTTC
CCCGTCGGTGAGCGGCGGGGGTGGCTCCAGCAACGGCTGGGCCCAAGCTGTGTAGAGGCCTTAACCAACGATAAC
GGCGGCGACGGCGAAACCTCGGAGCTCGCAGGGCGGGGGCAAGGCCCGGGCCTTGAGAGATGGAGAATTCTCAGTT
GTGTAAGCTGTTTCATCGGCGGCCTCAATGTGCAGACGAGTGAGTCGGGCCTGCGCGGCCACTTTGAGGCCTTTGG
GACTCTGACGGACTGCGTGGTGGTGGTGAATCCCCAGACCAAGCGCTCCCGTTGCTTTGGCTTCGTGACCTACTC
CAATGTGGAGGAGGCGGACGCCGCCATGGCCGCCCTCGCCCCATGCCGTGGACGGCAACACTGTGGAGCTGAAGCG
GGCGGTGTCCCGGGAGGATTGCGCGCGGGCCCGGTGCCACGCCAAGGTTAAGAAGCTCTTTGTGCGAGGCCTTAA
AGGAGACGTGGCTGAGGGCGACCTGATCGAGCACTTCTCGCAGTTTGGCACCGTGGAAGGCCGAGATTATTGC
CGACAAGCAGTCCGGCAAGAAGCGTGGATTGCGCTTCGTGTATTTCCAGAATCACGACGCGGCAGACAAGGCCGC
GGTGGTCAAGTTCCATCCGATTGAGGGCCATCGCGTGGAGGTGAAGAAAGCAGTCCCCAAGGAGGATATCTACTC
CGGTGGGGGTGGAGGCGGCTCCCGATCCTCCCGGGGCGGCCGAGGCGGCCGGGGCGCGGCGGTGGTTCGAGACCA
GAACGGCCTTTCCAAGGGCGGCGGCGGCGGTTACAACAGCTACGGTGGTTACGGCGGCGGCGGAGGCGGCGGCTA
CAATGCCTACGGAGGCGGCGGCGGCGGTTTCGTCTACGGTGGGAGCGACTACGGTAACGGCTTCGGCGGCTTCGG
CAGCTACAGCCAGCATCAGTCTCTCTATGGGCCCATGAAGAGCGGCGGCGGCGGCGGCGGTGGAGGCAGTAGCTG
GGCGGTTCGCAGTAATAGTGGACCTTACAGAGGCGGCTATGGCGGTGGGGGTGGCTATGGAGGCAGTCTCTCTTA
AAGAAAAATTTAAATGCCTGGGAGTGGCTATAGGGGTAGCTCTTTCCAACAGCCCAAGTGGGGTCAACTCCTAA
GCCCCACCCCTCACACACACCGCCTTCCCTGTTTTGCCCCCTGGGGGAGCCACTTCTAAGGCTGCTTACCCCTTGG
GGTGTTCCTCTATTTGCCGTGCCACCTCTCTTGTCTCTCCCTCTGAAGATGGACTCGGCCCCACATACACATTTT
TGTGTTACAGTCATTGATGGACTCTATTTTTTTATTATTACTTGGACCTTGGTCGTTTTTTATACTAGCAAAATGT
CTTGTTTTAATTTGTGTTTTTTGGGGGAGGGAGGGAGTGAACCTTGCTGATTCTGTAGCAAAACCTGGGTGGGG
TTGGGGTGGGGGTAGTTTACTTTGTTGTAAGGACTTGATAACCTGGCTACAGCGTTTTCTATGAAATCTACTTG
GATCCCATGCCTGAAATTTGGAAGCATATGTACACAAATCATTTTTTACGTTTTATTTTAATAAATCATTGTGTT
TGACCGTA

1821/6881
FIGURE 1688

MENSQ LCKLF IGGLNVQTSESGLRGHFEAFGTLTDCVVVVPQTKRSRCFGFVTYSNVEEADAAMAASPHAVDGN
TVELKRAVSREDSARPGAHAKVKKLFVGGLKGDVAEGDLIEHFSQFGTVEKAEIIADKQSGKKRGFGFVYFQNHD
AADKAAVVKFHPIQGHRVEVKKAVPKEDIYSGGGGGGSRSSRGGRGGRGRGGGRDQNGLSKGGGGGYNSYGGYGG
GGGGGYNAYGGGGGGSSYGGSDYGNGFGGFGSYSQHQSSYGPMKSGGGGGGGSSWGGRSNSGPYRGGYGGGGGY
GGSSF

1822/6881
FIGURE 1689

CCGCAGAACTTGGGGAGCCGCCGCCGCGCCATCCGCCGCCGCGAGCCAGCTTCCGCCGCCGCGAGGACCGGCCCTGCC
CCAGCCTCCGCGAGCCGCGGCGCGTCCACGCCCCGCGCGCCAGGGCGAGTCGGGGTCGCCGCTGCACGCTTCT
CAGTGTTCGCCGCGCCCCGCATGTAACCCGGCCAGGCCCGCCGCAACGGTGTCCCTGCAGCTCCAGCCCCGGCT
GCACCCCCCGCCCCGACACCAGCTCTCCAGCCTGCTCGTCCAGGATGGCCGCGGCCAAGGCCGAGATGCAGCTG
ATGTCCCGCTGCAGATCTCTGACCCGTTCCGATCCTTTCCTCACTCGCCACCATGGACAACCTACCCTAAGCTG
GAGGAGATGATGCTGCTGAGCAACGGGGCTCCCCAGTTCCTCGGCGCCGCGGGGGCCCCAGAGGGCAGCGGCAGC
AACAGCAGCAGCAGCAGCAGCGGGGGCGGTGGAGGCGGCGGGGGCGGCAGCAACAGCAGCAGCAGCAGCAGCACC
TTCAACCCTCAGGCGGACACGGGCGAGCAGCCCTACGAGCACCTGACCGCAGAGTCTTTTCCTGACATCTCTCTG
AACACGAGAAGGTGCTGGTGGAGACCAGTTACCCAGCCAAACCACTCGACTGCCCCCATCACCTATACTGGC
CGCTTTTCCTGGAGCCTGCACCCAACAGTGGCAACACCTTGTGGCCCGAGCCCCCTTTCAGCTTGGTCAGTGGC
CTAGTGAGCATGACCAACCCACCGCCTCCTCGTCTCAGCACCATCTCCAGCGGCCTCCTCCGCCTCCGCCTCC
CAGAGCCCACCCCTGAGCTGCGCAGTGCCATCCAACGACAGCAGTCCCATTTACTCAGCGGCACCCACCTTCCCC
ACGCCGAACACTGACATTTTCCCTGAGCCACAAAGCCAGGCCTTCCCGGGCTCGGCAGGGACAGCGTCCAGTAC
CCGCCTCCTGCCTACCCTGCCGCCAAGGGTGGCTTCCAGGTTCCCATGATCCCCGACTACCTGTTTCCACAGCAG
CAGGGGGATCTGGGCCTGGGCACCCCAGACCAGAAGCCCTTCCAGGGCCTGGAGAGCCGCACCCAGCAGCCTTCG
CTAACCCCTCTGTCTACTATTAAGGCCTTTGCCACTCAGTCGGGCTCCCAGGACCTGAAGGCCCTCAATACCAGC
TACCAGTCCCAGCTCATCAAACCCAGCCGCATGCGCAAGTATCCCAACCGGCCAGCAAGACGCCCCCCACGAA
CGCCCTTACGCTTGCCAGTGGAGTCCTGTGATCGCCGCTTCTCCCGCTCCGACGAGCTCACCAGCCACATCCGC
ATCCACACAGGCCAGAAGCCCTTCCAGTCCGCATCTGCATGCGCAACTTCAGCCGACGCGACCACCTCACCACC
CACATCCGCACCCACACAGGCGAAAAGCCCTTCGCCTGCGACATCTGTGGAAGAAAGTTTGCCAGGAGCGATGAA
CGCAAGAGGCATACCAAGATCCACTTGCGGCAGAAGGACAAGAAAGCAGACAAAAGTGTGTGGCCTCTTCGGCC
ACCTCCTCTCTCTCTTCTACCCGTCCCCGGTTGCTACCTCTTACCCGTCCCCGGTTACTACCTCTTATCCATCC
CCGGCCACCACCTCATACCCATCCCTGTGCCACCTCCTTCTCCTCTCCCGGCTCCTCGACCTACCCATCCCT
GTGCACAGTGGCTTCCCTCCCCGTCCGTGGCCACCACGTACTCCTCTGTTCCCCCTGCTTTCGGGCCCAGGTC
AGCAGCTTCCCTTCCCTCAGCTGTACCAACTCCTTCAGCGCCTCCACAGGGCTTTCGGACATGACAGCAACCTTT
TCTCCCAGGACAATTGAAATTTGCTAAAGGGGAAAGGGGAAAGAAAGGGAGAAAAAGAAACACAAGAGA
QTAAAGGACAGGAGGAGGAGATGGCCATAGGAGAGGAGGGTTCTCTTAGGTGAGATGGAGGTTCTCAGAGCCA
AGTCTCCCTCTCTACTGGAGTGAAGGTCTATTGGCCAACAATCCTTTCTGCCCCTTCCCTTCCCCAATTAC
TATTCCTTTGACTTCAGCTGCCTGAAACAGCCATGTCCAAGTTCTTACCTCTATCCAAAGAACTTGATTTGCA
TGGATTTGGATAAATCATTTTCAATATCATCTCCATCATATGCCTGACCCCTTGCTCCCTTCAATGCTAGAAAAT
CGAGTTGGCAAAATGGGGTTTGGGCCCCCTCAGAGCCCTGCCCTGCACCCCTGTACAGTGTCTGTGCCATGGATTT
CGTTTTTCTTGGGGTACTCTTGATGTGAAGATAATTGCATATTCTATTGTATTATTGGAGTTAGGTCCTCACT
TGGGGGAAAAAAAAAAAAAAAAAGCCAAGCAAACCAATGGTGATCCTCTATTTTGTGATGATGCTGTGACAATAAG
TTTGAACCTTTTTTTTTTGAACAGCAGTCCAGTATTCTCAGAGCATGTGTCAGAGTGTGTTCCGTTAACCTTT
TTGTAAATACTGCTTGACCGTACTCTCACATGTGGCAAAATATGGTTTGGTTTTTCTTTTTTTTTTTGAAAGTG
TTTTTTCTTCGTCCTTTTGGTTTAAAAAGTTTCACGTCTTGGTGCCTTTTGTGTGATGCCCTTGCTGATGGCTT
GACATGTGCAATTGTGAGGGACATGCTCACCTTAGCCTTAAGGGGGCAGGGAGTGATGATTGGGGGAGGCTT
TGGGAGCAAAATAAGGAAGAGGGCTGAGCTGAGCTTCGGTTCTCCAGAATGTAAGAAAACAAAATCTAAAACAAA
ATCTGAACCTCTCAAAGTCTATTTTTTAACTGAAAATGTAATTTATAAATATATTAGGAGTTGGAATGTTGT
AGTTACCTACTGAGTAGGCGCGATTTTTGTATGTTATGAACATGCAGTTCATTATTTTGTGGTTCTATTTTACT
TTGTACTTGTGTTTGTCTAAACAAAGTGACTGTTTGGCTTATAAACACATTGAATGCGCTTTATTGCCCATGGGA
TATGTGGTGTATATCTTCCAAAAAATTAACGAAAATAAAGTAGCTGCGATTGGG

1823/6881

FIGURE 1690

MAAAKAEMQLMSPLQISDPFGSFPHSPTMDNYPKLEEMLLSNGAPQFLGAAGAPEGSGSNSSSSSSSGGGGGGGG
GSNSSSSSSTFNPQADTGEQPYEHLTAESFPDISLNNEKVLVETSYPSQTTRLPPITYTGRFSLEPAFNSGNTLW
PEPLFSLVSGLVSMTNPPASSSSAPSPAASSASASQSPPLSCAVPSNDSSPIYSAAPTFTPTNTDIFPEPQSQAF
PGSAGTALQYPPPAYPAAGGFQVPMIPDYLFPPQQGDLGLGTPDQKPFQGLSRTQQPSLTPLSTIKAFATQSG
SQDLKALNTSYQSOLIKPSRMRKYPNRPSKTPPHERPYACPVESCDRRFSRDELTRHIRIHTGQKPFQCRICMR
NFSRSDHLTTHIRHTHTGEKPFACDICGRKFARSDEKRRHTKIHLRQKDKKADKSVVASSATSSLSSYPSPVATSY
PSPVTTSYSPATTSYPSPVPTSFS\$PGSSTYSPVHSGFPPSPSVATTYSSVPPAFPAQVSSFPSSAVTNSFSAS
TGLSDMTATFSPRTIEIC

1824/6881
FIGURE 1691

**ATGGCAAGAAAAGCTGGCAACTTCTATGTACCTGCAGAACCCAAATTGGCGTTTGTTCATCAGGATCAGAGGCATC
AATGGTGTGAGCCCCAAAGCCCTACAAGGCGCTTCCTCCCGGCCCCAGGCCCATACAAGGCGCTTCCTTCCCGGCG
CGGCTGGCTGGCGGCCCGCGGGCTGGGAGCCCGCCGGAGCACAGCACGCCCTGCCGGAGGTCTTTCAGCGGCCC
CAGCCCGGGACCTCCAGCCACACGGGCCTCCGAGCCTCGCCGGCCGCTCTCCCC**TGA****

1825/6881
FIGURE 1692

MARKAGNFYVPAEPKLAFVIRIRGINGVSPKPYKALPPGPRPIQGASFPARLAGGPRAGSPPGAQHALPEVFQRP
QPGTSSHTGLRASPAALP

1826/6881
FIGURE 1693

GGCACGAGGGGAGCGCTTGTTTGTCTGCCTCGTACTCCTCCATTTATCCGCCATGGATAAGTGCCAGCCGAGCTGCA
GCAGCCCCGTCTCGTGGGCGCCGCAGCCTCCCGGGGCCCTACGGCCGCCGCCACCAGGATAGCTGGAATGGCCTT
AGTCATGAGGCTTTTAGACTTGTTTCAAGGCGGGATTATGCATCAGAAGCAATCAAGGGAGCAGTTGTTGGTATT
GATTTGGGTACTACCAACTCCTGCGTGGCAGTTATGGAAGGTAAACGAGCAAAGGTGCTGGAGAATGCCGAAGGT
GCCAGAACCACCCCTTCAGTTGTGGCCTTTACAGCAGATGGTGAGCGACTTGTTGGAATGCCGGCCAAGCGACAG
GCTGTACCAACCCAAACAATACATTTTATGCTACCAAGCGTCTCATTGGCCGGCGATATGATGATCCTGAAGTA
CAGAAAGACATTAAAAATGTTCCCTTTAAAATTGTCCGTGCCTCCAATGGTGATGCCTGGGTTGAGGCTCATGGG
AAATTGTATTCTCCGAGTCAGATTGGAGCATTGTGTTGATGAAGATGAAAGAGACTGCAGAAAATTACTTGGGG
CGCACAGCAAAAAATGCTGTGATCACAGTCCCAGCTTATTTCAATGACTCGCAGAGACAGGCCACTAAAGATGCT
GGCCAGATATCTGGACTGAATGTGCTTCGGGTGATTAATGAGCCCACAGCTGCTGCTCTTGCTATGGTCTAGAC
AAATCAGAAGACAAAGTCATTGCTGTATATGATTTAGGTGGTGAACTTTTGATATTTCTATCCTGGAAATTCAG
AAAGGAGTATTTGAGGTGAAATCCACAAATGGGGATACCTTCTTAGGTGGGAAGACTTTGACCAGGCCCTTGCTA
CGGCACATTGTGAAGGAGTTCAAGAGAGAGACAGGGGTTGATTTGACTAAAGACAACATGGCACTTCAGAGGGTA
CGGGAAGCTGCTGAAAAGGCTAAGTGTGAACTCTCCTCATCTGTGCAGACTGACATCAATTTGCCCTATCTTACA
ATGGATTCTTCTGGACCCAAGCATTGTAATATGAAGTTGACCCGTGCTCAATTTGAAGGGATTGTCACTGATCTA
ATCAGAAGGACTATCGCTCCATGCCAAAAAGCTATGCAAGATGCAGAAGTCAGCAAGAGTGACATAGGAGAAGTG
ATTCTTGTGGGTGGCATGACTAGGATGCCAAAGGTTGAGCAGACTGTACAGGATCTTTTGGCAGAGCCCCAAGT
AAAGCTGTCAATCCTGATGAGGCTGTGGCCATTGGAGCTGCCATTGAGGGAGGTGTGTTGGCCGGCGATGTCACG
GATGTGCTGCTCCTTGATGTCACTCCCCTGTCTCTGGGTATTGAACTCTAGGAGGTGTCTTTACCAAACCTTATT
AATAGGAATACCACTATTCCAACCAAGAAGAGCCAGGTATTCTCTACTGCCGCTGATGGTCAAACGCAAGTGGA
ATTAAAGTGTGTCAGGGTGAAAGAGAGATGGCTGGAGACAACAACTCCTTGACAGTTTACTTTGATTGGAATT
CCACCAGCCCCCTCGTGGAGTTCCCTCAGATTGAAGTTACATTTGACATTGATGCCAATGGGATAGTACATGTTTCT
GCTAAAGATAAAGGCACAGGACGTGAGCAGCAGATTGTAATCCAGTCTTCTGGTGGATTAAGCAAAGATGATATT
GAAAATATGGTTAAAAATGCAGAGAAATATGCTGAAGAAGACCGGCGAAAGAAGGAACGAGTTGAAGCAGTTAAT
ATGGCTGAAGGAATCATTACGACACAGAAACCAAGATGGAAGAATTCAAGGACCAATTACCTGCTGATGAGTGC
AACAAGCTGAAAGAAGAGATTTCCAAAATGAGGGAGCTCCTGGCTAGAAAAGACAGCGAAACAGGAGAAAAATATT
AGACAGGCAGCATCCTCTCTTCAGCAGGCATCATTGAAGCTGTTGAAATGGCATACAAAAAGATGGCATCTGAG
CGAGAAGGCTCTGGAAGTTCTGGCACTGGGGGAACAAAAGGAAGATCAAAGGAGGAAAAACAGTAAATAATAGCAG
AAATTTTGAAGCCAGAAGGACAACATATGAAGCTTAGGAGTGAAGAGACTTCCTGAGCAGAAATGGGCGAACTTC
AGTCTTTTTACTGTGTTTTTGCAGTATTCTATATATAATTTCCCTTAATTTGTAAATTTAGTGACCATTAGCTAGT
GATCATTTAATGGACAGTGATTCTAACAGTATAAAGTTCACAATATTCTATGTCCCTAGCCTGTCATTTTTTCAGC
TGCATGTAAAAGGAGGTAGGATGAATTGATCATTATAAAGATTTAACTATTTTATGCTGAAGTGACCATATTTTC
AAGGGGTGAAACCATCTCGCACACAGCAATGAAGGTAGTCATCCATAGACTTGAAATGAGACCACATATGGGGAT
GAGATCCTTCTAGTTAGCCTAGTACTGCTGTACTGGCCTGTATGTACATGGGGTCCTTCAACTGAGGCCCTTGCAA
GTCAAGCTGGCTGTGCCATGTTTGTAGATGGGGCAGAGGAATCTAGAACAATGGGAACTTAGCTATTTATATTA
GGTACAGCTATTAAAAACAAGGTAGGAATGAGGCTAGACCTTTAACTTCCCTAAGGCATACTTTTCTAGCTACCTT
CTGCCCTGTGTCTGGCACCTACATCCTTGATGATTGTTCTCTTACCCATTCTGGAATTTTTTTTTTTTTTAAATA
AATACAGAAAGCATCTTGAAAAA

1827/6881
FIGURE 1694

MISASRAAAARLVGAAASRGPTAARHQDSWNGLSHEAFRLVSRDYASEAIKGAVVGIDLGTTNSCVAVMEGKRA
KVLNAEGARTTPSVVAFTADGERLVGMPAKRQAVTNPNTFYATKRLIGRRYDDPEVQKDIKNVPFKIVRASNG
DAWVEAHGKLYSPSQIGAFVLMKMKETAENYLGRTAKNAVITVPAYFNDSQRQATKDAGQISGLNVLRVINEPTA
AALAYGLDKSEDKVIAVYDLGGGTDFDISILEIQKGVFEVKSTNGDTFLGGEDFDQALLRHIVKEFKRETGVDLTK
DNMALQRVREAAEKAKCELSSSVQTDINLPYLTMDSSGPKHLNMKLTRAQFEGIVTDLIRRTIAPCQKAMQDAEV
SKSDIGEVILVGGMTRMPKVQQTVDLFGRAPSKAVNPDEAVAIGAIIQGGVLAGDVTDVLLLDVTPLSLGIETL
GGVFTKLINRNTTIPTKKSQVFSTAADGQTQVEIKVCQGEREMAGDNKLLGQFTLIGIPPAPRGVPQIEVTFDID
ANGIVHVSADKGTGREQQIVIQSSGGLSKDDIENMVKNAEKYAEEDRRKKERVEAVNMAEGIIHDTETKMEEFK
DQLPADECNKLKEEISKMRELLARKDSETGENIRQAASSLQQASLKLFEYKMMASEREGSGSSGTGEQKEDQK
EEKQ

1828/6881
FIGURE 1695

GAAATGACTGCTGTCCATGCAGGCAACATAAACTTCAAGTGGGATCCTAAAAGTCTAGAGATCAGGACTCTGGCA
GTTGAGAGACTGTTGGAGCCTCTTGTTACACAGGTTACAACCCTTGTAACACCAATAGTAAAGGGCCCTCTAAT
AAGAAGAGAGGTCGTTCTAAGAAGGCCCATGTTTTGGCTGCATCTGTTGAACAAGCAACTGAGAATTTCTTGGAG
AAGGGGGATAAAAATTGCGAAGGAGAGCCAGTTTCTCAAGGAGGAGCTTGTGGCTGCTGTAGAAGATGTTGAAAA
CAAGGTGATTTGATGAAGGCTGCTGCAGGAGAGTTTCGCAGATGATCCCTGCTCTTCTGTGAAGCGAGGCAACATG
GTTGCGGCGAGCTCGAGCTTTGCTCTCTGCTGTTACCCGGTTGCTGATTTTGGCTGACATGGCAGATGTCTACAAA
TTACTTGTTCAGCTGAAAGTTGTGGAAGATGGTATCTTGAAGTTGAGGAATGCTGGCAATGAACAAGACTTAGGA
ATCCAGTATAAAGCCCTAAAACCTGAAGTGGATAAGCTGAACATTATGGCAGCCAAAAGACAACAGGAATTGAAA
GATGTTGGCCATCGTGATCAGATGGCTGCAGCTAGAGGAATCCTGCAGAAGAACGTTCCGATCCTCTATACTGCA
TCCAGGCATGCCTACAGCACCTGATGTGCGAGCCTATAAGGCCAACAGGGACCTGATATACAAGCAGCTGCAG
CAGGCGGTACAGGCATTTCCAATGCAGCCAGGCCACTGCCTCAGACGATGCCTCACAGCACCAGGGTGGAGGA
GGAGGAGAAGTGGCATATGCACTCAATAACTTTGACAAACAAATCATTGTGGACCCCTTGAGCTTCAGCGAGGAG
CGCTTTAGGCCTTCCCTGGAGGAGCGTCTGGAAAGCATCATTAGTGGGGCTGCCTTGATGGCCGACTCGTCTGTC
ACGCGTGATGACCGTCTGTGAGCGAATTGTGGCAGAGTGTAAATGCTGTCCGCCAGGCCCTGCAGGACCTGCTTTCG
GAGTACATGGGCAATGCTGGACGTAAAGAAAGAAGTGATGCACTCAATTCTGCAATAGATAAAAATGACCAAGAAG
ACCAGGGACTTGCGTAGACAGCTCCGCAAAGCTGTGATGGACCACGTTTCAGATTCTTTCCTGGAAACCAATGTT
CCACTTTTGGTATTGATTGAAGCTGCAAAGAATGGAAATGAGAAAGAAGTTAAGGAGTATGCCCAAGTTTCCGT
GAACATGCCAACAAATTGATTGAGGTTGCCAAGCTTGGCCTGTTCCATCTCAAATAATGAAGAAGGTGTAAAGCTT
GTTGCAATGTCTGCAAGCCAGTTAGAAGCCCTCTGTCTCAGGTTATTAATGCTGCACTGGCTTTAGCAGCAAAA
CCACAGAGTAACTGGCCCAAGAGAACATGGATCTTTTTTAAAGAACAAATGGGAAAAACAAGTCCGTGTTCTCACA
GATGCTGTGATGACATTACTTCCATTGATGACTTCTTGGCTGTCTCAGAGAATCACATTTTGAAGATGTGAAC
AAATGTGTGCTGCTCTCCAAGAGAAGGATGTGGATGGCCTGGACCGCACAGCTGGTGCAATTCGAGGCCGGGCA
GCCCCGGTCAATTCAGTAGTCACCTCAGAGATGGACAACCTATGAGCCAGGAGTCTACACAGAGAAGGTTCTGGAA
GCCACTAAGCTGCTCTCCAACACAGTCATGCCACGTTTTTACTGAGCAAGTAGAAGCAGCCGTGGAAGCCCTCAGC
TCGGACCCTGCCCAGCCCATGGATGAGAAAGAGTTTATCGATGCTTCCCGCCTGGTATATGATGGCATCCGGGAC
ATCAGGAAAGCAGTGCTGATGATAAGGACCCCTGAGGAGTTGGATGACTCTGACTTTGAGACAGAAGATTTTGAT
GTCAGAAGCAGGACGAGCGTCCAGACAGAAGACGATCAGCTGATAGCTGGCCAGAGTGCCCCGGGCGATCATGGCT
CAGCTTCCCCAGGAGCAAAAAGCGAAGATTGCGGAACAGGTGGCCAGCTTCCAGGAAGAAAAGAGCAAGCTGGAT
GCTGAAGTGTCAAATGGGACGACAGTGGCAATGACATCATTGTGCTGGCCAAGCAGATGTGCATGATTATGATG
GAGATGACAGACTTTACCCGAGGTAAAGGACCACTCAAAAATACATCGGATGTCATCAGTGCTGCCAAGAAAATT
GCTGAGGCAGGATCCAGGATGGACAAGCTTGGCCGCACCATTCAGACCATTGCCCCGACTCGGCTTGCAAGCAG
GACCTGCTGGCCTACCTGCAACGCATCGCCCTCTACTGCCACCAGCTGAACATCTGCAGCAAGGTCAAGGCCGAG
GTGCAGAATCTCGGCCGGGAGCTTGTTGTCTCTGGGGTGGACAGCGCCATGTCCCTGATCCAGGCAGCCAAGAAC
TTGATGAATGCTGTGGTGCAGACAGTGAAGGCATCCTACGTGCGCTCTACCAAATACCAAAGTCAAGGGTATG
GCTTCCCTCAACCTTCTGCTGTGTGTCATGGAAGATGAAGGCACCAGAGAAAAAGCCATTGGTGAAGAGAGAGAAA
CAGGATGAGACACAGACCAAGATTAAACGGGCATCTCAGAAGAAGCACGTGAACCCGGTGCAGGCCCTCAGCGAG
TTCAAAGCTATGGACAGCATCTAAGTCTGCCAGGCCGGCCGCCCCCACCCTCGGGGCTCCTGAATATCAGTCA
CTGTTTCGTCACCTCAAATGAATTTGCTAAATACAACACTGATACTAGATTCCACAGGGAAATGGGCAGACTGAACC
AGTCCAGGTGGTGAATTTTCCAAGAACATAGTTTAAAGTTGATTAAAAATGCTTTTAGAATGCAGGAGCCTACTTC
TAGCTGTATTTTTTGTATGCTTAAATAAAAAATAAAATTCATAACCAAAGAGAATCCACATTAGCTTGTAGTA
ATGCTCTGACCAAGCCGAGATGCCCATTTCTTTAGTGATGGCGGCGTTAGGGTTTGAGAGAAGGGAATTTGGCTC
AACTTCAGTTGAGAGGGTGCAGTCCAGACAGCTTGACTGCTTTTTAAATGACCAAAGATGACCTGTGGTAAGCAAC
CTGGGCATCTTAGGAAGCAGTCCCTGGAGAAGGCATGTTCCAGAAAAGGTCTCTGGAGGGACAACTCACTCAGT
AAAACATAATGTATCATGAAGAAAAGTGAATCTCTATGACATGAAATGAAAAATTTTAAATGCATTGTTATAATTAC
TAATGTACGCTGCTGCAGGACATTAATAAAGTTGCTTTTTTAGGCTACAGTGCTCTCGATGCCATAATCAGAACAC
ACTTTTTTCTCTTTCTCCAGCTTCAAATGCAAATTCATCATTGGGCTCACTTCTAATAACTGCAGTGTTTCC
CGCCTTGGGCTTGCAG

1829/6881
FIGURE 1696

MTAVHAGNINFKWDPKSLEIRTLAVERLLEPLVTQVTTLVNTNSKGPSNKKRGRSCKAHVLAASVEQATENFLEK
GDKIATESQFLKEELVAAVEDVRKQGDLMKAAAGEFADDDPCSSVKGNMVRAARALLSAVTRLLILADMADVYL
LVQLKVVEDGILKLRNAGNEQDLGIQYKALKPEVDKLNIMAARKQOELKDVGHRDQMAAARGILQKNVPILYTAS
QACLQHPDVAAYKANRDLIYKQLQQAVTGISNAAQATASDDASQHQGGGGGELAYALNNFDKQIIVDPLSFSEER
FRPSLEERLESIISGAALMADSSCTRDDRERIVAECNAVRQALQDLLSEYMGNAGRKERSDALNSAIDKMTKKT
RDLRRQLRKAVMDHVSDFSLETNVP LLVLIEAAKNGNEKEVKEYAQVFREHANKLIEVANLACSI SNNEEGVKLV
RMSASQLEALCPQVINAALALAAKPQSKLAQENMDLFKEQWEKQVRVLTDAVDDITSIDDFLAVSENHILEDVNK
CVIALQEKDVGDLDRTAGAIRGRAARVIHVVTSEMDNYEPGVYTEKVLEATKLLSNTVMPRFTEQVEAAVEALSS
DPAQPMDENEFIDASRLVYDGI RDIRKAVLMIRTPPEELDDSDFETEDFDVRSRTSVQTEDDQLIAGQSARAIMAQ
LPQEQKAKIAEQVASFQEEKSKLDAEVSKWDDSGNDIIVLAKQMCIMMEMTDFTRGKGPLKNTSDVISAAKKIA
EAGSRMDKLGRTIADHCPDSACKQDLLAYLQRIALYCHQLNICKVKAQVQNLGGELVVSGVDSAMSLIQAAKNL
MNAVVQTVKASYVASTKYQKSQGMASLNLPAVSWKMKAPKPLVKREKQDETQTKIKRASQKKHVNPVQALSEF
KAMD SI

1830/6881
FIGURE 1697

GAATTCGGGCGGGGTTTGTACTATCCTCGGTGCTGTGGTGCAGAGCTAGTTCCTCTCCAGCTCAGCCGCGTAGGT
TTGGACATATTTACTCTTTTCCCCCAGGTTGAATTGACCAAAGCAATGGTGATGGAGAAGCCTAGTCCCCTGCT
GGTCGGGCGGGAATTTGTGAGACAGTATTACACACTGCTGAACCAGGCCCCAGACATGCTGCATAGATTTTATGG
AAAGAACTCTTCTTATGTCCATGGGGGATTGGATTCAAATGGAAAGCCAGCAGATGCAGTCTACGGACAGAAAGA
AATCCACAGGAAAAGTGATGTCACAAAACCTTCACCAACTGCCACACCAAGATTGCCATGTTGATGCTCATGCCAC
GCTAAATGATGGTGTGGTAGTCCAGGTGATGGGGCTTCTCTCTAACAACAACCAGGCTTTGAGGAGATTTCATGCA
AACGTTTGTCCCTTGCTCCTGAGGGGTCTGTTGCAAATAAATTCTATGTTACAATGATATCTTCAGATACCAAGA
TGAGGTCTTTGGTGGGTTTGTCACTGAGCCTCAGGAGGAGTCTGAAGAAGAAGTAGAGGAACCTGAAGAAAGACA
GCAAACACCTGAGGTGGTACCTGATGATTCTGGAACCTTCTATGATCAGGCAGTTGTCAGTAATGACATGGAAGA
ACATTTAGAGGAGCCTGTTGCTGAACCAGAGCCTGATCCTGAACCAGAACCAGAACAAGAACCTGTATCTGAAAT
CCAAGAGGAAAAGCCTGAGCCAGTATTAGAAGAACTGCCCTGAGGATGCTCAGAAGAGTTCTTCTCCAGCACC
TGCAGACATAGCTCAGACAGTACAGGAAGACTTGAGGACATTTTCTTGGGCATCTGTGACCAGTAAGAATCTTCC
ACCCAGTGGAGCTGTTCCAGTTACTGGGATACCACCTCATGTTGTTAAAGTACCAGCTTCACAGCCCCGTCCAGA
GTCTAAGCCTGAATCTCAGATTCCACCACAAAGACCTCAGCGGGATCAAAGAGTGCGAGAACAACGAATAAATAT
TCCTCCCCAAAGGGGACCCAGACCAATCCGTGAGGCTGGTGAGCAAGGTGACATTGAACCCCGAAGAATGGTGAG
ACACCCTGACAGTCACCAACTCTTCATTGGCAACCTGCCTCATGAAGTGGACAAATCAGAGCTTAAAGATTTCTT
TCAAAGTTATGGAAACGTGGTGGAGTTGCGCATTAACAGTGGTGGGAAATTACCCAATTTTGGTTTGTGTGT
TGATGATTCTGAGCCTGTTTCAAGAAAGTCCTTAGCAACAGGCCCATCATGTTTCAAGGTGAGGTCCGTCTGAATGT
CGAAGAGAAGAAGACTCGAGCTGCCAGGGAAGGCGACCGACGAGATAATCGCCTTCGGGGACCTGGAGGCCCTCG
AGGTGGGCTGGGTGGTGGAAATGAGAGGCCCTCCCCGTGGAGGCATGGTGCAGAAACCAGGATTTGGAGTGGGAAG
GGGGCTTGCGCCACGGCAGTAATCTTCATGGATCTTCATGCAGCCATACAAACCCTGGTTCCAACAGAAATGGTGA
ATTTTCGACAGCCTTTGGTATCTTGGAGTATGACCCAGTCTGTTATAAACTGCTTAAGTTTGTATAATTTTACT
TTTTTTGTGTGTTAATGGTGTGTGCTCCCTCTCCCTCTCTCCCTTTCCTGACCTTTAGTCTTTCACTTCCAATT
TTGTGGAATGATATTTTAGGAATAACGGACTTTTACCCGAATTC

1831/6881
FIGURE 1698

MVMEKPSPLLVGREFVRQYYTLLNQAPDMLHRFYGKNSSYVHGGLDSNGKPADAVYGQKEIHRKVMSQNFTNCHT
KIRHVDAHATLNDGVVVQVMGLLSNNNQALRRFMQTFVLAPEGSVANKFYVHNDIFRYQDEVFGGFVTEPQEESE
EEVEEPEERQQTFEVVDDSGTFYDQAVVSNDMEEHLEEFVAEPEPDPEPEPEQEPVSEIQEEKPEPVLEETAPE
DAQSSSPAPADIAQTVQEDLRTFSWASVTSKNLPPSGAVPVTGIPPHVVKVPASQPRPESKPESQIPPQRPQRD
QVRREQRINIPPQRGPRPIREAGEQGDIEPRRMVRHPDSHQLFIGNLPHEVDKSELKDDFFQSYGNVVELRINSGG
KLPNFGFVVFDSEPVQKVLNRPIMFRGEVRLNVEEKKTRAAREGDRRDNRRLRGPGGPRGGLGGGMRGPFRGGM
VQKPGFGVGRGLAPRQ

1832/6881
FIGURE 1699

GAGAGGCGCTGCTGACACCGCCGCCACACCGCCGCCACACCGCCGCTGCCTCAGTCATGCCGAAGCACGAGTTCT
CTGTGGACATGACCTGTGGAGGCTGTGCTGAAGCTGTCTCTCGGGTCCTCAATAAGCTTGGAGGAGTTAAGTATG
ACATTGACCTGCCCCAACAAAGAAGGTCTGCATTGAATCTGAGCACAGCATGGACACTCTGCTTGCAACCCTGAAGA
AAACAGGAAAGACTGTTTCCTACCTTGGCCTTGAGTAGCAGGGGCCTGGTCCCCACAGCCCACAGGATGGACCAA
AGGGGGCAGGATGCTGATCCTCCCGCTGGCTTCCAGACAGACCTGGGACTTGGCAGTCATGCCGGGTGATGGTGT
TCCTGCGGAGACCCTCAGTTGTCCTATTCCTTCCTAGCTTCCCTGCAATAAAATCAAGCTGCTTTTGTGG

1833/6881
FIGURE 1700

GGAGAGCGCGCTCTGCCTGCCGCTGCCTGCCACTGAGGGTTCCCAGCACCATGAGGGCCTGGATCTTCTT
TCTCCTTTGCCTGGCCGGGAGGGCCTTGGCAGCCCCCTCAGCAAGAAGCCCTGCCTGATGAGACAGAGGTGGTGG
AGAAACTGTGGCAGAGGTGACTGAGGTATCTGTGGGAGCTAATCCTGTCCAGGTGGAAGTAGGAGAATTTGATGA
TGGTGCAGAGGAAACCGAAGAGGAGGTGGTGGCGGAAAATCCCTGCCAGAACCACCACTGCAAAACACGGCAAGGT
GTGCGAGCTGGATGAGAACAACACCCCCATGTGCGTGTGCCAGGACCCCCACCAGCTGCCCAGCCCCCATTGGCGA
GTTTGAGAAGGTGTGCAGCAATGACAACAAGACCTTCGACTCTTCTGCCACTTCTTTGCCACAAAGTGCACCCCT
GGAGGGCACCAAGAAGGGCCACAAGCTCCACCTGGACTACATCGGGCCTTGCAAATACATCCCCCCTTGCCTGGA
CTCTGAGCTGACCGAATTCCCCCTGCGCATGCGGGACTGGCTCAAGAACGTCCTGGTCACCCCTGTATGAGAGGGA
TGAGGACAACAACCTTCTGACTGAGAAGCAGAAGCTGCGGGTGAAGAAGATCCATGAGAATGAGAAGCGCCTGGA
GGCAGGAGACCACCCCGTGGAGCTGCTGGCCCCGGGACTTCGAGAAGAACTATAACATGTACATCTTCCCTGTACA
CTGGCAGTTCGGCCAGCTGGACCAGCACCCCATTTGACGGGTACCTCTCCACACCGAGCTGGCTCCACTGCGTGC
TCCCCTCATCCCCATGGAGCATTGCACCACCCGCTTTTTTCGAGACCTGTGACCTGGACAATGACAAGTACATCGC
CCTGGATGAGTGGGCCGGCTGCTTCGGCATCAAGCAGAAGGATATCGACAAGGATCTTGTGATCTAAATCCA
CTTCCACAGTACCGGATTCTCTCTTTAACCCCTCCCTTCGTGTTTTCCCCAATGTTTTAAATGTTTGGATGGTTT
GTTGTTCTGCCCTGGAGACAAGGTGCTAACATAGATTTAAGTGAATACATTAACGGTGCTAAAAATGAAAATTCTA
ACCAAGACATGACATTCTTAGCTGTAACTTAACATTAAGGCCTTTTCCACACGCATTAATAGTCCCATTTTTTC
TCTTGCCATTTGTAGCTTTGCCCATTTGTCTTATTGGCACATGGGTGGACACGGATCTGCTGGGCTCTGCCTTAAA
CACACATTGCAGCTTCAACTTTTCTCTTTAGTGTTCTGTTTGAACTAATACTTACCGAGTCAGACTTTGTGTTT
ATTTCAATTTAGGGTCTTGGCTGCCTGTGGGCTTCCCCAGGTGGCCTGGAGGTGGGCAAAGGGAAGTAACAGACA
CACGATGTTGTCAAGGATGGTTTTTGGGACTAGAGGCTCAGTGGTGGGAGAGATCCCTGCAGAACCACCAACCAG
AACGTGGTTTTGCCTGAGGCTGTAACTGAGAGAAAAGATTCTGGGGCTGTGTTATGAAAAATATAGACATTCTCACAT
AAGCCCAGTTCATCACCATTTTCTCCTTTTACCTTTTCACTGTCAGTTTCTTTTTTACATTAGGCTGTTGGTTCAA
TTTGGGAGCACGGACTGTCAGTTCTCTGGGAAGTGGTCAGCGCATCCTGCAGGGCTTCTCCTCCTCTGTCTTTTG
GAGAACCAAGGGCTCTTCTCAGGGGCTCTAGGGACTGCCAGGCTGTTTTCAGCCAGGAAGGCCAAAATCAAGAGTGA
GATGTAGAAAGTTGTAAAATAGAAAAAGTGGAGTTGGTGAATCGGTTGTTCTTTTCTCACATTGGATGATTGTC
ATAAGGTTTTTAGCATGTTTCTCCTTTTCTTCCACCTCCCTTTTTTCTTCTATTAATCAAGAGAACTTCAAAG
TTAATGGGATGGTCGGATCTCACAGGCTGAGAACTCGTTCACCTCCAAGCATTTTCATGAAAAAGCTGCTTCTTAT
TAATCATACAACTCTCACCATGATGTGAAGAGTTTCAAAATCCTTCAAAATAAAAAGTAATGACTTAGAACT
G

1834/6881
FIGURE 1701

GCCACGTGTCCGGCTCGGAGCCACGGCTGTCTCCCGGTCCGCCCGCGCTGCGGTTGCTGCTGGGCTAACGGG
CTCCGATCCAGCGAGCGCTGCGTCTCGAGTCCCTGCGCCCGTGCGTCCGTCTGCGACCCGAGGCCTCCGCTGCG
CGTGGATTCTGCTGCGAACC GGAGACCATGGCCAAACCAGCACAGGGTGCCAAGTACCGGGGGCTCCATCCATGAC
TTCCCAGGCTTTGACCCCAACCAGGATGCCGAGGCTCTGTACACTGCCATGAAGGGCTTTGGCAGTGACAAGGAG
GCCATACTGGACATAATCACCTCACGGAGCAACAGGCAGAGGCAGGAGGTCTGCCAGAGCTACAAGTCCCTCTAC
GGCAAGGACCTCATTGCTGATTTAAAGTATGAATTGACGGGCAAGTTTGAACGGTTGATTGTGGGCCTGATGAGG
CCACCTGCCTATTGTGATGCCAAAGAAATTAAAGATGCCATCTCGGGCATTGGCACTGATGAGAAGTGCCCTCATT
GAGATCTTGGCTTCCCGGACCAATGAGCAGATGCACCAGCTGGTGGCAGCATACAAAGATGCCTACGAGCGGGAC
CTGGAGGCTGACATCATCGGCGACACCTCTGGCCACTTCCAGAAAGATGCTTGTGGTCTCTGCTCCAGGGAACCAGG
GAGGAGGATGACGTAGTGAGCGAGGACCTGGTACAACAGGATGTCCAGGACCTATACGAGGCAGGGGAAC TGAA
TGGGGAACAGATGAAGCCCAGTTCAATTTACATCTTGGGAAATCGCAGCAAGCAGCATCTTCGGTTGGTGTTTCAT
GAGTATCTGAAGACCACAGGGAAGCCGATTGAAGCCAGCATCCGAGGGGAGCTGTCTGGGGACTTTGAGAAGCTA
ATGCTGGCCGTAGTGAAGTGTATCCGGAGCACCCCGGAATATTTTGTGTAAGGCTCTTCAAGGCTATGAAGGGC
CTGGGGACTCGGGACAACACCCCTGATCCGCATCATGGTCTCCCGTAGTGAGTTGGACATGCTCGACATTCGGGAG
ATCTTCCGGACCAAGTATGAGAAGTCCCTCTACAGCATGATCAAGAATGACACCTCTGGCGAGTACAAGAAGACT
CTGCTGAAGCTGTCTGGGGGAGATGATGATGCTGCTGGCCAGTTCTTCCCGGAGGCAGCGCAGGTGGCCTATCAG
ATGTGGGAACCTTAGTGAGTGGCCCCGAGTAGAGCTGAAGGGAACGTGTGCGCCAGCCAATGACTTCAACCCTGAC
GCAGATGCCAAAGCGCTGCGGAAAGCCATGAAGGGACTCGGGACTGACGAAGACACAATCATCGATATCATCAG
CACCGCAGCAATGTCCAGCGGCAGCAGATCCGGCAGACCTTCAAGTCTCACTTTGGCCGGGACTTAATGACTGAC
CTGAAGTCTGAGATCTCTGGAGACCTGGCAAGGCTGATTCTGGGGCTCATGATGCCACCGGCCATTACGATGCC
AAGCAGTTGAAGAAGGCCATGGAGGGAGCCGGCACAGATGAAAAGGCTCTTATTGAAATCCTGGCCACTCGGACC
AATGCTGAAATCCGGGCCATCAATGAGGCCTATAAGGAGGACTATCACAAAGTCCCTGGAGGATGCTCTGAGCTCA
GACACATCTGGCCACTTCAGGAGGATCCTCATTTCTCTGGCCACGGGGCATCGTGAGGAGGGAGGAGAAAACCTG
GACCAGGCACGGGAAGATGCCCAGGTGGCTGCTGAGATCTTGGAAATAGCAGACACACCTAGTGAGACAAAACCT
TCCTTGGAGACACGTTTCATGACGATCCTGTGTACCCGGAGCTATCCGCACCTCCGGAGAGTCTTCCAGGAGTTC
ATCAAGATGACCAACTATGACGTGGAGCACACCATCAAGAAGGAGATGTCTGGGGATGTCAGGGATGCATTTGTG
GCCATTGTTCAAAGTGTCAAGAACAAGCCTCTCTTCTTTGCCGACAAACTTTACAAATCCATGAAGGGTGCTGGC
ACAGATGAGAAGACTCTGACCAGGATCATGGTATCCCGCAGTGAGATTGACCTGCTCAACATCCGAGGGAATTC
ATTGAGAAATATGACAAGTCTCTCCACCAAGCCATTGAGGGTGACACCTCCGGAGACTTCTGAAGGCCTTGCTG
GCTCTCTGTGGTGGTGAGGACTAGGGCCACAGCTTTGGCGGGCACTTCTGCCAAGAAATGGTTATCAGCACCAGC
CGCCATGGCCAAGCCTGATTGTTCCAGCTCCAGAGACTAAGGAAGGGGCAGGGGTGGGGGGAGGGGTTGGGTTGG
GCTCTTATCTTCAGTGAGCTTAGGAAACGCTCCCACTCCACGGGCCATCGAGGGCCAGCACGGCTGAGCGGC
TGAAAAACCGTAGCCATAGATCCTGTCCACCTCCACTCCCCTCTGACCCTCAGGCTTTCCAGCTTCTCCCCTT
GCTACAGCCTCTGCCCTGGTTTGGGCTATGTCAGATCCAAAAACATCCTGAACCTCTGTCTGT

1835/6881
FIGURE 1702

GTCGACCCACGCGTCCGTGCCAGTCTCCGGGGACTTTCCAGGGGTGGGGCGGCGTGTCCGGGCCCCGGCACTT
CCTCGTCTCTCGGCCCCGGGTGCCCTGCCCCGTCCAGGAGCCCTAGGAGTGCTACGGGGGGCCGGAGCCTTGCCCCG
GGCCGCTGCCCCGTCCCTGGATTTCGGGGCTGGACGCAGCAAGCGGGGCGCTGTGTCCCCAAGCTCCCCGTCTCG
CAGCGGGCACAGGCAGGGGCTGAGCTACCCTCATGGAAAGGGAGAGGACCGTACCGGATCTACGACCCTGGGGGCA
GCGTGCCCTCAGGAGAGGCATCCGCAGCTTTTGAGCGCCTAGTGAAGGAGAATTCCCGGCTGAAGGAAAAATGC
AAGGGATAAAGATGTTAGGGGAGCTTTTGGAAGAGTCCCAGATGGAAGCGACCAGGCTCCGGCAGAAGGCAGAGG
AGCTAGTGAAGGACAACGAGCTGCTCCACCACCTTCTCCCTCCTTGGGCTCCTTCGACCCCCCTGGCTGAGCTCA
CAGGAAAGGACTCAAATGTCACAGCATCTCCACAGCCCCCTGCATGCCCCAGTGACAAGCCAGCACCAGTCCAGA
AGCCTCCATCCAGTGGCACCTCCTCTGAATTTGAAGTGGTCACTCCTGAGGAGCAGAATTCACCAGAGAGCAGCA
GCCATGCCAATGCGATGGCGCTGGGCCCCCTGCCCCGTGAGGACGGCAACCTGATGCTGCACCTGCAGCGCCTGG
AGACCACGCTGAGTGTGTGTGCCGAGGAGCCGGACCACGGCCAGCTCTTACCCACCTGGGCCCGCATGGCCCTGG
AGTTCAACCGACTGGCATCCAAGGTGCACAAGAATGAGCAGCGCACCTCCATTCTGCAGACCCTGTGTGAGCAGC
TTCGGAAGGAGAAACGAGGCTCTGAAGGCCAAGTTGGATAAGGGCCTGGAACAGCGGGATCAGGCTGCCGAGAGGC
TGCGGGAGGAAAAATTTGGAGCTCAAGAAGTTGTTGATGAGCAATGGCAACAAAGAGGGTGCGTCTGGGCGGCCAG
GCTCACCGAAGATGGAAGGGACAGGCAAGAAGGCAGTGGCTGGACAGCAGCAGGCTAGTGTGACGGCAGGTAAGG
TCCCAGAGGTGGTGGCCTTGGGCGCACCCGAGAAGAAGGTGAAGATGCTGGAGCAGCAGCGCAGTGAGCTGCTGG
AAGTGAACAAGCAGTGGGACCAGCATTTCCGGTCCATGAAGCAGCAGTATGAGCAGAAGATCACTGAGCTGCGTC
AGAAGCTGGCTGATTTGCAGAAGCAGGTGACTGACCTGGAGGCCGAGCGGGAGCAGAAGCAGCGTGACTTTGACC
GCAAGCTCCTCCTGGCCAAGTCCAAGATTGAATGGAGGAGACCGACAAGGAGCAGCTGACAGCAGAGGCCAAGG
AGCTGCGCCAAAAGGTCAAGTACCTGCAGGATCAGCTGAGCCCACTCACCCGACAGCGTGAGTACCAGGAAAAGG
AGATCCAGCGGCTCAACAAGGCCCTGGAGGAAGCACTGAGCATCCAAACCCCGCCATCATCTCCACCAACAGCAT
TTGGGAGCCCAGAAGGAGCAGGGGCCCTCCTAAGGAAACAGGAGCTGGTCACGCAGAATGAGTTGCTGAAACAGC
AGGTGAAGATCTTCGAGGAGGACTTCAGAGGGAGCGCAGTGATCGTGAGCGCATGAATGAGGAGAAGGAAGAGC
TGAAGAAGCAAGTGGAAGAAGCTGCAGGCCCAGGTACCCTGTCAAATGCCCAGCTAAAAGCATTCAAAGATGAGG
AGAAGGCAAGAGAAGCCCTCAGACAGCAGAAGAGGAAAGCAAAGGCCCTCAGGAGAGCGTTACCATGTGGAGCCCC
ACCCAGAACATCTCTGCGGGGCCCTACCCCTACGCCTACCCGCCCATGCCAGCCATGGTGCCACACCATGGCTTCG
AGGACTGGTCCCAGATCCGCTACCCCCCTCCCCCATGGCCATGGAGCACCCGCCCCCACTCCCCAACTCGCGCC
TCTTCCATCTGCCGGAATACACCTGGCGTCTACCCTGTGGAGGGGTTGAAATCCAAATCAGAGCTCCCAAGTGA
TGGACCCTCCCACAGCCAGGCCTACAGAACCAGAGTCTCCAAAAAATGACCGTGAGGGGCCTCAGTGAGACCAGA
TTGTGTCAATTTGGCTCCACCTTCATCTTGAGAGCCAGCTGATCTCAATTGCCAAAACTAGAAGCCACTTGAC
GGTGTGGCCAGAGCCTCAGCTGGATGAGAGGCTGAGATGGGTGGCCAGCTTGTAACCACTCCCTGAACTGAGCT
GTTTACAGGACTGGGGAGGCTCCACCCAGAAGGCTTTTCAATTTGTAATCTGCTGGGAGTGACTGGGAAAACTCCT
TCCCTGCTGCTGAGTGAGAGAGGCTCATCCGGCTTTGACCCCCATCCTTGCAAGCCTCCAGGAGCAGCAAT
CCTAAGAGTGGGAGGCAGCCAAGACCCCTTCCCTTCAAAACCTCCCGGAAGTGGTTTCAGGCCCTCTAGTTGCCA
TGACCAATTTGTGTGTGTGTTTAAATTTTGTCTCAAGCTCTGTAGCAGGACCTGCCCCACGCACACCCCTACCCC
TCTGTGAGGAGCTGTGGGAAGTGTGGGTTTGTCTCCAGAACAGAAGAGAATGATGGATATTCTGGCTCTGGGGCC
CTCTCCACCACCACTCACAGTAGCCTTGCTGAAGCCATCACAGATGGGAGAAGGCCATGCCAGCCACGTCCGCCG
AGGGGCGCCAGCCTGAAGCTGCCAGGCCCTGAGGTTTCAAGCCCTGACCCCATAGCTGGAGGCCTGTGGTGCCAG
AAGCCCAGATTAGGGTGGCTGTCCATCCCTGGATAGCTATTTGCACGAATCATGGACATAAATCCAAGTTG

1836/6881
FIGURE 1703

MEGRGPYRIYDPGGSVPSGEASAAFERLVKENSRLKEKMQGIKMLGELLEESQMEATRLRQAEELVKDNELLPP
PSPSLGSFDPLAELTGKDSNVTASPTAPACPSDKPAPVQKPPSSGTSSEFEVVTPEEQNSPESSSHANAMALGPL
PREDGNLMLHLQRLETTLSVCAEEDHGQLFTHLGRMALEFNRLASKVHKNEQRTSILQTLCEQLRKENEALKAK
LDKGLEQRDQAAERLREENLELKKLLMSNGNKEGASGRPGSPKMEGTGKKAVAGQQQASVTAGKVPEVVALGAPE
KKVKMLEQQRSELLEVNKQWDQHFRSMKQQYEQKITELRQKLADLQKQVTDLEAEREQKQRDFDRKLLLAISKIE
MEETDKEQLTAEAKELRQKVLYLQDQLSPLTRQREYQEKEIQRLNKALEEALSITPPSSPPTAFGSPEGAGALL
RKQELVTQNELLKQQVKIFEEDFQRERSDRERMNEEKEELKKQVEKLQAQVTLNAQLKAFKDEEKAREALRQQK
RKAKASGERYHVEPHPEHLGAYPYAYPPMPAMVPHHGFEDWSQIRYPPPPMAMEHPPPLPNSRLFHLPEYTWRL
PCGGVRNPNQSSQVMDPPTARPTEPESPKNDREGPQ

1837/6881
FIGURE 1704

AGCCAAAAGAGGAAGGGACCGGCCTCCACGTCCACAGGGACCTGACTTCCACCTCTCTGCCCAGATTTGCTTAT
GTCACTGTCGCCCCGGGACGGGGAGGTGGGGAGCTGAGGGCAAGTCGCGCCCGCCCCTGAAATCCCAGCCGCCTA
GCGATTGGCTGCAAGGGTCTCGGCTTGGCCGCGGATTAATCACACCCGAGGGCTTGAAAGGTGGCTGGGAGCGCC
GGACACCTCAGACGGACGGTGGCCAGGGATCAGGCAGCGGCTCAGGCGACCCTGAGTGTGCCCCACCCCGCCAT
GGCCCGCTGCTGCAGGCGTCTGCTGCTTTCCCTGCTCCTGGCCGGCTTCGTCTCGCAGAGCCGGGGACAAGA
GAAGTCGAAGATGGACTGCCATGGTGGCATAAGTGGCACCATTACGAGTACGGAGCCCTCACCATTGATGGGGA
GGAGTACATCCCCTTCAAGCAGTATGCTGGCAAATACGTCTCTTTGTCAACGTGGCCAGCTACTGAGGCCTGAC
GGGCCAGTACATTGAACTGAATGCACTACAGGAAGAGCTTGACCAATTCGGTCTGGTCAATCTGGGCTTTCCCTG
CAACCAATTTGGAAAACAGGAACCAGGAGAGAACTCAGAGATCCTTCCTACCCCTCAAGTATGTCCGACCAGGTGG
AGGCTTTGTCCCTAATTTCCAGCTCTTTGAGAAAGGGGATGTCAATGGAGAGAAAGAGCAGAAATTCTACACTTT
CCTAAAGAACTCCTGTCTCCACCTCGGAGCTCCTGGGTACATCTGACCGCCTCTTCTGGGAACCCATGAAGGT
TCACGACATCCGCTGGAACCTTTGAGAAGTTCCTGGTGGGGCCAGATGGTATACCCATCATGCGCTGGCACCACCG
GACCACGGTCAGCAACGTCAAGATGGACATCCTGTCTACATGAGGCGGCAGGCAGCCCTGGGGGTCAAGAGGAA
GTAACTGAAGGCCGTCTCATCCCATGTCCACCATGTAGGGGAGGGACTTTGTTTCAGGAAGAAATCCGTGTCTCCA
ACCACACTATCTACCCATCACAGACCCCTTTCTATCACTCAAGGCCCCAGCCTGGCACAAATGGATGCATACAG
TTCTGTGTACTGCCAGGCATGTGGGTGTGGGTGCAATGTGGGTGTTTACACACATGCCTACAGGTATGCGTGATT
GTGTGTGTGTGCATGGGTGTACAGCCACGTGTCTACCTATGTGTCTTTCTGGGAATGTGTACCATCTGTGTGCCT
GCAGCTGTGTAGTGCTGGACAGTGACAACCCTTTCTCTCCAGTTCTCCACTCCAATGATAATAGTTCACTTATAC
CTAAACCCAAAGGAAAAACCAGCTCTAGGTCCAATTGTTCTGCTCTAACTGATACCTCAACCTTGGGGCCAGCAT
CTCCCACTGCCTCCAAATATTAGTAACTATGACTGACGTCCCCAGAAGTTTCTGGGTCTACCACACTCCCCAACC
CCCCACTCCTACTTCTGAAGGGCCCTCCCAAGGCTACATCCCCACCCACAGTTCTCCCTGAGAGAGATCAACC
TCCCTGAGATCAACCAAGGCAGATGTGACAGCAAGGGCCACGGACCCCATGGCAGGGGTGGCGTCTTCATGAGGG
AGGGGCCCAAAGCCCTTGTGGGCGGACCTCCCCTGAGCCTGTCTGAGGGGCCAGCCCTTAGTGCATTCAAGGCTAA
GGCCCTGGGCAGGGATGCCACCCCTGCTCCTTCGGAGGACGTGCCCTCACCCCTCACTGGTCCACTGGCTTGAG
ACTCACCCCGTCTGCCAGTAAAGCCTTTCTGCAGCAAAAAAAAAAAAAAAAAAAAAA

1838/6881
FIGURE 1705

MARLLQASCLLSLLLAGFVSQSRGQEKSKMDCHGGISGTIYEYGALTIDGEEYIPFKQYAGKYVLFVNVASYEGL
TGQYIELNALQEELAPFGLVILGFPCNQFGKQEPGENSEILPTLKYVRPGGGFVPNFQLFEKGDVNGEKEQKFYT
FLKNSCPPTSELLGTSDRLFWEPMKVHDIRWNFEKFLVGPDGIPIMRWHHRTTVSNVKMDILSYMRRQAALGVKR
K

1839/6881
FIGURE 1706

AGCCTCGGGGCTTGACGGGATTGTGGCGGTCCTCTCTCCCAATTCGGAAGCTACAGCTACCTCCGGACGCTCTCA
AGATGGCGACCTCTCTGGGTTCCAACACCTACAACAGGCAGAACTGGGAGGATGCGGACTTCCCCATTCTGTGCC
AGACATGTCTTGGAGAAAACCCATATATCCGAATGACCAAAGAAAAGTATGGGAAGGAATGCAAAATCTGTGCCA
GGCCATTACAGTGTTCGCTGGTGGCCTGGAGTCCGCATGCGTTTCAAGAAGACTGAAGTGTGCCAAACCTGCA
GTAAATTGAAGAATGTCTGTCAGACCTGCCTCTTAGACCTAGAGTATGGCCTGCCCATCCAGGTTTCGTGACGCAG
GATTGTCTTTTAAAGATGACATGCCAAAGTCAGATGTCAACAAAGAGTACTATACACAGAATATGGAGAGAGAGA
TTTCTAACTCTGATGGAACACGGCCAGTTGGCATGCTGGGGAAAGCCACATCTACCAGTGACATGCTGCTCAAAC
TGGCCCGGACCACACCCTACTACAAAAGGAATCGACCCACATTTGCTCCTTCTGGGTGAAAGGAGAGTGTAAAG
GAGGAGAGGAATGTCCATACAGACATGAGAAGCCTACAGATCCAGATGACCCCTTGCTGATCAGAATATTAAAG
ACCGTTATTACGGAATCAATGATCCTGTAGCTGACAAGCTTCTAAAGCGGGCTTCAACAATGCCTCGGCTGGACC
CACCAGAGGATAAACTATCACCACACTATATGTTGGTGGTCTAGGTGATACCATTACTGAGACAGATTTAAGAA
ATCATTTTCTACCAGTTCGGAGAGATCCGGACGATCACTGTTGTGTCAGAGACAGCAGTGTGCTTTTCATCCAGTTTG
CCACACGGCAGGCTGCAGAAGTGGCTGCTGAGAAGTCCTTTAATAAGTTGATTGTAAATGGCCGCAGACTGAATG
TGAAATGGGGAAGATCCCAGGCAGCCAGAGGAAAAGAAAAGAGAAAGATGGAACCTACAGACTCTGGGATCAAAC
TAGAACCTGTTCCAGGATTGCCAGGAGCTCTTCCTCCTCCTCCTGCAGCAGAAGAAGAAGCCTCTGCCAACTACT
TCAACTTGCCCCAAGTGGTCTCCAGCTGTGGTGAACATTGCTCTGCCACCGCCCCCTGGCATTGCTCCACCCC
CACCCCAGGTTTTGGGCCACACATGTTCCACCCAATGGGACCACCCCTCCTTTTCATGCGGGCTCCAGGACCAA
TCCACTATCCTTCTCAGGACCCTCAGAGGATGGGAGCTCATGCTGGAAAACACAGCAGCCCCCTAGCACCTTGTC
CCACTCTGGGGCTCTGTGGAAGAAAGGGCACTTAAAACTCCCAGTAAATCTTGGAATAAATATATTTTTCTTCC
CTTGTAGTTTCCATGGTAGCTGAATGTGCTCAGATGTGAGCAGTCAGAGACTGACAGCCATGCTTTCTATACTT
GTTCAAAGGATCGATGGACCGTAAATAAGCTGCCATTAACACATCTGGTTACTGCTGTAACATGACTAATAAAAC
CGAACGCCTGTTCCCTTACCCGTGTGGGGGACACGCAGATGAGTGAATTGGAATGTCCAGCAGAGTTACCTCC
CAATTATATGTTCATTTTGTATATTTTTTGGTGGGGGAAAAATTGACCTGCAGTAAAAAACCTTTGACCATTT
TTATGTCCATTGGATACTTTCCTTTTTATCATCTTAAAAAAGATAACTAGTACTAATCATTGTAGTGGCCTAAG
TGTGATTTAACTCTTGAAGTCACACCCTCCGAAAGATGAGTAGAAACCAGCACCAGCACAGCCCAGATCTTCTCT
TTCCTCTCCTTTTCTCATTTATTCCTAAAGGAATCTGACCATTTTACGTCTCTACGGCCCCAAAAAAGACAAAA
ATAAAAATTCTTTTTATTCTGTCAACTGGATGGAAACACAAATTTTCATGGAGCTGTGTACCATCGAAGAAACC
TGGTGTCTGGCATGAAATTACTGTAAAGAACTTCTGTAAAACACGTTCTTTAACAACTGAAATGAAAAGCATT
GGAGCGTCTGAATGAAAGACGTGACCTCCTGCTGGGACTCTGATGGTCTTCAGCATTACCTTCGTGTGTCTTCA
GTGTCTCATTGTATCCCTGCTTCTGTTTGGTCTTAGAGTGTGGATATAACTGAATTGTAGATGGTAAAGGAA
ATTTGATGTGTTTTTTGTTTTTAAATAATTAAAACGGGTCAATTTTT

1840/6881
FIGURE 1707

MATSLGSNTYNRQNWEDADFPILCQTCLGENPYIRMTKEKYGKECKICARPFTVFRWCPGVMRFRKKTEVCQTCS
KLKNVCQTCLLDLEYGLPIQVRDAGLSFKDDMPKSDVNKEYYTQNMEREISNSDGTRPVGMLGKATSTSDMLLKL
ARTTPYYKRNRPHICSFVWKGECKRGECPYRHEKPTDPDDPLADQNIKDRYYGINDPVADKLLKRASTMPRLDP
PEDKTITITLYVGGLGDTITETDLRNHFYQFGEIRTTITVVQRQQCAFIQFATRQAAEVAAEKSFNKLIVNGRRLNV
KWGRSQAARGKEKEKDGTTDGSIKLEPVPGLPALPPPPAAEEEEASANYFNLPPSGPPAVVNIALPPPPGIAPPP
PPGF GPHMFHPMGPPPPFMRAPGPIHYP SQDPQRMGAHAGKHSSP

1841/6881
FIGURE 1708

CTCCGCCCTCTCCCACTCTCTCTTTCCGGTGTGGAGTCTGGAGACGACGTGCAGAAATGGCACCTCGAAAGGGGA
AGGAAAAGAAGGAAGAACAGGTCATCAGCCTCGGACCTCAGGTGGCTGAAGGAGAGAATGTATTTGGTGTCTGCC
ATATCTTTGCATCCTTCAATGACACTTTTGTCCATGTCACTGATCTTTCTGGCAAGGAAACCATCTGCCGTGTGA
CTGGTGGGATGAAGGTAAAGGCAGACCGAGATGAATCCTCACCATATGCTGCTATGTTGGCTGCCCAGGATGTGG
CCCAGAGGTGCAAGGAGCTGGGTATCACCGCCCTACACATCAAACCTCCGGGCCACAGGAGGAAATAGGACCAAGA
CCCCTGGACCTGGGGCCCAGTCGGCCCTCAGAGCCCTTGCCCGCTCGGGTATGAAGATCGGGCGGATTGAGGATG
TCACCCCATCCCTCTGACAGCACTCGCAGGAAGGGGGGTCGCCGTGGTTCGCGTCTGTGAACAAGATTCCTCA
AAATATTTCTGTTAATAAATTGCCTTCATGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

1842/6881
FIGURE 1709

MAPRKGKEKKEEQVISLGPQVAEGENVFGVCHIFASFNDTFVHVTDLSGKETICRVTTGGMKVKADRDESSPYAAM
LAAQDVAQRCKELGITALHIKLRATGGNRTKTPGPGAQSALRALARSGMKIGRIEDVTPIPSDSTRRKGGRRGRRL

1843/6881
FIGURE 1710

ACCAAGTGGGCGGAGTGGCCTTCTGTGGACGAATCAGATTCTCTCCAGCACCGACTTTAAGAGGCGAGCCGGGG
GGTCAGGGTCCCAGATGCACAGGAGGAGAAGCAGGAGCTGTCGGGAAGATCAGAAGCCAGTCATGGATGACCAGC
GCGACCTTATCTCCAACAATGAGCAACTGCCCATGCTGGGCGGCGCCCTGGGGCCCCGGAGAGCAAGTGCAGCC
GCGGAGCCCTGTACACAGGCTTTTCCATCCTGGTGACTCTGCTCCTCGCTGGCCAGGCCACCACCGCCTACTTCC
TGTACCAGCAGCAGGGCCGGCTGGACAACTGACAGTCACCTCCCAGAACCTGCAGCTGGAGAACCTGCGCATGA
AGCTTCCCAAGCCTCCCAAGCCTGTGAGCAAGATGCGCATGGCCACCCCGCTGCTGATGCAGGCGCTGCCCCATGG
GAGCCCTGCCCCAGGGGCCCATGCAGAATGCCACCAAGTATGGCAACATGACAGAGGACCATGTGATGCACCTGC
TCCAGAATGCTGACCCCCCTGAAGGTGTACCCGCCACTGAAGGGGAGCTTCCCGGAGAACCTGAGACACCTTAAGA
ACACCATGGAGACCATAGACTGGAAGGTCTTTGAGAGCTGGATGCACCATTGGCTCCTGTTTGAAATGAGCAGGC
ACTCCTTGGAGCAAAAAGCCCACTGACGCTCCACCGAAAGTACTGACCAAGTGCCAGGAAGAGGTCAGCCACATCC
CTGCTGTCCACCCGGGTTCATTAGGCCCAAGTGCGACGAGAACGGCAACTATCTGCCACTCCAGTGCTATGGGA
GCATCGGCTACTGCTGGTGTGTCTTCCCCAACGGCACGGAGGTCCCCAACACCAGAAGCCGCGGGCACCATAACT
GCAGTGAGTCACTGGAAGTGGAGGACCCGTCTTCTGGGCTGGGTGTGACCAAGCAGGATCTGGGGCCAGTCCCCA
TGTGAGAGCAGCAGAGGCGGTCTTCAACATCCTGCCAGCCCCACACAGCTACAGCTTTCTTGCTCCCTTCAGCCC
CCAGCCCCCTCCCCCATCTCCCACCCTGTACCTCATCCCATGAGACCCTGGTGCCTGGCTCTTTCGTCACCCTTGG
ACAAGACAAACCAAGTCGGAACAGCAGATAACAATGCAGCAAGGCCCTGCTGCCCAATCTCCATCTGTCAACAGG
GGCGTGAGGTCCCAGGAAGTGGCCAAAAGCTAGACAGATCCCCGTTCCTGACATCACAGCAGCCTCCAACACAAG
GCTCCAAGACCTAGGCTCATGGACGAGATGGGAAGGCACAGGGAGAAGGGATAACCCTACACCCAGACCCAGGC
TGGACATGCTGACTGTCTCTCCCTCCAGCCTTTGGCCTTGGCTTTTCTAGCCTATTTACCTGCAGGCTGAGCC
ACTCTCTTCCCTTTCCCCAGCATCACTCCCCAAGGAAGAGCCAATGTTTTCCACCCATAATCCTTTCTGCCGACC
CCTAGTTCCCTCTGCTCAGCCAAGCTTGTTATCAGCTTTCAGGGCCATGGTTCACATTAGAATAAAAGGTAGTAA
TTAG

1844/6881
FIGURE 1711

ATAAGATCTGTCCCCAACTCTCCAGATCTGTGACCCACATTCTCTCTCCATAGGTGGAAAAGAGGCTGCTTC
AGGCACCACACCTCAGAAGTCCCGGAAGCCCAAGAAAGGGGCTGGGAACCCCAAGCCTCAACCCTGGCGCTGCA
AAGCAACATCACCCAGAGCAAGAAGAAGAAGAAGCTGGGGGCCGGGAAGGTGGGGAGGCCTCTGTTTCCCCAGA
AAAGACCTCCACGACTTCCAAGGGGAAAGCAAAGAGAGACAAAGCAAGTGGTGATGTCAAGGAGAAGAAAGGGAA
GGGGTCTCTTGGCTCCCAAGGGGCCAAGGACGAGCCAGAAGAGGAGCTTCAGAAGGGGATGGGGACGGTTGAAGG
TGGAGATCAAAGCAACCCAAAGAGCAAGAAGGAGAAGAAGAAATCCGACAAGA

1845/6881
FIGURE 1712A

GAAGGGCAGACAGAGTGTCCAAAAGCGTGAGAGCACGAAGTGAGGAGAAGGTGGAGAAGAGAGAAGAGGAAGAGG
AAGAGGAAGAGAGGAAGCGGAGGGAACTGCGGCCAGGCTAAAAGGGGAAGAAGAGGATCAGCCCAAGGAGGAGGA
AGAGGAAAACAAGACAAAACAGCCAGTGCAGAGGAGAGGAACGTGTGTCCAGTGTCCCGATCCCTGCGGAGCTAGT
AGCTGAGAGCTCTGTGCCCTGGGCACCTTGCAGCCCTGCACCTGCCTGCCACTTCCCCACCGAGGCCATGGGCCC
AGGAGTTCTGTCTGCTCCTGTGCTGGTGCCACAGCTTGGCATGGTCAGGGAATCCCAGTGATAGAGCCCAGTGTCCC
TGAGCTGGTTCGTGAAGCCAGGAGCAACGGTGACCTTGGCATGTGTGGGCAATGGCAGCGTGGAATGGGATGGCCC
CCCATCACCTCACTGGACCCGTACTCTGATGGCTCCAGCAGCATCCTCAGCACCAACAACGCTACCTTCCAAAA
CACGGGGACCTATCGCTGCACTGAGCCTGGAGACCCCCCTGGGAGGCAGCGCCGCCATCCACCTCTATGTCAAAGA
CCCTGCCCCGGCCCTGGAACGTGCTAGCACAGGAGGTGGTCGTGTTTCGAGGACCAGGACGCACTACTGCCCTGTCT
GCTCACAGACCCGGTGCTGGAAGCAGGCGTCTCGCTGGTGCGTGTGCGTGGCCGGCCCCCTCATGCGCCACACCAA
CTACTCCTTCTCGCCCTGGCATGGCTTACCATCCACAGGGCCAAGTTCATTTCAGAGCCAGGACTATCAATGCAG
TGCCCTGATGGGTGGCAGGAAGGTGATGTCCATCAGCATCCGGCTGAAAGTGCAGAAAGTCATCCCAGGGCCCCC
AGCCTTGACACTGGTGCCTGCAGAGCTGGTGCAGATTTCGAGGGGAGGCTGCCAGATCGTGTGCTCAGCCAGCAG
CGTTGATGTAACTTTGATGTCTTCCCTCCAACACAACAACACCAAGCTCGCAATCCCTCAACAATCTGACTTTCA
TAATAACCGTTACCAAAAAGTCTTGACCCTCAACCTCGATCAAGTAGATTTCCAACATGCCGGCAACTACTCCTG
CGTGGCCAGCAACGTGCAGGGCAAGCACTCCACCTCCATGTTCTTCCGGGTGGTAGAGAGTGCCTACTTGAACCTT
GAGCTCTGAGCAGAACCTCATCCAGGAGGTGACCGTGGGGGAGGGGCTCAACCTCAAAGTCATGGTGGAGGCCTA
CCCAGGCCTGCAAGGTTTTAACTGGACCTACCTGGGACCCCTTTTCTGACCACCAGCCTGAGCCCAAGCTTGCTAA
TGCTACCACCAAGGACACATACAGGCACACCTTACCCCTCTCTGCCCCGCCTGAAGCCCTCTGAGGCTGGCCG
CTACTCCTTCTGCGCCAGAAACCCAGGAGGCTGGAGAGCTCTGACGTTTGAGCTCACCTTTCGATACCCCCCAGA
GGTAAGCGTCATATGGACATTTCATCAACGGCTCTGGCACCCCTTTTGTGTGCTGCCTCTGGGTACCCCCAGCCAA
CGTGACATGGCTGCAGTGCAGTGGCCACACTGATAGGTGTGATGAGGCCCAAGTGTGTCAGGTCTGGGATGACCC
ATACCCTGAGGTCTGAGCCAGGAGCCCTTCCACAAGGTGACGGTGCAGAGCCTGCTGACTGTTGAGACCTTAGA
GCACAACCAAAACCTACGAGTGCAGGGCCCAACAGCGTGGGGAGTGGCTCCTGGGCCTTCATACCCATCTCTGC
AGGAGCCCACACGCATCCCCCGGATGAGTTCTCTTACACCAGTGGTGGTGCCTGCATGTCCATCATGGCCTT
GCTGCTGCTGCTGCTCCTGTGCTATTGTACAAGTATAAGCAGAAGCCCAAGTACCAGGTCCGCTGGAAGATCAT
CGAGAGCTATGAGGGCAACAGTTATACTTTTCATCGACCCACGCAGCTGCCTTACAACGAGAAGTGGGAGTTCCC
CCGGAACAACCTGCAGTTTGGTAAGACCTCGGAGCTGGAGCCTTTGGGAAGGTGGTGGAGGCCACGGCCTTTGG
TCTGGGCAAGGAGGATGCTGTCTGAAGGTGGCTGTGAAGATGCTGAAGTCCACGGCCCATGCTGATGAGAAGGA
GGCCCTCATGTCCGAGCTGAAGATCATGAGCCACCTGGGGCCAGCACGAGAACATCGTCAACCTTCTGGGAGCCTG
TACCCATGGAGGCCCTGTACTGGTCATCACGGAGTACTGTTGCTATGGCGACCTGCTCAACTTTCTGCGAAGGAA
GGCTGAGGCCATGCTGGGACCCAGCCTGAGCCCCGGCCAGGACCCCGAGGGAGGCGTCGACTATAAGAACATCCA
CCTCGAGAAGAAATATGTCCGCAGGGACAGTGGCTTCTCCAGCCAGGGTGTGGACACCTATGTGGAGATGAGGCC
TGTCTCCACTTCTTCAAATGACTCCTTCTCTGAGCAAGACCTGGACAAGGAGGATGGACGGCCCCCTGGAGCTCCG
GGACCTGCTTCACTTCTCCAGCCAAGTAGCCAGGGCATGGCCTTCCCTCGCTTCCAAGAATTGCATCCACCGGGA
CGTGGCAGCGCGTAACGTGCTGTTGACCAATGGTCATGTGGCCAAGATTGGGGACTTCGGGCTGGCTAGGGACAT
CATGAATGACTCCAACCTACATTGTCAAGGGCAATGCCCCGCTGCCTGTGAAGTGGATGGCCCCAGAGAGCATCTT
TGACTGTGTCTACACGGTTCAGAGCGACGTCTGGTCCTATGGCATCCTCCTCTGGGAGATCTTCTCACTTGGGCT
GAATCCCTACCCTGGCATCCTGGTGAACAGCAAGTTCTATAAACTGGTGAAGGATGGATAACCAATGGCCCAGCC
TGCAATTTGCCCCAAAGAATATATACAGCATCATGCAGGCCTGCTGGGCCTTGGAGCCCACCCACAGACCCACCTT
CCAGCAGATCTGCTCCTTCTCAGGAGCAGGCCCAAGAGGACAGGAGAGAGCGGGACTATACCAATCTGCCGAG
CAGCAGCAGAAGCGGTGGCAGCGGCAGCAGCAGCAGTGAAGTGGAGGAGGAGCTCTAGTGAGCACCTGACCTG
CTGCGAGCAAGGGGATATCGCCCAGCCCTTGTGTCAGCCCAACAACCTATCAGTTCTGCTGAGGAGTTGACGACAG
GGAGTACCACTCTCCCTTCCCACAACTTCAACTCCTCCATGGATGGGGCGACACGGGGAGAACATACAACTCT
GCCTTCCGGTCATTTCACTCAACAGCTCGGCCAGCTCTGAACTTGGGAAGGTGAGGGATTGAGGGGAGGTCAGA
GGATCCCACTTCTGAGCATGGGCCATCACTGCCAGTCAGGGGCTGGGGGCTGAGCCCTCACCCCCCTCCCT
ACTGTTCTCATGGTGTGGCCTCGTGTGTTGCTATGCCAACTAGTAGAACCTTCTTTCCTAATCCCTTATCTTCA
TGGAATGGACTGACTTTATGCCTATGAAGTCCCCAGGAGCTACACTGATACTGAGAAAACAGGCTCTTTGGGG

1846/6881
FIGURE 1712B

CTAGACAGACTGGCAGAGAGTGAGATCTCCCTCTCTGAGAGGAGCAGCAGATGCTCACAGACCACACTCAGCTCA
GGCCCCCTTGGAGCAGGATGGCTCCTCTAAGAATCTCACAGGACCTCTTAGTCTCTGCCCTATACGCCGCCTTCAC
TCCACAGCCTCACCCTCCACCCCCATACTGGTACTGCTGTAATGAGCCAAGTGGCAGCTAAAAGTTGGGGTG
TTCTGCCCAGTCCCGTCATTCTGGGCTAGAAGGCAGGGGACCTTGGCATGTGGCTGGCCACACCAAGCAGGAAGC
ACAAACTCCCCCAAGCTGACTCATCCTAACTAACAGTCACGCCGTGGGATGTCTCTGTCCACATTAACTAACAG
CATTAAATGC

1847/6881
FIGURE 1713

TTTTTCCGGCTGGAACCATGGAGGGTGTAGAAGAGAAGAAGAAGGAGGTTCCCTGCTGTGCCAGAAACCCTTAAGA
AAAAGCGAAGGAATTTTCGCAGAGCTGAAGATGAAGCGCCTGAGAAAGAAGTTTGCCAAAAGATGCTTCGAAAGG
CAAGGAGGAAGCTTATCTATGAAAAAGCAAAGCACTATCACAAAGGAATATAGGCAGATGTACAGGACTGAAATTC
GAATGGCGAGGATGGCAAGAAAAGCTGGCAACTTCTATGTACCTGCAGAACCCAAATTGGCGTTTGTTCATCAGAA
TCAGAGGTATCAATGGAGTGAGCCCAAAGGTTGAAAGGTGTTGCAGCTTCTTCGCCTTCGTCAAATCTTCAATG
GAACCTTTGTGAAGCTCAACAAGGCTTCGATTAAACATGCTGAGGATTGTAGAGCCATATATTGCATGGGGGTACC
CCAATCTGAAGTCAGTAAATGAACTAATCTACAAGCGTGGTTATGGCAAAATCAATAAGAAGCGAATTGCTTTGA
CAGATAACGCTTTGATTGCTCGATCTCTTGGTAAATACGGCATCATCTGCGTGGAGGATTTGATTCATGAGATCT
ATACTGTTGGAAAACGCTTCAAAGAGGCAAATAACTTCCTGTGGCCCTTCAAATTGTCTTCTCCACGAGGTGGAA
TGAAGAAAAAGACCACCCATTTTGTAGAAGGTGGAGATGCTGGCAACAGGGAGGACCAGATCAACAGGCTTATTA
GAAGAATGAACTAAGGTGTCTACCATGATTATTTTTCTAAGCTGGTTGGTTAATAAACAGTACCTGCTCTCAAAT
TGG

1848/6881
FIGURE 1714

ATGGCCGAGGCCAGGAAGCGGCGGGAGCTACTTCCCCTGATCTACCACCATCTGCTGCGGGCTGGCTATGTGCGT
GCGGCGCGGGAAAGTGAAGGAGCAGAGCGGCCAGTGGGTTGGGCCAGAAAGTGTGCTCGCAGGGGCCGAACTTTGT
AATTCCCGCTTCCCTTACCTCCACGCCCTTCCCTGGTAGCGGGTATTTTAAGTTTCCTAAGTCTCCCCGCCACGTGG
CTAGGCTCTGCGCGGCCCCCCTGGGGCAAGGAGGTTGCTGCGAGTCTCGGGGGTGGATTGCGACCAGCCCCCTCG
GGGAGCGCCTGGAAGAGGACCCTACAGCCTCTTAGTTGAGCTGGAACCTCAGGCCTTTAGCGATTGTCTGTACT
GAGACGGTCAGCTTTGGTACTCGAAGTCTGTTGAGTACAGTCATTTCTTACTTGATTAATTCAACTGTTAATCCGGTA
CTCAGGGTGCTTCTGTTGTTTGAATGAAGTGTTCCTGGCTCAGCCCGTAACCCCTTCTGGACATCTATACACAC
TGGCAACAAACCTCAGAGCTTGGTCGGAAGCGGAAGGCAGAGGAAGATGCGGCACTGCAAGCTAAGAAAACCCGT
GTGTGACACCCCATCAGCACCTCGGAGAGCTCGGAAGAGGAGGAAGAAGCAGAAGCCGAAACCGCCAAAGCCAGT
AAGAGCCTTGACGCTTTGGGAACAGGCTATGGAATATTGATTGTTCTAGGTTTCTATGACCCCTTCTCTCCTACT
TTCTATGAAATGGGGGAAGCCCAAGGTCCCAGTCTCCTAACTCCTGGTGTACGGATTGAATTGTGTTTCCCCA
AAAGGTGTTGTGCTGAGCCTCTGGCTGACAGCTGTGTTTTCTCTGCTCAGCAAAGGCTTTAACCATAAACAGGAG
AAATCGGGCCAGACAGTTGCTGGTACTTTCTGCCCAGTACTACTTCACAGAGTCAGTGTCCAGCTTCCGAACAGC
ATGGAGGCAGCTCTGAGTCATCCGAATCCAGTGGCCCCACAGCCTGCTCAGCTTCGGCTACCTGTCTTGGGAC
TGGGCCAAGCCGAGCTTCGTGGCCGACGGGCCCGGGGAGGCTGGCGAGCAGCCCTCGGCCGCTCCGCCCCAGCCT
CCCCACATCATCTTCATCCTCACGGACGACCAAGGCTACCACGACGTGGGCTACCATGGTTTCAGATATCGAGACC
CCTACGCTGGACAGGCTGGCGGCCAAGGGGTCAAGTTGGAGAATTATTACATCCAGCCCATCTGCACGCCTTCG
CGGAGCCAGCTCCTCACTGGCAGGTACCAGATCCACACAGGACTCCAGCATTCCATCATCCGCCCCACAGCAGCCC
AACTGCCTGCCCCCTGGACCAGGTGACACTGCCACAGAAGCTGCAGGAGGCAGGTTATTCCACCCATATGGTGGGC
AAGTGGCACCTGGGCTTCTACCGGAAGGAGTGTCTGCCCCACCCGTGCGGGCTTCGACACCTTCTGGGCTCGCTC
ACGGGCAATGTGGACTATTACACCTATGACAACCTGTGATGGCCCAGGCGTGTGCGGCTTCGACCTGCACGAGGGT
GAGAATGTGGCCTGGGGGCTCAGCGGCCAGTACTCCACTATGCTTTATGCCAGCGCGCCAGCCATATCCTGGCC
AGCCACAGCCCTCAGCGTCCCCTCTTCTCTATGTGGCCTTCCAGGCAGTACACACACCCCTGCAGTCCCCCTCGT
GAGTACCTGTACCGCTACCGCACCATGGGCAATGTGGCCCGGCGGAAGTACGCGGCCATGGTGACCTGCATGGAT
GAGGCTGTGCGCAACATCACCTGGGCCCTCAAGCGCTACGGTTTCTACAACAACAGTGTTCATCATCTTCTCCAGT
GACAATGGTGGCCAGACTTTCTCGGGGGGCAGCAACTGGCCGCTCCGAGGACGCAAGGGCACTTATTGGGAAGGT
GGCGTGGGGGCTTAGGCTTTGTCCACAGTCCCCTGCTCAAGCGAAAGCAACGGACAAGCCGGGCACTGATGCAC
ATCACTGACTGGTACCCGACCCTGGTGGTCTGGCAGGTGGTACCACCTCAGCAGCCGATGGGCTAGATGGCTAC
GACGTGTGGCCGGCCATCAGCGAGGGCCGGGCTCACCACGCACGGAGATCCTGCACAACATTGACCCACTCTAC
AACCATGCCCAGCATGGCTCCCTGGAGGGCGGCTTTGGCATCTGGAACACCGCCGTGCAGGCTGCCATCCGCGTG
GGTGAGTGGAAGCTGCTGACAGGAGACCCGGCTATGGCGATTGGATCCCACCGCAGACACTGGCCACCTTCCCG
GGTAGCTGGTGGAACTGGAACGAATGGCCAGTGTCCGCCAGGCCGTGTGGCTCTTCAACATCAGTGTGACCCT
TATGAACGGGAGGACCTGGCTGGCCAGCGGCTGATGTGGTCCGCACCCTGCTGGCTCGCCTGGCCGAATATAAC
CGCACAGCCATCCCGGTACGCTACCCAGCTGAGAACCCCGGGCTCATCCTGACTTTAATGGGGGTGCTTGGGGG
CCCTGGGCCAGTGATGAGGAAGAGGAGGAAGAGGAAGGGAGGGCTCGAAGCTTCTCCCGGGGTGCTCGCAAGAAA
AAATGCAAGATTTGCAAGCTTCGATCCTTTTTCCGTAAACTCAACACCAGGCTAATGTCCCAACGGATCTGA

1849/6881
FIGURE 1715

LDRLAAKGVKLENYYIQPICTPSRSQLLTGRIYQIHTGLQHSIIRPQQPNCLPLDQVTLPOKLQEAGYSTHMGKW
HLGFYRKECLPTRRGFDITLGLSLTGNVDYYTYDNCDGPGVCGFDLHEGENVAWGLSGQYSTMLYAQRASHILASH
SPQRPLFLYVAFQAVHTPLQSPREYLY

1850/6881
FIGURE 1716

ATGGGGATAATCAGGCACAGGTCTTTCCGCCAATGCGTTATGATGATTAAAGAAGTTGTCATATTTGTGAACTCG
CGGCAAATCTGGCCTCTCTGTGATTTTCATCACTGTGCACACTCCTCTCCTGCCCTCCACGACAGGCTTGCTGAAT
GACAACACCTTTGCCCAGTGCAAGAAGGGGGTGCGTGTGGTGAACGTGTGCCCGTGGAGGGATCGTGGACGAAGGC
GCCCTGCTCCGGGCCCTGCAGTCTGGCCAGTGTGCCGGGGCTGCACTGGACGTGTTTACGGAAGTAAGTGCCTGG
CAGCCTCAGCGTCAGGAGGACGGGAGAGATAGGGAGCAGAGAGGCCCATGGCAGGGAAAGCCTGGCGTTTTACAG
AAAGCCTATAGCTTATTGTCTCTTTTCATCCATGGTAAAAGGAGAAAACGTGTGTTGCCAAAAACACACCTTTGTGG
TTTGAGGAGTCCTTGCGGAGCCTGTACCTGCTTCTTGCCCGAGGTGTGGCTGTGCAGAGGGGCTCCCTAACTGC
ATCCTGAGGGTGCTCCCACTATGCACCCTGTGCCAAGCCTGGACACCTGAGGGATCTGTGCCCAATGCTACTGGA
GCCAAGGCTGGGGCTACCTTTAGTGATAGTGTTATTATTGTAATTATTGTAACCATTGTCACAGAATGTCCAGAC
TGGTATGCAGGTATAGCTCATTACCAGGAGGAAAACACAGAAGGTCTTTGTGCAGTTGCTGTGGTTTTGAGTTTC
TCTGGGATAGCTTGTATTTTGCCAGCAAATGAAAGCTTTGGACCTCTGCAGATGTCACTTGGAGGAGCAGTCAAA
GACATCTTCAGGTTTCATGGTCATATTCATTATGGTGTGTTGTGGCCTTTATGATTGGAACGTACAACCTTCTACTCC
TACTACATTGGTGCAAAACAAAATGAAGCCTTCACAACAGTTGAAGAGAGTTTTAAGACACTGTTCTGGGGCTATA
TTTGGACTTGCTGAAGTGAAATCAGTGGTCATCAACTATAACCACAAATTCATTGAAAATATTGGTTATGTTTCGT
TATGGAGTCTATAATGTTACAGTGGTCATTGTTTTGCTAAATGTGTTAATTGCCATGATCAACAATTCATTCCAG
GAAATTGAGGATGATGCTGATGTGGAGTAG

1851/6881
FIGURE 1717

MGIIRHRSFRQCVMMIKEATFSDSVIIVIIIVTIVTECPDWYAGIAHYQEENTEGLCAVAVVLSFSGIACILPANE
SFGPLQMSLGGAVKDI FRFMVIFIMVFVAFMIGTYNFYSYYIGAKQNEAFTTVEESFKTLFWAIFGLAEVKSIVI
NYNHKFIENIGYVRYGVYNVTVVIVLLNVLIAMINNSFQEIEDDADVE

1852/6881
FIGURE 1718

ATGGCGACTGCGACCCCCGTGCCGCCGCGGATGGGCAGCCGCGCTGGCGGGCCCCACCACGCCGCTGAGCCCCACG
CGCCTGTCGCGGCTCCAGGAGAAGGAGGAGCTGCGCGAGCTCAATGACCGGCTGGCGGTGTACATCGACAAGGTG
CGCAGCCTGGAGACGGAGAACAGCGCGCTGCAGCTGCAGGTGACGGAGCGCGAGGAGGTGCGCGGCCGTGAGCTC
ACCGGCCTCAAGGCGCTCTACGAGACCGAGCTGGCCGACGCGCGACGCGCGCTCGACGACACGGCCCCGCGAGCGC
GCCAAGCTGCAGATCGAGCTGGGCAAGTGCAAGGCGGAACACGACCAGCTGCTCCTCAACTATGCTAAGAAGGAA
TCTGATCTTAATGGCGCCAGATCAAGCTTCGAGAATATGAAGCAGCACTGAATTCGAAAGATGCAGCTCTTGCT
ACTGCACTTGGTGACAAAAAAGTTTAGAGGGAGATTTGGAGGATCTGAAGGATCAGATTGCCAGTTGGAAGCC
TCCTTAGCTGCAGCCAAAAACAGTTAGCAGATGAAACTTTACTTAAAGTAGATTTGGAGAATCGTTGTCAGAGC
CTTACTGAGGACTTGGAGTTTCGCAAAAGCATGTATGAAGAGGAGATTAACGAGACCAGAAGGAAGCATGAAACG
CGCTTGGTAGAGGTGGATTCTGGGCGTCAAATTGAGTATGAGTACAAGCTGGCGCAAGCCCTTCATGAGATGAGA
GAGCAACATGATGCCCAAGTGAGGCTGTATAAGGAGGAGCTGGAGCAGACTTACCATGCCAACTTGAGAATGCC
AGACTGTCATCAGAGATGAATACTTCTACTGTCAACAGTGCCAGGGAAGAACTGATGGAAAGCCGCATGAGAATT
GAGAGCCTTTTCATCCCAGCTTTCTAATCTACAGAAAGAGTCTAGAGCATGTTTGGAAAGGATTCAAGAATTAGAG
GACTTGCTTGCTAAAGAAAAAGACAACCTCTCGTCGCATGCTGACAGACAAAGAGAGAGAGATGGCGGAAATAAGG
GATCAAATGCAGCAACAGCTGAATGACTATGAACAGCTTCTTGATGTAAAGTTAGCCCTGGACATGGAAATCAGT
GCTTACAGGAAACTCTTAGAAGGCGAAGAAGAGAGGTTGAAGCTGTCTCCAAGCCCTTCTTCCCGTGTGACAGTA
TCCCAGCATCCTCAAGTCGTAGTGTACGTACAAC TAGAGGAAAGCGGAAGAGGGTTGATGTGGAAGAATCAGAG
GCGAGTAGTAGTGTAGCATCTCTCATTCCGCCTCAGCCACTGGAAATGTTTGCATCGAAGAAATTGATGTTGAT
GGGAAATTTATCCGCTTGAAGAACACTTCTGAACAGGATCAACCAATGGGAGGCTGGGAGATGATCAGAAAAATT
GGAGACACATCAGTCAGTTATAAATATACCTCAAGATATGTGCTGAAGGCAGGCCAGACTGTTACAATTTGGGCT
GCAAACGCTGGTGTACAGCCAGCCCCCACTGACCTCATCTGGAAGAACCAGAACTCGTGGGGCACTGGCGAA
GATGTGAAGGTTATATTGAAAAATTCTCAGGGAGAGGAGGTTGCTCAAAGAAGTACAGTCTTTAAAACAACCATA
CCTGAAGAAGAGGAGGAGGAGGAAGAAGCAGCTGGAGTGGTTGTTGAGGAAGAACTTTTCCACCAGCAGGGAACC
CCAAGAGCATCCAATAGAAGCTGTGCAATTATGTAAAATTTTCAACTGTCTTCCTCAAATAAAGAAGTATGGTA
ATCTTTACCTGTATACAGTGCAGAGCCTTCTCAGAAGCACAGAATATTTTATATTTCTTTATGTGAATTTTGA
AGCTGCAAATCTGATGGCCTTAATTTCTTTTTTGACACTGAAAGTTTTGTAAAAGAAATCATGTCCATACACTTT
GTTGCAAGATGTGAATTATTGACACTGAACTTAATAACTGTGTACTGTTCCGAAGGGGTTCTCAAATTTTTTGA
CTTTTTTTGTATGTGTGTTTTTTCTTTTTTTTAAAGTTCTTATGAGGAGGGGAGGGTAAATAAACCAGTGTGCGT
CTTGGTGTAAATTTGAAGATTGCCCCATCTAGACTAGCAATCTCTTCATTATTCTCTGCTATATATAAACGGTGC
TGTGAGGGAGGGGAAAAAGCATTTTTCAATATATTGAACTTTTGTACTGAATTTTTTTGTAAATAAGCAATCAAGGT
TATAATTTTTTTTAAAAATAGAAATTTTGTAAAGAAGGCAATATTAACCTAATCACCATGTAAGCACTCTGGATGAT
GGATTCCACAAAACCTTGGTTTTATGGTTACTTCTTCTCTTAGATTCTTAATTCATGAGGAGGGTGGGGAGGGAG
GTGGAGGGAGGGGAAGGGTTTTCTCTATTAAATGCATTCTGTTGTGTTTTTTAAGATAGTGTAACTTGCTTAAATTT
CTTATGTGACATTAAACAAATAAAAAAGCTCTTTT

1853/6881
FIGURE 1719

MATATPVPPRMGSRAGGPTTPLSPTRL SRLQEKEELRELNDRLAVYIDKVRSL ETENSALQLQVTEREEVGRREL
TGLKALYETELADARRALDDTARERAKLQIELGKCKAEHDQLLLNYAKKESDLNGAQIKLREYEAALNSKDAALA
TALGDKKSLEGDLEDLKDQIAQLEASLAAAKQLADETLLKVDLENRCQSLTEDLEFRKSMYEEEINETRRKHET
RLVEVD SGRQIEY EYKLAQALHEMREQHDAQVRLYKEELEQTYHAKLENARLSSEMNTSTVNSAREELMESRMRI
ESLSSQLSNLQKESRACLERIQELEDLLAKEKDNSRRLTDKEREMAEIRDQMQQQLNDYEQLLDVKLALDMEIS
AYRKLL EGEEERLKLSPSPSSRVTVSRASSRSVRTTRGKRKRVDVEESEASSSVSISHSASATGNVCIEEIDVD
GKFIRLKNTSEQDQPMGGWEMIRKIGDTSVSYKYTSRYVLKAGQTVTIWAANAGVTASPTD LIWKNQNSWGTGE
DVKVILKNSQGEEVAQRSTVFKTTIPEEEEEEEEAAGVVVEEELFHQQGTPRASNRSCAIM

1854/6881
FIGURE 1720

GGTCTCTGGTCTCCCCTCTCTGAGCACTCTGAGGTCCTTATGTCTGTCAGAAAGATCGAGAAGCTCAGGAGGATGAA
TTGCTGGCCCTGGCAAGTATTTACGATGGAGATGAATTTAGAAAAGCAGAGTCTGTCCAAGGTGGAGAAACCAGG
ATCTATTTGGATTTGCCACAGAATTTCAAGATATTTGTGAGCGGCAATTCAAATGAGTGTCTCCAGAATAGTGGC
TTTGAATACACCATTTGCTTTCTGCCTCCACTTGTGCTGAACTTTGAACTGCCACCAGATTATCCATCCTCTTCC
CCACCTTCATTACACTTAGTGGCAAATGGCTGTCACCAACTCAGCTATCTGCTCTATGCAAGCACTTAGACAAC
CTATGGGAAGAACACCGTGGCAGCGTGGTCCTGTTTGCCTGGATGCAATTTCTTAAGGAAGAGACCCTAGCATAC
TTGAATATTGTCTCTCCTTTTGAGCTCAAGATTGGTTCTCAGAAAAAAGTGCAGAGAAGGACAGCTCAAGCTTCT
CCCAACACAGAGCTAGATTTTGGAGGAGCTGCTGGATCTGATGTAGACCAAGAGGAAATTGTGGATGAGAGAGCA
GTGCAGGATGTGGAATCACTGTCAAATCTGATCCAGGAAATCTTGGACTTTGATCAAGCTCAGCAGATAAAATGC
TTAATAGTAAATTGTTCCCTGTGCAGTATCTGTTTCTGTGAGAAAGCTGGGTAGTGAATGCATGTACTTCTTGGAG
TGCAGGCATGTGTACTGCAAAGCCTGTCTGAAGGACTACTTTGAAATCCAGATCAGAGATGGCCAGGTTCAATGC
CTCAACTGCCCAGAACCAAAGTGCCCTTCGGTGGCCACTCCTGGTCAGGTCAAAGAGTTAGTGAAGCAGAGTTA
TTTGCCCGTTATGACCGCCTTCTCCTCCAGTCCTCCTTGGACCTGATGGCAGATGTGGTGTACTGCCCCCGGCCG
TGCTGCCAGCTGCCTGTGATGCAGGAACCTGGCTGCACCATGGGTATCTGCTCCAGCTGCAATTTTGCCTTCTGT
ACTTTGTGCAGGTTGACCTACCATGGGGTCTCCCCATGTAAGGTGACTGCAGAGAAATTAATGGACTTACGAAAT
GAATACCTGCAAGCGGATGAGGCTAATAAAAGACTTTTGGATCAAAGGTATGGTAAGAGAGTGATTCAGAAGGCA
CTGGAAGAGATGGAAAAGTAAGGAGTGGCTAGAGAAGAACTCAAAGAGCTGCCCATGTTGTGGAACCTCCCATAGAG
AAATTAGACGGATGTAACAAGATGACATGTACTGGCTGTATGCAATATTTCTGTTGGATTTGCATGGGTTCTCTC
TCTAGAGCAAACCTTACAAACATTTCAATGACCCTGGTTACCATGTTTTAACCGGCTGTTTTATGCTGTGGAT
GTTGACGACGATATTTGGGAAGATGAGGTAGAAGACTAGTTAACTACTGCTCAAGATATGGAAGTGGATTGTTTT
TCCCTAATCTTCCGTCAAGTACACAAAGTAACCTTTGCGGGATATTTAGGGTACTATTCACTTCTTCTGCGT
AGAAGATATGGAAGAACGAGGTTTATATTTTCATGTGGTACTACTGAAGAAGGTGCATTGATACATTTTTAAATG
TAAGTTGAGAAAAATTTATAAGCCAAAGGTTCAAGAAATTAACTACAGAA

1855/6881
FIGURE 1721

CGCGGCGGCCTTTCTAGCCGCTGTCCCAAGGGTTGGTCTCGCGCTTTTCGGCTGCGAGCTCTCTGTGGTGCTGGCA
GCGACATGTGGCGCCTCCCGGGACTCCTGGGCCGAGCTCTTCCCGTACACTGGGACCTAGCCTCTGGAGGGTGA
CTCCTAAGTCCACCAGCCCAGATGGGCCTCAGACTACCTCCTCCACTTTGCTGGTTCTGTGCCTAACCTCGACA
GGTCAGGTCCCCATGGCCCAGGCACGAGCGGGGGTCCAAGGTCCCATGGATGGAAGGATGCCTTCCAATGGATGT
CTTCCCGTGTCTCCCCGAACACCCTATGGGATGCCATATCTTGGGGCACTCTGGCCGTGCTGGCCCTGCAGCTGG
CAAGGCAGATCCACTTCCAGGCATCCCTGCCAGCAGGACCTCAGCGGGTAGAACACTGCTCCTGGCACAGTCCCC
TGGACCGTTTCTTCTCATCTCCCTTGTGGCACCCATGCTCCTCACTGCGACAACACATCCTCCCCAGCCCCGATG
GCCCAGCTCCCAGGCACACTGGCCTCAGGGAACCCAGGCTTGGCCAGGAAGAAGCCTCAGCTCAGCCCCGGAAC
TCTCACACAACCTCTTTGAGAGGAGCTCGTCTCAGGACCCCTCTGAGGAAGGTCCCGGTGATTTTGGCTTCTGCTG
ATGCCAGTAGTAGCATCGAGTCCGAGGCAAAACCAGCCCAGCCTCAGCCCCTGGTGAAAAGGAACAAGATAAAT
CAAAAACCTCTTTCCCTTGGAGAGGCTGTGACTTCCATTGAGCAGCTCTTCCAGCTCAGTGTTCATCGCTTTCA
ACTTCTGGGAACAGAGAACATGAAGAGTGGCGACCACACGGCAGCCTTTTCTTACTTCCAGAAAAGCTGCAGCCC
GCGGCTACAGCAAAGCGCAGTACAATGCGGGCTTGTGTCATGAGCATGGCAGAGGCACCCCCAGGGACATTAGCA
AGGCGGTCTCTTATTATCAGTTGGCTGCCAGCCAGGGCCACAGCCTGGCTCAGTACCGCTATGCCAGGTGCCTAC
TACGAGACCCAGCCTCTTCGTGGAACCTGAGCGGCAGAGGGCAGTGTCTTGTGAAGCAGGCTGCAGACTCAG
GCTTGAGAGAGGCCAAGCTTTTCTCGGGGTGCTTTTACCAAGGAGCCCTACCTGGATGAGCAGAGAGCTGTGA
AATATCTTTGGCTTGCAGCCAACAATGGGGACTCACAGAGCAGGTACCACCTTGGAAATTTGCTATGAGAAAGGCC
TTGGTGTGCAGAGGAATCTGGGAGAGGCCTTGAGATGTTACCAGCAGTCAGCCGCTCTGGGAAATGAGGCCGCC
AGGAGAGGCTGCGAGCCCTCTTTTCCATGGGGGCTGCAGCCCCGGGGCCAGCGACCTGACAGTTACAGGACTGA
AGTCTTTTCTCCAGCCCCCTCCCTCTGCAGCTTGAACACCTGCTAGCAGGAACCTCACGCCTACCACATGCCTCGA
GCACAGGCAACCTTGGCCTCCTCTGCAGAAGTGGGCATCTCGGAGCCAGCCTGGAAGCCTCCAGCAGGGCTATTC
CCCCACACCCCTACCCACTGGAAAGGAGTGTGTGAAGACTAGGTTTTTGGCTTAAGGTGAGATAAAACATAGTCCCT
GGTGCCTCTTAGGGGCCAGAGCGGGCAGGAGGTTGGATAACAAAAATAGAGCATCAGCAACCCCTTTCAGGTAGA
AATTCCAGCGGGAGTTCAGGTTCCCAAGCAATTTACGTACATGGCTGGTAAGTGAAGTACTGATCTTTCCCCCGCTT
GGTAGCCTCACAGATGAGTCTTGGATGCATTACAGTCATTTCTGGTCTGTGCACCAAAGGATGCATTCAGTGAC
CTATGAAAAACCCCTACTGAAGGTCCAGAGACCCTGGTGCTCACCTTAGCCTTTGTCTTTGAGCAAATAACTTAC
CTTCTTCCTTCTTATGCCTGGGTTTTCTCACACTTAAATCTGTACTACTGTTTGCCAATGTCTGATGTGTGTATC
CCTGGTTCACAAGAAGATTTTAGATGGTATTCAAATTAATATTTTCTATTTAGTTATATATTTAATGTATAATAT
AAAAATATGATTAGCATATTGACCTGTAGTTTGATAGATGTTCTGTCTAGGATAAAGCTAACTGTAAAAAAAAT
AGTGAATCAGTTTAAAGAAAAACATAACGTAAAAGTGGGCACAGATCCAGAGAGGTAGCAAAAATCACAGGGGTG
GTTCCATGAATGGCTGACACTTAGGAACTCTGAATTAGGCCATCCTCGAGACTAGCCCACCATTACCTCTGTT
CATCCCCCGTGGGCTCATAATCGTTTTCATTTACCTTTGATTTGGAAGGAAGAAGTTTCTTGCCCAAATGCCTG
GATGTGTCTGCTTGACTTTCAGAACTTCTCACCTCAGCCCTAAAGAGGGAGCCTGTGGGTTCTCAGAGAGATATC
ACAATTTGAGTCCCAAAGAAGAGGCCAGATACCCACCCACCTTCCCCCAAATCTTAAGCACCTGCGCCAGTACAG
TCAAGAAGAGGAAAGTGTGTGAAGACCCAGGTCTGGCTCTGCCACTTGCTGGCCATGTACCTTGAAGCTGTGA
CCTGACTCCCTATATTGTTTCTCAGTTGTAGACCAAAGGCAATGGTGTCTGCCCTCCTACCTTAGAAGACAAAT
GCAAGGGCATTTCACCACAGAGAGGACCTTTGTGCTCACTTTGGCCCAGGAGGCAGTGATGCTCATGGTTGCATG
ACTTTATGAGTCGCTGGGCCAGGGTGGAGACCTGGGCCTCCTGACTCCTGGCCCAGAGTTCTTGTCCATCAGTTC
ATACTGCAATTTTATGTGAAAGCATTATGACTGTCTACCCATGGGAGAGTAAATGTAGATTGAATGCTAGGAGT
CTTAAAGCTGGAGAGTATAGATTTTGGAGTCCCCATTTGGGAAACATGTGCCAGAAATGTCTAGGTGTTTAATAA
AACAGATATTGGATTATCTC

1856/6881
FIGURE 1722

MWRLPGLLGRALPRTLGPSTLWRVTPKSTSPDGPQTTSSTLLVPVNLDRSGPHGPGTSGGPRSHGWKDAFQWMSS
RVSPNTLWDAISWGTLAVLALQLARQIHFAQSLPAGPQORVEHCSWHSPLDRFFSSPLWHPCSSLRQHILPSPDGP
APRHTGLREPRLGQEEASAQPRNFSHNSLRGARPQDPSEEGPGDFGFLHASSSIESEAKPAQPQPTGEKEQDKSK
TSLLEEAVTSIQQLFQLSVSIAFNFLGTENMKSGDHTAAFSYFQKAAARGYSKAQYNAGLCHEHGRGTFRDISKA
VLYYQLAASQGHSLAQYRYARCLLRDPASSWNPERQRAVSLLKQAADSGLREAQAFGLGVLFTEPEYLDEQRAVKY
LWLAANNQDSQSRYHLGICYEKGLGVQRNLGEALRCYQQAALGNEAAQERLRALFSMGAAAPGPSDLTVTGLKS
FSSPSLCSLNTLLAGTSRLPHASSTGNLGLLCRSGHLGASLEASSRAIPHPYPLERSVVRLGFG

1857/6881
FIGURE 1723A

GCCCTCCTGATTCTGGGGCCTCCCAGGATGGAGCACCTGAGGCACAGCCCAGGCCCTGGGGGGCAACGGCTACTG
CTGCCCTCCATGCTGCTAGCACTGCTGCTCCTGCTGGCTCCATCCCCAGGCCACGCCACTCGGGTAGTGTAACA
GTGCCGGAGGAACAGCCACCCAACACCCCTCATTGGGAGCCTCGCAGCCGACTATGGTTTTCCAGATGTGGGGCAC
CTGTACAAGCTAGAGGTGGGTGCCCCGTACCTTCGCGTGGATGGCAAGACAGGTGACATTTTCACCACCGAGACC
TCCATCGACCGTGAGGGGGCTCCGTGAATGCCAGAACCAGCTCCCTGGTGATCCCTGCATCCTGGAGTTTGAGGTA
TCTATCACAGACCTCGTGCGAATGGCAGCCCCCGGTGCTAGAGGGCCAGATAGAAGTACAAGACATCAATGAC
AACACACCCAACCTTCGCTCACCAGTCACTACTCTGGCCATCCCTGAGAACACCAACATCGGCTCACTCTTCCCC
ATCCCGCTGGCTTCAGACCGTGATGCTGGTCCCAACGGTGTGGCATCCTATGAGCTGCAGGTGGCAGAGGACCAG
GAGGAGAAGCAACCACAGCTCATTGTGATGGGCAACCTGGACCGTGAGCGCTGGGACTCCTATGACCTCACCATC
AAGGTGCAGGATGGCGGCAGCCCCCACGCGCCAGCAGTGCCCTGCTGCGTGTACCGTGCTTGACACCAATGAC
AACGCCCCCAAGTTTGAGCGGCCCTCCTATGAGGCCGAATATCTGAGAAATAGCCCCATAGGCCACTCGGTCATC
CAGGTGAAGGCCAATGACTCAGACCAAGGTGCCAATGCAGAAATCGAATACACATTCCACCAGGCGCCCGAAGTT
GTGAGGCGTCTTCTTCGACTGGACAGGAACACTGGACTTATCACTGTTTCAGGGCCCGGTGGACCGTGAGGACCTA
AGCACCCCTGCGCTTCTCAGTGCTTGCTAAGGACCGAGGCACCAACCCCAAGAGTGCCCGTGCCAGGTGGTTGTG
ACCGTGAAGGACATGAATGACAATGCCCCACCATTGAGATCCGGGGCATAGGGCTAGTGACTCATCAAGATGGG
ATGGCTAACATCTCAGAGGATGTGGCAGAGGAGACAGCTGTGGCCCTGGTGCAGGTGTCTGACCGAGATGAGGGA
GAGAATGCAGCTGTCACTGTGTGGTGGCAGGTGATGTGCCCTTCAGCTGCGCCAGGCCAGTGAGACAGGCAGT
GACAGCAAGAAGAAGTATTTCTGCAGACTACCACCCCGCTAGACTACGAGAAGGTCAAAGACTACACCATTGAG
ATTGTGGCTGTGGACTCTGGCAACCCCCACTCTCCAGCACTAACTCCCTCAAGGTGCAGGTGGTGGACGTCAAT
GACAACGCACCTGTCTTCACTCAGAGTGTCACTGAGGTGCGCTTCCCGAAAACAACAAGCCTGGTGAAGTGATT
GCTGAGATCACTGCCAGTGATGCTGACTCTGGCTCTAATGCTGAGCTGGTTTACTCTCTGGAGCCTGAGCCGGCT
GCTAAGGGCCTCTTACCATCTCACCAGAGCTGGAGAGATCCAGGTGAAGACATCTCTGGATCGGGAACAGCGG
GAGAGCTATGAGTTGAAGGTGGTGGCAGCTGACCGGGGAGTCCTAGCCTCCAGGGCACAGCCACTGTCTTGTG
AATGTGCTGGACTGCAATGACAATGACCCCAATTTATGCTGAGTGGCTACAACCTTCTCAGTGATGGAGAACATG
CCAGCACTGAGTCCAGTGGGCATGGTGAAGTGTCACTGATGGAGACAAGGGGAGAATGCCAGGTGCAGCTCTCA
GTGGAGCAGGACAACGGTGACTTTGTTATCCAGAATGGCACAGGCACCATCCTATCCAGCCTGAGCTTTGATCGA
GAGCAACAAAGCACCTACACCTTCCAGCTGAAGGCAGTGGATGGTGGCGTCCACCTCGCTCAGCTTACGTTGGT
GTCACCATCAATGTGCTGGACGAGAATGACAACGCACCCTATATCACTGCCCCCTTCTAACACCTCTCACAAGCTG
CTGACCCCCCAGACACGTCTTGGTGAGACGGTCAGCCAGGTGGCAGCCGAGGACTTTGACTCTGGTGTCAATGCT
GAGCTGATCTACAGCATTGCAGGTGGCAACCCCTTATGGACTCTTCCAGATTGGGTACATTTCAGGTGCCATCACC
CTGGAGAAGGAGATTGAGCGGCGCCACCATGGGCTACACCGCCTGGTGGTGAAGGTGAGTACCGCGGCAAGCCC
CCACGCTATGGCACAGCCTTGGTCCATCTTTATGTCAATGAGACTCTGGCCAACCGCACGCTGCTGGAGACCCTC
CTGGGCCACAGCCTGGACACGCGCGCTGGATATTGACATTGCTGGGGATCCAGAATATGAGCGCTCCAAGCAGCGT
GGCAACATTCTCTTTGGTGTGGTGGCTGGTGTGGTGGCCGTGGCCTTGCTCATCGCCCTGGCGGTTCTTGTGCGC
TACTGCAGACAGCGGGAGGCCAAAAGTGGTTACCAGGCTGGTAAGAAGGAGACCAAGGACCTGTATGCCCCCAAG
CCAGTGGCAAGGCCTCCAAGGGAAACAAAAGCAAAGGCAAGAAGAGCAAGTCCCCAAAGCCCGTGAAGCCAGTG
GAGGACGAGGATGAGGCCGGGCTGCAGAAGTCCCTCAAGTTCAACCTGATGAGCGATGCCCCTGGGGACAGTCCC
CGCATCCACCTGCCCCCTCACTACCCACCAGGCAGCCCTGACCTGGGCGGCCACTATCGCTCTAACTCCCCACTG
CCTTCCATCCAGCTGCAGCCCCAGTCACCCCTCAGCCTCCAAGAAGCACAGGTGGTACAGGACCTGCCACCTGCA
AACACATTCTGTGGGCACCGGGGACACCAGTCCACGGGCTCTGAGCAGTACTCCGACTACAGCTACCGCACCAAC
CCCCCAAATACCCAGCAAGCAGTTACCTCACCAGCGCGCTCACCTTCTCGGCCACCAGCCAGGCCCAGGAGCTG
CAGGACCCATCCCAGCACAGTTACTATGACAGTGGCCTGGAGGAGTCTGAGACGCCGTCCAGCAAGTCATCTCA
GGGCTCGACTCGGTCCCCTGGCCCTGCCTGAGGATCACTATGAGCGCACCAACCCCTGATGGCAGCATAGGAGAG
ATGGAGCACCCCGAGAATGACCTTCGCCCTTTGCCTGATGTGCGCATGACAGGCACATGTACCCGGGAGTGCACT
GAGTTTGGCCACTCTGACACATGCTGGATGCCTGGCCAGTCATCTCCCAGCCGCGGACCAAGAGCAGCGCCCTC
AAACTCTCCACCTTCGTGCCCTTACCAGGACCGAGGAGGGCAGGAGCCTGCGGGCGCCGGCAGCCCCAGCCCCCG
GAAGACCGGAACACCAAAACGGCCCCCGTGCGCCTCCTGCCCTCTACAGTGCCCTTCTCCACAGTAGCCATGAT
TCTGCAAGGACTCGGCCACCTTGGAGGAAATCCCCCTGACCCAGACCTCGGACTTCCACCCGAGCCACACCG

1858/6881
FIGURE 1723B

GCATCTGCCCAGACGGCCAAGCGCGAGATCTACCTGTGAGCCCCCTACTGGCCGGCCGGCCCCCTCCCCCAGCC
GCCGGCCAGCTCCCAAATGGCCCATTCAGGGCCTCACTCTCCACCCCTTCAGCGTGGACTTCCTGGCCAGGGCC
CCAAGTGGGGGTATCACTGACCTCATGACCACGCTGGCCCTTCTCCCATGCAGGGTCCAGGTCTCTCCCTCAT
TTCCATCTCCCAGCCCCAGGGGCCCTTCCCCTTTATGGGGCTTCCCCATCTGATGCCCAAGAGGGCTCCTCT
GCAATGACTGGGCTCCTTCCCTTGACTTCCAGGGAGCACCCCTCGATTTGGGCAGATGGTGGAGTCAAGGGTGG
GCAGCGTACTTCTAACTCATTGTTTCCCTCATGGCCGACCAGGGCGGGGATAGCATGCCCAATTTAGCCCTGAA
GCAGGGCTGAACTGGGGAGCCCCCTTCCCTGGGAGCTCCAGAGGAACTCTTGACCACCAGTGGCTCCCTGAAG
GGCTTTTGTTACCAAAGGTGGGGTAGGGACGGGGGTGGGAGTGGAGCGGAGGCCTTGTTTTCCCGTG

1859/6881
FIGURE 1724

GGAGACGCTTCTTCCTCTTGCTGCTCTTCTCGTTCCCCGAGATCAGCGGCGGCGGTGACCGCGAGTGGGTGCGGCAC
CGTCTCCGGCTCCGGGTGCGAACAATGCTGACTGATAGCGGAGGCGGCGGCACCTCCTTTGAGGAGGACCTGGAC
TCTGTGGCTCCGCGATCCGCCCCAGCTGGGGCCTCGGAGCCGCTCCGCCGGGAGGGGTCTGGTCTGGGGATCCGC
ACCGTGAGGCTCTTTGGGGAGGCCGGGCCAGCGTCGGGAGTCGGCAGCAGCGGCGGCGGCGGCAGCGGCAGCGGT
ACGGGCGGAGGGGACGCGGCGCTGGATTTCAAGTTGGCGGCTGCCGTGCTGAGGACCGGGGTGGAGGTGGTGCC
TCTGGCAGTGACGAGGACGAAGTGTCCGAGGTTGAATCATTTATTTTGACCAAGAAGATCTGGATAACCCAGTG
CTTAAACAACATCAGAGATATTCTTATCAAGTACTGCAGAAGGAGCAGACTTACGCACTGTGGATCCAGAGACA
CAGGCACGACTAGAAGCATTGCTAGAAGCAGCAGGAATTGGCAAATTGTCAACTGCTGATGGTAAAGCTTTTGCA
GATCCTGAGGTACTCCGGAGACTGACATCCTCAGTTAGTTGTGCACTGGATGAAGCTGCTGCTGCACTGACACGG
ATGAAGCAGAAAAACAGCCACAATGCAGGACAAGTGGACACTCGCAGTCTAGCAGAAGCTTGTTTCAGATGGGGAT
GTTAATGCTGTTTCGTAAATTGCTAGATGAAGGCAGAAGTGTAATGAACATACAGAAGAAGGAGAAAGCCTGCTG
TGTTTGGCTTGTTTCAGCAGGGTATTATGAATTAGCACAAAGTATTGCTTGCTATGCATGCTAATGTTGAAGATCGA
GGGAATAAAGGAGACATAACTCCCCTGATGGCAGCTTCCAGTGGAGGTTACTTAGATATTGTGAAATTATTACTT
CTTCATGATGCTGATGTCAACTCCCAGTCTGCAACAGGAAAACACTGCGCTAACTTATGCATGTGCTGGAGGATTT
GTTGACATTGTTAAAGTGCTCCTTAATGAAGGTGCAAATATAGAAGATCATAATGAAAATGGACATACTCCCTTA
ATGGAAGCAGCCAGTGCAGGTCATGTGGAAGTTGCAAGAGTTCTTTTAGATCATGGTGCAGGCATCAACACTCAT
TCTAATGAATTCAAAGAAAGTGCTCTAACACTTGCTTGCTACAAAGGCCATTTGGATATGGTTTCGCTTTCTACTT
GAAGCTGGTGCAGATCAAGAGCACAAAACAGATGAGATGCACACTGCCTTAATGGAGGCCTGCATGGATGGACAT
GTAGAGGTGGCACGTTTGCTTTTGGATAGTGGTGCTCAAGTGAACATGCCTGCAGATTCATTTGAATCTCCATTG
ACGCTAGCTGCCTGTGGAGGACATGTTGAATTGGCAGCTCTACTTATTGAAAGGGGAGCAAATCTTGAAGAAGTT
AATGATGAAGGATACACTCCCTTGATGGAAGCTGCCCCGGAAGGACATGAAGAAATGGTGGCACTACTCTTAGCA
CAAGGAGCAAATATAAATGCCAGACAGAAGAACTCAAGAACTGCTCTTACTTTGGCTTGCTGTGGAGGATTT
TCTGAAGTTGCAGACTTTCTTATTAAGGCAGGGGCTGATATAGAACTTGGCTGCTCCACACCTCTGATGGAGGCA
TCTCAGGAGGGACACCTGGAATTGGTTAAATATTTGCTGGCTTCTGGCGCTAATGTGCATGCTACAACAGCAACA
GGAGACACAGCCTTAACCTATGCTTGTGAAAATGGACATACGGATGTTGCAGATGTTTTACTTCAAGCAGGGGCT
GATTTAGACAAGCAGGAGGACATGAAGACTATTTTGGAGGGCATAGATCCGGCCAAGCATCAGGTGAGGGTGGCC
TTTGATGCTTGTAAGCTACTACGTAAAGAATAGATGTTGTAGGTAACCAGAACTCTGGATATCTGAATTCCAGCC
AAGAAGTTCCAGGACCCTGCTGGGTGACAAAGGAAATCCTCTTCAATTGAAAAAGATTATGAAGTCCCAATAAAA
AGAGATTTGTATTGCTGGTAAAAAAAAAAAAAAAAAAAAA

1860/6881
FIGURE 1725

MKAENSHNAGQVDTRSLAEACSDGDVNAVRKLLDEGRSVNEHTEEGESLLCLACSAGYYELAQVLLAMHANVEDR
GNKGDITPLMAASSGGYLDIVKLLLLHDADVNSQSATGNTALTYACAGGFVDIVKVLLNEGANIEDHNENGHTPL
MEAASAGHVEVARVLLDHGAGINTHSNEFKESALTACYKGHLDMVRFLLEAGADQEHKTDEMHTALMEACMDGH
VEVARLLLD SGAQVNMPADSFESPLTLAACGGHVLAALLIERGANLEEVNDEGYTPLMEAAREGHEEMVALLLA
QGANINAQTEETQETALTACCGGFSEVADFLIKAGADIELGCSTPLMEASQEGHLELVKYLILASGANVHATTAT
GDTALTYACENGHTDVADVLLQAGADLDKQEDMKTILEGIDPAKHQVRVAFDACKLLRKE

1861/6881
FIGURE 1726

GGCACGAGGGCGGGGAAGATGGCGGATGACAAGGATTCTCTGCCTAAGCTTAAGGACCTGGCATTCTCTCAAGAAC
CAGCTGGAAAGCCTGCAGCGGCGTGTAGAAGACGAAGTCAACAGTGGAGTGGGCCAGGATGGCTCGCTGTTGTCC
TCCCCGTTCTCAAGGGATTCTCTGGCTGGCTATGTGGTGGCCAAACTGAGGGCATCAGCAGTATTGGGCTTTGCT
GTGGGCACCTGCACTGGCATCTATGCGGCTCAGGCATATGCTGTGCCAACGTGGAGAAGACATTAAGGGACTAT
TTGCAGTTGCTACGCAAGGGGCCCCGACTAGCTCTAGGTGCCATGGAAGAGGCAGGATGAGCAGCTCAGCCTTCAG
GTGGAGACACTTTATCTGGATTCCCCAGCTGTCACTCCATTTGCTATCTCCAACCTTCCCTGCCACCTTCATCCTTG
CCTCCCTTCTGCAAGATTGTGGACAGTAGTTCTCTCAGCCTGCACCCTGGATTCCCTTCTTCCCCTTCTAGCTCCA
TGGGACTCGCCCCAAGACTGTGGCTTCAAGGACCACCAGCCCCCTTACTCTTCAAGCCCTGACTGTGGAGTTGGTA
GATGCCTCTGATCCTCAGTATTCTCTCTGGCAATGTTCCACGGCTTCTCCTTCTGGGAGCTGGCTCCATAACTT
GATTTTCCCCAAACGTGTTGCAATCCCTGCTGCCCCCTTAGCCACCCAGGGTCTTGTGTGGGTATGAGTGTAGAGG
ATGGGGGTATGCCAGGCCCTGGGCGCTCCCAGGCAGGCCCGCTGGACCCTGATGCTACTCCTATCCACTGCCATGT
ACGGTGCCCATGCCCATTTGCTGGCACTGTGCCATGTGGACGGCCGAGTGCCCTTCCGGCCCTCCTCAGCCGTGC
TGCTGACTGAGCTGACCAAGCTACTGTTATGCGCCTTCTCCCTTCTGGTAGGCTGGCAAGCATGGCCCCAGGGGC
CCCCACCCTGGCGCCAGGCTGCTCCCTTCGCACTATCAGCCCTGCTCTATGGCGCTAACAACAACCTGGTGATCT
ATCTTCAGCGTTACATGGACCCCAGCACCTACCAGGTGCTGAGTAATCTCAAGATTGGAAGCACAGCTGTGCTCT
ACTGCCTCTGCC'TCCGGCACCGCCTCTCTGTGCGTCAGGGGTTAGCGCTGCTGCTGCTGATGGCTGCGGGAGCCT
GCTATGCAGCAGGGGGCCTTCAAGTTCCCGGGAACACCCTTCCCAGTCCCCCTCCAGCAGCTGCTGCCAGCCCCA
TGCCCCCTGCATATCACTCCGCTAGGCCTGCTGCTCCTCATTCTGTACTGCCTCATCTCAGGCTTGTCTCAGTGT
ACACAGAGCTGCTCATGAAGCGACAGCGGCTGCCCTGGCACTTCAGAACCTCTTCTCTACACTTTTGGTGTGC
TTCTGAATCTAGGTCTGCATGCTGGCGGCGGCTCTGGCCCAGGCCTCCTGGAAGGTTTCTCAGGATGGGCAGCAC
TCGTGGTGCTGAGCCAGGCCTAAATGGACTGCTCATGTCTGCTGCTCATGAAGCATGGCAGCAGCATCACACGCC
TCTTTGTGGTGTCTGCTCGCIGGTGGTCAACGCCGTGCTCTCAGCAGTCTGCTACGGCTGCAGCTCACAGCCG
CCTTCTTCTGGCCACATTGCTCATTGGCCTGGCCATGCGCCTGTACTATGGCAGCCGCTAGTCCCTGACAACTT
CCACCCTGATTCGGACCCTGTAGATTGGGCGCCACCACCAGATCCCCCTCCAGGCCTTCTCCTCTCCCATC
AGCAGCCCTGTAACAAGTGCCTTGTGAGAAAAGCTGGAGAAGTGAGGGCAGCCAGGTTATTCTCTGGAGGTTGGT
GGATGAAGGGGTACCCCTAGGAGATGTGAAGTGTGGGTTTGGTTAAGGAAATGCTTACCATCCCCACCCCCAAC
CAAGTTCTTCCAGACTAAAGAATTAAGGTAACATCAATACCTAGGCCTGAGAAATAACCCCATCCTTGTTGGGCA
GCTCCCTGCTTTGTCTGCTGATGAACAGAGTTGATGAAAGTGGGGTGTGGGCAACAAGTGGCTTTCTTGCCTACT
TTAGTCACCCAGCAGAGCCACTGGAGCTGGCTAGTCCAGCCCAGCCATGGTGCATGACTCTTCCATAAGGGATCC
TCACCCTTCCACTTTTCATGCAAGAAGGCCAGTTGCCACAGATTATACAACCATTACCCAAACCACTCTGACAGT
CTCCTCCAGTTCCAGCAATGCCTAGAGACATGCTCCCTGCCCTCTCCACAGTGCTGCTCCCCACACCTAGCCTTT
GTTCTGGAAACCCAGAGAGGGCTGGGCTTGACTCATCTCAGGGAATGTAGCCCCTGGGCCCTGGCTTAAGCCGA
CACTCCTGACCTCTCTGTTACCCCTGAGGGCTGTCTTGAAGCCCGCTACCCACTCTGAGGCTCCTAGGAGGTACC
ATGCTTCCCACTCTGGGGCCTGCCCTGCTAGCAGTCTCCCAGCTCCCAACAGCCTGGGGAAGCTCTGCACAGA
GTGACCTGAGACCAGGTACAGGAAACCTGTAGCTCAATCAGTGTCTCTTTAACTGCATAAGCAATAAGATCTTAA
TAAAGTCTTCTAGGCTGTAGGGTGGTTCTACAACCACAGCAAAAAAAAAAAAAAAAAAAAAA

1862/6881
FIGURE 1727

MSVEDGGMPGLGRPRQARWTLMLLLSTAMYGAHAPLLALCHVDGRVPFRPSSAVLLTELTKLLLCAFSLLVGWQA
WPQGPPPWQAAPFALSALLYGANNNLVIYLQRYMDPSTYQVLSNLKIGSTAVLYCLCLRHRLSVRQGLALLLLM
AAGACYAAGGLQVPGNTLPSPPAAAAASPMPPLHITPLGLLLLLILYCLISGLSSVYTELLMKRQRLPLALQNLFY
TFGVLLNLGLHAGGGSGPGLLEGFSGWAALVVLSQALNGLLMSAVMKHGSSITRLFVVSCSLVVNAVLSAVLLRL
QLTAAFFLATLLIGLAMRLYYGSR

1863/6881
FIGURE 1728A

CAGAAAGCCATGTCGGACTCGGCGCCAGCGCCCAAGCGCTAACCCGCTGAAAGTTTCTCAGCGAAATCTCAGGG
ACGATCTGGACCCCGCTGAGAGGAACTGCTTTTGAGTGAGATGGTCCCAGAGGCCTGGAGGAGCGGACTGGTAAG
CACCGGGAGGGTAGTGGGAGTTTTGCTTCTGCTTGGTGCCCTTGAACAAGGCTTCCACGGTCATTCACTATGAGAT
CCCGGAGGAAAGAGAGAAGGGTTTTGCTGTGGGCAACGTGGTCGCGAACCTTGGTTTGGATCTCGGTAGCCTCTC
AGCCCGCAGGTTCCGGGTGGTGTCTGGAGCTAGCCGAAGATTCTTTGAGGTGAACCGGGAGACCGGAGAGATGTT
TGTGAACGACCGTCTGGATCGAGAGGAGCTGTGTGGGACACTGCCCTCTTGCACTGTAACCTCTGGAGTTGGTAGT
GGAGAACCCGCTGGAGCTGTTTCAAGCTGGAAGTGGTGATCCAGGACATCAACGACAACAATCCTGCTTTCCCTAC
CCAGGAAAATGAAATTGGAGATTAGCGAGGCCGTGGCTCCGGGGACGCGCTTTCCGCTCGAGAGCGCGCACGATCC
CGATGTGGGAAGCAACTCTTTACAAACCTATGAGCTGAGCCGAAATGAATACTTTGCGCTTCGCGTGCAGACGCG
GGAGGACAGCACCAAGTACGCGGAGCTGGTGTGGAGCGCGCCCTGGACCGAGAACGGGAGCCTAGTCTCCAGTT
AGTGCTGACGGCGTTGGACGGAGGGACCCAGCTCTCTCCGCCAGCCTGCCTATTACATCAAGGTGCTGGACGC
GAATGACAATGCGCCTGTCTTCAACCAGTCCTTGTACCGGGCGCGCGTCTGGAGGATGCACCCCTCCGGCACGCG
CGTGGTACAAGTCTTGAACGGATCTGGATGAAGGCCCAACGGTGAAATTATTTACTCCTTCGGCAGCCACAA
CCGCGCCGGCGTGCAGCAACTATTGCGCTTAGACCTTGTAAACGGGATGCTGACAATCAAGGGTCGGCTGGACTT
CGAGGACACCAAACCTCCATGAGATTTACATCCAGGCCAAAGACAAGGGCGCAATCCCGAAGGAGCACATTGCAA
AGTGTGGTGGAGTTGTGGATGTGAATGACAACGCCCCGAGATCACAGTCACCTCCGTGTACAGCCAGTACC
CGAGGATGCCCTCTGGGACTGTCATCGCTTGTCTAGTGTGACTGACCTGGATGCTGGCGAGAACGGGCTGGT
GACCTGCGAAGTTCCACCGGTCTCCCTTTACGCTTACTTCTTCCCTCAAGAATTACTTCACTTTGAAAACAG
TGCAGACCTGGATCGGGAGACTGTGCCAGAATAACAACCTCAGCATCACCGCCGAGACGCCGGAACCCCTTCCCT
CTCAGCCCTTACAATAGTGCCTGTTCAAGTGTCCGACATCAATGACAACCCCTCCACAATCTTCTCAATCTTCTTA
CGACGTTTACATTGAAGAAAACAACCTCCCCGGGGCTCCAATACTAAACCTAAGTGTCTGGGACCCCGACGCCCC
GCAGAATGCTCGGCTTTCTTTCTTCTTCTTGGAGCAAGGAGCTGAAACCGGGCTAGTGGGTGCTATTTTACAAT
AAATCGTGACAATGGCATAGTGTATCCTTAGTGCCCTTAGACTATGAGGATCGGCGGGAATTTGAATTAACAGC
TCATATCAGCGATGGGGGACCCCGGTCTAGCCACCAACATCAGCGTGAACATATTTGTCACTGATCGCAATGA
CAATGCCCCCAGTCTATATCCTCGGCCAGGTGGGAGCTCGGTGGAGATGCTGCCTCGAGGTACCTCAGCTGG
CCACCTAGTGTACGGGTGGTAGGCTGGGACGCGGATGCAGGGCACAATGCCTGGCTCTCCTACAGTCTCTTGGG
ATCCCTTAACCAGAGCCTTTTTGCCATAGGGCTGCACACTGGTCAAATCAGTACTGCCCGTCCAGTCCAAGACAC
AGATTACCCAGGCAGACTCTCACGGTCTTGATCAAAGACAATGGGGAGCCTTCGCTCTCCACCACTGCTACCCT
CACTGTGTAGTAACCGAGGACTCTCCTGAAGCCCCGAGCCGAGTTCCCTCTGGCTCTGCCCCCGGGAGCAGAA
AAAAAATCTCACCTTTTATCTACTTCTTTCTCTAATCCTGGTTTCTGTGGGGTTTGTGGTTCAGTGTTCGGAGT
AATCATATTCAAAGTTTACAAGTGGAAGCAGTCTAGAGACCTATACCGAGCCCCGGTGAGCTCACTGTACCGAAC
ACCAGGGCCCTCCTTGCACGCGGACGCCGTGCGGGGAGGCTGATGTGCGCGCACCTTTACCATCAGTGTATCT
CACCACGGACTCCCGCCGACGCGACCCGCTGCTGAAGAAACCTGGTGCAGCCAGTCCACTGGCCAGCCGCCAGAA
CACGCTGCGGAGCTGTGATCCGGTGTCTATAGGCAGGTGTTGGGTGCAGAGAGCGCCCTCCCGGACAGCAAGC
CCCGCCCAACACGACTGGCGTTTCTCTCAGGCCAGAGACCCGGCACCAGCGGCTCCCAAAATGGCGATGACAC
CGGCACCTGGCCCAACAACAGTTTGACACAGAGATGCTGCAAGCCATGATCTTGGCGTCCGCCAGTGAAGCTGC
TGATGGGAGCTCCACCCTGGGAGGGGGTGCCGGCACCATGGGATTGAGCGCCCGCTACGGACCCAGTTCACCT
GCAGCACGTGCCGACTACCGCCAGAATGTCTACATCCAGGCAGCAATGCCACACTGACCAACGCAGCTGGCAA
GCGGGATGGCAAGGCCCCAGCAGGTGGCAATGGCAACAAGAAGTGGGCAAGAAGGAGAAGAAGTAAACATGG
AGGCCAGGCCAAGAGCCACAGGGCGGCTCTCCCCAACAGCCAGCTTCTCCTTACCTGCACCCAGGCTCAGA
GTTTCAGGGCTAACCCCAAGAATACTGGTAGGGGCAAGGCCATGCTCCCTTGGGAAACAGAAACAAGTGCCCA
GTCAGCACCTACCCCTTCCCCCAGGGGGTTGAATATGCAAAAGCAGTTCCGCTGGGAACCCCATCCAATCAA
CTGCTGTACCCATGGGGGTAGTGGGGTTACTGTAGACACCAAGAACCATTGTCACACCCCGTTTAGTTACAGCT
GAACTCCTCCATCTTCCAAATCAATCAGGCCATCCATCCCATGCCTCCCTCCTCCCCACCCACTCCAACAGTT
CCTCTTTCCCGAGTAAGGTGGTGGGGTGTGAAAGTACCAAGTAACCTACAAGCCTCCTAGTTCTGAAAAGTTGG
AAGGGCATCATGACCTCTTGGCCTCTCCTTTGATTCTCAATCTTCCCCAAAGCATGGTTTGGTGCCAGCCCCCTT
CACCTCCTTCCAGAGCCCAAGATCAATGCTCAAGTTTTGGAGGACATGATCACCATCCCCATGGTACTGATGCTT
GCTGGATTTAGGGAGGGCATTCTTGTACCAAGCCTCTTCCCAACGCCCTGGGGACCAGTCTTCTGTTTTGTTTT

1864/6881
FIGURE 1728B

CATTGTTTGACGTTTCCACTGCATGCCTTGACTTCCCCACCTCCTCCTCAAACAAGAGACTCCACTGCATGTTT
CAAGACAGTATGGGGTGGTAAGATAAGGAAGGGAAGTGTGTGGATGTGGATGGTGGGGGCATGGACAAAGCTTGA
CACATCAAGTTATCAAGGCCTTGGAGGAGGCTCTGTATGTCCTCAGGGGACTGACAACATCCTCCAGATTCCAGC
CATAAACCAATAACTAGGCTGGACCCTTCCCACTACATAATAGGGCTCAGCCCAGGCAGCCAGCTTTGGGGCTGAG
CTAACAGGACCAATGGATTAACTGGCATTTCAGTCCAAGGAAGCTCGAAGCAGGTTTAGGACCAGGTCCCCCTTG
AGAGGTGAGAGGGGGCCTCTGTGGGTGCTGGGTACTCCAGAGGTGCCACTGGTGGAAGGGTCAGCGGAGCCCCAGC
AGGAAGGGTGGGCCAGCCAGGCCATTCTTAGTCCCTGGGTTGGGGAGGCAGGGAGCTAGGGCAGGGACCAAATGA
ACAGAAAGTCTCAGCCCAGGATGGGGCTTCTTCAACAGGGCCCCCTGCCCTCCTGAAGCCTCAGTCCTTCACCTTG
CCAGGTGCCGTTTCTCTTCCGTGAAGGCCACTGCCCAGGTCCCCAGTGCGCCCCCTAGTGGCCATAGCCTGGTTA
AAGTTCCCCAGTGCTCCTTGTGCATAGACCTTCTTCTCCACCCCCCTTCTGCCCCCTGGGTCCCCGGCCATCCAG
CGGGGCTGCCAGAGAACCCAGACCTGCCCTTACAGTAGTGTAAGCGCCCCCTCCCTCTTTTCGGCTGGTGTAGAAT
AGCCAGTAGTGTAAGTGCGGTGTGCTTTTACGTGATGGCGGGTGGGCAGCGGGCGGCGGGCTCCGCGCAGCCGTCT
GTCCTTGATCTGCCGCGGCGGCCCGTGTGTGTTTTGTGCTGTGTCCACGCGCTAAGGCGACCCCCCTCCCCGT
ACTGACTTCTCCTATAAGCGCTTCTCTTCGCATAGTCACGTAGCTCCCACCCACCCTCTTCTGTGTCTCACGC
AAGTTTTATACTCTAATATTTATATGGCTTTTTTTCTTCGACAAAAAATAATAAAACGTTTCTTCTGAAAAGCT
G

1865/6881
FIGURE 1729

MVPEAWRSGLVSTGRVVGVLALLGALNKASTVIHYEIPEREKGFVGNVAVNLGLDLGSLSSARRFRVVS GASRR
FFEVRNRETGEMFVNDRDLREELCGTLPSCVTLELVVENPLELFSVEVVIQDINDNNPAFPTQEMKLEISEAVAP
GTRFPLESAHDPDVGSNSLQTYELSRNEYFALRVQTREDSTKYAELVLERALDREREPSLQLVLTALDGGTPALS
ASLPIHIKVL DANDNAPVFNQSLYRARVLEDAPSGTRVVQVLATDLDEGPNGEIIYSFGSHNRAGVRQLFALDLV
TGMLTIKGRDLDFEDTKLHEIYIQAKDKGANPEGACHCKVLVEVVDVNDNAPEITVTSVYSPVPEDAPLGTVIALLS
VTDLDAGENGLVTCEVPPGLPFSLTSSLKNYFTLTKTSADLDRETVP EYNLSITARDAGTPSLSALTIVRVQVSDI
NDNPPQSSQSSYDVYIEENNLP GAPILNLSVWDPDAPQNARLSFFLLEQGAETGLVGRYFTINRDNGIVSSLVPL
DYEDRREFELTAHISDGGTPVLATNISVNIFVTDNRNDNAPQVLYPRPGGSSVEMLPRGTSAGHLVSRVVGWDADA
GHNAWLSYSLLGSPNQSLFAIGLHTGQISTARPVQD TDS PRQTLTVLIKDNGEPSLSTTATLTVSVTEDSPEARA
EFPSGSAPREQKNLTFYLLLSLILVSVGFVVTVFGV IIFKVYKWKQSRDLYRAPVSSLYRTPGPSLHADAVRGG
LMSPHLYHQVYLTTDSRRSDPLLKKPGAASPLASRQNTLRSCDPVFYRQVLGAESAPPGQQAPPNTDWRFSQAQR
PGTSGSQNGDDTGTWPNNQFDTEMLQAMILASASEAADGSSTLGGGAGTMGLSARYGPQFTLQHVPDYRQNVYIP
GSNATLTNAAGKRDGKAPAGGNGNKKKSGKKEKK

1866/6881
FIGURE 1730A

ACGCGCCTGAAGCACAAAGCAGATAGCTAGGAATGAACCATCCCTGGGAGTATGTGGAAACAACGGAGGAGCTCT
GACTTCCCAACTGTCCCATTCTATGGGCGAAGGAAGTGTCTCTGACTTCAGTGGTTAAGGGCAGAATTGAAAATA
ATTCTGGAGGAAGATAAGA**ATG**ATTCTCTGCGCGACTGCACCGGGACTACAAAGGGCTTGCTCTGCTGGGAATCCT
CCTGGGGACTCTGTGGGAGACCGGATGCACCCAGATACGCTATTTCAGTTCCGGAAGAGCTGGAGAAAAGGCTCTAG
GGTGGGCGACATCTCCAGGGACCTGGGGCTGGAGCCCCGGGAGCTCGCGGAGCGCGGAGTCCGCATCATCCCCAG
AGGTAGGACGCAGCTTTTCGCCCTGAATCCGCGCAGCGGCAGCTTGGTCACGGCGGGCAGGATAGACCGGGAGGA
GCTCTGTATGGGGGCCATCAAGTGTCAATTAAATCTAGACATTCTGATGGAGGATAAAGTGAAAATATATGGAGT
AGAAGTAGAAGTAAGGGACATTAACGACAATGCGCCTTACTTTCTGTGAAAGTGAATTAGAAATAAAAAATTAGTGA
AAATGCAGCCACTGAGATGCGGTTCCCTCTACCCCCACGCCTGGGATCCGGATATCGGGAAGAACTCTCTGCAGAG
CTACGAGCTCAGCCCGAACACTCACTTCTCCCTCATCGTGCAAAATGGAGCCGACGGTAGTAAGTACCCCGAATT
GGTGCTGAAACGCGCCCTGGACCGCGAAGAAAAGGCTGCTCACCACCTGGTCCTTACGGCCTCCGACGGGGGCGA
CCCGGTGCGCACAGGCACCGCGCGCATCCGCGTGATGGTTCTGGATGCGAACGACAACGCACCAGCGTTTGCTCA
GCCCCAGTACCGCGCGAGCGTTCCGGAGAATCTGGCCTTGGGCACGCAGCTGCTTGTAGTCAACGCTACCGACCC
TGACGAAGGAGTCAATGCGGAAGTGAGGTATTCTTCCGGTATGTGGACGACAAGGCGGCCCAAGTTTCAAACCT
AGATTGTAATTCAGGGACAATATCAACAATAGGGGAGTTGGACCACGAGGAGTCAGGATTCTACCAGATGGAAGT
GCAAGCAATGGATAATGCAGGATATTCTGCGCGAGCCAAAGTCTGATCACTGTTCTGGACGTGAACGACAATGC
CCCAGAAGTGGTCTCTCACCTCTCTCGCCAGCTCGGTTCCCGAAAACCTCTCCAGAGGGACATTAATTGCCCTTTT
AAATGTAAATGACCAAGATTCTGAGGAAAACGGACAGGTGATCTGTTTCATCCAAGGAAATCTGCCCTTTAAATT
AGAAAAATCTTACGGAAATTACTATAGTTTAGTCACAGACATAGTCTTGGATAGGGAACAGGTTCTAGCTACAA
CATCACAGTGACCGCCACTGACCGGGGAACCCCGCCCCTATCCACGGAACTCATATCTCGCTGAACGTGGCAGA
CACCAACGACAACCCGCGGTCTTCCCTCAGGCCTCTATTCCGCTTATATCCCAGAGAACAATCCCAGAGGAGT
TTCCCTCGTCTCTGTGACCGCCACGACCCCGACTGTGAAGAGAACGCCAGATCACTTATTCCCTGGCTGAGAA
CACCATCCAAGGGGCAAGCCTATCGTCTACGTGTCCATCAACTCCGACACTGGGGTACTGTATGCGCTGAGCTC
CTTCGACTACGAGCAGTTCCGAGACTTGCAAGTGAAAGTGATGGCGCGGACAACGGGCACCCGCCCCCTCAGCAG
CAACGTGTCTGTTGAGCCTGTTCTGTGCTGGACCAGAACGACAATGCGCCCGAGATCCTGTACCCCGCCCCCTCCCCAC
GGACGGTTCCACTGGCGTGGAGCTGGCTCCCCGCTCCGCAGAGCCCGGCTACCTGGTGACCAAGGTGGTGGCGGT
GGACAGAGACTCCGGCCAGAACGCCTGGCTGTCTTACCGTCTGCTCAAGGCCAGCGAGCCGGGACTCTTCTCGGT
GGGTCTGCACACGGGCGAGGTGCGCACGGCGCGAGCCCTGCTGGACAGAGACGCGCTCAAGCAGAGCCTCGTAGT
GGCCGTCCAGGACCACGGCCAGCCCCCTCTCTCCGCCACTGTACGCTCACCGTGGCCGTGGCCGACAGCATCCC
CCAAGTCTTGCGGACCTCGGCAGCCTCGAGTCTCCAGCTAACTCTGAAACCTCAGACCTCACTCTGTACCTGGT
GGTAGCGGTGGCCGCGGTCTCCTGCGTCTTCTTGGCCTTCGTCTCTTGTCTGCTGGCGCTCAGGCTGCGGCGCTG
GCACAAGTCACGCTGCTGCAGGCTTCAGGAGCGGCTTGACAGGAGCGCCGGCGTGCACCTTTGTGGGCGTGGA
CGGGGTGCAGGCTTTCTGCGAGACCTATTCCACGAGGTTTCCCTCACCACGGAAGTGCAGGAGTACCTGAT
CTTCCCCCAGCCCAACTATGCAGACATGCTCGTCAGCCAGGAGAGCTTTGAAAAAGCGAGCCCCCTTTGCTGTC
AGGTGATTCCGTATTTTCTAAAGACAGTCATGGGTTAATTGAGCAAGCCCCGCCAACACGGACTGGCGTTTCTC
TCAGGCCCAGAGACCCGGCACCAGCGGCTCCCAAAATGGCGATGACACCGGCACCTGGCCCAACAACAGTTTGA
CACAGAGATGCTGCAAGCCATGATCTTGGCGTCCGCCAGTGAAGCTGCTGATGGGAGCTCCACCCTGGGAGGGGG
TGCCGGCACCATGGGATTGAGCGCCGCTACGGACCCAGTTCACCTGCAGCACGTGCCCCACTACCGCCAGAA
TGTCTACATCCCAGGCAGCAATGCCACACTGACCAACGCAGCTGGCAAGCGGGATGGCAAGGCCCCAGCAGGTGG
CAATGGCAACAAGAAGAAGTCGGGCAAGAAGGAGAAGAAG**TAA**CATGGAGGCCAGGCCAAGAGCCACAGGGCGGC
CTCTCCCCAACCCAGCCAGCTTCTCCTTACCTGCACCCAGGCCCTCAGAGTTTTCAGGGCTAACCCCCAGAATACTG
GTAGGGGCCAAGGCCATGCTCCCCTTGGGAAACAGAAACAAGTGCCAGTCAGCACCTACCCCTTCCCCCCCAGG
GGGTTGAATATGCAAAAGCAGTTCCGCTGGGAACCCCCATCCAATCAACTGCTGTACCCATGGGGGTAGTGGGGT
TACTGTAGACACCAAGAACCATTGTGCCACACCCCGTTTAGTTACAGCTGAACCTCCTCCATCTTCCAAATCAATCA
GGCCCATCCATCCCATGCCTCCCTCCTCCCCACCCCACTCCAACAGTTCTCTTTCCCGAGTAAGGTGGTTGGGG
TGTTGAAGTACCAAGTAACCTACAAGCCTCCTAGTTCTGAAAAGTTGGAAGGGCATCATGACCTCTTGGCCTCTC
CTTTGATTCTCAATCTTCCCCCAAAGCATGGTTTGGTGCCAGCCCCCTTACCTCCTTCCAGAGCCCCAAGATCAAT
GCTCAAGTTTTTGAGGACATGATCACCATCCCCATGGTACTGATGCTTGTGATTTAGGGAGGGCATTTTGCTA

1867/6881
FIGURE 1730B

CCAAGCCTCTTCCCAACGCCCTGGGGACCAGTCTTCTGTTTTGTTTTTCATTGTTTGACGTTTCCACTGCATGCC
TTGACTTCCCCCACCTCCTCCTCAAACAAGAGACTCCACTGCATGTTCCAAGACAGTATGGGGTGGTAAGATAAG
GAAGGGAAGTGTGTGGATGTGGATGGTGGGGGCATGGACAAAGCTTGACACATCAAGTTATCAAGGCCTTGGAGG
AGGCTCTGTATGTCCTCAGGGGACTGACAACATCCTCCAGATTCCAGCCATAAACCATAACTAGGCTGGACCCT
TCCCACTACATAATAGGGCTCAGCCCAGGCAGCCAGCTTTGGGCTGAGCTAACAGGACCAATGGATTAAACTGGC
ATTTCAGTCCAAGGAAGCTCGAAGCAGGTTTAGGACCAGGTCCCCCTTGAGAGGTGAGAGGGGCTCTGTGGGTGC
TGGGTACTCCAGAGGTGCCACTGGTGGAAGGGTCAGCGGAGCCCCAGCAGGAAGGGTGGGCCAGCCAGGCCATTC
TTAGTCCCTGGGTGTTGGGGAGGCAGGGAGCTAGGGCAGGGACCAAATGAACAGAAAGTCTCAGCCCAGGATGGGGC
TTCTTCAACAGGGCCCCCTGCCCTCCTGAAGCCTCAGTCCTTCACCTTGCCAGGTGCCGTTTTCTCTTCCGTGAAGG
CCACTGCCCAGGTCCCCAGTGCGCCCCCTAGTGCCCATAGCCTGGTTAAAGTTCCCCAGTGCCCTCCTTGTGCATA
GACCTTCTTCTCCCACCCCCTTCTGCCCCCTGGGTCCCCGGCCATCCAGCGGGGCTGCCAGAGAACCCCAGACCTG
CCCITACAGTAGTGTAGCGCCCCCTCCCTCTTTTCGGCTGGTGTAAGATAGCCAGTAGTGTAGTGCAGGTGTGCTTT
TACGTGATGGCGGGTGGGCAGCGGGCGGCGGGCTCCGCGCAGCCGTCTGTCTTGATCTGCCCCGCGGCGGCCCGT
GTTGTGTTTTGTGCTGTGTCCACGCGCTAAGGCGACCCCCCTCCCCCGTACTGACTTCTCCTATAAGCGCTTCTCT
TCGCATAGTCACGTAGCTCCACCCACCCCTCTTCTGTGTCTCAGCAAGTTTTATACTCTAATATTTATATGG
CTTTTTTCTTCGACAAAAAATAATAAACGTTTCTTCTGAAAAGCTG

1868/6881
FIGURE 1731

MIPARLHRDYKGLVLLGILLGTLWETGCTQIRYSVP EELEKGSRVGDISRDLGLEPRELAERGVRIIPRGRTQLF
ALNPRSGSLVTAGRIDREELCMGAIKCQLNLDILMEDKVKIYGVEVEVRDINDNAPYFRESELEIKISENAATEM
RFPLPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGADGSKYPELVLKRALDREEKAAHHLVLTASDGGDPVRTGT
ARIRVMVLDANDNAPAFAPQPEYRASVPENLALGTQLLVVNATDPDEGVNAEVRYSFYVDDKAAQVFKLDCNSGT
ISTIGELDHEESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTSASSVPENSPRGTLIALLVNDQD
SEENGQVICFIQGNLPFKLEKSYGNYYSLVTDIVLDREQVPSYNITVTATDRGTPPLSTETHISLNVADTNDNPP
VFPQASYSAYIPENNPBGVSLVSVTAHDPDCEENAQITYSLAENTIQGASLSSYVSINSDTGVLIALSSFDYEQF
RDLQVKVMARDNGHPPLSSNVSLSLFVLDQNDNAPEILYPALPTDGSTGVELAPRSAEPGYLVTKVVAVDRDSGQ
NAWLSYRLLKASEPGLFSVGLHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTLTVAVADSIPQVLADL
GSLESPANSETSDLTLYLVVAVAAVSCVFLAFVILLALLRLRRWHKSRLQASGGGLTGAPASHFVGVDGVQAF
QTYSHEVSLTTDSRKSHLIFPQPNYADMLVSQESFEKSEPLLLSGDSVFSKDSHGLIEQAPPNTDWRFSQAQRP
TSGSQNGDDTGTWPNNQFDTEMLQAMILASASEAADGSSTLGGGAGTMGLSARYGPQFTLQHVDPDYRQNVYIPGS
NATLTNAAGKRDGKAPAGGNGNKKKSGKKEKK

1869/6881
FIGURE 1732A

ATGGGGAGCGGCGCCGGGGAGCTGGGCGGGCTGAGAGGCTGCCAGTGCTCTTTCTCTTCCTGCTGTCTTTGTTC
TGCCCGGCGCTCTGTGAGCAGATCCGCTACAGGATTCCCGAGGAAATGCCCAAGGGCTCCGTAGTGGGGAACCTC
GCCACGGACCTGGGGTTTACGCGTCCAGGAGTTACCGACTCGAAAATGCGCGTCAGTTCGGAGAAGCCTTACTTC
ACCGTGAGCGCAGAGAGCGGGGAGTTGCTTGTGAGCAGCAGGCTAGACAGGGAGGAGATATGCGGGAAGAAGCCA
GCTTGTGCTCTGGAATTTGAGGCTGTTGCTGAAAATCCACTGAACTTTTATCACGTGAATGTGGAGATCGAGGAC
ATTAATGACCACACGCCAAAATTCACGCAAAATTCCTTTGAGCTGCAAAATAAGTGAGTCTGCACAGCCTGGCACA
CGATTTATATTAGGATCTGCCCATGATGCGGATATTGGTAGCAACACACTGCAGAATTACCAACTCAGTCCCAGT
GATCATTTTCTCACTGATAAATAAAGAGAAATCAGATGGCAGTAAATACCCTGAGATGGTATTGAAGACACCTTTG
GACAGAGAAAAGCAGAAAATCCTACCACTTGACTTTGACTGCCTTGGACTTTGGAGCTCCACCCCTAAGCAGCACT
GCACAGATACACGTTCTAGTGACTGATGCCAATGATAATGCTCCAGTGTTTCAAGACGTATACAGGGTGAGC
CTTTTCAGAAAACGTGTACCCGGGGACCACGGTGCTACAGGTGACTGCCACGGACCAGGATGAGGGTGTCAATGCC
GAGATTACTTTCTCTTTCAGTGAAGCTAGCCAGATCACCCAATTTGACCTGAACTCTAACACCGGGGAAATTACT
GTTTTAAATACATTAGATTTTGAAGAAGTCAAAGAATATTCCATAGTTTGGGAAGCAAGGGACGGTGGAGGAATG
ATTGCGCAATGCACAGTGGAGGTAGAAGTCATAGATGAAAATGACAACGCCCCAGAAGTGATATTCCAGTCTCTA
CCCAACCTAATTATGGAGGACGCCGAGCTGGGAACACATATTGCTTTGCTCAAAGTCCGTGACAAGGATTCCAGA
CACAATGGAGAAGTGACTTGTAATTTGAAGGTGATGTTCCATTTAAAATATTAACCTTCTTCAAGAAACACGTAT
AAATTAGTGACAGATGCTGTTCTAGACCGCGAGCAGAATCCAGAGTACAATATAACCGTTACGGCAACAGATCGG
GGCAAGCCTCCCCTCTCCTCCAGTTCACGATCACCTGCACATTGGTGATGTAAATGACAACGCTCCGGTTTTTC
TCACAGTCTTCTATATAGTCCACGTGGCCGAGAACAACCCGCCTGGAGCCTCTATTTACAAGTCAGGGCTTCT
GATCCGGACTTGGGGCCCCAACGGCCAAGTCTCTTACTGCATCATGGCCAGTGACCTGGAGCAGCGGGAGCTGTCA
TCCTACGTGTCCATAAGCGCGGAGAGCGGGGTGGTGTTCGCGCAGCGCGCCTTCGACCACGAGCAGCTGCGCGCC
TTCGAACTCACACTGCAGGCCCCGCGACCAGGGCTCGCCAGCGCTCAGCGCGAACGTGAGCCTGCGCGTGTTAGTG
GACGACCGCAACGACAATGCGCCACGGGTGCTGTACCCCGCGCTGGGTCCCGACGGCTCTGCGCTCTTCGATATG
GTGCCGACGCTGCAGAGCCTGGCTACTTGGTGACCAAGGTAGTGGCGGTGGACGCAGACTCAGGACACAACGCC
TGGCTGTCTTACCACGTGCTGCAGGCTAGCGAGCCCGGGCTCTTCAGCCTGGGGCTGCGCACGGGCGAAGTGCGC
ACAGCGCGTGCCCTTAGGCGACAGGGACGCCGTCCGCCAGCGCCTTCTGGTTCGCCGTGCGTGACGGTGGACAGCCA
CCACTCTCGGCCACTGCCACGTTGCACCTGGTCTTCGCCGACAGCTTGCAGGAGGTGCTGCCGGATATCACTGAC
CGCCCCGACCCCTCTGACCTCCAGGCTGAGCTGCAGTTTTACCTAGTGGTGGCCTTGGCCTTGATCTCAGTGCTC
TTCTCGTGGCCATGATTCTGGCCATTGCCTTGCGCCTGCGACGCTCCTCCAGCCCCGCTCCTGGAGCTGCTTC
CAGCCTGGTCTCTGTGTTAAATCCGAATCCGTGGTTCCCCCAACTACAGCGAGGGGACTTTGCCTTATTCTTAC
AATCTATGTGTTGCACATACAGGAAAGACGGAGTTTAATTTCTTAAATGTAGTGAGCAGTTGAGTTTCAGGACAA
GACATACTTTGCGGTGATTCATCTGGGGCCTTATTTCCACTTTGTAATTCCAGTGAATTGACTTCCCATCAGCAA
GCCCCGCCCAACACGGACTGGCGTTTTCTCTCAGGCCCAGAGACCCGGCACCAGCGGCTCCCAAAATGGCGATGAC
ACCGGCACCTGGCCCAACAACCAGTTTGACACAGAGATGCTGCAAGCCATGATCTTGGCGTCCGCCAGTGAAGCT
GCTGATGGGAGCTCCACCCTGGGAGGGGGTGCCGGCACCATGGGATTGAGCGCCGCTACGGACCCAGTTCACC
CTGCAGCACGTGCCCGACTACCGCCAGAATGTCTACATCCCAGGCAGCAATGCCACACTGACCAACGCAGCTGGC
AAGCGGGATGGCAAGGCCCCAGCAGGTGGCAATGGCAACAAGAAGAAGTCGGGCAAGAAGGAGAAGAAGTAAACAT
GGAGGCCAGGCCAAGAGCCACAGGGCGGCCTCTCCCCAACAGCCAGCTTCTCCTTACCTGCACCCAGGCCTCA
GAGTTTCAGGGCTAACCCCCAGAATACTGGTAGGGGCCAAGGCCATGCTCCCCTTGGGAAACAGAAACAAGTGCC
CAGTCAGCACCTACCCCTTCCCCCCCAGGGGGTTGAATATGCAAAAGCAGTTCGGCTGGGAACCCCCATCCAATC
AACTGCTGTACCCATGGGGGTAGTGGGGTACTGTAGACACCAAGAACCATTTCGCCACACCCCGTTTAGTTACAG
CTGAACTCCTCCATCTTCCAAATCAATCAGGCCCATCCATCCCATGCCTCCCTCCTCCCCACCCCACTCCAACAG
TTCTCTTTTCCCGAGTAAGGTGGTGGGGTGTGAAAGTACCAAGTAACCTACAAGCCTCCTAGTTCTGAAAAGTT
GGAAGGGCATCATGACCTCTTGGCCTCTCCTTTGATTCTCAATCTTCCCCAAAGCATGGTTTGGTGCCAGCCCC
TTCACCTCCTTCCAGAGCCCAAGATCAATGCTCAAGTTTTGGAGGACATGATCACCATCCCCATGGTACTGATGC
TTGCTGGATTTAGGGAGGGCATTTTGTACCAAGCCTCTTCCCAACGCCCTGGGGACCAGTCTTCTGTTTTGTTT
TTCATTGTTTGACGTTTTCCACTGCATGCCTTGACTTCCCCACCTCCTCCTCAAACAAGAGACTCCACTGCATGT
TCCAAGACAGTATGGGGTGGTAAGATAAGGAAGGGAAGTGTGTGGATGTGGATGGTGGGGGCATGGACAAAGCTT

1870/6881
FIGURE 1732B

GACACATCAAGTTATCAAGGCCTTGGAGGAGGCTCTGTATGTCCTCAGGGGACTGACAACATCCTCCAGATTCCA
GCCATAAACCAATAACTAGGCTGGACCCTTCCCCTACATAATAGGGCTCAGCCCAGGCAGCCAGCTTTGGGCTG
AGCTAACAGGACCAATGGATTAACTGGCATTTCAGTCCAAGGAAGCTCGAAGCAGGTTTAGGACCAGGTCCCCT
TGAGAGGTCAGAGGGGCCTCTGTGGGTGCTGGGTACTCCAGAGGTGCCACTGGTGGAAGGGTCAGCGGAGCCCCA
GCAGGAAGGGTGGGCCAGCCAGGCCATTCTTAGTCCCTGGGTTGGGGAGGCAGGGAGCTAGGGCAGGGACCAAAT
GAACAGAAAGTCTCAGCCCAGGATGGGGCTTCTTCAACAGGGCCCCCTGCCCTCCTGAAGCCTCAGTCCTTCACCT
TGCCAGGTGCCGTTTCTCTTCCGTGAAGGCCACTGCCCAGGTCCCCAGTGCGCCCCCTAGTGGCCATAGCCTGGT
TAAAGTTCCCCAGTGCCCTCCTTGTGCATAGACCTTCTTCTCCCACCCCCTTCTGCCCTTGGGTCCCCGGCCATCC
AGCGGGGCTGCCAGAGAACCCAGACCTGCCCTTACAGTAGTGTAGCGCCCCCTCCCTCTTTCGGCTGGTGTAGA
ATAGCCAGTAGTGTAGTGCGGTGTGCTTTTACGTGATGGCGGGTGGGCAGCGGGCGGCGGGCTCCGCGCAGCCGT
CTGTCTTTGATCTGCCCGCGGCGGCGCCGTGTTGTGTTTTGTGCTGTGTCCACGCGCTAAGGCGACCCCCCTCCCCC
GTACTGACTTCTCCTATAAGCGCTTCTCTTCGCATAGTCACGTAGCTCCCACCCACCCCTCTTCCTGTGTCTCAC
GCAAGTTTTATACTCTAATATTTATATGGCTTTTTTCTTCGACAAAAAATAATAAAACGTTTCTTCTGAAAAG
CTG

1871/6881
FIGURE 1733

MSGAGELGRAERLPVLFLFLSLFCPALCEQIRYRIPEEMPKGSVVGNLATDLGFSVQELPTRKLRVSSEKPYF
TVSAESGELLVSSRLDREEICGKKPACALEFEAVAENPLNFYHVNVEIEDINDHTPKFTQNSFELQISESAQPGT
RFILGSAHDADIGSNTLQNYQLSPSDHFSLINKEKSDGSKYPEMVLKTPLDREKQKSYHLTLTALDFGAPPLSST
AQIHVLVTDANDNAPVFSQDVYRVSLSENVYPGTTVLQVTATDQDEGVNAEITFSFSEASQITQFDLNSNTGEIT
VLNTLDFEEVKEYSIVLEARDGGGMIAQCTVEVEVIDENDNAPEVIFQSLPNLIMEDAELGTHIALLKVRDKDSR
HNGEVTCKLEGDVPFKILTSSRNTYKLVTDVLDREQNPEYNITVTATDRGKPLSSSSSITLHIGDVNDNAPVF
SQSSYIVHVAENNPPGASISQVRASDPDLGPNGQVSYCIMASDLEQRELSSYVSISAESGVVFAQRAFDHEQLRA
FELTLQARDQGSPALSANVSLRVLVDDRNDNAPRVLYPALGPDGSALFDMVPHAAEPGYLVTKVVAVDADSGHNA
WLSYHVLQASEPGLFSLGLRTGEVRTARALGDRDAVRQRLLVAVRDGGQPPLSATATLHLVFADSLQEVLPDITD
RPDPSDLQAEHQFYLVVALALISVFLVAMILAIALRLRRSSSPASWSCFQPGLCVKSESVVPPNYSEGTLPPSY
NLCVAHTGKTEFNFLKCSEQLSSGQDILCGDSSGALFPLCNSSELTSHQQAPPNTDWRFSQAQRPGTSGSQNGDD
TGTWPNNQFDTEMLQAMILASASEAADGSSTLGGGAGTMGLSARYGPQFTLQHVPDYRQNVYIPGSNATLTNAAG
KRDGKAPAGNGNKKKSGKKEKK

1872/6881
FIGURE 1734A

ATGAAGATTCAGAAAAAGCTGACTGGCTGCAGCAGGCTGATGCTTCTGTGTCTTTCTCTGGAGCTGCTGTTGGAA
GCTGGGGCTGGGAATATTCACACTACTCAGTGCCGGAAGAGACAGACAAAGGTTCCCTTCGTAGGCAACATCGCCAAAG
GACCTAGGGCTGCAACCCAGGAGCTGGCAGATGGCGGAGTCCGCATCGTCTCCAGAGGTAGGATGCCGCTTTTC
GCTCTGAATCCTAGAAAGTGGCAGCTTGATCACCGCGCGCAGGATAGACCGGGAGGAGCTCTGCGCTCAGAGCATG
CCGTGTCTCGTGAGTTTTAATATCCTTGTTGAGGATAAAATGAAGCTTTTTCCTGTTGAAGTAGAAATAATTGAT
ATTAATGACAACACTCCCCAATTCCAGTTAGAGGAACTGGAGTTTAAATGAATGAAATAACGACTCCAGGTACC
AGAGTCTCATTGCCTTTTGGGCAAGACCTTGATGTGGGTATGAACTCACTCCAGAGCTACCAACTCAGCTCTAAC
CCTCATTCTCCCTGGATGTGCAACAGGGAGCCGATGGGCCTCAACATCCAGAGATGGTGCTGCAGAGTCCCTTA
GACAGAGAAGAAGAAGCTGTCCACCACCTCATCCTCACAGCTTCTGATGGGGGTGAACCAGTCCGTTTCAGGGACC
CTCAGAATTTACATTTCAGGTGGTGGATGCAAATGACAATCCTCCAGCATTTACTCAGGCACAATACCATATAAAT
GTCCCCGAAAACGTGCCGCTGGGTACTCAGCTGCTCATGGTAAATGCCACTGACCCTGATGAGGGAGCCAATGGG
GAAGTAACGTACTCCTTTCACAATGTAGACCACAGAGTGGCCCAAATATTTTCGTTTAGATTCTTACACAGGAGAA
ATATCAAATAAAGAACCCTAGATTTTGAAGAATACAAAATGTATTCAATGGAAGTTCAAGCCCAGGATGGTGCG
GGGCTCATGGCTAAAGTTAAGGTACTGATCAAAGTTTTGGATGTAAATGATAATGCCCCAGAAGTGACCATCACC
TCTGTCAACCACTGCAGTTCCAGAAAACCTTTCCCTCCTGGGACCATAATTGCTCTTATCAGTGTGCATGACCAGGAC
TCAGGAGACAATGGCTACACCACATGTTTCATTCTGAAATTTACCCTTTAAATTGGAAAAGTTAGTTGATAAT
TATTACCGTTTAGTGACTGAAAGAACACTGGACAGAGAACTTATCTCTGGGTACAACATCACAATAACAGCAATA
GACCAAGGAACTCCAGCTCTATCTACTGAAACTCACATTTCACTACTAGTGACAGATATCAATGACAACCTCCCCA
GTCTTCCATCAGGACTCCTACTCTGCCTACATTCCCGAAAACAACCCCAAGAGGAGCCTCCATCTTCTCTGTGAGG
GCCCCAGACTTGGACAGCAATGAGAATGCACAAATCACTTACTCCCTAATAGAGGACACTATCCAGGGGGCACCC
CTATCTGCCTACCTCTCCATCAACTCCGACACTGGGGTCTGTATGCGCTGCGATCCTTCGACTATGAGCAGTTC
CGGGACATGCAACTGAAAGTGATGGCGCGGGACAGTGGGGATCCGCCCTCAGCAGCAACGTGTCTCTCAGCCTA
TTCTTGCTGGACCAGAACGACAACGCGCCCGAGATCCTGTACCCCGCCCTCCCCACAGATGGTTCTACCGGCGTG
GAGCTGGCGCCCTCTCCGACAGAGCCCGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACAGAGACTCGGGCCAG
AACGCTGGCTGTCTACCGCCTGCTCAAGGCCAGCGAGCCGGGACTCTTCTCGGTGGGTCTGCACACGGGCGAG
GTGCGCACGGCGCGAGCCCTGCTGGACAGAGACGCGCTCAAGCAGAGTCTCGTGGTGGCCGTCCAGGACCACGGC
CAGCCCCCGCTCTCCGCCACTGTACGCTCACCGTGGCCGTGGCCGACAGGATCTCCGACATCTGGCCGACCTG
GGCAGCCTCGAGCCCTCCGCCAAACCCAAACGATTCCGACCTCACTCTGTACCTGGTGGTGGCGCGGCCGCGGTC
TCCTGCGTCTTCTTGGCCTTCGTATCGTGCTGCTGGCGCACAGGCTGCGGCGCTGGCACAAGTCACGTCTGCTA
CAGGCTTCCGGGAGGCGGCTTAGCGAGCATGCCCGGTTTCGCACTTTGTGGGCGTGGACGGGGTTCCGGGCTTTCTG
CAGACCTATTCCCACGAGGTCTCCCTCACTGCGGACTCGCGGAAGAGCCACCTGATTTTCCCCCAGCCCACTAT
GCGGACACACTCATCAGCCAGGAGAGCTGTGAGAAAAAGGGTTTTCTATCAGCACCCCACTCTTTACTTGAAGAC
AAAAAGGAACCATTTTTCTCAGCAAGCCCCGCCAAACACGGACTGGCGTTTCTCTCAGGCCCAGAGACCCGGCACC
AGCGGCTCCCCAAAATGGCGATGACACCGGCACCTGGCCCAACAACAGTTTGACACAGAGATGCTGCAAGCCATG
ATCTTGGCGTCCGCCAGTGAAGCTGCTGATGGGAGCTCCACCCTGGGAGGGGGTGCCGGCACCATGGGATTGAGC
GCCCCGTACGGACCCCACTTACCCTGCAGCACGTGCCCGACTACCGCCAGAATGTCTACATCCCAGGCAGCAAT
GCCACACTGACCAACGCAGCTGGCAAGCGGGATGGCAAGGCCCCAGCAGGTGGCAATGGCAACAAGAAGAAGTCG
GGCAAGAAGGAGAAGAAGTAACATGGAGGCCAGGCCAAGAGCCACAGGGCGGCTCTCCCCAACCAGCCAGCTT
CTCCTTACCTGCACCCAGGCCCTCAGAGTTTCAGGGCTAACCCCAAGAATACTGGTAGGGGGCAAGGCCATGCTCC
CCTTGGGAAACAGAAACAAGTGCCAGTCAGCACCTACCCCTTCCCCCAGGGGGTTGAATATGCAAAAGCAGT
TCCGCTGGGAACCCCATCCAATCAACTGCTGTACCCATGGGGGTAGTGGGGTTACTGTAGACACCAAGAACCAT
TTGCCACACCCCGTTTAGTTACAGCTGAACTCCTCCATCTTCAAATCAATCAGGCCCCATCCATCCCATGCCTCC
CTCCTCCCCACCCCACTCCAACAGTTCTCTTCCCGAGTAAGGTGGTTGGGGTGTGAAGTACCAAGTAACCTA
CAAGCCTCCTAGTTCTGAAAAGTTGGAAGGGCATCATGACCTCTTGGCCTCTCCTTTGATTCTCAATCTTCCCC
AAAGCATGGTTTGGTGCCAGCCCTTACCTCCTTCCAGAGCCCAAGATCAATGCTCAAGTTTGGAGGACATGA
TCACCATCCCCATGGTACTGATGCTTGGATTTAGGGAGGGCATTGTGCTACCAAGCCTCTTCCCAACGCCCT
GGGGACCAGTCTTCTGTTTTGTTTTTTCATTGTTTGACGTTTCCACTGCATGCCTTGACTTCCCCACCTCCTCCT
CAAACAAGAGACTCCACTGCATGTTCCAAGACAGTATGGGGTGGTAAGATAAGGAAGGGGAAGTGTGTGGATGTGG

1873/6881
FIGURE 1734B

ATGGTGGGGGCATGGACAAAGCTTGACACATCAAGTTATCAAGGCCTTGGAGGAGGCTCTGTATGTCCTCAGGGG
ACTGACAACATCCTCCAGATTCCAGCCATAAACCAATAACTAGGCTGGACCCTTCCCCTACATAATAGGGCTCA
GCCCAGGCAGCCAGCTTTGGGCTGAGCTAACAGGACCAATGGATTAAACTGGCATTTCAGTCCAAGGAAGCTCGA
AGCAGGTTTAGGACCAGGTCCCCCTTGAGAGGTCAGAGGGGCCTCTGTGGGTGCTGGGTACTCCAGAGGTGCCACT
GGTGGAAGGGTCAGCGGAGCCCCAGCAGGAAGGGTGGGCCAGCCAGGCCATTCTTAGTCCCTGGGTGGGGAGGC
AGGGAGCTAGGGCAGGGACCAAATGAACAGAAAGTCTCAGCCCAGGATGGGGCTTCTTCAACAGGGCCCCTGCCC
TCCTGAAGCCTCAGTCCTTCACCTTGCCAGGTGCCGTTTCTCTTCCGTGAAGGCCACTGCCCAGGTCCCCAGTGC
GCCCCCTAGTGGCCATAGCCTGGTTAAAGTTCCCCAGTGCCCTCCTTGTGCATAGACCTTCTTCTCCACCCCCTT
CTGCCCCCTGGGTCCCCGGCCATCCAGCGGGGCTGCCAGAGAACCCCAGACCTGCCCTTACAGTAGTGTAGCGCCC
CCTCCCTCTTTTCGGCTGGTGTAGAATAGCCAGTAGTGTAGTGCGGTGTGCTTTTACGTGATGGCGGGTGGGCAGC
GGGCGGCGGGCTCCGCGCAGCCGTCTGTCCTTGATCTGCCCAGCGCGGCCCGTGTGTGTTTTGTGCTGTGTCCA
CGCGCTAAGGCGACCCCTCCCCGTAAGTCTCTCTATAAGCGCTTCTCTTCGCATAGTCACGTAGCTCCCA
CCCCACCTCTTCTGTGTCCTCACGCAAGTTTTATACTCTAATATTTATATGGCTTTTTTTCTTCGACAAAAAA
TAATAAACGTTTCTTCTGAAAAGCTG

1874/6881
FIGURE 1735

MKIQKKLTGCSRLMLLCLSELELLLEAGAGNIHYSVPEETDKGSFVGNIAKDLGLQPQELADGGVRIVSRGRMPLE
ALNPRSGSLITARRIDREELCAQSMPCLVSFNILEVEDKMKLFPVEVEIIDINDNTPQFQLEEELEFKMNEITTPGT
RVSLPFGQDLVDVGMNSLQSYQLSSNPHFSLDVQQGADGPHPEMVLQSPLDREEEAVHHLILTASDGGEFVRS
LRIYIQVVDANDNPPAFTQAQYHINVPENVPLGTQLLMVNATDPDEGANGEVTYSFHNVDHRVAQIFRLDSY
TGEISNKEPLDFEYKMYSMQVQAQDGAGLMAKVVKLIKVLVDVNDNAPEVTITSVTTAVPENFPPTIIALISV
HDQD SGDNQYTTCTFIPGNLFPKLEKLVDNYYRLVTERTLDRELISGYNITITAITDQGTPALSTETHISLLV
TDINDNSP VFHQDSYSAYIPENNPRGASIFSVRAHDLDSENENAQITYSLIEDTIQGAPLSAYLSINSDTG
VLYALRSFDYEQF RDMQLKVMARDSGDPPLSSNVSLSLFLLDQNDNAPEILYPALPTDGSTGVELAPLSAEP
GYLVTKVVAVDRDSGQ NAWLSYRLLKASEPGLFSVGLHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLS
ATVTLTVAVADRISDILADL GSLEPSAKPNDSDLTLYLVVAAA VSCVFLAFVIVLLAHLRRWHKSRL
LQASGGGLASMPGSHFVGVDGVRAFL QTY SHEVSLTADSRKSHLIFPQPNYADTLISQESCEKKGFLSAPQ
SLEDKKEPFSQQAPPNTDWRFSQAQRPGT SGSQNGDDTGTWPNNQFDTEMLQAMILASASEAADGSSTLGGGAG
TMGLSARYGPQFTLQHVDPYRQNVYIPGSN ATLTNAAGKRDGKAPAGNGNKKKSGKKEK

1875/6881
FIGURE 1736A

ATGCCCGCTCAAAGGAATCGCTCAAAGGAATCAAAGGATTGCAGCGGGCTGGTCCTGCTCTGCCTTTTCTTCGGG
ATTCCATGGGAGGCTGGAGCCCGGCAGATCTCCTACTCAATTCCTGAGGAATTAGAGAAAGGCTCTTTTCGTGGGC
AACATCTCCAAGGACTTGGGTCTGGCGCCCCGGGAGCTGGCGGAGCGCGGAGTCCGCATAGTCTCCAGAGGTAGG
ACGCAGCTTTTCTCTCTGAACCCGCGCAGCGGCAGCTTGATCACCGCGGGCAGGATAGACCGGGAGGAGCTCTGC
GCTCAGAGCGCGCGGTGCGTGGTGAGTTTTAATATCCTTGTGGAAGACAGGGTGAACTTTTGGGATAGAAATA
GAAGTAACTGATATCAATGACAATGCTCCAAAATTCCAAGCAGAAAATCTAGACGTAAAAATTAATGAAAATGTC
GCTGCGGGAATGCGTTTTTCTCTCCCGGAAGCTATTGATCCGGATGTGGGCGTGAACTCCCTGCAGAGCTATCAG
CTCAGCCCCAATAAGCACTTCTCCCTAAGAGTTCAGAGCCGTGCCAATGGCGTCAAGTACCCGGAGCTGGTACTG
GAGCACTCCCTAGATCGCGAGGAAGAGGCCATTACCACCTGGTCCTCACCGCCTCCGACGGGGGTGACCCTCTC
CGATCTGGCACTGTCTTGTGAGTGTGACTGTCTTCGATGCAAATGACAACGCGCCGGTCTTCACCTTGCCAGAA
TACCGAGTGAGTGTCTTGAGAATTTGCCTGTGGGCACTCAGCTGCTGACAGTCACAGCCACCGACAGGGACGAA
GGTGCCAAATGGAGAAGTGACATATTCATTCCGAAAATTACCTGACACGCAATTGTTGAAGTTCCAATAAACAAA
TATACTGGAGAAAATAAAAATATCAGAAAATCTAGATTATGAAGAAACCGGTTTCTATGAAATAGAAAATACAAGCA
GAAGATGGAGGAGCATATCTTGCAACTGCAAAAGTGTTGATTACAGTAGAAGATGTAAATGACAACAGTCCAGAG
CTGACCATCACGTCTCTATTTAGTCCAGTGACTGAAGATTCACCTCTGGGAACAGTCGTAGCCCTTTTAAATGTG
CATGATTTAGACTCTGAGCAGAATGGACAGGTAACTGTTCATTTTGGCGTATCTACCATTTAAATTAGAAAAG
TCCATTGACAGTTATTACAGATTGGTGATACACAGAGCCCTTGACAGGGAACAGGTATCCTCTTACAATATCACA
GTGACAGCCACAGATGGGGGAAGTCCTCCTCTATCAACGGAAAGCTCACTTTATGCTACAAGTGGCAGATATCAAT
GACAACCCACCTACCTTCTCTCAAGTCTCCTACTTTACCTATATCCCAGAGAACAACGCCAGGGGTGCCTCCATC
TTCTCAGTGACAGCGCTGGACCCGGACAGCAAAGAGAATGCCAGATTATTTACTCCCTGGCTGAAGACACCATC
CAGGGGGTACCTCTGTCTCATACATATCCATCAACTCAGACACTGGCGTCTGTATGCACTCAGATCCTTCGAC
TATGAGCAGTTTCATGAGCTACAGATGCAGGTGACAGCCAGCGACAGCGGGGATCCTCCACTCAGCAGCAACGTG
TCGTTGAGCCTGTTTGTGCTGGACCAGAACGACAATGCGCCCGAGATCCTGTACCCCGCCCTCCCCACAGACGGT
TCCACAGGCGTGAGCTGGCGCCCCGCTCCGCAGAGCCCCGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACAGA
GACTCCGGCCAGAACGCCTGGCTGTCTACCGTCTGTCTCAAGGCCAGCGAGCCGGGACTCTTCGCGGTGGGGGAG
CACACGGGCGAGGTGCGCACGGCGCGAGCCCTGCTGGACAGAGACGCGCTCAAGCAAAGCCTCGTAGTGGCCGTC
CAGGACCACGGCCAGCCCCCTCTCTCCGCCACTGTACGCTCACCGTGGCCGTGGCCGACAGCATCCCCAAGTC
CTGGCGGACCTCGGCAGCTTCGAGTCTCCAGCTAACTCTGAAACCTCAGACCTCACTCTGTACCTGGTGGTAGCG
GTGGCCGCGGTCTCCTGCGTCTTCTGCGCTTCGTCATCGTGTCTGGCGCACAGGCTGCGGCGCTGGCACAAG
TCACGCCTGCTGCAGGCTTCAGGAGGCGGCTTGACAGGTGTGTCCGGCTCGCACTTTGTGGGCGTGGACGGGGTT
CGGGCTTTCTGCGAGACCTATTCCCACGAGGTCTCTCTACCGCGGACTCGCGAAAGAGTCACCTGATCTTCCCC
CAGCCCAATTATGCGGACACGCTCATCAGCCAGGAGAGCTGTGAGAAAAACGATCCTTTGTCTTTGTTAGATGAT
TCGAAGTTTCTATAGAGGATACCCATTGGTTCCACAAGCCCCGCCAACACGGACTGGCGTTTCTCTCAGGCC
CAGAGACCCGGCACCAGCGGCTCCCAAAATGGCGATGACACCGGCACCTGGCCCAACAACCAGTTTGACACAGAG
ATGCTGCAAGCCATGATCTTGCGCTCCGCCAGTGAAGCTGCTGATGGGAGCTCCACCCTGGGAGGGGGTGCCGGC
ACCATGGGATTGAGCGCCCGCTACGGACCCAGTTTACCCTGCAGCACGTGCCGACTACCGCCAGAATGTCTAC
ATCCCAGGCAGCAATGCCACACTGACCAACGCAGCTGGCAAGCGGGATGGCAAGGCCCCAGCAGGTGGCAATGGC
AACAAGAAGAAGTCGGGCAAGAAGGAGAAGAAGTAACATGGAGGCCAGGCCAAGAGCCACAGGGCGGCCTCTCCC
CAACCAGCCCAGCTTCTCCTTACCTGCACCCAGGCCTCAGAGTTTTCAGGGCTAACCCCCAGAATACTGGTAGGGG
CCAAGGCCATGCTCCCCCTTGGGAAACAGAAACAAGTGCCAGTCAGCACCTACCCCTTCCCCCCAGGGGGTTGA
ATATGCAAAAGCAGTTCCGCTGGGAACCCCATCCAATCAACTGCTGTACCCATGGGGGTAGTGGGGTTACTGTA
GACACCAAGAACCATTGTCACACCCCGTTTAGTTACAGCTGAACTCCTCCATCTTCCAAATCAATCAGGCCCAT
CCATCCCATGCTCCTCCTCCCCACCCCACTCCAACAGTTCTCTTTCCCGAGTAAGGTGGTTGGGGTGTGAA
GTACCAAGTAACCTACAAGCCTCCTAGTTCTGAAAAGTTGGAAGGGCATCATGACCTCTTGGCCTCTCCTTTGAT
TCTCAATCTTCCCCAAAGCATGGTTTGGTGCCAGCCCTTACCTCCTTCCAGAGCCCAAGATCAATGCTCAAG
TTTGGAGGACATGATACCATCCCCATGGTACTGATGCTTGTGATTTAGGGAGGGCATTGCTACCAAGCC
TCTTCCCAACGCCCTGGGGACAGTCTTCTGTTTTGTTTTTCATTGTTTGACGTTTCCACTGCATGCCTTGACTT
CCCCACCTCCTCCTCAAACAAGAGACTCCACTGCATGTTCCAAGACAGTATGGGGTGGTAAGATAAGGAAGGA

1876/6881
FIGURE 1736B

AGTGTGTGGATGTGGATGGTGGGGGCATGGACAAAGCTTGACACATCAAGTTATCAAGGCCTTGGAGGAGGCTCT
GTATGTCCTCAGGGGACTGACAACATCCTCCAGATTCCAGCCATAAACCAATAACTAGGCTGGACCCTTCCCCT
ACATAATAGGGCTCAGCCCAGGCAGCCAGCTTTGGGCTGAGCTAACAGGACCAATGGATTAACTGGCATTTCAG
TCCAAGGAAGCTCGAAGCAGGTTTAGGACCAGGTCCCCTTGAGAGGTCAGAGGGGCCTCTGTGGGTGCTGGGTAC
TCCAGAGGTGCCACTGGTGGGAAGGGTCAGCGGAGCCCCAGCAGGAAGGGTGGGCCAGCCAGGCCATTCTTAGTCC
CTGGGTGGGGAGGCAGGGAGCTAGGGCAGGGACCAAATGAACAGAAAGTCTCAGCCCAGGATGGGGCTTCTTCA
ACAGGGCCCCCTGCCCTCCTGAAGCCTCAGTCCTTACCTTGCCAGGTGCCGTTTCTCTTCCGTGAAGGCCACTGC
CCAGGTCCCCAGTGCGCCCCCTAGTGGCCATAGCCTGGTTAAAGTTCCCCAGTGCCCTCCTTGTGCATAGACCTTC
TTCTCCCACCCCCTTCTGCCCCCTGGGTCCCCGGCCATCCAGCGGGGCTGCCAGAGAACCCAGACCTGCCCTTAC
AGTAGTGTAGCGCCCCCTCCCTCTTTTCGGCTGGTGTAGAATAGCCAGTAGTGTAGTGCGGTGTGCTTTTACGTGA
TGGCGGGTGGGCAGCGGGCGGGCGGGCTCCGCGCAGCCGTCTGTCTTGATCTGCCCGCGGGCGGCCCGTGTGTGT
TTTGTGCTGTGTCCACGCGCTAAGGCGACCCCCTCCCCCGTACTGACTTCTCCTATAAGCGCTTCTCTTCGCATA
GTCACGTAGCTCCCACCCCACCCCTCTTCTGTGTCTCACGCAAGTTTATACTCTAATATTTATATGGCTTTTTT
TCTTCGACAAAAAATAATAAACGTTTCTTCTGAAAAGCTG

1877/6881
FIGURE 1737

MAAQRNRSKESKDCSGLVLLCLFFGIPWEAGARQISYSIPEELEKGSFVGNISKDLGLAPRELAERGVRIVSRGR
TQLFSLNPRSGSLITAGRIDREELCAQSARCVVSFNILVEDRVKLFGEIEVTDINDNAPKFQAE NL DVKINENV
AAGMRFP LPEAIDPDVG VNSLQSYQLSPNKHFSLRVQSRANGVKYPELVLEHSLDREEEAIIHHLVLTASDGGDPL
RSGTVLVSVTVFDANDNAPVFTLPEYRVSVPENLPVGTQLLTVTATDRDEGANGEVTYSFRKL PDTQLLKFQ LNK
YTGEIKISENL DYEETGFYEIEIQAEDGGAYLATAKV LITVEDVNDNSPELTITSLFSPVTEDSPLGTVVALLNV
HDLDSEQNGQVTCSILAYLPFKLEKSIDSYYRLVIHRA LDREQVSSYNITVTATDGGSPPLSTEAHFMLQVADIN
DNPPTFSQVSYFTYIPENNARGASIFSVTALDPDSKENAQIIYSLAEDTIQGVPLSSYISINSDTGVL YALRSFD
YEQFH ELMQV TASD SGDPPLSSNVSLSLFVLDQNDNAPEILYPALPTD GSTGV ELAPRSAEPGYLVTKVAVDR
DSGQNAWLSYRLLKASEPGLFAVGEHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTLTVAVADSIPQV
LADLGSFESPANSETSDLTLYLVVAVAAVSCVFLAFVIVLLAHLRRWHKSRL LQASGGGLTGVS GSHFVGVDGV
RAFLQTYSHEVSLTADSRKSHLIFPQPNYADTLISQESCEKNDPLSLDDSKFP IEDTPLVPQAPPNTDWRFSQA
QRPGTSGSQNGDDTGTWPNNQFDTEMLQAMILASASEAADGSSTLGGGAGTMGLSARYGPQFTLQHVPDYRQNVY
IPGSNATLTNAAGKRDGKAPAGGNGNKKKSGKKEKK

1878/6881
FIGURE 1738A

AGAATGGGCTCTAGGCGCCGCTGCTCACCAATCAGGGAATGGGAAGCTGCGCGCCATTGAGTCCCTCCCTCCCC
GCCTCTACCACACAAAGCGGAATGAGATGGATACTCACAGATCCTGACACTGGAGACTTAGAAGTATTTTCCTTC
GCTTTCTGATATATTTTGGATGTAGTCGGCCTAGGACTTCATAGATACATAAGCCGATTACAACCAACCAGCTC
GAGAAACCGCGGAATATCGGCTTAGAGCCTGCCATGGCGAATCGGCTACAGCGCGGGGACCAGTCGGCTGCTG
CTGCTGCTGTGCATTTTCTGGGGACGCTGCGGGGGTTCCGGGCCAGGCAGATCCGATATTCGGTGCCAGAAGAG
ACCGAAAAGGGCTCCTTCGTGGGCAATATCTCCAAGGACCTGGGGCTGGAGCCCCGGGAGCTGGCGAAGCGCGGA
GTCCGCATCGTCTCCAGAGGGAAGACACAGCTTTTCGCTGTGAATCCGCGAAGCGGCAGCTTGATCACGGCAGGC
AGGATAGACCGGGAGGAGCTCTGTGAGACGGTGTCTCTCTGTTTTTAAATATGGAACCTTCTCGTGAAGACACC
TTGAAGATTTACGGAGTGGAGGTGGAAATAATAGATATTAATGATAACGCCCCAGCTTCCAGGAGGACGAAGTG
GAGATAAAAGTCAGTGAGCACGCAATTCCTGGGGCGCGATTTGCTCTTCTTAATGCTAGGGATCCAGATGTGGGC
GTGAACCTCCCTCCAGAGCTACCAGCTCAGCCCTAATAATTACTTTTCTTGCAACTGCGGGGCAGAACGGATGGG
GCCAAGAATCCAGAGCTAGTACTGGAGGGAAGCCTGGACCGAGAGAAAGAGGCTGCTCACCTGCTCCTCTCACA
GCTTTAGATGGAGGCGATCCCATCCGAAAGGGCGCAGTTCCCATTCGTGTGGTGGTCTCGATGTAAATGATCAC
ATCCCAATGTTTACACAGTCCGTATATCGCGTGAGTGTTCCAGAAAACATCAGCTCCGGAACCTCGGGTGCTGATG
GTTAATGCAACGGATCCAGACGAGGGAATCAACGGGGAAGTAATGTATTCAATTCGGAACATGGAAAGCAAGGCT
TCTGAAATATTCCAATTGGATTCAAACTGGAGAAGTTCAAGTACGGGGGTCTCTGGATTTTGAAAAATATAGA
TTCTATGAGATGGAAATTCAGGCCAAGATGGTGGAGGTCTCTTTACCACCACGACGATGTTGATCACTGTTGTG
GATGTGAATGATAACGCTCCAGAAATAACTATCACCTCTTCTATTAATTCAATTCTGGAAGAACTCTCTCCAGGT
ACAGTGATTGCTCTTCTAAATGTGCAAGATCAAGATTCTGGAGAAAATGGTCAAGTCTCTGTTTTATTCTAAC
CACCTGCCTTTTAAATTAGAAAAGACTTATGGAAATTATTACAAATTGATAACAAGCAGAGTGCTGGACAGGGAG
TTGGTCCAGAGCTACAATATAACGTTGACAGCCACAGACCAGGGAAGCCCGCTTTGTCTGCAGAACTCATGTC
TGGCTGAATGTGGCAGATGACAACGATAACCCCTCCCGTTTTTCTCACTCTCTTACTCTGCCTACATTCCCGAA
AACAAACCCAGGGGTGCCTCCATCTTCTCAGTGACCGCCCTCGACCCGGACAGCAAACAGAATGCCCTGGTCACT
TACTCTCTGACGGATGACACTGTCCAGGGGTGCCTCTGTCTCTCTATGTCTCTATTAACCTCAACACTGGTGT
CTCTATGCCCTACAATCCTTCGACTATGAGCAGTTTCGAGACTTAGAACTGAGAGTGATAGCACGTGACAGCGGG
GACCCGCCCCCTCAGCAGCAACGTGTGCTGAGCCTGTTCTGTCTGGACCAGAACGACAATGCGCCCCGAGATCCTG
TACCTGCCCCCTCCACAGACGGCTCCACTGGCGTGGAGCTGGCGCCCCGCTCTGCGGAACCTGGCTACCTGGTG
ACCAAGGTGGTTGCGGTGGACAAAAGATTAGGCCAGAACGCCTGGCTGTCTATCGCCTGCTTAAGGCCAGCGAG
CCGGGACTCTTTCGCGGTGGGGGAGCACAGGGCGAGGTGCGTACAGCGCGGGGCACTGCTGGACAGAGACGCGCTC
AAGCAGAGCCTCGTGGTGGCCGTCCAGGACCACGGCCAGCCCCCTCTCTCGGCCACCGTCACGCTCACCGTGGCT
GTGGCCGACAGCATCCCCGAAGTCTGGCGGACCTCGGCAGCCTCGAGTCTCTGGCTAACTCTGAAACCTCAGAC
CTCTCGCTGTACTTGGTGGTGGCGGTGGCCGAGTCTCTGCTATCTTCTGGTCTTTGTATCGTGTCTGGCA
CTCAGGCTGTGGCGCTGGCATAAGTCACGCCTGCTGCAGGCTTCTGAAGGCGGGTGGCAGGTATGCCACGTCA
CATTTTGTAGGCGTGGACGGGTACAGGCTTTTCTGCAAACCTATTCCCACGAGGTCTCTCTCATTGCGGACTCG
CAGAAGAGTCACCTGATTTTCCCCAGCCCACTATGGGGACACGCTCATCAGCCAGGAGAGCTGTGAGAAAAGC
GAGCCACTCTTGATAGCTGAAGACTCAGCTATCATTTTAGGCAAATGTGACCCGACAAGTAATCAGCAAGCCCCG
CCCAACACGGACTGGCGTTTCTCTCAGGCCAGAGACCCGGCACCAGCGGCTCCCAAAATGGCGATGACACCGGC
ACCTGGCCCAACAACAGTTTGACACAGAGATGCTGCAAGCCATGATCTTGGCGTCCGCCAGTGAAGCTGCTGAT
GGGAGCTCCACCTTGGGAGGGGGTGCCGGCACCATGGGATTGAGCGCCCCGTACGGACCCCACTTACCCTGCAG
CACGTGCCCCGACTACCGCCAGAATGTCTACATCCCAGGCAGCAATGCCACACTGACCAACGCAGCTGGCAAGCGG
GATGGCAAGGCCCCAGCAGGTGGCAATGGCAACAAGAAGAAGTCGGGCAAGAAGGAGAAGAAGTAACATGGAGGC
CAGGCCAAGAGCCACAGGGCGGCTCTCCCCAACAGCCAGCTTCTCTTACCTGCACCCAGGCCTCAGAGTTT
CAGGGCTAACCCCCAGAATACTGGTAGGGGCCAAGGCCATGCTCCCTTGGGAAACAGAAACAAGTGCCCACTCA
GCACCTACCCCTTCCCCCCCCAGGGGGTTGAATATGCAAAAGCAGTTCCGCTGGGAACCCCATCCAATCAACTGC
TGTACCCATGGGGGTAGTGGGGTTACTGTAGACACCAAGAACCATTGCCACACCCCGTTTAGTTACAGCTGAAC
TCCTCCATCTTCCAAATCAATCAGGCCCATCCATCCCATGCCTCCCTCCTCCCCACCCCACTCCAACAGTTCCCTC
TTTCCCGAGTAAGGTGGTTGGGGTGTGAAGTACCAAGTAACCTACAAGCCTCCTAGTTCTGAAAAGTTGGAAGG
GCATCATGACCTCTTGGCCTCTCCTTTGATTCTCAATCTTCCCCCAAAGCATGGTTTGGTGCCAGCCCCCTTACC

1879/6881
FIGURE 1738B

TCCTTCCAGAGCCCCAAGATCAATGCTCAAGTTTTGGAGGACATGATCACCATCCCCATGGTACTGATGCTTGCTG
GATTTAGGGAGGGCATTTTGCTACCAAGCCTCTTCCCAACGCCCTGGGGACCAGTCTTCTGTTTTGTTTTTCATT
GTTTGACGTTTCCACTGCATGCCTTGACTTCCCCCACCTCCTCCTCAAACAAGAGACTCCACTGCATGTTCCAAG
ACAGTATGGGGTGTAAGATAAGGAAGGGAAGTGTGTGGATGTGGATGGTGGGGGCATGGACAAAGCTTGACACA
TCAAGTTATCAAGGCCTTGAGGAGGCTCTGTATGTCCTCAGGGGACTGACAACATCCTCCAGATTCCAGCCATA
AACCAATAACTAGGCTGGACCCTTCCCACTACATAATAGGGCTCAGCCCAGGCAGCCAGCTTTGGGCTGAGCTAA
CAGGACCAATGGATTAAACTGGCATTTCAGTCCAAGGAAGCTCGAAGCAGGTTTAGGACCAGGTCCCCCTTGAGAG
GTCAGAGGGGCTCTGTGGGTGCTGGGTACTCCAGAGGTGCCACTGTTGGAAGGGTCAGCGGAGCCCCAGCAGGA
AGGGTGGGCCAGCCAGGCCATTCTTAGTCCCTGGGTGGGGAGGCAGGGAGCTAGGGCAGGGACCAAATGAACAG
AAAGTCTCAGCCCAGGATGGGGCTTCTTCAACAGGGCCCCCTGCCCTCCTGAAGCCTCAGTCCTTCACCTTGCCAG
GTGCCGTTTCTCTTCCGTGAAGGCCACTGCCCAGGTCCCCAGTGCGCCCCCTAGTGGCCATAGCCTGGTTAAAGT
TCCCCAGTGCCCTCCTTGTCATAGACCTTCTTCTCCACCCCCCTTCTGCCCCCTGGGTCCCCGGCCATCCAGCGGG
GCTGCCAGAGAACCCCAGACCTGCCCTTACAGTAGTGTAGCGCCCCCTCCCTCTTTCGGCTGGTGTAGAATAGCC
AGTAGTGTAGTGCAGGTGTGCTTTTACGTGATGGCGGGTGGGCAGCGGGCGGGGGCTCCGCGCAGCCGTCTGTCC
TTGATCTGCCCCGCGGCGGCCCGTGTGTGTTTTGTGCTGTGTCCACGCGCTAAGGCGACCCCCCTCCCCGTACTG
ACTTCTCCTATAAGCGCTTCTCTTCGCATAGTCACGTAGCTCCACCCCCACCCTCTTCCTGTGTCTCACGCAAGT
TTTATACTCTAATATTTATATGGCTTTTTTTCTTCGACAAAAAAATAATAAACGTTTCTTCTGAAAAGCTG

1880/6881
FIGURE 1739

MANRLQRGDRSRLLLLLCIFLGLRGFRARQIRYSVPEETEKGSFVGNISKDLGLEPRELAKRGVRIVSRGKTQL
FAVNPRSGSLITAGRIDREELCETVSSCFLNMELLVEDTLKIYGVEVEIIDINDNAPSFQEDEVEIKVSEHAIPG
ARFALPNARDPDVGVNSLQSYQLSPNNYFSLQLRGRDGAKNPELVLEGSLDREKEAAHLLLLTALDGGDPPIRKG
AVPIRVVVLVDNDHIPMFTQSVYRVSVPENISSGTRVLMVNATDPDEGINGEVMYSFRNMESKASEIFQLDSQTG
EVQVRGSLDFEKYRFYEMEIQQQDGGGLFTTTTMLITVVDVNDNAPEITITSSINSILENSPPGTVIALLNVDQDQ
DSGENGQVSCFIPNHLFPKLEKTYGNYYKLITSRVLDRELVSYNITLTATDQGSPPLSAETHVWLVNADDNDNP
PVFPHSSYSAYIPENNPRGASIFSVTALDPPDSKQNALVTYSLTDDTVQGVPLSSYVSINSNTGVLYALQSFDYEQ
FRDLELRVIARDSGDPPLSSNVSLSLFVLDQNDNAPEILYPALPTDGSTGVELAPRSAEPGYLVTKVVAVDKDSG
QNAWLSYRLLKASEPGLFAVGEHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTLTVAVADS IPEVLAD
LGSLESLANSETSDLSLYLVVAVAAVSCIFLVFVIVLLALRLWRWHKSRLQASEGGLAGMPTSHFVGVDGVQAF
LQYSHEVSLIADSQKSHLIFPQPNYGDTLISQESCEKSEPLLIAEDSAIILGKCDPTSNQQAPPNTDWRFSQAQ
RPGTSGSQNGDDTGTWPNNQFDTEMLQAMILASASEAADGSSTLGGGAGTMGLSARYGPQFTLQHVPDYRQNVYI
PGSNATLTNAAGKRDGKAPAGGNGNKKKSGKKEKK

1881/6881
FIGURE 1740A

AAGGGGGTGGAGGTTTGGCCCTAAAGCTTCAGGACACCAAAGAAATTCAGTCGAACAGCCCACCAGTTCTCTCCA
TAGGGACCTGGGTCCCGTGAATGCTGGTTATCTCACACCCTGAGGAATAAAGATTGGAATCCGCACTGGATGCTG
GAAGTTGACTCGGAGAAAATTGCGACAGGAGGGAAATGGCGGCTCTGCAAAAGTTGCCACACTGCAGAAAGCTGG
TCCTGCTGTGCTTCCTTTTGGCGACCCTGTGGGAGGCCAGGGCCGGGCAGATTTCGCTATTCTGTGCGGGAAGAGA
TCGACAGAGGCTCCTTCGTAGGCAACATCGCCAAGGACTTGGGTTTGGAGCCCTGGCACTGGCAGAGCAGGGAG
TCCGCATCGTCTCCAGAGGTAGGTCCCAGCTCTTTGCTCTGAACCCGCGAAGCGGCAGCTTGGTCACTGCGAACA
GGATAGACCAGGGAGGAGCTCTGCGCTCAGAGCGCACCCTGTCTGTGAATTTTAACATTCTGCTGGAGGATAAAT
TGACTATTTATTAGTAGAGGTGGAAATAACAGATATTAACGATAATGCCCTCGCTTTGGAGTAGAGGAACTGG
AGCTAAAAATCAGTGAAACCACTACGCCAGGATTCCGGATTCTCTTAAGAATGCGCATGATGCAGACGTAGGTG
AGAACGCCCTTCAGAAGTACGCACTCAACCCAAATGACCATTCTCCCTGGACGTGCGAAGGGGAGCTGATGGGA
ACAAGTACCCAGAAGTGGTGTGAGAGCGTCTCTGGACCGCGAGGAAGAGGCTGTTACCACCTCGTTCTCGTGG
CTTCTGATGGGGGTGACCCAGTGCTATCTGGCACCTCCCGCATCTGCGTGAAGGTCCTGGATGCGAACGACAATG
CGCTGTTTTTACACAGCCCGAGTACCGCATAAGCATTCCGGAGAATACGCTCGTGGGCACCCGGATACTCACGG
TGACCGCCACTGACGCAGATGAGGGCTACTACGCTCAAGTGGTATATTTTCTAGAGAAAAGCCCTGGAGAAACCT
CAGAGGTATTTGAGCTTAAGTCAACATCTGGAGAACTGACAATCATAAAAGATCTAGATTATGAGGATGCTACAT
TCCATGAAATTGATATTGAAGCTCAGGATGGTCCGGGCCCTTCTAACCAGAGCGAAGGTTATCGTCACGGTCTTG
ATGTGAATGACAATGCCCCAGAATTTTACATGACATCTGCTACTAGCTCAGTTTCTGAAGACTCTCTTCCAGGAA
CCATAATTGGGCTTTTTAATGTACATGATAGAGACTCTGGGCAGAACGCATTACCCACCTGTTCACTCCCCGAGG
ATCTTCCTTTTAAGTTAGAAAAGTCAGTAGACAATTACTACCGACTGGTTACAACCAGAGCCCTTGACAGGGAAC
AGTTTTCTTTTACAACATCACTCTAACCGCTAAAGATGGAGGGAACCCCTCCCTGTCCACGGATGCTCACATTT
TGCTCCAGGTGGCAGACATCAACGACAACGCACCCGCCCTTCTCCCGCACATCCTACTCCACCTACATTCCCGAAA
ACAACCCAGAGGAGCCTCTGTCTTCTCAGTGACGGCCCATGACCCGACAGCAACGACAATGCTCATGTAACCT
ACTCTTTCGCGGAGGACACTGTTTCAGGGGGCACCCCTATCCTCTTACATCTCTATCAACTCCGACACTGGAGTAC
TCTATGCACTGCGCTCCTTTGATTATGAGCAGTTGCGAGACTTGCAAGTGTGGGTGATAGCGCGGGACAGCGGGA
ACCCCTCCACTCAGTAGCAATGTATCATTAAAGCCTGTTCTGTCTGGACCAGAACGACAACGCGCCCGAGATCCTGT
ACCCCTGCCTTCCCCACAGACGGTTCCACTGGCGTGGAGCTGGCGCCCCGCTCCGCAGAGCCCGGCTACCTGGTGA
CCAAGGTGGTGGCGGTGGACAGAGACTCGGGCCAGAACGCCTGGCTGTCTTACCACCTGCTCAAGGCCAGCGAGC
CGGGACTCTTCTCGGTGGGTCTGCACACGGGCGAGGTGCGCACGGCGCGAGCCCTGCTGGACAGAGACGCGCTCA
AGCAGAGCCTCGTGGTGGCCATCCAGGACCACGGCCAGCCCCCTCTCTCCGCCACTGTACGCTCACCGTGGCCG
TGGCCGACAGGATCCCCGACATCCTGGCCGACCTGGGCAGCCTCGAGCCCTCCGCCATACCCAACGATTCCGGACC
TCACTCTGTACCTGGTGGTGGCGGTGGCCGCGGTCTCCTGCGTCTTCTGGCCTTCGTCATCGTGTGCTGGCGC
ACAGGCTGCGGCGCTGGCACAAGTCACGCCTGCTGCAGGCTTCAGGAGGCAGCTTGACAGGCATGCAGAGCTCGC
ACTTTGTGGGCGTGGACGGGGTTCGGGCTTTCCTGCAGACCTATTCCACGAGGTCTCCCTCACTGCGGACTCGC
GGAAGAGCCACCTGATTTTCCCCAGCCCAACTATGCGGACACGCTCATCAGCCAGGAGAGCTGTGAGAAAAGG
ATTTTTTATCAGCGCCTCAATCTCTACTCGAAGAAGAAAAGAGAAGAAACGTTTTCTCAGCAAGCCCCGCCCAACA
CGGACTGGCGTTTCTCTCAGGCCCAGAGACCCGGCACCAGCGGCTCCCAAAATGGCGATGACACCGGCACCTGGC
CCAACAACCAGTTTGACACAGAGATGCTGCAAGCCATGATCTTGGCGTCCGCCAGTGAAGCTGCTGATGGGAGCT
CCACCCCTGGGAGGGGGTGC CGGCACCATGGGATTGAGCGCCCGCTACGGACCCCACTTACCCTGCAGCACGTGC
CCGACTACCGCCAGAATGTCTACATCCAGGCAGCAATGCCACACTGACCAACGCAGCTGGCAAGCGGGATGGCA
AGGCCCCAGCAGGTGGCAATGGCAACAAGAAGAAGTCGGGCAAGAAGGAGAAGAAGTAAACATGGAGGCCAGGCCA
AGAGCCACAGGGCGGCCTCTCCCCAACCAGCCAGCTTCTCCTTACCTGCACCCAGGCCTCAGAGTTTTCAGGGCT
AACCCCAAGAATACTGGTAGGGGCCAAGGCCATGCTCCCCTTGGGAAACAGAAACAAGTGCCAGTCAGCACCTA
CCCCTTCCCCCCCCAGGGGGTTGAATATGCAAAAGCAGTTCCGCTGGGAACCCCATCCAATCAACTGCTGTACCC
ATGGGGGTAGTGGGGTTACTGTAGACACCAAGAACCATTGCCACACCCCGTTTAGTTACAGCTGAACTCCTCCA
TCTTCCAAATCAATCAGGCCCATCCATCCCATGCTCCCTCCTCCCCACCCCACTCCAACAGTTCTCTTTCCCG
AGTAAGGTGGTTGGGGTGTGAAGTACCAAGTAACCTACAAGCCTCCTAGTTCTGAAAAGTTGGAAGGGCATCAT
GACCTCTTGGCCTCTCCTTTGATTCTCAATCTTCCCCCAAAGCATGGTTTGGTGCCAGCCCTTACCTCCTTCC
AGAGCCCAAGATCAATGCTCAAGTTTTGGAGGACATGATCACCATCCCCATGGTACTGATGCTTGCTGGATTAG

1882/6881
FIGURE 1740B

GGAGGGCATTTTGCTACCAAGCCTCTTCCCAACGCCCTGGGGACCAGTCTTCTGTTTTGTTTTTCATTGTTTGAC
GTTTCCACTGCATGCCTTGACTTCCCCACCTCCTCCTCAAACAAGAGACTCCACTGCATGTTCCAAGACAGTAT
GGGGTGGTAAGATAAGGAAGGGAAGTGTGTGGATGTGGATGGTGGGGGCATGGACAAAGCTTGACACATCAAGTT
ATCAAGGCCCTTGGAGGAGGCTCTGTATGTCTCAGGGGACTGACAACATCCTCCAGATTCCAGCCATAAAACCAAT
AACTAGGCTGGACCTTCCCACTACATAATAGGGCTCAGCCAGGCAGCCAGCTTTGGGCTGAGCTAACAGGACC
AATGGATTAAACTGGCATTTCAGTCCAAGGAAGCTCGAAGCAGTTTAGGACCAGGTCCCCTTGAGAGGTGAGAG
GGGCTCTGTGGGTGCTGGGTACTCCAGAGGTGCCACTGGTGGAAAGGTCAGCGGAGCCCCAGCAGGAAGGGTGG
GCCAGCCAGGCCATTCTTAGTCCCTGGGTTGGGGAGGCGAGGAGCTAGGGCAGGGACCAAATGAACAGAAAGTCT
CAGCCCAGGATGGGGCTTCTTCAACAGGGCCCCCTGCCCTCCTGAAGCCTCAGTCCCTTACCTTGCCAGGTGCCGT
TTCTCTTCCGTGAAGGCCACTGCCCAGGTCCCCAGTGCGCCCCCTAGTGGCCATAGCCTGGTTAAAGTTCCCCAG
TGCCCTCCTTGTGCATAGACCTTCTTCTCCCACCCCCTTCTGCCCTGGGTCCCCGGCCATCCAGCGGGGCTGCCA
GAGAACCCCAGACCTGCCCTTACAGTAGTGATAGCGCCCCCTCCCTCTTTCGGCTGGTGTAGAATAGCCAGTAGTG
TAGTGCGGTGTGCTTTTACGTGATGGCGGGTGGGCAGCGGGCGGCGGGCTCCGCGCAGCCGTCTGTCTTGAICT
GCCCCGCGCGGCCCGT
CTATAAGCGCTTCTCTTCGCATAGTCACGTAGCTCCCACCCCACCTTCTCTGTGTCTCACGCAAGTTTTATAC
TCTAATATTTATATGGCTTTTTTTTCTTCGACAAAAAATAATAAAACGTTTCTTCTGAAAAGCTG

1883/6881
FIGURE 1741

MAALQKLPHCRKLVLLCFLLATLWEARAGQIRYSVREEIDRGSFVGNIAKDLGLEPLALAEQGVRIVSRGRSOLF
ALNPRSGSLVTANRIDREELCAQSAPCLLNFNILLEDKLTIIYSVEVEITDINDNAPRFGVEELELKISETTTTPGF
RIPLKNAHDADVGENALQKYALNPNDHFSLDVRRGADGNKYPELVLESLDREEEAVHHLVLVASDGGDPVLSGT
SRICVKVLDANDNAPVFTQPEYRISIPENTLVGTRILTVTATDADEGYAQVVYFLEKSPGETSEVFELKSTSGE
LTIKDLDYEDATFHEIDIEAQDGPGLLTRAKVIVTVLDVNDNAPEFYMTSATSSVSEDSLPGTIIIGLFNVHDRD
SGQNAFTTCSLPEDLPFKLEKSVDNYYRLVTTRALDREQFSFYINITLTAKDGGNPSLSTDAHILLQVADINDNAP
AFSRTSYSTYIPENNPRGASVFSVTAHDPDSNDNAHVITYSFAEDTVQGAPLSSYISINSDTGVLYALRSFDYEQ
RDLQVWVIARDSGNPPLSSNVSLSLFVLDQNDNAPEILYPAFPTDGSTGVELAPRSAEPGYLVTKVVAVDRDSGQ
NAWLSYHLLKASEPGLFSVGLHTGEVRTARALLDRDALQSLVVAIQDHGQPPLSATVTTLTVAVADRIPDILADL
GSLEPSAIPNDSDLTLYLVVAVAAVSCVFLAFVIVLLAHLRRWHKSRLQASGGSLTGMQSSHFGVDGVRAFL
QTYSHVSLTADSRKSHLIFPQPNYADTLISQESCEKKDFLSAPQSLLEEEEREETFSQQAPPNTDWRFSQAQRPG
TSGSQNGDDTGTWPNNQFDTEMLQAMILASASEAADGSSTLGGGAGTMGLSARYGPQFTLQHVPDYRQNVYIPGS
NATLTNAAGKRDGKAPAGGNGNKKKSGKKEKK

1884/6881
FIGURE 1742A

ATGACCAATTGCCTGAGTTTCCGAAATGGCAGAGGACTGGCCCTGCTGTGCGCGCTCCTGGGGACGCTGTGCGAA
ACAGGATCCGGTCAGATCCGCTACTCGGTGTCTGAGGAGCTAGATAAAGGTTCTTCGTGGGCAACATCGCTAAC
GACCTGGGGCTAGAGCCCCGGGAGCTGGCGGAGCGCGGAGTCCGCATCGTCTCCAGAGGTAGGACGCGAGCTTTTC
TCTCTGAATCCGCAAAGCGGCAGCTTGGTCACCCGCGGAGAGGATAGACCGGGAGGAGCTCTGCGCTCAGATCCCG
CTGTGTCTGGTAAAAATTAACATTCTGGTTGAGGATAAAATTGAAAATTTTGAAGTAGAAAATAGAAAATTAAAGAT
ATTAATGATAATGCTCCTAATTTCCCAACAGAGGAATTGGAATAAAAAATTGGTGAACATAACGGTTCTTGGAACC
CGATTTCCAATTAAAAGTCTTTTGAACCCAGATGTAGGCATTAACCTCCCTGCAGAACTACAAGCTTAGCCCCAAT
GACTACTTCTCTCTGGCTGTGAATAGCGTCTCTGAGGGGGGCCAAGTATCCAGAGCTGGTGCTGGAGCGGGCCCTG
GACCGTGAGAAAAAAGAAATTCACCAGCTTGTCTGGTTGCCTCTGATGGTGGCGACCCCTGTCCACTCTGGCAAC
TTGCACATCCAAGTGATAGTCCTGGATGCAAATGACAACCCACCAATGTTTACTCAGCCTGAGTACCGTGTGAGT
GTTTGGGAGAACGTGCCTGTGGGTACCCGGCTGCTCACGGTGAATGCCACTGACCCTGACGAGGGATTCAATGCT
CAAGTGCTTATATTCTAGATAAAATGCCTGGGAAAAATCGCTGAGATTTTCCATCTTAACCTCAGTGAGTGGAGAA
GTATCAATATTAAAAAGTCTAGATTATGAGGATGCCATGTTCTATGAAATTAAAATTGAAGCACAGGATGGACCA
GGTCTTCTTTCAAGAGCCAAGATTCTAGTCACGGTTCTGGATGTGAATGACAATGCTCCAGAAATTACAATCACG
TCTCTCACAAGCTCAGTCCAGAAGAGGGCACCGTTGGAAGAGAAATTGCTCTTATCGACGTGCATGACCGAGAT
TCTGGGCAGAATGGGCAGGTTGAAGTTTTTGTCTGGGAAATCTGCCATTTAAGTTAGAAAAATCAATAGATCAA
TATTACCGCTTAGTGACGGCCACATCCCTGGACCGGAACAAATATCAGAATATAACATTAGTCTGAGAGCCTCA
GATGGGGGAAGCCCGCCACTGTCCACAGAACTCACATCACCCCTGCATGTGATTGACATCAATGACAACCCACCC
ACCTTCCCTCATTTATCCTACTCCGCCTACATTCAGAAAAACAACCCCAAGAGGAGCCTCCATCTTCTCAGTGACA
GCCCAGGACCCAGATAGCAACAACAACGCCCGCATCACTTATGCATTGACCGAGGACACTCTCCAGGGGGCGCCC
CTGTCTCTCTCGTCTCTATCAACTCCAACACTGGCGTCTTATACGCGCTGAGATCCTTCGACTACGAGCAATTT
AGAGACTTAAAGCTACTGGTGACAGCCAGCGACAGCGGGAACCCCTCCACTCAGCAGCAACGTGTGCTGAACCTG
TTCGTGCTGGACCAGAACGACAACGCGCCCGAGATCCTGTACCCCGCCCTCCCCACAGACGGTTCCACTGGCGTG
GAGCTGGCGCCTCGCTCCGCAGAGCCCGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACAGAGACTCGGGCCAG
AACGCTGGCTGTCTTACCGCCTGCTCAAGGCCAGCGAGCCGGGACTCTTCTCGGTGGGTCTGCACACGGGCGAG
GTGCGCACGGCGCGAGCCCTGCTGGACAGAGACGCGCTCAAGCAGAGCCTCGTGGTGGCCGTCCAGGACCACGGC
CAGCCCCCTCTCTCCGCCACTGTACGCTCACCGTGGCCGTGGCCGACAGGATCCCCGACATCCTGGCCGACCTG
GGCAGCCTCGAGCCCTCCGCCAAACCCAACGATTCCGACCTCACTCTGTACCTGGTGGTGGCGGTGGCCGCGGTC
TCCTGCGTCTTCTTGGCCTTCGTCATCGTGCTGCTGGCGCTCAGGCTGCGGCGCTGGCACAAGTCACGCCTGCTG
CAGGCTTCCGGAGGCGGCTTGGCGAGTACGCCCCGCTCGCACTTTGTGGGCGCGGACGGGGTTTCGGGCTTTCTCTG
CAGACCTATTCCCACGAGGTCTCCCTCACTGCGGACTCGCGGAAGAGCCACCTGATTTTCCCCAGCCCAACTAT
GCGGACACGCTCATCAGCCAGGAGAGCTGTGAGAAAAGCGAGCCTCTTCTGATAACTCAGGATTTACTTGAAATG
AAAGGAGATTCCAACCTACTTCAGCAAGCCCCGCCAACACGGACTGGCGTTTCTCTCAGGCCCAGAGACCCGGC
ACCAGCGGCTCCCAAATGGCGATGACACCGGCACCTGGCCCAACAACAGTTTGACACAGAGATGCTGCAAGCC
ATGATCTTGGCGTCCGCCAGTGAAGCTGCTGATGGGAGCTCCACCCTGGGAGGGGGTGCCGGCACCATGGGATTG
AGCGCCCGCTACGGACCCCAAGTTACCCCTGCAGCACGTGCCCGACTACCGCCAGAATGTCTACATCCCAGGCAGC
AATGCCACACTGACCAACGCAGCTGGCAAGCGGGATGGCAAGGCCCCAGCAGGTGGCAATGGCAACAAGAAGAAG
TCGGGCAAGAAGGAGAAGAAGTAAATGAGGAGCCAGGCCAAGAGCCACAGGGCGGCCTCTCCCCAACAGCCAG
CTTCTCCTTACCTGCACCCAGGCCTCAGAGTTTCAAGGGCTAACCCCCAGAATACTGGTAGGGGCCAAGGCCATGC
TCCCCTTGGGAAACAGAAACAAGTGCCAGTCAGCACCTACCCCTTCCCCCAGGGGGTTGAATATGCAAAAGC
AGTTCCGCTGGGAACCCCCATCCAATCAACTGCTGTACCCATGGGGGTAGTGGGGTTACTGTAGACACCAAGAAC
CATTTGCCACACCCCGTTTAGTTACAGCTGAACTCCTCCATCTTCCAAATCAATCAGGCCCATCCATCCCATGCC
TCCCTCCTCCCCACCCCACTCCAACAGTTCTCTTTCCCGAGTAAGGTGGTTGGGGTGTGAAAGTACCAAGTAAC
CTACAAGCCTCCTAGTTCTGAAAAGTTGGAAGGGCATCATGACCTCTTGGCCTCTCCTTTGATTCTCAATCTTCC
CCCAAAGCATGGTTTGGTGCCAGCCCTTCACTCCTTCCAGAGCCCAAGATCAATGCTCAAGTTTTGGAGGACA
TGATCACCATCCCCATGGTACTGATGCTTGTGGAATTTAGGGAGGGCATTTTGTACCAAGCCTCTTCCCCAACGC
CCTGGGGACAGTCTTCTGTTTTGTTTTTCAATTGTTTGACGTTTCCACTGCATGCCTTGACTTCCCCACCTCCT
CCTCAAACAAGAGACTCCACTGCATGTTCCAAGACAGTATGGGGTGGTAAGATAAGGAAGGGAAGTGTGTGGATG

1885/6881

FIGURE 1742B

TGGATGGTGGGGGCATGGACAAAGCTTGACACATCAAGTTATCAAGGCCTTGGAGGAGGCTCTGTATGTCCTCAG
GGGACTGACAACATCCTCCAGATTCCAGCCATAAACCAATAACTAGGCTGGACCCTTCCCACTACATAATAGGGC
TCAGCCCAGGCAGCCAGCTTTGGGCTGAGCTAACAGGACCAATGGATTAACTGGCATTTCAGTCCAAGGAAGCT
CGAAGCAGGTTTAGGACCAGGTCCCCTTGAGAGGTCAGAGGGGCCTCTGTGGGTGCTGGGTACTCCAGAGGTGCC
ACTGGTGGAAAGGGTCAGCGGAGCCCCAGCAGGAAGGGTGGGCCAGCCAGGCCATTCTTAGTCCCTGGGTGGGGA
GGCAGGGAGCTAGGGCAGGGACCAAATGAACAGAAAGTCTCAGCCCAGGATGGGGCTTCTTCAACAGGGCCCCTG
CCCTCCTGAAGCCTCAGTCCTTCACCTTGCCAGGTGCCGTTTCTCTTCCGTGAAGGCCACTGCCCAGGTCCCCAG
TGCGCCCCCTAGTGGCCATAGCCTGGTTAAAGTTCCCCAGTGCCCTCCTTGTGCATAGACCTTCTTCTCCACCCC
CTTCTGCCCCCTGGGTCCCCGGCCATCCAGCGGGGCTGCCAGAGAACCCAGACCTGCCCTTACAGTAGTGTAGCG
CCCCCTCCCTCTTTTCGGCTGGTGTAGAATAGCCAGTAGTGTAGTGCGGTGTGCTTTTACGTGATGGCGGGTGGGC
AGCGGGCGGCGGGCTCCGCGCAGCCGTCTGTCTTGATCTGCCCAGCGCGGCCCGTGTGTGTTTTGTGCTGTGT
CCACGCGCTAAGGCGACCCCTCCCCCGTACTGACTTCTCCTATAAGCGCTTCTCTTCGCATAGTCACGTAGCTC
CCACCCACCCCTCTTCTGTGTCTCAGCAAGTTTTATACTCTAATATTTATAATGGCTTTTTTTCTTCGACAAAA
AAATAATAAAACGTTTCTTCTGAAAAGCTG

1886/6881
FIGURE 1743

MTNCLSFNRNGRLALLCALLGTLCTGSGQIRYSVSEELDKGSFVGNIANDLGLEPRELAERGVRIVSRGRTQLF
SLNPQSGSLVTAERIDREELCAQIPLCLVKINILVEDKLKIFEVEIEIKDINDNAPNFPTEELEIKIGELTVPGT
RFPIKTAFDPDVGINSLQNYKLSNDYFSLAVNSVSEGAKEYPELVLERALDREKKEIHQLVLVASDGGDPVHSGN
LHIQVIVLDANDNPPMFTQPEYRVSVWENVPVGTRLLTVNATDPDEGFNAQVSYILDKMPGKIAEIFHLNSVSGE
VSILKSLDYEDAMFYEIKIEAQDGPGLLSRAKILVTVLDVNDNAPEITITSLTSSVPEEGTVGREIALIDVHDRD
SGQNGQVEVFVLGNLPFKLEKSIDQYYRLVTATSLDREQISEYNISLRASDGGSPPLSTETHITLHVIDINDNPP
TFPHLSYSAYIPENNNPRGASIFSVTAQDPDSNNNARITYALTEDTLQGAPLSSFVSINSNTGVLYALRSFDYEQF
RDLKLLVTASDSGNPPLSSNVSLNLFVLDQNDNAPEILYPALPTDGSTGVELAPRSAEPGYLVTKVVAVDRDSGQ
NAWLSYRLLKASEPGLFSVGLHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTLTVAVADRIPDILADL
GSLEPSAKPNDSDLTLYLVVAVAAVSCVFLAFVIVLLALRLRRWHKSRLQASGGGLASTPGSHFVGADGVRAFL
QTYSHVSLTADSRKSHLIFPQPNYADTLISQESCEKSEPLITQDLLEMKGDSNLLQQAPPNTDWRFSQAQRPG
TSGSQNGDDTGTWPNNQFDTEMLQAMILASASEAADGSSTLGGGAGTMGLSARYGPQFTLQHVPDYRQNVYIPGS
NATLTNAAGKRDGKAPAGGNGNKKKSGKKEKK

1887/6881
FIGURE 1744A

ATGGCGGCGCCTCCTGCTCGCCAGACCACACCCGGCTGCTCCAGATCTGCCTTCTCCTGGGGGTTCCTGGTGGA
ATCAGGGCCGAACAGATTCTCTACTCGGTGTTTGAGGAGCAGGAAGAAGGCTCAGTGGTGGGCAACATCGCCAAG
GACCTGGGGTTGGCGCCCCGGGAGCTGGCGGAGCGCGGAGTCCGCATCGTCTCCAGAGGTAGGACGCAGCTTTTC
GCCCTGAACCCGCGCAGCGGCACCTTGGTCACCGCGGGTAGGATAGACAGGGAGGAGCTCTGCGACAGATCTCCA
AACTGTGTGACAAACCTGGAGATTCTTCTAGAAGATACAGTGAAGATTTTGCGGGTAGAGGTGGAAATAATCGAT
GTTAATGATAACCCACCCAGTTTTGGGACAGAACAGAGGGAAATAAAAGTTGCTGAAAATGAAAATCCTGGGGCA
AGATTTCTCTCTCCTGAAGCTTTTGATCCGGATGTAGGTGTAACTCCCTGCAGGGTTACCAGCTCAACTCAAAC
GGTTACTTTTCCCTGGACGTGCAAAGTGGGGCCGATGGGATTAAGTACCCAGAGCTGGTGCTGGAACGCGCTCTA
GATCGCGAGGAAGAGGCGGTTACCCACCTCGTTCTCACGGCCTTCGATGGAGGTGACCCGGTTCGCTCTGGCACT
GCCAGGATTCTCATAATACTTGTGGATACCAACGATAATGCTCCCGTGTTCACTCAGCCGAGTACCACGTAAGT
GTTCTGTGAGAACGTTTCTGTAGGCACTCGGCTACTCACCGTAAAAGCCACTGATCCAGATGAAGGAGCCAATGGA
GACGTGACGTAATTTCTTCCGGAAAAGTAAGAGACAAAATATCACAGCTATTTCAAGTTGAATCTCTGAGTGGGGAT
ATAACAATATTGGGGGGTCTAGATTATGAGGACTCTGGATTCTATGACATAGATGTAGAAGCCCATGATGGGCCT
GGTCTCCGAGCTAGAAGCAAGGTACTGGTGACAGTTCTGGATGAAAATGACAACGCACCAGAAGTCACAGTTACA
TCTCTCACCAGCTCAGTCCAGGAATCTTCTTCCCGGGTACAGTAATTGCACTTTTCAACGTGCATGACAGTGAC
TCAGGAGGAAATGGCCTAGTCACATGTTCTATTCCAGATAATCTGCCATTCACTTGAAGACCTATGGAAAT
TATTATCGGTTGTTGACACACAGAACTGGACAGGGAAGAAGTCTCAGAATATAACATCACTGTAAGTGGCACT
GACCAGGGAACCTCCTCCACTGTCTACAGAACTCATATTTCACTGCAAGTGATGGACATCAATGACAACCCACCC
ACTTTCCCTCATGCTTCTACTCTGCTTACATTCCTGAAAACAACCCAGAGGAGCCTCCATCTTATCTATGACT
GCTCAAGACCCTGACAGTGGTGACAATGCCCGAATCACTTACTCCCTGGCCGAAGACACCTTCCAGGGTGCACCT
CTGTCTCCTATGTCTCCATCAACTCCAATACAGGGATCCTATATGCTCTTTGCTCCTTCGACTATGAGCAGTTT
AGAGACCTGCAGCTGCTGATGACAGCCAGTGACAGTGGAGACCCTCCACTCAGCAGCAATGTGTCACTGAGCCTC
TTTGTGCTGGACCAGAACGACAATGTCCCTGAGATCCTGTACCCACCTTCCCTACTGATGGCTCCACTGGTGTG
GAGCTGGCACCCCGCTCCGCAGATTCCGGCTACCTGGTGACCAAAGTGGTGGCAGTGGACAGAGACTCAGGTCAG
AATGCCTGGCTGTCTACAGCCTACTCAAGTCCAGCGAGCCGGGACTATTTGCAGTGGGGCTGCACACAGGCGAG
GTGCGCACCGCACGGGCCCTGCTGGACAGAGACGCGCTCAAGCAGAGGCTTGTAGTGGTCTCCAGGACCATGGC
CAGCCCCCTCTCTCGGCCACCGTCACACTCACTGTGGCTGTGGCCGACAGCATCCAGATGTCTGGCTGACTTG
GGCAGCCTCAAGCCTTCAGCAGACCCAGACGACTCGGGCCTCACACTCTATCTCGTGGTGGCAGTGGCCGCTGTC
TCCTGCGTCTTCTGGCTTTTGTACGGTGCTGTAGCACTCAAGCTGAGACGCTGGCACAAGTCACGCCTGCTT
CACGCTGAAGGCAGCAGGTTGGCAGGTGTGCCTGCCTCGCACTTTGTGGGCGTGGACGGGGTTGGGGCTTTCTCTG
CAGACCTATTCCACGAGGTCTCCCTCACC GCGGACTCGCGGAAGAGTCACCTGATCTTCTCCCAACCCAGCTAT
GCAGACAGCTCATCAGCCGGGAGAGTTGTGAGAAAAGCGAGCCTCTTCTGATAACTCAGGATTTACTTGAAACA
AAAGGAGACCCTAATCTTCAGCAAGCCCCGCCAACACGGACTGGCGTTTCTCTCAGGCCCAGAGACCCGGCACC
AGCGGCTCCCAAAATGGCGATGACACCGGCACCTGGCCCCAACAAACCAGTTTGACACAGAGATGCTGCAAGCCATG
ATCTTGGCGTCCGCCAGTGAAGCTGCTGATGGGAGCTCCACCCTGGGAGGGGGTGCCGGCACCATGGGATTGAGC
GCCCCTACGGACCCCACTTACCCTGCAGCACGTGCCCGACTACCGCCAGAATGTCTACATCCAGGCAGCAAT
GCCACACTGACCAACGCAGCTGGCAAGCGGGATGGCAAGGCCCCAGCAGGTGGCAATGGCAACAAGAAGAAGTCG
GGCAAGAAGGAGAAGAAGTAAATCATGGAGGCCAGGCCAAGAGCCACAGGGCGGCCTCTCCCCAACCAGCCAGCTT
CTCCTTACCTGCACCCAGGCCTCAGAGTTTACGGGCTAACCCCCAGAATACTGGTAGGGGCCAAGGCCATGCTCC
CCTTGGGAAACAGAAACAAGTGCCAGTCAGCACCTACCCCTTCCCCCCCAGGGGGTTGAATATGCAAAAGCAGT
TCCGCTGGGAACCCCATCCAATCAACTGCTGTACCCATGGGGGTAGTGGGGTTACTGTAGACACCAAGAACCAT
CTCCTCCCCACCCCACTCCAACAGTTCTCTTTCCGAGTAAGGTGGTGGGGTGTGAAGTACCAAGTAACCTA
CAAGCCTCCTAGTTCTGAAAAGTTGGAAGGGCATCATGACCTCTTGGCCTCTCCTTTGATTCTCAATCTTCCCC
AAAGCATGGTTTGGTGCCAGCCCCCTCACCTCCTTCCAGAGCCCAAGATCAATGCTCAAGTTTGGAGGACATGA
TCACCATCCCCATGGTACTGATGCTTGTGGATTTAGGGAGGGCATTTTGTCTACCAAGCCTCTTCCCAACGCCCT
GGGGACCAGTCTTCTGTTTTGTTTTTCAATGTTTGACGTTTCCACTGCATGCCTTGACTTCCCCACCTCCTCCT
CAAACAAGAGACTCCACTGCATGTTCCAAGACAGTATGGGGTGGTAAGATAAGGAAGGGAAGTGTGTGGATGTGG

1888/6881
FIGURE 1744B

ATGGTGGGGGCATGGACAAAGCTTGACACATCAAGTTATCAAGGCCTTGGAGGAGGCTCTGTATGTCCTCAGGGG
ACTGACAACATCCTCCAGATTCCAGCCATAAACCAATAACTAGGCTGGACCCTTCCCCTACATAATAGGGCTCA
GCCCAGGCAGCCAGCTTTGGGCTGAGCTAACAGGACCAATGGATTAACTGGCATTTCAGTCCAAGGAAGCTCGA
AGCAGGTTTAGGACCAGGTCCCCCTTGAGAGGTCAGAGGGGCCTCTGTGGGTGCTGGGTACTCCAGAGGTGCCACT
GGTGGAAGGGTCAGCGGAGCCCCAGCAGGAAGGGTGGGCCAGCCAGGCCATTCTTAGTCCCTGGGTTGGGGAGGC
AGGGAGCTAGGGCAGGGACCAAATGAACAGAAAGTCTCAGCCCAGGATGGGGCTTCTTCAACAGGGCCCCCTGCCC
TCCTGAAGCCTCAGTCCTTCACCTTGCCAGGTGCCGTTTTCTCTTCCGTGAAGGCCACTGCCCAGGTCCCCAGTGC
GCCCCCTAGTGGCCATAGCCTGGTTAAAGTTCCCCAGTGCCCTCCTTGTGCATAGACCTTCTTCTCCCACCCCCTT
CTGCCCCCTGGGTCCCCGGCCATCCAGCGGGGCTGCCAGAGAACCCAGACCTGCCCTTACAGTAGTGTAGCGCCC
CCTCCCTCTTTTCGGCTGGTGTAGAAATAGCCAGTAGTGTAGTGCAGGTGTGCTTTTACGTGATGGCGGGTGGGCAGC
GGGCGGCGGGCTCCGCGCAGCCGTCTGTCCTTGATCTGCCCAGCGCGGCCCGTGTGTTGTGTTTTGTGCTGTGTCCA
CGCGCTAAGGCGACCCCTCCCCGTAAGTCTCTCCTATAAGCGTTCTCTTCGCATAGTCACGTAGCTCCCA
CCCCACCTCTTCTGTGTCTCAGCAAGTTTTATACTCTAATATTTATATGGCTTTTTTTCTTCGACAAAAAAA
TAATAAACGTTTCTTCTGAAAAGCTG

1889/6881
FIGURE 1745

MAAPPARPDHTRLLQICLLLGVLVEIRAEQILYSVFEEQEESVVGNIAKDLGLAPRELAERGVRIVSRGRTQLF
ALNPRSGTLVTAGRIDREELCDRSPNCVTNLEILLED TVKILRVEVEIIDVNDNPPSFGTEQREIKVAENENPGA
RFPLPEAFDPDVG VNSLQGYQLNSNGYFSLDVQSGADGIKYPELVLERALDREEEAVHHLVLTAFDGGDPVRS GT
ARILIIILVD TNDNAPVFTQPEYHVS VRENVPGTRLLTVKATDPDEGANGDV TYSF RKVRDKISQLFQLNSLSGD
ITILGGLDYEDSGFYDIDVEAHDGPGLRARSKVLVTVLDENDNAPEVTVTSLTSSVQESSSPGTVIALFNVHDS D
SGGNGLVTCSIPDNLPFTLEKTYGNYRLLTHRTLDREEVSEYNITVTATDQGT PPLSTETHISLQVMDINDNPP
TFPHASYSAYIPENNPRGASILSMTAQDPDSGDNARITYSLAEDTFQGAPLSSYVSINSNTGILYALCSFDYEQF
RDLQLLMTASDSGD PPLSSNVSLSLFVLDQNDNVPEILYPTFTPDTGSTGVELAPRSADSGYLVTKVVAVD RDSGQ
NAWLSYSLKKSSEPGLFAVGLHTGEVRTARALLDRDALKQRLVVVVQDHGQPPLSATVTLTVAVADSIPDVLADL
GSLKPSADPDDSGLTLYLVVAVAAVSCVFLAFVTVLLALKLRRWHKSRL LHAEGSRLAGVPASHFVGVDGVRAFL
QTY SHEVSLTADSRKSHLIFSQPSYADTLISRESCEKSEPLLI TQDLLET KGDPNLQQAPPNTDWRFSQAQRPGT
SGSQNGDDTGTWPNNQFDTEMLQAMILASASEAADGSSTLGGGAGTMGLSARYGPQFTLQHVPDYRQNVYIPGSN
ATLTNAAGKRDGKAPAGGNGNKKKSGKKEKK

1890/6881
FIGURE 1746A

ATGGCGAGTCCACCTAGGGGCTGGGGCTGCGGAGAGCTGCTGCTGCCCTTCATGCTCCTGGGGACGCTGTGCGAG
CCAGGATCCGGGCAGATCCGCTACTCGATGCCGGAGGAGCTGGACAAAGGCTCCTTCGTCGGCAACATAGCCAAAG
GACCTTGGGCTGGAGCCCCAGGAGCTGGCGGAGCGCGGAGTCCGCATCGTCTCCAGAGGTAGGACGCAGCTTTTT
GCCCTGAACCCGCGAAGCGGCAGCTTGGTACCCGCGGGCAGGATAGACCGGGAGGAGCTCTGCGCTCAGAGCCCA
CTGTGTGTGGTGAACCTTTAACATCTTGGTTGAGAACAAAATGAAAATTTATGGAGTAGAAGTAGAAAATAATCGAT
ATTAATGATAACTTCCCGCGTTTCCGGGATGAAGAGTTAAAAAGTAAAAGTTAATGAAAATGCGGCTGCAGGGACA
CGGTTAGTGCTTCCCTTCGCGCGGGATGCGGATGTGGGTGTGAACCTCTCTCCGGAGTTACCAGCTCAGCTCCAAT
CTGCACTTCTCTCTGGATGTGGTAAGCGGAACCTGATGGACAAAAGTATCCGGAGCTGGTGTGGAACAGCCCCTA
GACCGCGAGAAAGAGACTGTTACGACCTCCTCCTCACAGCTTTAGATGGCGGAGACCCGGTACTCTCCGGCACC
ACGCACATCCGTGTTACGGTCCTCGACGCAAACGACAATGCGCCCTGTTACCCCATCCGAGTACAGCGTGAGT
GTTCCAGAGAACATACCTGTGGGCACTCGGCTGCTCATGCTAACCGCCACGGATCCAGATGAGGGAATAAACGGG
AAATTGACCTACTCTTTTCGCAATGAAGAAGAAAAAATTTTCGGAGACTTTCCAACCTTGATTCCAACCTGGGGGAA
ATCTCAACTCTACAATCACTGGACTATGAAGAATCCAGATTCTACCTCATGGAAGTGGTAGCTCAGGATGGAGGC
GCTCTTGTGTCAGCGCTAAGGTGGTGGTCACAGTACAGGACGTGAATGACAATGCCCCCGAAGTGATCCTCACC
TCTCTGACCAGTTGATCTCTGAAGACTGTCTTCCCGAACTGTAATCGCGCTGTTTAGCGTACATGATGGTGAT
TCTGGAGAAAATGGTGAGATTGCATGCTCTATTCTAGGAATTTGCCTTTTAAATTGGAGAAGTCAGTTGATAAT
TACTATCACCTATTAACAACCTAGGGACCTGGACAGAGAAGAGACTTCAGATTATAATATCACTTTAACCGTCATG
GACCATGGAACCCCGCCCCCTCTCTACAGAAAGCCACATCCCCTTGAAAGTAGCAGACGTTAATGACAACCCACCC
AATTTCCCTCAAGCCTCCTACTCCACCTCTGTACAGAAAACAATCCCAGAGGTGTCTCTATCTTCTCTGTGACA
GCCCATGACCCCGACAGCGGCGACAACGCTCGAGTCACCTACTCCCTGGCTGAAGACACATTTTCAGGGGGCGCCC
TTGTCTCTCTATGTATCCATTAACCTCTGACACCGGTGTCTGTATGCTCTGAGATCCTTCGACTATGAGCAGTTG
AGAGACCTACAGTTGTGGGTGACAGCAGCGACAGTGGGAACCCCTCCACTTAGCAGCAACGTGTGCTGAGCCTG
TTTGTGCTGGACCAGAACGACAATACGCTGAGATCCTGTACCCCGCCCTCCCCACAGACGGTTCCACGGGCGTG
GAGCTGGCGCCTCGCTCCGCAGAACCTGGCTACCTGGTGACCAAGGTGGTAGCGGTGGACAAAGATTTCAGGCCAG
AACGCCTGGCTGTCTTACC GCCTGCTTAAGGCCAGCGAGCCAGGACTCTTTGCGGTTGGGCTGCACACGGGCGAG
GTGCGCACAGCGCGAGCCCTGCTGGACAGAGACGCGCTCAAGCAGAGCCTCGTGGTGGCCGTGGAAGACCATGGC
CAGCCCCCTCTGTACGCCACCTTCACGGTCACCGTTGCCGTGGCCGACAGGATCCCTGACATCCTGGCTGACCTA
GGCAGTATCAAGACCCCCATTGACCCTGAGGATCTGGACCTCACACTCTATCTTGTGGTGGCAGTGGCTGCAGTC
TCCTGCGTCTTCTTGGCCTTCGTCTATCGTGCTGCTGGTGCTCAGACTGAGGCGCTGGCACAAGTCACGCCCTGCTT
CAGGCTGAAGGCAGCAGGTTGGCGGGTGTGCCCGCCTCGCACTTTGTGGGCGTGGATGGGGTTTCGGGCTTTCCCTG
CAGACCTATTCCACGAGGTCTCCCTCACC CGGACTCGAGGAAGAGTCACCTGATCTTTCCCCAGCCCAACTAC
GCAGACACGCTCCTTAGTGAAGAGAGCTGTGAGAAAAGCGAGCCTCTTCTGATGTCTGATAAGGTAGATGCAAAC
AAAGAAGAACGGCGAGTTCAGCAAGCCCCGCCAACACGGACTGGCGTTTCTCTCAGGCCCAGAGACCCGGCACC
AGCGGCTCCCAAAATGGCGATGACACCGGCACCTGGCCCAACAACCAAGTTTGACACAGAGATGCTGCAAGCCATG
ATCTTGGCGTCCGCCAGTGAAGCTGCTGATGGGAGCTCCACCCTGGGAGGGGGTGCCGGCACCATGGGATTGAGC
GCCCCTACGGACCCCAAGTTACCCCTGCAGCACGTGCCCGACTACCGCCAGAATGTCTACATCCCAGGCAGCAAT
GCCACACTGACCAACGCAGCTGGCAAGCGGGATGGCAAGGCCCCAGCAGGTGGCAATGGCAACAAGAAGAAGTCG
GGCAAGAAGGAGAAGAAGTAAACATGGAGGCCAGGCCAAGAGCCACAGGGCGGCCTCTCCCCAACCCAGCCCAGCTT
CTCCTTACCTGCACCCAGGCCTCAGAGTTTTCAGGGCTAACCCCCAGAATACTGGTAGGGGCCAAGGCCATGCTCC
CCTTGGGAAACAGAAACAAGTGCCAGTCAGCACCTACCCCTTCCCCCCCAGGGGGTTGAATATGCAAAAGCAGT
TCCGCTGGGAACCCCCATCCAATCAACTGCTGTACCCATGGGGGTAGTGGGGTTACTGTAGACACCAAGAACCAT
TTGCCACACCCCGTTTAGTTACAGCTGAACTCCTCCATCTTCCAAATCAATCAGGCCCATCCATCCCATGCTCC
CTCCTCCCCACCCCACTCCAACAGTTCTCTTTCCCGAGTAAGGTGGTTGGGGTGTGAAGTACCAAGTAACCTA
CAAGCCTCCTAGTTCTGAAAAGTTGGAAGGGCATCATGACCTCTTGGCCTCTCCTTTGATTCTCAATCTTCCCCC
AAAGCATGGTTTTGGTGCCAGCCCTTACCTCCTTCCAGAGCCCAAGATCAATGCTCAAGTTTTTGGAGGACATGA
TCACCATCCCCATGGTACTGATGCTTGGTGGATTTAGGGAGGGCATTTTGCTACCAAGCCTCTTCCCAACGCCCT
GGGGACCAGTCTTCTGTTTTGTTTTTTCATTGTTTGACGTTTCCACTGCATGCCTTGACTTCCCCACCTCCTCCT
CAAACAAGAGACTCCACTGCATGTTCCAAGACAGTATGGGGTGTAAGATAAGGAAGGGAAGTGTGTGGATGTG

1891/6881
FIGURE 1746B

ATGGTGGGGGCATGGACAAAGCTTGACACATCAAGTTATCAAGGCCTTGGAGGAGGCTCTGTATGTCCTCAGGGG
ACTGACAACATCCTCCAGATTCCAGCCATAAACCAATAACTAGGCTGGACCCTTCCCACTACATAATAGGGCTCA
GCCCAGGCAGCCAGCTTTGGGCTGAGCTAACAGGACCAATGGATTAACTGGCATTTCAGTCCAAGGAAGCTCGA
AGCAGGTTTAGGACCAGGTCCCCTTGAGAGGTGAGAGGGGCCTCTGTGGGTGCTGGGTACTCCAGAGGTGCCACT
GGTGGAAGGGTCAGCGGAGCCCCAGCAGGAAGGGTGGGCCAGCCAGGCCATTCTTAGTCCCTGGGTGAGGGAGGC
AGGGAGCTAGGGCAGGGACCAAATGAACAGAAAGTCTCAGCCCAGGATGGGGCTTCTTCAACAGGGCCCCCTGCCC
TCCTGAAGCCTCAGTCCTTCACCTTGCCAGGTGCCGTTTCTCTTCCGTGAAGGCCACTGCCAGGTCCCCAGTGC
GCCCCCTAGTGGCCATAGCCTGGTTAAAGTTCCCCAGTGCCCTCCTTGTCATAGACCTTCTTCTCCACCCCCCTT
CTGCCCCCTGGGTCCCCGGCCATCCAGCGGGGCTGCCAGAGAACCCAGACCTGCCCTTACAGTAGTGTAGCGCCC
CCTCCCTCTTTTCGGCTGGTGTAGAAATAGCCAGTAGTGTAGTGCGGTGTGCTTTTACGTGATGGCGGGTGGGCAGC
GGGCGGCGGGCTCCGCGCAGCCGTCTGTCCTTGATCTGCCCCGCGGCGGCCCGTGTGTGTTTTGTGCTGTGTCCA
CGCGCTAAGGCGACCCCTCCCCCGTACTGACTTCTCCTATAAGCGCTTCTCTTCGCATAGTCACGTAGCTCCCA
CCCCACCCTCTTCTGTGTCTCACGCAAGTTTTATACTCTAATATTTATATGGCTTTTTTTCTTCGACAAAAAAA
TAATAAAACGTTTCTTCTGAAAAGCTG

1892/6881
FIGURE 1747

MASPPRGWGCCELLLPFMLLGTLCPEPGSGQIRYSMPHEELDKGSFVGNIAKDLGLEPQELAERGVRIVSRGRTQLF
ALNPRSGSLVTAGRIDREELCAQSPLCVVNFNILVENKMKIYGVEVEIIDINDNFPRFRDEELKVKNENAAAGT
RLVLPFARDADVGVNSLSYQLSSNLHFSLDVVSGTDGQKYPELVLEQPLDREKETVHDLTALDGGDPVLSGT
THIRVTVLDANDNAPLFTPSEYSVSVPENIPVGTRLLMLTATDPDEGINGKLTYSFRNEEEKISETFQLDSNLGE
ISTLQSLDYEESRFYLMVVVAQDGGALVASAKVVVTVQDVNDNAPEVILTSLTSSISEDCLPGTVIALFSVHDGD
SGENGEIACSI PRNLFPKLEKSVDNYYHLLTTRDLREETS DYNITLTVM DHGTPPLSTESHIP LKVADVNDNPP
NFPQASYSSTVTENNPRGV SIFSVTAHDPDSGDNARVTYSLAEDTFQGAPLSSYVSINSDTGVLIALRSFDYEQ
RDLQLWVTASDSGNPPLSSNVSLSLFVLDQNDNTPEILYPALPTDGSTGVELAPRSAEPGYLVTKVVAVDKDSGQ
NAWLSYRLLKASEPGLFAVGLHTGEVRTARALLDRDALKQSLVVAVEDHGGPPLSATFTVTVAVADRIPDILADL
GSIKTPIDPEDLDLTLYLVVAVAAVSCVFLAFVIVLLVLRRLRRWHKSRLQLAEGSRLAGVPASHFVGVDGVRAFL
QTYSHEVSLTADSRKSHLIFPQPNYADTLLSEESCEKSEPLMSDKVDANKEERRVQQAPPNTDWRFSQAQRPQT
SGSQNGDDTGTPNNQFDTEMLQAMILASASEAADGSSTLGGGAGTMGLSARYGPQFTLQHVDPYRQNVYIPGSN
ATLTNAAGKRDGKAPAGGNGNKKKSGKKEKK

1893/6881
FIGURE 1748A

ATGGCGCCTCCGCAGAGGCATCCGCAGCGCAGCGAGCAGGTCCTGCTCCTCACGCTCCTGGGGACGCTGTGGGGG
GCCGCGGCAGCGCAGATCCGCTACTCTATTCCCGAGGAGCTGGAGAAAGGCTCCTTCGTAGGCAACATCGTCAAG
GATCTGGGACTGGAGCCCCAGGAGTTGGCGGAGCACGGAGTCCGCATCGTCTCCAGAGGTAGGATGCAGCTTTTC
TCTCTGAATCCGCGAAACGGCAGCTTGGTCACCGCGGGTAGGATAGACCGCGAGGAGCTCTGTGCTCAGAGCCCCG
CGGTGTCTGGTGAGTTTTAACATCCTTGTCGAGGATAAACTGAATCTTTATCCCGTGGAAGTGGAATAAGTGGAC
ATTAATGACAATACACCCCGATTCTTAAAGGAAGAATTGGAAGTGAAAATTCTCGAAAACGCAGCTCCATCCTCT
CGTTTTCCACTAATGGAGGTCTATGACCCTGATGTGGGAATGAACTCCCTTCAGGGATTTAAGCTCAGTGGTAAT
AGTCACTTCTCAGTGGACGTGCAAAGCGAAGCCCATGGGCCCCAAGTACCCGGAGCTGGTGCTGGAGGGGCACACTG
GACCGGGAAGGAGAAGCCGTTTACCGCCTGGTCCTTACTGCCATGGATGGCGGCGACCCCTGTCCGCTCAAGCGTC
GCCCAAATTCTGGTAACAGTTCTAGATGTGAATGACAACACTCCAATGTTTACTCAGCCTGTCTACCGTGTAAGT
GTTCTGAAAACCTGCCAGTAGGCACACCAAGTGTGGCAGTGACTGCCACCGACCAGGATGAAGGAGTCCACGGG
GAAGTAACCTATTCCCTTTGTGAAGATTACAGAAAAGATCTCACAATTTTCTGTTTGAATGTTTGGACTGGAGAA
ATTTCAACTTCTGCAAATCTAGACTATGAGGACTCGAGTTTTTATGAGCTGGGTGTTGAAGCCCCGGGATGGGCCA
GGTCTTCGAGACAGAGCGAAAGTCTTAATAACTATCTTGGATGTCAATGATAATGTACCAGAAGTGGTTGTTACA
TCTGGAAGCAGAACAATTGCTGAAAGTGCACCTCCAGGAACAGTAATCGCCCTTTTTCAAGTGTTGCATCGAGAC
TCTGGCCTGAATGGCCTGGTAACCTGTTCCATCCCGAGAAGTCTCCCATTTGAATTGAAAAATCAGTTGGCAAT
TATTATCGATTAGTGACAAATGCAGCTCTAGACCGGGAAGAGGTATTCTTGTACAACATCACTGTGACAGCCACG
GACAAAGGAACACCACCTCTGTCTACAGAAACAATCATCTCTCTAAATGTGGCAGACACCAACGACAACCCGCC
ACCTTCCCCCATTCATCCTACTCAGTCTATGTCTTGA AAAACAACCCAGGGGTGCCTCCATCTTCTCTGTGAAT
GCACTGGACCCTGACGTGGACCAGAACGCCCAAGTCTCTACTCACTGGCAGAAGACACCCTCCAGGGGGCGCCC
CTGTCTCTCTACGTGTCCATCAACTCCGACACTGGGATTCTGTACGCCCTGCGCTCCTTCGACTATGAGCAGTTG
AGAGACCTACAGCTGTGGGTGACAGCCAGCGACAGCGGGGACCCGCCCTCTAGCAGCAACGTGTCACTGAGCCTG
TTTGTGCTGGACCAGAATGACAATGCGCCGAGATCCTGTACCCCGCCCTCCCCACAGACGGTTCCACTGGCGTG
GAGCTGGCGCCCCGCTCCGCAGAGCCCGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACAGAGACTCGGGCCAG
AACGCCTGGCTGTCTTACC GCCTGCTCAAGGCCAGCGAGCCAGGACTTTTTCTCAGTGGGCCTGCACACGGGCGAG
GTGCGCACGGCGCGCGCCCTGCTGGACAGAGACGCGCTCAAGCAGAGCCTAGTGGTGGCCGTCCAGGACCACGGC
CAGCCCCCTCTCTCCGCCACTGTACGCTCACCGTGGCCGTGGCCGACAGGATCCCCGACATCCTGGCCGACCTG
GGCAGCCTCGAGCCCTCCGCCAAACCCAAACGATTTCGGACCTCACTCTGTACCTGGTGGTGGCGGTGGCCGCGGT
TCCTGCGTCTTCTGGCCTTTCGTATCGTGCTGCTGGCGCTCAGACTGCAGCGCTGGCACAAGTCACGCCTGCTG
CAGGCTTTCGGGAGGTGGCTTAGCGAGCATGCCCGGCTCGCACTTTGTGGGCGTGGAAGGGGTTTCGGGCTTTCCTG
CAGACCTATTCCACGAGGTCTCACTCACTGCAGACTCGCGTAAGAGTCATCTGATTTTCCCCAGCCCACTAT
GCCGACACGCTTATCAACCAGGAGAGCTATGAGAAAAGCGAGCCTCTTCTGATAACTCAGGATTTACTTGAAACG
AAAGGAGAACCCAGGCAACTTCAGCAAGCCCCGCCAACACGGACTGGCGTTTCTCTCAGGCCAGAGACCCGGC
ACCAGCGGCTCCCAAAATGGCGATGACACCGGCACCTGGCCCAACAACAGTTTGACACAGAGATGCTGCAAGCC
ATGATCTTGGCGTCCGCCAGTGAAGCTGCTGATGGGAGCTCCACCCTGGGAGGGGTGCCGGCACCATGGGATTG
AGCGCCCGCTACGGACCCAGTTTACCCTGCAGCACGTGCCCGACTACCGCCAGAATGTCTACATCCCAGGCAGC
AATGCCACACTGACCAACGCAGCTGGCAAGCGGGATGGCAAGGCCCCAGCAGGTGGCAATGGCAACAAGAAGAAG
TCGGGCAAGAAGSAGAAGAAGTAACATGGAGGCCAGGCCAAGAGCCACAGGGCGGCCTCTCCCAACAGCCAG
CTTCTCCTTACCTGCACCCAGGCCTCAGAGTTTCAAGGCTAACCCCCAGAATACTGGTAGGGGCCAAGGCCATGC
TCCCTTGGGAAACAGAAACAAGTGGCCAGTCAGCACCTACCCCTTCCCCCCCAGGGGGTTGAATATGCAAAAGC
AGTTCCGCTGGGAACCCCCATCCAATCAACTGCTGTACCCATGGGGGTAGTGGGGTTACTGTAGACACCAAGAAC
CATTTGCCACACCCCGTTTAGTTACAGCTGAACCTCCTCCATCTTCCAAATCAATCAGGCCCATCCATCCCATGCC
TCCCTCCTCCCCACCCCACTCCAACAGTTCTCTTTCCCGAGTAAGGTGGTTGGGGTGTGAAAGTACCAAGTAAC
CTACAAGCCTCCTAGTTCTGAAAAGTTGGAAGGGCATCATGACCTCTTGGCCTCTCCTTTGATTCTCAATCTTCC
CCCAAAGCATGGTTTGGTGCCAGCCCTTACCTCCTTCCAGAGCCCCAAGATCAATGCTCAAGTTTTGGAGGACA
TGATCACCATCCCCATGGTACTGATGCTTGGTGGATTTAGGGAGGGCATTTTGCTACCAAGCCTCTTCCCAACGC
CCTGGGGACAGTCTTCTGTTTTGTTTTTCATTGTTTGACGTTTCCACTGCATGCCTTGACTTCCCCACCTCCT
CCTCAAACAAGAGACTCCACTGCATGTTCCAAGACAGTATGGGGTGGTAAGATAAGGAAGGAAGTGTGTGGATG

1894/6881
FIGURE 1748B

TGGATGGTGGGGGCATGGACAAAGCTTGACACATCAAGTTATCAAGGCCTTGGAGGAGGCTCTGTATGTCCTCAG
GGGACTGACAACATCCTCCAGATTCCAGCCATAAACCAATAACTAGGCTGGACCCTTCCCACTACATAATAGGGC
TCAGCCCAGGCAGCCAGCTTTGGGCTGAGCTAACAGGACCAATGGATTAAACTGGCATTTCAGTCCAAGGAAGCT
CGAAGCAGGTTTAGGACCAGGTCCCCTTGAGAGGTCAGAGGGGCCTCTGTGGGTGCTGGGTACTCCAGAGGTGCC
ACTGGTGGAAGGGTCAGCGGAGCCCCAGCAGGAAGGGTGGGCCAGCCAGGCCATTCTTAGTCCCTGGGTGTTGGGGA
GGCAGGGAGCTAGGGCAGGGACCAAATGAACAGAAAGTCTCAGCCCAGGATGGGGCTTCTTCAACAGGGCCCCCTG
CCCTCCTGAAGCCTCAGTCCTTACCTTGCCAGGTGCCGTTTCTCTTCCGTGAAGGCCACTGCCCAGGTCCCCAG
TGCGCCCCCTAGTGGCCATAGCCTGGTTAAAGTTCCCCAGTGCCCTCCTTGTGCATAGACCTTCTTCTCCCACCCC
CTTCTGCCCCCTGGGTCCCCGGCCATCCAGCGGGGCTGCCAGAGAACCCAGACCTGCCCTTACAGTAGTGTAGCG
CCCCCTCCCTCTTTCGGCTGGTGTAGAATAGCCAGTAGTGTAGTGCGGTGTGCTTTTACGTGATGGCGGGTGGGC
AGCGGGCGGCGGGCTCCGCGCAGCCGTCTGTCTTGATCTGCCGCGGCGGCCCGTGTGTGTTTTGTGCTGTGT
CCACGCGCTAAGGCGACCCCTCCCCCGTACTGACTTCTCCTATAAGCGCTTCTCTTCGCATAGTCACGTAGCTC
CCACCCACCCCTCTTCTGTGTCTCACGCAAGTTTTATACTCTAATATTTATATGGCTTTTTTCTTCGACAAAA
AAATAATAAAACGTTTCTTCTGAAAAGCTG

1895/6881
FIGURE 1749

MAPPQRHPQRSEQVLLLLTLLGTLWGAAAAQIRYSIPEELEKGSFVGNIVKDLGLEPQELAEHGVRIVSRGRMQLF
SLNPRNGSLVTAGRIDREELCAQSPRCLVSFNILVEDKLNLYPVEVEIVDINDNTPRFLKEELEVKILENAAPSS
RFPLMEVYDPDVG MNSLQGFKLSGNSHF SVDVQSEAHGPKYPELVLEGTLDREGEAVYRLVLTAMDGGDPVRSSV
AQILVTVLVDVNDNTPMFTQPVYRVSVPENLPVGTPVLAVTATDQDEGVHGEVTYSFVKITEKISQIFCLNVL TGE
ISTSANLDYEDSSFYELGVEARDGPGLRDRAKVLITILDVNDNVPEVVVTSGSRTIAESAPPGTVIALFQVFD RD
SGLNGLVTCSIPRSLPFELEKSVGNYYRLVTNAALDREEVFLYNITVTATDKGTPPLSTETIISLNVADTNDNPP
TFPHSSYSVYVLENNPRGASIFSVNALDPDQNAQVSYS LAEDTLQGAPLSSYVSINSDTGILYALRSFDYEQ L
RDLQLWVTASDSGDPPLSSNVSLSLFVLDQNDNAPEILYPALPTDGSTGVELAPRSAEPGYLVTKVVAVD RDSGQ
NAWLSYRLLKASEPGLFSVGLHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTLTVAVADRI PDILADL
GSLEPSAKPNDSDLTLYLVVAVAAVSCVFLAFVIVLLALRLQRWHKSRL LQASGGGLASMPGSHFVGVEGVRAFL
QTY SHEVSLTADSRKSHLIFPQPNYADTLINQESYEKSEPL LITQDLLETKGEP RQLQQAPPNTDWRFSQAQRPG
TSGSQNGDDTGTWPNNQFDTEMLQAMILASASEAADGSSTLGGGAGTMGLSARYGPQFTLQHVPDYRQNVYIPGS
NATLTNAAGKRDGKAPAGGNGNKKKSGKKEKK

1896/6881
FIGURE 1750A

ATGGCGGCTCAGCCGAGGGGCGGGGACTACAGAGGATTCTTCTGCTCTCCATCCTCCTGGGGACCCCCTGGGAA
GCCTGGGCAGGACGTATTCTCTACTCCGTGTCTGGAGGAGACGGACAAAGGGTCCTTTGTGGGAGACATCGCCAAG
GACCTGGGGCTGGAGCCCCGGGAGCTGGCGGAGCGCGGAGTCCGCATCATCTCCAGAGGTAGGACGCAGCTTTTC
GCCCTGAACCAGCGCAGCGGCAGCTTGGTCACTGCGGGCAGGATAGACCGGGAAGAGATCTGCGCTCAGAGTGCG
CGGTGTCTGGTAAACTTTAACATCCTGATGGAAGATAAAATGAATCTTTACCCTATAGACGTGGAAATAATAGAT
ATTAATGACAACGTTCCAAGATTCTTGACGGAAGAAATAAATGTAAAAATAATGGAGAATACAGCTCCTGGGGTT
CGGTTTTCCGTTAAGCGAGGCTGGGGATCCAGATGTGGGCACGAACTCCCTCCAGAGTTACCAGCTCAGCCCCAAT
CGCCACTTCTCCCTGGCTGTGCAAAGTGGAGACGATGAAACTAAGTACCCGGAACGGTGCTGGAGCGGGTGCTG
GACCGGGAGGAAGAGCGGGTTACCACCTGGTCTCAGACGCTCTGATGGCGGCGACCCGCCCCGATCCAGCACC
GCCACATCCAGGTGACAGTGGTGGATGTGAATGACCACACGCCTGTCTTCTCTGCTCAGTACCAAGTAACT
GTCCCCGAGAATGTGCCAGTGGGTACAAGACTGCTCAGGTACATGCTATCGACCTGGACGAGGGAGTCAATGGG
GAAGTGACATATTCTTTTCGGAATAAATACTCCTAACTTCCAAAGATGTTTCATCTGAACTCGCTTACAGGAGAA
ATATCAACTTTAGAAGGATTAGATTATGAAGAACTGCCTTCTATGAAATGGAGGTTCAAGGCTCAAGATGGTCCT
GGTAGTCTGACAAAGGCAAAAGTACTGATCAGATTTTAGATGTAAATGATAATGCTCCAGAAGTGACTATGACG
TCTTTAAGTAGCTCAATCCCTGAAGACACACCTCTTGGGACAGTCATTGCTCTTTTCTACCTACAAGACAGAGAT
TCTGGAAAGAATGGTGAGGTGACCTGCACCATTCCAGAAAACCTACCTTTTAAATTAGAAAAATCAATAGATAAT
TATTATAGATTGGTCACAACCAAAAACCTTGGACCGGGAACACTCTCTTTGTATAACATCACACTGAAAGCCACA
GATGGTGGAACCTCTCCCTTGTCCAGGGAAACTCACATATTCATGCAGGTGGCAGACACCAACGATAACCCACCC
ACCTTCCCCCACTCATCCTACTCAGTCTACATCGCTGAGAACAACCCAGAGGGGCTCCATTTTCTTAGTGACT
GCACAGGACCACGACAGTGAGGATAATGCCAGATCACTTATTCTTGGCCGAAGACACCATCCAGGGGGCTCCA
GTGTCCTCCTATGTCTCCATAAACTCTGACACTGGAGTCTGTACGCGCTGCAATCCTTTGATTATGAGCAGTTG
AGAGAACTACAATAAGAGTGACTGCACATGACAGCGGGGACCCGCTCTCAGCAGCAACATGTCACTGAGCCTG
TTCGTGCTGGACCAGAATGACAACCCGCCGAGATCCTGTACCCGGCCCTCCCCACAGATGGTTCTACTGGCATG
GAGCTGGCACCCCGCTCCGCAGAGCCCGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACAAAGATTCAAGCCAG
AACGCCTGGCTGTACATACCTCCTGCTTAAGGCCAGCGAGCCAGGACTCTTTGCGGTTGGGCTGTACACGGGCGAG
GTGCGCACGGCTCGGGCCCTGCTGGACAGAGATGCCCTCAAGCAGAGCCTCGTGGTGGCCGTCCAGGACCACGGT
CAGCCTCCTCTGTACGCCACCGTCACACTCACCGTGGCTGTGGCTGACAGCATCCCCGAAGTCTTGGCCGACCTG
GGCAGCCTTGAGCCCTCCGACGGTCTTACAACATATGACCTCACGTTGTACCTGGTGGTGGCGGTGGCCACAGTC
TCCTGCGTCTTCTAGCCTTCGTCTCGTACTGCTGGCGCTCAGGCTGCGGCGCTGGCACAAGTCACGCCTGCTG
CAGGCTTCAGAAGGTGGCTTGGCGAACGTGCCACCTCGCACTTTGTGGGCATGGACGGGGTGCAGGCTTTTCTG
CAGACCTATTCCCATGAGGTCTCCCTCACCGCGGACTCTCGGAAGAGTCACCTGATCTTCCCCAGCCCACTAT
GTAGACATGCTCATCAGCCAGGAGAGCTGTGAGAAAAATGATTCTTTGCTAACATCCGTAGATTTTCAGGAATGT
AAAGAAAACCTGCCAAGTATTAGCAAGCCCCGCCAACACGGACTGGCGTTTCTCTCAGGCCAGAGACCCGGC
ACCAGCGGCTCCCCAAAATGGCGATGACACCGGCACCTGGCCCAACAACAGTTTGACACAGAGATGCTGCAAGCC
ATGATCTTGGCGTCCGCCAGTGAAGCTGCTGATGGGAGCTCCACCCTGGGAGGGGTGCCGGCACCATGGGATTG
AGCGCCCGCTACGGACCCAGTTCACCTGTCAGCACGTGCCCCACTACCGCCAGAATGTCTACATCCCAGGCAGC
AATGCCACACTGACCAACGCAGCTGGCAAGCGGGATGGCAAGGCCCCAGCAGGTGGCAATGGCAACAAGAAGAAG
TCGGGCAAGAAGGAGAAGAAGTAACATGGAGGCCAGGCCAAGAGCCACAGGGCGGCCTCTCCCCAACAGCCAG
CTTCTCCTTACCTGCACCCAGGCCCTCAGAGTTTCAGGGCTAACCCCCAGAATACTGGTAGGGGCAAGGCCATGC
TCCCCTTGGGAAACAGAAACAAGTGCCAGTCAGCACCTACCCCTTCCCCCCCAGGGGGTTGAATATGCAAAAGC
AGTTCCGCTGGGAACCCCCATCCAATCAACTGCTGTACCCATGGGGGTAGTGGGGTTACTGTAGACACCAAGAAC
CATTTGCCACACCCCGTTTAGTTACAGCTGAACTCCTCCATCTTCCAAATCAATCAGGCCCATCCATCCCATGCC
TCCCTCCTCCCCACCCCACTCCAACAGTTCTCTTTCCCGAGTAAGGTGGTTGGGGTGTGAAGTACCAAGTAAC
CTACAAGCCTCCTAGTTCTGAAAAGTTGGAAGGGCATCATGACCTCTTGGCCTCTCCTTTGATTCTCAATCTTCC
CCCAAAGCATGGTTTGGTGCCAGCCCTTCACCTCCTTCCAGAGCCCCAAGATCAATGCTCAAGTTTTGGAGGACA
TGATCACCATCCCCATGGTACTGATGCTTGTGGATTTAGGGAGGGCATTGCTACCAAGCCTCTTCCCAACGC
CCTGGGGACAGTCTTCTGTTTTGTTTTTATTGTTTGCAGTTTCCACTGCATGCCTTGACTTCCCCACCTCCT
CCTCAAACAAGAGACTCCACTGCATGTTCCAAGACAGTATGGGGTGGTAAGATAAGGAAGGAAGTGTGTGGATG

1897/6881
FIGURE 1750B

TGGATGGTGGGGGCATGGACAAAGCTTGACACATCAAGTTATCAAGGCCTTGGAGGAGGCTCTGTATGTCCTCAG
GGGACTGACAACATCCTCCAGATTCCAGCCATAAACCAATAACTAGGCTGGACCCTTCCCCTACATAATAGGGC
TCAGCCCAGGCAGCCAGCTTTGGGCTGAGCTAACAGGACCAATGGATTAACTGGCATTTCAGTCCAAGGAAGCT
CGAAGCAGGTTTAGGACCAGGTCCCCTTGAGAGGTCAGAGGGGCTCTGTGGGTGCTGGGTACTCCAGAGGTGCC
ACTGGTGGAAAGGTCAGCGGAGCCCCAGCAGGAAGGGTGGGCCAGCCAGGCCATTCTTAGTCCCTGGGTGGGGA
GGCAGGGAGCTAGGGCAGGGACCAAATGAACAGAAAGTCTCAGCCCAGGATGGGGCTTCTTCAACAGGGCCCCCTG
CCCTCCTGAAGCCTCAGTCCTTACCTTGCCAGGTGCCGTTTCTCTTCCGTGAAGGCCACTGCCCAGGTCCCCAG
TGCGCCCCCTAGTGGCCATAGCCTGGTTAAAGTTCCCCAGTGCCCTCCTTGTGCATAGACCTTCTTCTCCCACCCC
CTTCTGCCCCCTGGGTCCCCGGCCATCCAGCGGGGCTGCCAGAGAACCCAGACCTGCCCTTACAGTAGTGTAGCG
CCCCCTCCCTCTTTCGGCTGGTGTAGAATAGCCAGTAGTGTAGTGCGGTGTGCTTTTACGTGATGGCGGGTGGGC
AGCGGGCGGCGGGCTCCGCGCAGCCGTCTGTCCTTGATCTGCCGCGGCGGCCCGTGTGTGTTTTGTGCTGTGT
CCACGCGCTAAGGCGACCCCTCCCCGTACTGACTTCTCCTATAAGCGCTTCTCTTCGCATAGTCACGTAGCTC
CCACCCACCCCTCTTCTGTGTCTCAGCAAGTTTTATACTCTAATATTTATATGGCTTTTTTTCTTCGACAAAA
AAATAATAAAACGTTTCTTCTGAAAAGCTG

1898/6881
FIGURE 1751

MAAQPRGGDYRGFFLLSILLGTPWEAWAGRILYSVSEETDKGSFVGDIAKDLGLEPRELAERGVRIISRGRQTQLF
ALNQSRGSLVTAGRIDREEICAQSARCLVNFNLMEDKMNLYPIDVEIIDINDNVPRFLTEEINVKIMENTAPGV
RFPLSEAGDPDVGTSLSQSYQLSPNRHFS LAVQSGDDETKYPELVLERVLDREEERVHHLVLTASDGGDPPRSST
AHIQVTVVDVNDHTPVFSLPQYQVTVPENVPVGTRLLTVHAIDLDEGVNGEVTYSFRKITPKLPKMFHLNSLTGE
ISTLEGLDYEETAFYEMEVQAQDGPGLTKAKVLITVLDVNDNAPEVTMTSLSSSIPEDTPLGTVIALFYQLQDRD
SGKNGEVTCTIPENLPFKLEKSIDNYYRLVTTKNLDRETLSLYNITLKATDGGTPPLSRETHIFMQVADTNDNPP
TFPHSSYSVYIAENNPRGASIFLVTAQDHDSEDNAQITYSLAEDTIQGAPVSSYVSINSDTGVLIALQSFDYEQL
RELQLRVTAHDSGDPPLSSNMSLSLFLVDQNDNPPEILYPALPTDGSTGMELAPRSAEPGYLVTKVAVDKDSGQ
NAWLSYLLLLKASEPGLFAVGLYTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTLTVAVADSIPEVLADL
GSLEPSDGPYNYDLTLYLVVAVATVSCVFLAFVLVLLALRLRRWHKSRLQASEGGLANVPTSHFVGMDGVQAFL
QTYSHEVSLTADSRKSHLIFPQPNYVDMLISQESCEKNDSSLTSVDFQECKENLPSIQQAPPNTDWRFSQAQRPG
TSGSQNGDDTGTWPNNQFDTEMLQAMILASASEAADGSSTLGGGAGTMGLSARYGPQFTLQHVPDYRQNVYIPGS
NATLTNAAGKRDGKAPAGGNGNKKKSGKKEKK

1899/6881
FIGURE 1752A

ATGGCGAGCTCCAAACCAAATGCCAGCTCCGCGGAAGATTAGTCCTGCTATGCTCGCTCCTGGGGATGCTATGGGAG
GCCAGGGCCAGTCAGATTTCGCTACTCAGTGCCTGAAGAGACAGAAAAGGGCTATATTGTGGGCAACATCTCCAAG
GACCTGGCTCTGGAGCCCCGGGAGCTGGCGGAGCGCCGAGTCCGCATCGTCTCTAGAGGTAGGACGCGAGCTTTTC
TCTCTGAACCCGCGCAGCGGCACCTTGGTCACCGCGGGTAGGATAGACCGGGAGGAGCTCTGTGCTCAGAGCCCCG
CGGTGTCTGGTGAACCTTTAAAGTCCTGGTTGAAGACAGAGTGAACTGTACGGAATAGAAAATAGAACTAACTGAT
ATTAACGACAGCGCCCCAAAGTTCCAGGCCGAAAGTCTGGAAGTAAAAATTAACGAAATCGCGGTTCTCTGGAGCA
CGTTATCCACTTCCAGAAGCTATTGATCCGGATGTTGGCGTGAACCTCCCTCCAGAGCTACCAGCTCAGCCCCAAT
CACCACCTTCTCCCTGAACGTGCAGACTGGAGACAATGGAGCCATAAACCCAGAGCTGGTGCTGGAGCGCGCCCTG
GACAGGGGAGGAGGCAACTGCCCCACCACCTGGTCCCTCACGGCCTCGGATGGCGGCGAGCCGCGTCCGCTCCAGCACA
GTGCGCATCCATGTGACAGTGTTGGATACAAATGATAATGCCCGGTTTTTGTCTCAACGGATTTACCGAGTTAAA
GTCCTTGAGAACGTGCCCCAGGCACCTGGCTGCTTACTGCAACAGCCAGCGACCTGGATGAGGGAATCAACGGA
AAAGTGGCATACAAATTTCTGGAATAATGAAAAACAATCTCTGCTATTCCAGCTTAATGAAAATACTGGGGAA
ATATCAACAGCAAAAAGTCTAGATTATGAAGAATGTTCATTTTATGAAATGGAATACAAGCTGAAGATGGTGGG
GGATTGAAAGGGTGGACAAAAGTGCTCATTTTCGGTGGAAAGATGTAAATGACAATAGACCTGAAGTGACCATTACA
TCTCTGTTTAGCCAGTGAGAGAAGACGCACCTCAGGGAACAGTAATTCTTCTTTTCAATGCTCATGACCGAGAC
TCCGGGAAGAATGGTCAAGTTGTCTGTTCTATCCAGGAGAATCTATCTTTTACATTAGAAAATTCAGAAGAAGAT
TATTACAGATTGTTGACGGCCCAAATTTCTTGACCGAGAAAAAGCCTCAGAATATAATATCACGGTGACTGCAACA
GACAGAGGAACTCCGCCCCGTGCCACAGAAATTCACATCACCTGCAAGTGACTGACATCAATGATAATCCACCT
GCTTTCTCTCAAGCCTCCTACTCAGTCTACCTCCCGGAAAAACAACGCCAGAGGTACTTCCATCTTCTCCGTGATT
GCCTATGACCCTGATAGCAATGAGAATTCTAGAGTTATTTACTCCTTGGCAGAGGATACCATCCAAGGGTCTCCT
CTCTCCACCTATGTCTCTATTAACTCAGACACTGGTGTGCTGTATGCTCTGTGCTCCTTTGACTATGAGCAGTTT
AGAGATTTGCAAATGCAGGTGACGGCAAGTGACAGTGGAAGCCCCACCCTTAGCAGCAATGTGTCAATTGAGACTG
TTTGTTTTGGACCAGAATGACAATGCCCCAGAAATCCTGTACCCTGCCCTCCCCACTGATGGTTCTACTGGTGTG
GAGCTGGCACCCCGCTCTGCAGAGCCTGGCTACCTGGTGACCAAGGTGGTGGCAGTGGACAGAGACTCAGGCCAG
AATGCTTGGCTCTCCTACCGCCTATTCAAGGCCAGTGAGCCAGGGCTCTTCTCGGTGGGGCTGCACACAGGTGAA
GTGCGCACAGCTCGGGCCCTGCTAGATAGAGATGCGCTCAAACAGAGCCTTGTGGTGGCTGTACAGGACCATGGC
CAGCCCCCTCTCTCGGCCACTGTACGCTCACAGTAGCCATAGCTGACAGCATCCCAGACATCCTGGCTGACCTG
GGCAGTCTTCAGATCCCTGCAGACCTGGAGGCCTCAGACCTTACCCTCTACCTCGTTGTGGCTGTGGCAGTCGTC
TCCTGTGTCTTCTCACCTTCGTTATCACGCTGCTGGCCCTCAGGCTGAGGCACTGGCACTCCTCGCATCTGCTG
CGGGCTACCAGTGATGGGTTGGCTGGTGTGCCACCTCACACTTTGTGGGTGTAGATGGGGTTTCAGCTTTTCCFA
CAGACCTATTCTCAGGAGTTCTCCCTCACCGCTGACTCAAGGAAGAGTCACCTGATCTTCCCCAGCCCACTAT
GCAGACACACTCATCAGCCAGCAGAGCTGTGAGAAAAATGAGCCTTTGTGCGTCTCTGTTGATTCCAAGTTTCCT
ATAGAAGACACCCCTTTGGTTCCGCAAGCCCCGCCAACACGGACTGGCGTTTCTCTCAGGCCCAGAGACCCGGC
ACCAGCGGCTCCCAAAATGGCGATGACACCGGCACCTGGCCCAACAACAGTTTGACACAGAGATGCTGCAAGCC
ATGATCTTGGCGTCCGCCAGTGAAGCTGCTGATGGGAGCTCCACCCTGGGAGGGGGTGCCGGCACCATGGGATTG
AGCGCCCGCTACGGACCCCGAGTTACCCCTGCAGCACGTGCCCCGACTACCGCCAGAATGTCTACATCCCAGGCAGC
AATGCCACACTGACCAACGCAGCTGGCAAGCGGGATGGCAAGGCCCCAGCAGGTGGCAATGGCAACAAGAAGAAG
TCGGGCAAGAAGGAGAAGAAGTAACATGGAGGCCAGGCCAAGAGCCACAGGGCGGCCTCTCCCAACCAGCCAG
CTTCTCCTTACCTGCACCCAGGCCTCAGAGTTTCAGGGCTAACCCCCAGAATACTGGTAGGGGCCAAGGCCATGC
TCCCTTGGGAAACAGAAACAAGTGCCAGTCAGCACCTACCCCTTCCCCCCCAGGGGGTTGAATATGCAAAAGC
AGTTCCGCTGGGAACCCCCATCCAATCAACTGCTGTACCCATGGGGGTAGTGGGGTTACTGTAGACACCAAGAAC
CATTTGCCACACCCCGTTTAGTTACAGCTGAACCTCCTCCATCTTCCAAATCAATCAGGCCCATCCATCCCATGCC
TCCCTCCTCCCCACCCCACTCCAACAGTTCTCTTTCCCGAGTAAGGTGGTGGGGTGTGAAAGTACCAAGTAAC
CTACAAGCCTCCTAGTTCTGAAAAGTTGGAAGGGCATCATGACCTCTTGGCCTCTCCTTTGATTCTCAATCTTCC
CCCAAAGCATGGTTTGGTGCCAGCCCCCTTACCTCCTTCCAGAGCCCCAAGATCAATGCTCAAGTTTTGGAGGACA
TGATCACCATCCCATGGTACTGATGCTTGTGAGTTTAGGGAGGGCATTTTGCTACCAAGCCTCTTCCCAACGC
CCTGGGGACAGTCTTCTGTTTTGTTTTTCAATTGTTTGACGTTTCCACTGCATGCCTTGACTTCCCCACCTCCT
CCTCAAACAAGAGACTCCACTGCATGTTCCAAGACAGTATGGGGTGGTAAGATAAGGAAGGAAGTGTTGTGGATG

1900/6881

FIGURE 1752B

TGGATGGTGGGGGCATGGACAAAGCTTGACACATCAAGTTATCAAGGCCTTGGAGGAGGCTCTGTATGTCCTCAG
GGGACTGACAACATCCTCCAGATTCCAGCCATAAACCAATAACTAGGCTGGACCCTTCCCACTACATAATAGGGC
TCAGCCCAGGCAGCCAGCTTTGGGCTGAGCTAACAGGACCAATGGATTAAACTGGCATTTCAGTCCAAGGAAGCT
CGAAGCAGGTTTAGGACCAGGTCCCCTTGAGAGGTCAGAGGGGCCTCTGTGGGTGCTGGGTACTCCAGAGGTGCC
ACTGGTGGAAAGGGTCAGCGGAGCCCCAGCAGGAAGGGTGGGCCAGCCAGGCCATTCTTAGTCCCTGGGTGGGGA
GGCAGGGAGCTAGGGCAGGGACCAAATGAACAGAAAGTCTCAGCCCAGGATGGGGCTTCTTCAACAGGGCCCCCTG
CCCTCCTGAAGCCTCAGTCCTTCACCTTGCCAGGTGCCGTTTCTCTTCCGTGAAGGCCACTGCCCAGGTCCCCAG
TGCGCCCCCTAGTGGCCATAGCCTGGTTAAAGTTCCCCAGTGCCCTCCTTGTCATAGACCTTCTTCTCCACCCC
CTTCTGCCCCCTGGGTCCCCGGCCATCCAGCGGGGCTGCCAGAGAACCCAGACCTGCCCTTACAGTAGTGTAGCG
CCCCCTCCCTCTTTTCGGCTGGTGTAGAATAGCCAGTAGTGTAGTGCGGTGTGCTTTTACGTGATGGCGGGTGGGC
AGCGGGCGGCGGGCTCCGCGCAGCCGTCTGTCTTGATCTGCCCAGCGCGGCCCGTGTGTGTTTTGTGCTGTGT
CCACGCGCTAAGGCGACCCCCCTCCCCCGTACTGACTTCTCCTATAAGCGCTTCTCTTCGCATAGTCACGTAGCTC
CCACCCACCCCTCTTCTGTGTCTCACGCAAGTTTTATACTCTAATATTTATATGGCTTTTTTTCTTCGACAAAA
AAATAATAAAACGTTTCTTCTGAAAAGCTG

1901/6881
FIGURE 1753

MAAPTCKQLRGRVLVLLCSLLGMLWEARASQIRYSVPEETEEKGYIVGNISKDLALEPRELAERRVRIVSRGRTQLF
SLNPRSGTLVTAGRIDREELCAQSPRCLVNFKVLVEDRVKLYGIEIEVTDINDSAPKFQAESLEVKINEIAVPGA
RYPLPEAIDPDVGVNSLQSYQLSPNHHFSLNVQTGDNGAINPELVLERALDREEATAHHLVLTASDGGEPRRSST
VRIHVTVLDTNDNAPVFAQRIYRVKVLENVPPGTWLLTATASDLDEGINGKVAYKFWKINEKQSLLFQLNENTGE
ISTAKSLDYEECSFYEMEIQAEDGGGLKGWTKVLISVEDVNDNRPEVTITSLFSPVREDAPQGTVILLFNAHDRD
SGKNGQVVCSIQENLSFTLEENSEEDYYRLLTAQILDREKASEYNITVTATDRGTPPLSTEIHTLQVTDINDNPP
AFSQASYSVYLPENNARGTSIFSUIAYDPDSNENSRIYISLAEDTIQGSPLSTYVSINSDTGVLIALCSFDYEQF
RDLQMQVTASDSGSPPLSSNVSLRFLVLDQNDNAPEIILYPALPTDGSTGVELAPRSAEPGYLVTKVAVDRDSGQ
NAWLSYRLFKASEPGLFSVGLHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTLTVAIADSIPDILADL
GSLQIPADLEASDLTLYLVAVAVVSCVFLTFVITLLALRLRHHSSHLLRATSDGLAGVPTSHFVGVDGVRAFL
QTYSQEFSLTADSRKSHLIFPQPNYADTLISQQSCEKNEPLCVSVDSEKPIEDTPLVPQAPPNTDWRFSQAQRPG
TSGSQNGDDTGTWPNNQFDTEMLQAMILASASEAADGSSTLGGGAGTMGLSARYGPQFTLQHVPDYRQNVYIPGS
NATLTNAAGKRDGKAPAGGNGNKKKSGKKEKK

1902/6881
FIGURE 1754A

ATGCAGAGAGCCAGAGAAGCCGAAATGATGAAAAGTCAGGTACTGTTTCCCTTCCTGCTGTCTTTGTTCTGCGGG
GCCATCTCCCAGCAGATCCGATACACGATTCCAGAGGAGCTAGCCAACGGCTCACGGGTGGGGAAACTTGCCAAG
GATCTGGGGCTCAGTGTCCGGGAGTTGCCAACTCGAAAACCTGCGGGTTAGTGCAGAGGATTATTTCAACGTTAGT
TTGGAGAGCGGGGATTTGTTAGTGAACGGTAGGATAGATCGAGAGAAGATTTGCGGAAGGAACTTGAGTGTGCA
CTAGAATTCGAAACGGTCGCTGAAAACCCAATGAATGTTTTCCACGTGGTTGTTGTAATCCAAGATATTAATGAC
AATGCACCACGTTTCGTTGCAAAGGCATTGACTTAGAAATTTGTGAGTCAGCCTTACCCGGGGTAAAATTCTCT
CTGGATTCTGCTCAAGATGCAGATGTGGAAGGCAATTCAGTGAAGTTATACACCATCAACCCCAATCAATACTTC
TCTCTGTCAACGAAGGAAAGTCCTGATGGAAGTAAATATCCGGTATTACTGCTGGAAAAACCTCTAGACAGGGAA
CATCAGAGCTCTCATCGCTTAATCCTGACTGCCATGGATGGCGGGGACCCGCCTCTAAGCGGCACCACCCATATC
TGGATCCGAGTTACGGATGCCAATGATAATGCTCCCGTGTTTAGCCAGGAGGTATACAGGGTTAGCCTCCAAGAA
AACGTACCGTGGGGAACCTCCGTGCTGCGGGTGATGGCCACAGACCAGGATGAGGGCATTAAATGCAGAGATCACC
TATGCCTTCCTCAATTCCCCAATAAGTACCAGCCTCTTCAATCTCAATCCAAATACTGGCGACATCACAACCAAT
GGCACATTGGATTTTGAAGAGACAAGTAGATATGTGTTGAGTGTGGAAGCTAAGGATGGAGGAGTACACACAGCT
CACTGTAATGTTCAAATAGAAAATTGTTGACGAGAATGACAATGCCCCAGAGGTGACATTCATGTCCTTCTCTAAC
CAGATTCCAGAGGATTTCAGACCTTGGAACGTGAATAGCCCTCATAAAAGTGCAGACAAGGATTCTGGGCAAAAT
GGCATGGTGACATGCTATACTCAGGAAGAAGTTCCTTTCAAATTAGAATCCACCTCGAAGAATTATTACAAGCTG
GTGATTGCTGGAGCCCTAAACCGGGAGCAGACAGCAGACTACAACGTACAATCATAGCCACCGACAAGGGCAAA
CCAGCCCTTTCTCCAGGACAAGCATCACCTGCACATCTCCGACATCAACGACAATGCACCTGTTTTCCATCAG
GCCTCCTATGTGGTCCACGTGTCTGAGAACAACCCACCTGGCGCCTCCATTGCACAAGTAAGCGCCTCCGACCCG
GATTTGGGACCCAACGGCAGAGTCTCCTACTCTATTCTGGCCAGTGACCTGGAGCCGCGGGAGCTGTTGTCTAC
GTGTCCGTGAGCCCGCAGAACCGGGTGTTGTCGCGCAGCGCGCCTTCGACCACGAGCAGCTGCGCGCCTTCGAG
CTCACACTGCAGGCCAGGGACCAGGGCTCCCCGCGCTCAGCGCCAACGTGAGCCTGCGCGTGTGGTGGGCGAC
CTCAATGACAATGCGCCACGGGTGCTGTACCCGCGCTGGGGCCTGATGGCTCCGCCCTCTTCGATATGGTGCCA
CGCGCCGACAGAGCCCGGTACCTGGTGACCAAGGTGGTGGCGGTGGACGCAAGTCTAGGACACAACGCTTGGCTG
TCCTACCACGTGCTGCAGGCCAGCGAGCCCGGGCTCTTACGCTGGGGTTGCGCACGGGTGAGGTGCGCACAGCG
CGTGCTTGGGCGACAGGGACGCGGCCCGCCAGCGCTGCTGGTCTGCTGTGCGTGATGGAGGACAGCCGCCACTC
TCCGCCACCGCCACGCTGCACCTAATCTTCGCGGATAGCCTGCAAGAGGTATTGCCAGACCTCAGCGACCGCCCT
GAGCCCTCTGACCCCAAGACGGAAGTGCAGTTTTACCTGGTTGTGGCCTTGGCCTTGATCTCAGTGTCTTTCTC
CTCGCGGTGATTCTAGCGATCGCCCTGCGCCTGCGACGTTCTCCAGCCTCGACACTGAGGGCTGCTTTCAAACC
GGTCTCTGCTCCAAGTCTGGGCCCGGGTTCCTCCCAACCACAGCGAGGGGACTTTGCCCTATTCTTACAATCTA
TGTATTGCCCTCTCATTCTGCAAAGACAGAGTTTAATTCTCTCAACCTGACACCGGAAATGGCTCCCCCTCAGGAT
CTGCTGTGTGATGATCCTTCTATGGTTGTATGTGCCAGTAATGAAGATCACAATAATCGCTTATGACCTTCTTTG
TCTTCGCACCAAGCCCCGCCAACACGGACTGGCGTTTCTCTCAGGCCAGAGACCCGGCACCAGCGGCTCCCAA
AATGGCGATGACACCGGCACCTGGCCCAACAACAGTTTGACACAGAGATGCTGCAAGCCATGATCTTGGCGTCC
GCCAGTGAAGCTGCTGATGGGAGCTCCACCCTGGGAGGGGTGCCGGCACCATGGGATTGAGCGCCCGCTACGGA
CCCCAGTTACCCCTGCAGCACGTGCCCCGACTACCGCCAGAATGTCTACATCCCAGGCAGCAATGCCACACTGACC
AACGCAGCTGGCAAGCGGGATGGCAAGGCCCCAGCAGGTGGCAATGGCAACAAGAAGAAGTCGGGCAAGAAGGAG
AAGAAGTAAACATGGAGGCCAGGCCAAGAGCCACAGGGCGGCTCTCCCAACCAGCCAGCTTCTCCTTACCTGC
ACCCAGGCCTCAGAGTTTCAGGGCTAACCCCAAGAACTAGTGGTAGGGGCCAAGGCCATGCTCCCTTGGGAAACA
GAAACAAGTGGCCAGTACGACCTACCCCTTCCCCCAAGGGGTTGAATATGAAAAGCAGTTCCGCTGGGAAAC
CCCCATCCAATCAACTGCTGTACCCATGGGGGTAGTGGGGTTACTGTAGACACCAAGAACCATTGCCACACCCC
GTTTAGTTACAGCTGAACCTCCTCCATCTTCAAATCAATCAGGCCCATCCATCCCATGCCTCCCTCCTCCCCACC
CCACTCCAACAGTTCTCTTTCCCGAGTAAGGTGGTTGGGGTGTGTAAGTACCAAGTAACCTACAAGCCTCCTAG
TTCTGAAAAGTTGGAAGGGCATCATGACCTCTTGGCCTCTCCTTTGATTCTCAATCTTCCCCCAAAGCATGGTTT
GGTGCCAGCCCCCTCACCTCCTTCCAGAGCCCAAGATCAATGCTCAAGTTTTGGAGGACATGATCACCATCCCCA
TGGTACTGATGCTTGCTGGATTTAGGGAGGGCATTGCTACCAAGCCTCTTCCCAACGCCCTGGGGACCAAGTCT
TCTGTTTTGTTTTTCATTGTTTGACGTTTCCACTGCATGCCTTGACTTCCCCCACCTCCTCCTCAAACAAGAGAC
TCCACTGCATGTTCCAAGACAGTATGGGGTGGTAAGATAAGGAAGGGAAGTGTGTGGATGTGGATGGTGGGGCA

1903/6881
FIGURE 1754B

TGGACAAAGCTTGACACATCAAGTTATCAAGGCCTTGGAGGAGGCTCTGTATGTCCTCAGGGGACTGACAACATC
CTCCAGATTCCAGCCATAAACCAATAACTAGGCTGGACCCCTCCCCTACTACATAATAGGGCTCAGCCCAGGCAGCC
AGCTTTGGGCTGAGCTAACAGGACCAATGGATTAACTGGCATTTCAGTCCAAGGAAGCTCGAAGCAGGTTTAGG
ACCAGGTCCCCCTTGAGAGGTCAGAGGGGCCTCTGTGGGTGCTGGGTACTCCAGAGGTGCCACTGGTGGAAAGGTC
AGCGGAGCCCCAGCAGGAAGGGTGGGCCAGCCAGGCCATTCTTAGTCCCTGGGTGAGGAGGCAGGGAGCTAGGG
CAGGGACCAAATGAACAGAAAGTCTCAGCCCAGGATGGGGCTTCTTCAACAGGGCCCCCTGCCCTCCTGAAGCCTC
AGTCCTTACCTTGCCAGGTGCCGTTTTCTTCCGTGAAGGCCACTGCCAGGTCCCCAGTGCGCCCCCTAGTGG
CCATAGCCTGGTTAAAGTTCCCCAGTGCCCTCCTTGTGCATAGACCTTCTTCTCCCACCCCCTTCTGCCCTGGGT
CCCCGGCCATCCAGCGGGGCTGCCAGAGAACCCAGACCTGCCCTTACAGTAGTGTAGCGCCCCCTCCCTCTTTC
GGCTGGTGTAGAATAGCCAGTAGTGTAGTGCGGTGTGCTTTTACGTGATGGCGGGTGGGCAGCGGGCGGCGGGCT
CCGCGCAGCCGTCTGTCCTTGATCTGCCCGCGGCGGCGGCGTGTGTGTTTTGTGCTGTGTCCACGCGCTAAGGCG
ACCCCTCCCCCGTACTGACTTCTCCTATAAGCGCTTCTCTTCGCATAGTCACGTAGCTCCCACCCACCCTCTT
CCTGTGTCTCACGCAAGTTTTATACTCTAATATTTATATGGCTTTTTTCTTCGACAAAAAATAATAAACGTT
TCTTCTGAAAAGCTG

1904/6881
FIGURE 1755

MQRAREAEEMMKSQVLFPFLLSLFCGAISQQIRYTIPEELANGSRVGKLA KDLGLSVREL PTRKLRVSAEDYFNVS
LESGDLLVNGRIDREKICGRKLECALEFETVAENPMNVFHVVVVIQDINDNAPRFVAKGIDLEICESALPGVKFS
LDSAQDADVEGNSLKLYTINPNQYFSLSTKESPDGSKYPVLLLEKPLDREHQSSHRLILTAMDGGDPPLSGTTHI
WIRVTDANDNAPVFSQEVYRVSLQENVPWGTSVLRVMATDQDEGINAEITYAFLNSPISTSLFNLNPNTGDITTN
GTLDFEETSRYVLSVEAKDGGVHTAHCNVQIEIVDENDNAPEVTFMSFSNQIPEDSDLGTVIALIKVRDKDSGQN
GMVTCYTQEEVFPKLESTSKNYYKLVIAGALNREQTADYNVTIIATDKGKPALSSRTSITLHISDINDNAPVFHQ
ASYVVHVSENNPPGASIAQVSASDPDLGPNGRVSYSLASDLEPRELLSYVSVSPQSGVVFAQRAFDHEQLRAFE
LTLQARDQGSPALSANVSLRVLVGDLNDNAPRVLYPALGPDGSALFDMVPRAAEPGYLVTKVVAVDADSGHNAWL
SYHVLQASEPGLFSLGLRTGEVRTARALGDRDAARQRLLVAVRDGGQPPLSATATLHLIFADSLQEVLPDLSDRP
EPSPDQTELQFYLVVALALISVLFLLAVILAIALRLRRSSSLDTEGCFQTGLCSKSGPGVPPNHSEGTLPYSYNL
CIASHSAKTEFNSLNLTPEMAPPQDLLCDDPSMVVCASNEDHKIAYDPSLSSHQAPPNTDWRFSQAQRPGTSGSQ
NGDDTGTPNPNQFDTEMLQAMILASASEAADGSSTLGGGAGTMGLSARYGPQFTLQHVPDYRQNVYIPGSNATLT
NAAGKRDGKAPAGGNGNKKKSGKKEKK

1905/6881
FIGURE 1756A

ATGAAGCGAGCTCAGGGAGGTGCGGGCTGGTGCGGTGGCTGCAGGTACTGTTGCCCTTCCTGTTGTCTTTGTTTC
CCCCGGGCTCTCCCAGTCCAGATCCGCTATTCAATTCCAGAGGAGCTGGCCAAAACTCGGTCGTAGGAAACCTC
GCCAAGGATCTGGGGCTCAGCGTCCGGGACTTGCCAGCCCGGAAGCTGCGGGTTAGCGCGGAGAAGGAATATTTTC
ACAGTAAACCCAGAAAGCGGAGACTTACTTGTGAGTGACAGAATAGACCGAGAACAGATATGCGGGGAGCAGCCT
CTGTGTGTTCTGGATTTCGATACTGTGCTGAAAAATCCACTAAATATTTTCTACATAGCAGTAATTGTGCAGGAT
ATAAATGATAATACCCCGCTATTCAAACAGACTAAGATTAATTTAAAAATGGCGAATCCACTAAGCCAGGTACA
ACATTTCCACTTGACCCAGCCCTGGATTGAGATGTTGGTCTTAACCTCACTACAAAGATAACCACCTTAATGACAAC
GAGTACTTTGATCTCGCTGAGAAACAGACTCCAGATGGTCTGTAATATCCTGAGTTGATTCTAAAAACTCTCTG
GACAGAGAAGAGCACAGTTTACATCAATTGGTCTCAGAGCTGTGGATGGCGGAGACCCACCTCAAAGTGGCAGC
ACCCAAATCCGAATCAAAGTCACGGATGCCAACGATAACCTCCAGTGTTCAGCCAGGACGTGTACAGGGTCACC
CTGAGGGGAGGACGTGCCGCCGGGCTTCTTTGTGCTTCAAGTGACAGCCACCGACCGGGATGAAGGCATAAACGCA
GAGATCACCTACTCCTTTTCATAATGTGGACGAACAAGTGAAACACTTTTTTCAACTTAAATGAAAAACAGGAGAA
ATCACGACAAAGGATGATTTGGATTTTGAGATTGCAAGTAGTTACACTCTGAGTATCGAAGCAAAAGATCCTGGA
GATCTAGCAGCCCACTGCAGTATCCAAGTTGAAATCTTGATGACAACGATTGTGCACCTGAAGTTATTGTGACT
TCAGTATCTACTCCCTACCGGAGGATTGCCACCAGGAACAGTGATCGCCTTGATAAAAACGAGAGACAGAGAC
TCTGGAGAAAATGGAGAAGTTTACTGCCAAGTGTTGGGAAATGCCAAGTTATTTTGAAATCTTCTCAAAGAAC
TATTACAAACTAGTGACAGACGGCGCTCTGGACCGGGAGGAGATCCAGAATACAATCTCACCATCACAGCCACC
GACGGGGGCAAGCCGCCCTCTCCTCCAGCATAATTGTCACCCTGCACATCTCCGACGTCAACGATAATGCCCCA
GTTTTCCAACAGACTTCCTACATGGTTACAGTGGCAGAGAACAATCCTCCTGGCGCCTCTATCGCTCAAATCAGT
GCCTCTGACCCTGACTTGGGCCCCAGTGGCCAAGTTTCTACTCCATCGTAGCGAGCGACCTGAAGCCGCGGGAG
ATTTTATCCTACGTGTCCGTGAGCGCGCAGAGCGGGGTGGTGTTCGCGCAGCGCGCCTTCGATCATGAGCAGCTG
CGCGCCTTCGAGCTCACACTGCAGGCCCGCGACCAGGGCTCGCCCGCGCTCAGCGCCAACGTGAGCCTGCGCGTG
TTAGTGGGCGACCTCAATGACAATGCGCCACGGGTGCTGTACCCCGCGCTGGGGCCTGATGGCTCCGCCCTCTTC
GATA¹GGTGCCACGCGCCGAGAGCCCGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACGCAGACTCAGGACAC
AACGCTTGGCTGTCTTACCAGTGCTGCAGGCCAGCGAGCCCGGGCTCTTCAGCCTGGGGTTGCGCACGGGTGAG
GTGCGCACAGCGCTGCCCTTGGGCGACAGGGACCGGGCCCGCCAGCGCCTGCTGGTCTGTGCGTGATGGAGGA
CAGCCGCCACTCTCCGCTACGGCCACGCTGCACCTAATCTTCGCGGATAGCCTGCAAGAGGTATTGCCAGACCTC
AGCGACCGCGGGGAGCCCTCTGACCCCCAGGCAAACTGCAGTTTTACCTGGTTGTGGCCTTGGCCTTGATCTCA
GTGCTCTTCTTCTCGCGGTGATTCTGGCAATCTCCCTGCGCCTGCGACTCTCTTCAGGTGAGATGCTTGGGAC
TGTTTTTCAGCCTGGTCTCAGCTCCAAGCCTGGACCTGGGGTTCTCCCCAATTACAGTGAGGGTACATTGCCCTAT
TCCTACAACCTGTGTGTTGCCTCACAATCAGCCAAGACAGAGTTCAATTTTCTGAACATAACCCCGGAATTGGTT
CCCGCGCAAGATCTCGTCTGTGACAATGCCTCTTGGGAACAAAATACAAATCATGGAGCCGCTGGGGTCCCTTTT
GCCTCAGATACTATTTTGAAGCAAGCCCCGCCCAACACGGACTGGCGTTTCTCTCAGGCCAGAGACCCGGCACC
AGCGGCTCCCAAAATGGCGATGACACCGGCACCTGGCCCAACAACCAAGTTTGACACAGAGATGCTGCAAGCCATG
ATCTTGGCGTCCGCCAGTGAAGCTGCTGATGGGAGCTCCACCTGGGAGGGGGTGCCGGCACCATGGGATTGAGC
GCCCCTACGGACCCCACTTACCCTGCAGCACGTGCCCGACTACCGCCAGAATGTCTACATCCAGGCAGCAAT
GCCACACTGACCAACGCAGCTGGCAAGCGGGATGGCAAGGCCCCAGCAGGTGGCAATGGCAACAAGAAGAAGTCG
GGCAAGAAGGAGAAGAAGTTAACATGGAGGCCAGGCCAAGAGCCACAGGGCGGCCTCTCCCCAACCAGCCCAGCTT
CTCCTTACCTGCACCCAGGCCTCAGAGTTTACAGGGCTAACCCCCAGAATACTGGTAGGGGCCAAGGCCATGCTCC
CCTTGGGAAACAGAAACAAGTGCCAGTCAGCACCTACCCCTTCCCCCCAGGGGGTTGAATATGCAAAAGCAGT
TCCGCTGGGAACCCCATCCAATCAACTGCTGTACCCATGGGGGTAGTGGGGTTACTGTAGACACCAAGAACCAT
TTGCCACACCCCGTTTAGTTACAGCTGAACTCCTCCATCTTCCAAATCAATCAGGCCCATCCATCCCATGCCTCC
CTCTCCCCACCCCACTCCAACAGTTCTCTTTCCCGAGTAAGGTGGTGGGGTGTGAAGTACCAAGTAACCTA
CAAGCCTCCTAGTTCTGAAAAGTTGGAAGGGCATCATGACCTCTTGGCCTCTCCTTTGATTCTCAATCTTCCCC
AAAGCATGGTTTGGTGCCAGCCCCCTCACCTCCTTCCAGAGCCCAAGATCAATGCTCAAGTTTGGAGGACATGA
TCACCATCCCCATGGTACTGATGCTTGTGGATTAGGGAGGGCATTTTGTCTACCAAGCCTCTTCCCAACGCCCT
GGGAGCCAGTCTTCTGTTTTGTTTTTCAATTGTTTGACGTTTTCCACTGCATGCCTTGACTTCCCCACCTCCTCCT
CAAACAAGAGACTCCACTGCATGTTCCAAGACAGTATGGGGTGGTAAGATAAGGAAGGGAAGTGTGTGGATGTGG

1906/6881
FIGURE 1756B

ATGGTGGGGGCATGGACAAAGCTTGACACATCAAGTTATCAAGGCCTTGGAGGAGGCTCTGTATGTCCTCAGGGG
ACTGACAACATCCTCCAGATTCCAGCCATAAACCAATAACTAGGCTGGACCCTTCCCACTACATAATAGGGCTCA
GCCAGGCAGCCAGCTTTGGGCTGAGCTAACAGGACCAATGGATTAACTGGCATTTCAGTCCAAGGAAGCTCGA
AGCAGGTTTtaggaccaggtcccccttgagaggtcagaggggcctctgtgggtgctgggtactccagaggtgccact
GGTGGAAAGGGTCAGCGGAGCCCCAGCAGGAAGGGTGGGCCAGCCAGGCCATTCTTAGTCCCTGGGTGGGGAGGC
AGGGAGCTAGGGCAGGGACCAAATGAACAGAAAGTCTCAGCCCAGGATGGGGCTTCTTCAACAGGGCCCCTGCCC
TCCTGAAGCCTCAGTCCTTACCTTGCCAGGTGCCGTTTCTCTTCCGTGAAGGCCACTGCCCAGGTCCCAGTGC
GCCCCCTAGTGGCCATAGCCTGGTTAAAGTCCCCAGTGCCTCCTTGTGCATAGACCTTCTTCTCCACCCCCTT
CTGCCCCCTGGGTCCCCGGCCATCCAGCGGGGCTGCCAGAGAACCCAGACCTGCCCTTACAGTAGTGTAGCGCCC
CCTCCCTCTTTCGGCTGGTGTAGAATAGCCAGTAGTGTAGTGCAGTGTGCTTTTACGTGATGGCGGGTGGGCAGC
GGGCGGCGGGCTCCGCGCAGCCGTCTGTCTTGATCTGCCGCGGCGGCCCGTGTGTGTTTTGTGCTGTGTCCA
CGCGCTAAGGCGACCCCTCCCCCGTACTGACTTCTCCTATAAGCGCTTCTCTTCGCATAGTCACGTAGCTCCCA
CCCCACCTCTTCTGTGTCTCACGCAAGTTTTATACTCTAATATTTATATGGCTTTTTTTCTTCGACAAAAAA
TAATAAAACGTTTCTTCTGAAAAGCTG

1907/6881
FIGURE 1757

MKASSGRCGLVRWLQVLLPFLLSLFPGALPVQIRYSIPEELAKNSVVGNLAKDLGLSVRDL PARKLRVSAEKEYF
TVNPESGDL LVSDRIDREQICGKQPLCVLDFDTVAENPLNIFYIAVIVQDINDNTPLFKQTKINLKIGESTKPGT
TFPLDPALDS DVGPNSLQRYHLNDNEYFDLAEKQTPDGRKYPELILKHSLDREEHSLHQLVLTAVDGGDPPQSGT
TQIRIKVTDANDNPPVFSQDVYRVTLREDVPPGFFVLQVTATDRDEGINAEITYSFHNVDEQVKHFFNLNEKTGE
ITTKDDLD FEIASSYTLSIEAKDPGDLAAHCSIQVEILDDNDCAPEVIVTSVSTPLPEDSPPGTVIALIKTRDRD
SGENGEVYCQVLGNAKFILKSSSKNYYKLVTDGALDREEIPEYNLTITATDGGKPPLSSSIIVTLHISDVNDNAP
VFQQTSYMHVAENNP PGASIAQISASDPDLGPGSQVSYSIVASDLKPREILSYVSVSAQSGVVFAQRAFDHEQL
RAFELTLQARDQGSPALSANVSLRVLVGDLNDNAPRVLYPALGPDGSALFDMVPRAAEPGYLVTKVVAVDADSGH
NAWLSYHVLQASEPGLFSLGLRTGEVRTARALGDRDAARQRLLVAVRDGGQPPLSATATLHLIFADSLQEVL PDL
SDRREPSDPQAKLQFYLVALALISVLFFLAVILAI SLRLRLSSRSDAWDCFQPLSSKPGPGVLPNYSEGTLPY
SYNLCVASQSAKTEFNFLNITPELVPAQDLVCDNASWEQNTNHGAAGVPFASDTILKQAPPNTDWRFSQAQRPGT
SGSQNGDDTGTPNPNQFDTEMLQAMILASASEAADGSSTLGGGAGTMGLSARYGPQFTLQHVDPDYRQNVYIPGSN
ATLTNAAGKRDGKAPAGGNGNKKKSGKKEKK

1908/6881
FIGURE 1758A

ATGGGAAATAGCTCCGGATGGAGGGGCCAGCAGGGCAGAGGCGAATGCTATTTCTCTTCCTGCTCTCTTTGTTA
GACCAGGTTCTCTCCGAACCGATCCGCTACGCTATTCCCAGAGGAGCTGGACAGGGGCTCGCTGGTAGGGAAACCTC
GCCAAGGACCTGGGGTTTGGCGTGGGGGATTTACCTACTAGGAACCTGCGGGTTATTGCAGAGAAGAAATTCCTT
ACCGTGAGCCCCGAAAATGGGAACCTTACTTGTGAGCGACCGTATAGACCGAGAGGAGATTTGTGGCAAGAAGTCG
ACGTGTGTTCTGGAATTTGAAATGGTTGCTGAAAAGCCTTTAAACTTTTTTTCATGTAAGTGTGCTGATCCAGGAT
ATTAACGACAACCCACCGACCTTTAGCCAAAATATCACTGAGCTGGAAATCAGCGAACTGGCTCTCACTGGAGCC
ACATTTGCCCTGGAATCTGCGCAAGATCCTGATGTAGGTGTCAATTCGCTGCAGCAGTACTACCTCAGCCCTGAT
CCGCACTTCTCTTTGATTGAGAAGGAGAACCTGGATGGCAGTAGGTACCCAGAGCTAGTACTGAAAGCACCCCTG
GACAGGGAAGAGCAGCCACATCACCACCTGGTCCTCAGAGCTGTGGATGGGGGCGAGCCCTCCAGAAGCTGTACC
ACCCAGATCAGGGTAATTGTGCGAGATGCAAATGATAACCCCCAGTATTTACTCAGGACATGTACAGGGTCAAT
GTTGCAGAGAACCTGCCCCGCTGGCTCCTCCGTATTAAAAGTGATGGCCATTGACATGGATGAGGGCATCAATGCC
GAAATCATCTATGCCTTCATCAATATTGGCAAGGAAGTGAGACAACCTGTTCAAGCTGGACAGTAAAACGGGGGAA
CTCACCACCTATTGGAGAACTGGACTTTGAAGAGAGAGATAGCTACACAATTGGGGTGAAGCAAAGGATGGTGA
CATCACACTGCATATTGTAAAGTACAGATAGATATTTAGATGAAAATGACAATGCCCCGAGATAACCCCTGGCT
TCTGAATCCCAACATATACAAGAAGATGCTGAGCTGGGGACTGCCGTTGCCCTGATCAAAACACATGATCTAGAT
TCTGGATTTAATGGAGAAATCCTATGCCAACTAAAAGGAACTTCCCCTTTAAAATCGTTCAAGATACCAAAAAC
ACATACAGGTTGGTGACAGATGGAGCCCTGGACCGGGAGCAGATCCCAGAATACAATGTGACGATCACAGCTACC
GACAAAGGCAATCCACCGCTCTCCTCCAGCAAGACCATCACTCTGCACATCCTTGATGTCAACGACAACGTTCCC
GTTTTCCACCAGGCCTCTACACCGTGCATGTAGCTGAGAACAATCCGCCTGGAGCCTCCATTGCGCATGTGAGA
GCCTCGGATCCCGACTTGGGACCTAATGGCCTTGTCTCCTACTACATCGTGGCCAGTGACCTGGAGCCGCGGGAG
CTGTCGTCTACGTGTCCGTGAGCGCGGAGCGGGGTGGTGTTCGCGCAGCGAGCCTTCGACCACGAGCAGCTG
CGTGCCTTCGAGCTCACTCTGCAGGCCCGCGACCAGGGCTCGCCTACGCTCAGCGCCAACGTGAGCCTGCGCGTG
TTGGTGGACGACCGCAACGACAATGCACCGCTGGTGTGTACCCAGCTCTGGGGCCCGAAGGCTCTGCGCTCTTC
GATATGGTGCCGCGCTCTGCAGAGCCTGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACGCAGACTCGGGATAC
AACGCCTGGCTGTCTTACCACATTGTGCAGGCCAGCGAGCCCGGGCTGTTTCAGCCTGGGCCTGCGCACGGGTGAG
GTGCGCACGGCGCGTACCTTGGGCGACAGGGAGGCCCGCCGAGCGCCTGCTGGTCACTGTGCGTGATGGAGGA
CAGCAGCCTCTTTAGCCACCGTCATGCTGCACCTAATCTTCGAGATAGCTTGCAAGAGATACAACCTGACCTT
AGCGACCGCCCCACTCCCTCTGACCCCTCAGGCGGAGCTACAGTTTTACCTAGTAGTGGCGTTGGCCTTGATCTCA
GTGCTCTTCTCCTCGCGGTGATTCTGGCAATCTCCCTGCGCCTGCGATGCTCCTCCAGACCCGCCACTGAGGGC
TACTTTAGCCTGGTGTCTGCTTCAAGACTGTACCTGGAGTTCTCCCCACCTACAGCGAAAGGACTTTGCCTTAT
TCCTACAATCCGTGTGCTGCCTCACATTCTCAAACACCGAGTTTTAAATTTCTCAATATAAAGGCTGAAAATGCT
GCACCACAAGATCTTCTATGTGATGAAGCCTCTTGTTTTGAAAGTAATGACAATCCAGAAATGCCTTCTAATTCA
GGCAATTTGAAAAGCAAGCCCCGCCAACACGGACTGGCGTTTTCTCTCAGGCCAGAGACCCGGCACCAGCGGC
TCCCAAAATGGCGATGACACCGGCACCTGGCCCAACAACAGTTTTGACACAGAGATGCTGCAAGCCATGATCTTG
GCGTCCGCCAGTGAAGCTGCTGATGGGAGCTCCACCCTGGGAGGGGTGCCGGCACCATGGGATTGAGCGCCCGC
TACGGACCCCACTTACCCCTGCAGCACGTGCCCGACTACCGCCAGAATGTCTACATCCCAGGCAGCAATGCCACA
CTGACCAACGCAGCTGGCAAGCGGGATGGCAAGGCCCCAGCAGGTGGCAATGGCAACAAGAAGTGGGGCAAG
AAGGAGAAGAAG**TAAC**ATGGAGGCCAGGCCAAGAGCCACAGGGCGGCCTCTCCCCAACAGCCAGCTTCTCCTT
ACCTGCACCCAGGCCTCAGAGTTTCAGGGCTAACCCCAAGAACTAGGTAGGGGCCAAGGCCATGCTCCCTTGG
GAAACAGAAACAAGTGCCAGTCAGCACCTACCCCTTCCCCCAGGGGGTTGAATATGCAAAAGCAGTTCCGCT
GGGAACCCCATCCAATCAACTGCTGTACCCATGGGGGTAGTGGGGTTACTGTAGACACCAAGAACCATTGCGCA
CACCCCGTTTAGTTACAGCTGAACCTCCATCTTCCAAATCAATCAGGCCATCCATCCCATGCCTCCCTCCTC
CCCACCCCACTCCAACAGTTCTCTTTCCCGAGTAAGGTGGTGGGGTGTGAAAGTACCAAGTAACCTACAAGCC
TCCTAGTTCTGAAAAGTTGGAAGGGCATCATGACCTCTTGGCCTCTCCTTTGATTCTCAATCTTCCCCAAAGCA
TGGTTTGGTGCCAGCCCTTCACTCCTTCCAGAGCCCAAGATCAATGCTCAAGTTTTGGAGGACATGATACCA
TCCCCATGGTACTGATGCTTGTGATTTAGGGAGGGCATTTTGTACCAAGCCTCTTCCCCAACGCCCTGGGGAC
CAGTCTTCTGTTTTGTTTTTCAATTGTTTGACGTTTCCACTGCATGCCTTGACTTCCCCCACCTCCTCCTCAAACA
AGAGACTCCACTGCATGTTCCAAGACAGTATGGGGTGGTAAGATAAGGAAGGAAGTGTGTGGATGTGGATGGTG

1909/6881
FIGURE 1758B

GGGGCATGGACAAAGCTTGACACATCAAGTTATCAAGGCCTTGGAGGAGGCTCTGTATGTCCTCAGGGGACTGAC
AACATCCTCCAGATTCCAGCCATAAACCAATAACTAGGCTGGACCCTTCCCCTACATAATAGGGCTCAGCCCAG
GCAGCCAGCTTTGGGCTGAGCTAACAGGACCAATGGATTAAACTGGCATTTCAGTCCAAGGAAGCTCGAAGCAGG
TTTAGGACCAGGTCCCCCTTGAGAGGTGAGAGGGGCTCTGTGGGTGCTGGGTACTCCAGAGGTGCCACTGGTGA
AGGGTCAGCGGAGCCCCAGCAGGAAGGGTGGGCCAGCCAGGCCATTCTTAGTCCCTGGGTGGGGAGGCAGGGAG
CTAGGGCAGGGACCAAATGAACAGAAAGTCTCAGCCCAGGATGGGGCTTCTTCAACAGGGCCCCTGCCCTCCTGA
AGCCTCAGTCCTTCACCTTGCCAGGTGCCGTTTCTCTTCCGTGAAGGCCACTGCCAGGTCCCCAGTGCGCCCC
TAGTGGCCATAGCCTGGTTAAAGTTCCCCAGTGCCTCCTTGTGCATAGACCTTCTTCTCCACCCCCCTTCTGCC
CTGGGTCCCCGGCCATCCAGCGGGGCTGCCAGAGAACCCAGACCTGCCCTTACAGTAGTGTAGCGCCCCCTCCC
TCTTTCGGCTGGTGTAGAATAGCCAGTAGTGTAGTGCGGTGTGCTTTTACGTGATGGCGGGTGGGCAGCGGGCGG
CGGGCTCCGCGCAGCCGTCTGTCCTTGATCTGCCCGCGGCGGCCCGTGTGTGTTTTGTGCTGTGTCCACGCGCT
AAGGCGACCCCTCCCCCGTACTGACTTCTCCTATAAGCGCTTCTCTTCGCATAGTCACGTAGCTCCCACCCAC
CCTCTTCCTGTGTCTACGCAAGTTTATACTCTAATATTTATATGGCTTTTTTTCTTCGACAAAAAATAATAA
AACGTTTCTTCTGAAAAGCTG

1910/6881
FIGURE 1759

MGNSSGWRGPAGQRRMLFLFLLSLLDQVLSEPIRYAIPeelDRGSLVGNLAKDLGFGVGDLPTRNLRVIAEKKFF
TVSPENGNNLLVSDRIDREEICGKKSTCVLEFEMVAEKPLNFFHVTVLIQDINDNPPTFSQNITELEISELALTGA
TFALESAQDPDVGVNSLQQYYLSPDPHFSLIQKENLDGSRYPELVLKAPLDREEQPHHHLVLTAVDGGEPSRSCT
TQIRVIVADANDNPEVFTQDMYRVNVAENLPAGSSVLKVMaidMDEGINAEIIYAFINIGKEVRQLFKLDSKTGE
LTTIGELDFEERDSYTIgVEAKDGGHHTAYCKVQIDISDENDNAPEITLASESQHIQEDAELGTAVALIKTHDL
SGFNGEILCQLKGNFPFKIVQDTKNTYRLVTDGALDREQIPEYNVTITATDKGNPPLSSSKTITLHILDVNDNVP
VFHQASYTVHVAENNPpGASIAHVrasDPDLGPNGLVSYIIVASDLEPRELSSYVSVSARSGVVFAQRAFDEQL
RAFELTLQARDQGSPTLSANVSLRVLVDDRNDNAPLVLYPALGPEGSALFDMVPRSAEPGYLVTKVVAVDADSGY
NAWLSYHIVQASEPGLFSLGLRTGEVRTARTLGdREAARQRLlVTVRDGGQQPLSATVMLHLIFADSLQEIQPD
SDRPTPSDPQaelQFHLVVALALISVLFLLAVILAIslRLRCSSRPATEGYFQPGVCFTVPGVLPTYSERTLPY
SYNPCAASHSSNTEFKFLNIKAENAApQDLLCDEASWFESNDNPEmpSNsgNLQKQAPPNTDWRFSQAQRPGTSG
SQNGDDTGTWPNNQFDTEMLQAMILASASEAADGSSTLGGGAGTMGLSARYGPQFTLQHVDPYRQNVYIPGSNAT
LTNAAGKRDGKAPAGGNGNKKKSGKKEKK

1911/6881
FIGURE 1760A

ATGGGGAGCGGCGCCGGGGAGCTGGGCCGGGCTGAGAGGCTGCCAGTGCTCTTTCTCTTCCTGCTGTCTTTGTTCTGCCCCGGCGCTCTGTGAGCAGATCCGCTACAGGATTCCCGAGGAAATGCCAAGGGCTCCGTAAGTGGGGAAACCTCGCCACGGACCTGGGGTTCAGCGTCCAGGAGTTACCGACTCGAAAACCTGCGCGTCAGTTCGGAGAAGCCTTACTTCACCGTGAGCGCAGAGAGCGGGGAGTTGCTTGTGAGCAGCAGGCTAGACAGGGAGGAGATATGCGGGAAGAAGCCAGCTTGTGCTCTGGAATTTGAGGCTGTTGCTGAAAATCCACTGAACTTTTATCACGTGAATGTGGAGATCGAGGACATTAATGACCACACGCCAAAATTCACGCAAATTCCTTTGAGCTGCAAATAAGTGAGTCTGCACAGCCTGGCACAAGATTTATACTAGAAGTAGCAGAAGATGCAGATATTGGCTTAAACTCTCTGCAGAAGTATAAACTCTCTCTTAACCCAAGTTTCTCATTAAATAATTAAGGAGAAACAGGATGGTAGTAAATACCCGGAAGTGGCACTGGAGAAAACCTTAGACCGGGAACAACAGAGTTACCATCGTTTAGTCCTGACTGCCTTGGACGGTGGACATCCACCCCTAAGCGGCACCCTGAGCTCCGGATCCAGGTAACCGACGCCAATGATAATCCCCCGGTATTCAACCGAGACGTGTACAGAGTCAGCCTTCGGGAAAACGTGCCACCAGGCACCACTGTGTTGCAAGTGTGAGCCACTGACCAAGACGAGGGCATCAACTCAGAAATTACTTATTCTTCTACAGAACCGGGCAAATCTTTAGTCTGAATTCAAAGAGCGGAGAAATTACCACTCAAAGAAACTGGATTTTGAAGAGACCAAGGAATATTCAATGGTTGTAGAAGGGAGGGATGGTGGTGGACTGGTTGCACAATGTACAGTTGAAATTAATATTCAAGATGAAAATGACAATAGCCCAGAAGTTACATTCCATTCTCTACTTGAAATGATTCTGGAAAACGCGGTGCCTGGAACACTAATTGCTTTGATCAAATAACATGACCAAGATTCTGGGGAAAATGGGGAGGTTAATTGTCAATTACAAGGCGAAGTCCCTTTTAAGATTATCTCTTCATCCAAAATTCGTATAAGTTGGTAACAGATGGAACCCTAGACCGAGAGCAAACCCCGGAGTACAATGTCACCATCACAGCCACAGACAGGGGCAAGCCGCCCTCTCCTCCAGCATAAGCGTCATCTACATATCAGAGACGTCAACGATAACGCTCCGGTTTTCCACCAGCGCTCCTACTTAGTCAGTGTACCCGAAAACAACCTCCTGGGGCCTCCATCGCGCAAGTCTGCGCCTCGGACCTGACTTGGGGTTGAACGGCCAAGTCTCCTACTCTATCATGGCCAGCGACCTAGAGCCTCTGGCACTGGCCTCTTACGTGTCCATGAGCGCGCAAAGTGGGGTGGTGTTCGCGCAGCGCGCCTTTGACTACGAGCAGCTGCGCACCTTCGAATCACACTACAGGCCCGCGACCAGGGCTCGCCTGCGCTCAGCGCAAACGTGAGCCTGCGCGTGTGGTGGGCGACCGAAACGACAACGCACCGCGGGTGTGTACCCCGCGCTGGGTCCCGACGGCTCTGCGCTCTTCGATATGGTGCCGCGCGCTGCAGAGCCCGGTACCTGGTGACCAAGGTAGTGGCCGTGGACGCAGACTCAGGACACAACGCCTGGCTGTCTACACGTGCTGCAGGCTAGCGAGCCCGGGCTCTTCAGCCTGGGGCTGCGCACAGGAGAGGTGCGCACAGCGCGTGCCCTTGGGCGACAGGGACGCGGCCCCGCCAGCGCCTGCTGGTTGCTGTGCGTGATGGTGGACAGCCGCCACTCTCCGCCACCGCCACGTGCACTTGGTCTTTGCTGACAGCTTGCAGGAGGTGCTGCCGGATATCACTGACCGCCCTGTACCCTCTGACCCCCAGGCTGAGCTGCAGTTTTACCTAGTGGTGGCCTTGGCCTTGATCTCAGTGCTCTTCCTCTGGCCGTGATTCTGGCCGTGCTTGCCTTGCCTGCGCTGCGACGCTCCTCCAGCCCTGCCGCTGGAGCTGCTTCCAACCTGGTCTCTGTGTCAAGTCTGGACCTGTGGTTCCCCCAACTACAGTCAGGGGACTTTGCCTTATTCTACAACCTATGTGTTGCACATACAGGAAAAGACGGAGTTTAATTTCTAAAATGTAGTGAGCAATTGAGTTCAGGACAAGACATACCTTGTGGTGATTCACTGCGGGCTTATTTCCACTTTGTAATTCCAGCGAGTCGACTTCCCATCCTGAGTTGCAAGCCCCGCCAACACGGACTGGCGTTTCTCTCAGGCCCAGAGACCCGGCACCAGCGGCTCCCAAATGGCGATGACACCGGCACCTGGCCCAACAACCAAGTTTGACACAGAGATGCTGCAAGCCATGATCTTGGCGTCCGCCAGTGAAGCTGCTGATGGGAGCTCCACCCTGGGAGGGGTGCCGGCACCATGGGATTGAGCGCCCGCTACGGACCCAGTTTACCCTGCAGCACGTGCCCGACTACCGCCAGAATGTCTACATCCCAGGCAGCAATGCCACACTGACCAACGCAGCTGGCAAGCGGGATGGCAAGGCCCCAGCAGGTGGCAATGGCAACAAGAAGAAGTCGGGCAAGAAGGAGAAGAAG**TAA**CATGGAGGCCAGGCCAAGAGCCACAGGGCGGCCTCTCCCCAACAGCCAGCTTCTCCTTACCTGCACCCAGGCCTCAGAGTTTCAGGGCTAACCCCCAGAATACTGGTAGGGGCCAAGGCCATGCTCCCTTGGGAAACAGAAACAAGTGCCAGTTCAGCACCTACCCCTTCCCCCCCAGGGGTTGAATATGCAAAAGCAGTTCCGCTGGGAACCCCCATCCAATCACTGCTGTACCCATGGGGGTAGTGGGGTACTGTAGACACCAAGAACCATTGCCACACCCCGTTTAGTTACAGCTGAACCTCCTCCATCTTCCAATCAATCAGGCCCATCCATCCCATGCCTCCCTCCTCCCCACCCCACTCCAACAGTTCTCTTTCCCGAGTAAGGTGGTTGGGGTGTGAAGTACCAAGTAACCTACAAGCCTCCTAGTTCTGAAAAGTTGGAAGGGCATCATGACCTCTTGGCCTCTCCTTTGATTCTCAATCTTCCCCAAAGCATGGTTTGGTGCCAGCCCCTTACCTCCTTCCAGAGCCCCAAGATCAATGCTCAAGTTTTGGAGGACATGATCACCATCCCCATGGTACTGATGCTTGCTGGATTTAGGGAGGGCATTGCTACCAAGCCTCTTCCCAACGCCCTGGGGACCACTTCTGTTTTGTTTTTTCATTGTTTGACGTTTCCACTGCATGCCTTGACTTCCCCACCTCCTCCTCAAACAAGAGACTCCACTGCATGTCCAAGACAGTATGGGGTGGTAAGATAAGGAAGGGAAGTGTGTGGATGTGGATGGTGGGGGCATGGACAAAGCTT

1912/6881
FIGURE 1760B

GACACATCAAGTTATCAAGGCCTTGGAGGAGGCTCTGTATGTCCTCAGGGGACTGACAACATCCTCCAGATTCCA
GCCATAAACCAATAACTAGGCTGGACCCTTCCCACTACATAATAGGGCTCAGCCCAGGCAGCCAGCTTTGGGCTG
AGCTAACAGGACCAATGGATTAACTGGCATTTCAGTCCAAGGAAGCTCGAAGCAGGTTTAGGACCAGGTCCCCT
TGAGAGGTCAGAGGGGCCTCTGTGGGTGCTGGGTACTCCAGAGGTGCCACTGGTGGAAGGGTCAGCGGAGCCCCA
GCAGGAAGGGTGGGCCAGCCAGGCCATTCTTAGTCCCTGGGTTGGGGAGGCAGGGAGCTAGGGCAGGGACCAAAT
GAACAGAAAGTCTCAGCCCAGGATGGGGCTTCTTCAACAGGGCCCCCTGCCCTCCTGAAGCCTCAGTCCTTCACCT
TGCCAGGTGCCGTTTCTCTTCCGTGAAGGCCACTGCCCAGGTCCCCAGTGCGCCCCCTAGTGGCCATAGCCTGGT
TAAAGTTCCCCAGTGCCCTCCTTGTGCATAGACCTTCTTCTCCCACCCCCTTCTGCCCCTGGGTCCCCGGCCATCC
AGCGGGGCTGCCAGAGAACCCAGACCTGCCCTTACAGTAGTGTAGCGCCCCCTCCCTCTTTTCGGCTGGTGTAGA
ATAGCCAGTAGTGTAGTGCGGTGTGCTTTTACGTGATGGCGGGTGGGCAGCGGGCGGCGGGCTCCGCGCAGCCGT
CTGTCCTTGATCTGCCCCGCGCGGCCCGTGTGTGTTTTGTGCTGTGTCCACGCGCTAAGGCGACCCCCCTCCCC
GTACTGACTTCTCCTATAAGCGCTTCTCTTCGCATAGTCACGTAGCTCCCACCCACCCCTCTTCCTGTGTCTCAC
GCAAGTTTTTATACTCTAATATTTATATGGCTTTTTTTTCTTCGACAAAAAATAATAAACGTTTCTTCTGAAAAG
CTG

1913/6881
FIGURE 1761

MSGAGELGRAERLPVLFLLSLFCPALCEQIRYRIPEEMPKGSVVGNLATDLGFSVQELPTRKLRVSSEKPYF
TVSAESGELLVSSRLDREEICGKKPACALEFEAVAENPLNFYHVNVEIEDINDHTPKFTQNSFELQISESAQPGT
RFILEVAEDADIGLNSLQKYKLSLNPFSFLIIKEKQDGSKYPELALEKTLTREQQSYHRLVLTALDGGHPPLSGT
TELRIQVTDANDNPPVFNRDVYRVSLRENVPPGTTVLQVSATDQDEGINSEITYSFYRTGQIFSLNSKSGEITTQ
KKLDFEETKEYSMVVEGRDGGGLVAQCTVEINIQDENDNSPEVTFHSLLEMILENAVPGTLIALIKIHDQDSGEN
GEVNCQLQGEVPFKIISSSKNSYKLVTGTLTREQTPEYNVTITATDRGKPPPLSSSISVILHIRDVNDNAPVFHQ
ASYLVSVPENPPGASIAQVCASDLGLNGQVSYSIMASDLEPLALASYVSMSAQSGVVFAQRAFDYEQLRTFE
LTLQARDQGSPALSANVSLRVLVGDRNDNAPRVLYPALGPDGSALFDMVPRAAEPGYLVTKVVAVDADSGHNAWL
SYHVLQASEPGLFSLGLRTGEVRTARALGDRDAARQRLLVAVRDGGQPPLSATATLHLVFADSLQEVLPDITDRP
VPSDPQAELOFYLVVALALISVLFLLAVILAVALLRRLRSSSPAAWSCFQPGLCVKSGPVVPPNYSQGTLPYSYNL
CVAHTGKTEFNFLKCSEQLSSGQDILCGDSSGALFPLCNSSESTSHPELQAPPNTDWRFSQAQRPGTSGSQNGDD
TGTWPNNQFDTEMLQAMILASASEAADGSSTLGGGAGTMGLSARYGPQFTLQHVPDYRQNVYIPGSNATLTNAAG
KRDGKAPAGGNGNKKKSGKKEKK

1914/6881
FIGURE 1762A

ATGGGAGGGAGCTGCGCGCAGAGGCGCCGGGCGGCCGCGGCAGGTGCTATTTCCCTTTGCTGCTGCCTTTGTTC
TACCCACCCCTGAGTGAGCCGATCCGCTACTCGATTCCGGAGGAGCTGGCCAAGGGCTCGGTGGTGGGGAACCTC
GCTAAGGATCTAGGGCTCAGTGTCCTGGATGTGTGGCTCGCAAGCTGCGAGTGAGCGCGGAGAAAGCTGCACTTC
AGCGTAGACGCGGAGAGCGGGGACTTACTTGTGAAGAACCGAATAGACCGTGAGCAAATATGCAAAAGAGAGAAGA
AGATGTGAGTTGCAATTGGAAGCTGTGGTGGAAAAATCCTTTAAATATTTTTTCATGTCAATTGTGGTGATTGAGGAT
GTTAATGACCACGCCCCCTCAATTTGATAAAAAAGGAAATACATTTAGAAATTTTCGAATCTGCATCCGCTGGTACA
CGACTATCGCTTGACCCCTGCCACGGATCCTGATATAAAACATAAACTCAATTAAAGATTATAAGATAAACTCTAAT
CCTTATTTTTTCATTAAATGGTTAGAGTTAATTCCGATGGTGGCAAATACCCAGAGTTATCTCTGGAGAACTCCTA
GACCGGGAAGAACAGAGATCTCATAGCTTGATATTGACTGCCTTGGACGGAGGGGACCCACCAAGAAGTGCCACC
GCTCACATAGAAATTTCTGTCAAGGATACCAATGATAACCCCCCGGTTTTTCAGCAGAGACGAATATAGAATTAGT
CTTAGTGAAAATCTGCCCCCTGGGTCCCTGTGTTGCAAGTGACAGCCACTGACCAGGATGAGGGGGTCAATGCT
GAGATAAACTACTACTTCCGAAGCACTGCCCAGAGCACAAAACATATGTTCTCATTGGATGAGAAAACAGGTATG
ATTAAGAATAACCAGTCATTTGATTTTGAAGATGTAGAAAGGTACACCATGGAAGTGGAAGCGAAGGACGGAGGT
GGTCTCTCTACCCAGTGTAAGTAATCATAGAAATCCTTGATGAAAACGACAACAGCCCAGAAATAATCATCACT
TCTCTCTCTGATCAGATTTTGGAGAATTCACCTCCAGGAATGGTTGTTGCCCTCTTCAAAACACGGGATCTGGAT
TTCGGAGGAAATGGAGAAGTCAGGTGTÀATATAGAAACAGACATTCCATTCAAGATTTATTCTTCTTCCAATAAC
TACTACAACTGGTGACAGATGGAGCCCTGGACCGAGAGCAGACACCAGAATACAATGTCACCATCGTAGCCACT
GACAGGGGCAAGCCGCTCTTTCTTCCAGTAGAAGCATCACCTTGATGTGCTGACATCAACGACAACGCCCCA
GTTTTTCGACCAGACGTCCTACGTGGTCCACGTGGCCGAGAACAACCCGCCAGGAGCCTCCATTGCGCAAGTGAGC
GCCTCTGACCCGGATTGTTGGGGCTCAATGGCCACATCTCCTACTCTATAGTGGCGAGTGACCTAGAGCCCCCTGGCG
GTGTGCTCATACGTGTCAGTGAGCGCGCAGAGCGGGGTGGTGTTCGCGCAGCGCGCCTTTGATCACGAGCAGCTG
CGCGCCTTCGCGCTCACGCTGCAGGCCCGCGACCACGGCTCGCCACGCTCAGCGCCAACGTGAGCCTGCGCGTG
TTGGTGGGAGACCGCAATGACAACGCACCGCGGGTGCTGTACCCAGCTCTGGGTCTGACGGCTCCGCGTTCTTC
GATATGGTACCTCGC'CTGCGAGAGCCCGGCTACCTAGTGACTAAGGTGGTAGCGGTGGACGCCGACTCGGGACAC
AACGCCTGGCTGTCTTACCACGTGCTGCAGGCCAGTGAGCCCGGACTCTTCAGCCTGGGGCTGCGCACTGGGGAG
GTGCGCACGGCTCGAGCCTTAGGCGACAGGGACGCAGCCCGCCAGCGCCTGCTGGTCTGTGCGTGACGGTGGA
CAGCCGCCACTCTCTGCCACCGCCACGCTTCATCTGGTCTTCGCGAGACAACCTTGCAAGAGATACTGCCAGACCTC
AGCGACCGCCCTGTACTCTCTGACCCCCAGGCTGAACTGCAGTTTTACCTGGTGGTGGCCTTGGCCTTAATCTCA
GTGCTCTTCTCCTCGCCGTGATTCTGGCCATTGCCTTTCGCGCTGCGACGCTCTCTCAGCCCTGCTACTTGGGAC
TGCTTCCATCCTGGTCTCTGTGTCAAGTCTGGACCTGTAGTTCCCCCAACTACAGTGAGGGGACTTTGCCTTAT
TCTTATAATCTGTGCATTGCACATACGGGTACAAAAGAGTTTAATTTCCATAAATGCAGTGTGCCCTACATTCC
AATGAAGACATGGTTTGAGTGTCTCTCTGGAGCCTTAATCCACCTCATGGTGGGAGGATTGACTTCACAT
CCTGAGACTCTGACTTCGCAAGCCCCGCCAACACGGACTGGCGTTTCTCTCAGGCCAGAGACCCGGCACCAGC
GGCTCCCAAAATGGCGATGACACCGGCACCTGGCCCAACAACAGTTTGACACAGAGATGCTGCAAGCCATGATC
TTGGCGTCCGCCAGTGAAGCTGCTGATGGGAGCTCCACCCTGGGAGGGGTGCGGACCATGGGATTGAGCGCC
CGCTACGGACCCAGTTACCCCTGCAGCACGTGCCCCGACTACCGCCAGAATGTCTACATCCCAGGCAGCAATGCC
ACACTGACCAACGCAGCTGGCAAGCGGGATGGCAAGGCCCCAGCAGGTGGCAATGGCAACAAGAAGAAGTCGGGC
AAGAAGGAGAAGAAGTAAATCATGGAGGCCAGGCCAAGAGCCACAGGGCGGCCTCTCCCAACCAGCCAGCTTCTC
CTTACCTGCACCCAGGCCCTCAGAGTTTCAGGGCTAACCCCCAGAATACTGGTAGGGGCCAAGGCCATGCTCCCT
TGGGAAACAGAAACAAGTGCCAGTCAGCACCTACCCCTTCCCCCAGGGGGTTGAATATGCAAAAGCAGTTCC
GCTGGGAACCCCATCCAATCAACTGCTGTACCCATGGGGGTAGTGGGGTTACTGTAGACACCAAGAACCATTG
CCACACCCCGTTTAGTTACAGCTGAACTCCTCCATCTTCCAAATCAATCAGGCCATCCATCCCATGCCTCCCTC
CTCCCCACCCCACTCCAACAGTTCTCTTTCCCGAGTAAGGTGGTTGGGGTGTGAAAGTACCAAGTAACCTACAA
GCCTCCTAGTTCTGAAAAGTTGGAAGGGCATCATGACCTCTTGGCCTCTCCTTTGATTCTCAATCTTCCCCAAA
GCATGGTTTGGTGCCAGCCCCCTTACCTCCTTCCAGAGCCCCAAGATCAATGCTCAAGTTTTGGAGGACATGATCA
CCATCCCCATGGTACTGATGCTTGTGGATTTAGGGAGGGCATTTTGCTACCAAGCCTCTTCCCAACGCCCTGGG
GACCAGTCTTCTGTTTTGTTTTTCAATTGTTTGACGTTTCCACTGCATGCCTTGACTTCCCCACCTCCTCCTCAA
ACAAGAGACTCCACTGCATGTTCCAAGACAGTATGGGGTGGTAAGATAAGGAAGGAAGTGTGTGGATGTGGATG

1915/6881
FIGURE 1762B

GTGGGGGCATGGACAAAGCTTGACACATCAAGTTATCAAGGCCTTGGAGGAGGCTCTGTATGTCCTCAGGGGACT
GACAACATCCTCCAGATTCCAGCCATAAACCAATAACTAGGCTGGACCCTTCCCACTACATAATAGGGCTCAGCC
CAGGCAGCCAGCTTTGGGCTGAGCTAACAGGACCAATGGATTAAACTGGCATTTCAGTCCAAGGAAGCTCGAAGC
AGGTTTAGGACCAGGTCCCCTTGAGAGGTGAGAGGGGCTCTGTGGGTGCTGGGTACTCCAGAGGTGCCACTGGT
GGAAGGGTCAGCGGAGCCCCAGCAGGAAGGGTGGGCCAGCCAGGCCATTCTTAGTCCCTGGGTGGGGAGGCAGG
GAGCTAGGGCAGGGACCAAATGAACAGAAAGTCTCAGCCCAGGATGGGGCTTCTTCAACAGGGCCCCCTGCCCTCC
TGAAGCCTCAGTCCTTCACCTTGCCAGGTGCCGTTTCTCTTCCGTGAAGGCCACTGCCCAGGTCCCCAGTGCGCC
CCCTAGTGGCCATAGCCTGGTTAAAGTTCCCCAGTGCCTCCTTGTGCATAGACCTTCTTCTCCCACCCCTTCTG
CCCCTGGGTCCCCGGCCATCCAGCGGGGCTGCCAGAGAACCCCAGACCTGCCCTTACAGTAGTGTAGCGCCCCCT
CCCTCTTTCGGCTGGTGTAGAAATAGCCAGTAGTGTAGTGCAGGTGTGCTTTTACGTGATGGCGGGTGGGCAGCGGG
CGGCGGGCTCCGCGCAGCCGCTGTCTTGTATCTGCCCAGCGCGGCCCCGTGTTGTGTTTTGTGCTGTGTCCACGC
GCTAAGGCGACCCCTCCCCCGTACTGACTTCTCTATAAGCGTTCTCTTCGCATAGTCACGTAGCTCCCACCC
CACCCTCTTCTGTGTCTCACGCAAGTTTTATACTCTAATATTTATATGGCTTTTTTCTTCGACAAAAAATAA
TAAAACGTTTCTTCTGAAAAGCTG

1916/6881
FIGURE 1763

MGGSCAQRRRAGPRQVLFPLLLPLFYPTLSEPIRYSIPEELAKGSVVGNLAKDLGLSVLDVSARKLRVSAEKLHF
SVDAESGDLLVKNRIDREQICKERRRCELQLEAVVENPLNIFHVIVVIEDVNDHAPQFDKKEIHLEIFESASAGT
RLSLDPATDPDININSIKDYKINSNPYFSLMVRVNSDGGKYPELSLEKLLDREEQRSHSLILTALDGGDPPRSAT
AHIEISVKDTNDNPPVFSRDEYRISLSENLPFGSPVLQVTATDQDEGVNAEINYYFRSTAQSTKHMFSLDEKTGM
IKNNQSFD FEDVERYTMEVEAKDGGGLSTQCKVIEILDENDNSPEIIITSLSDQILENSPFGMVVALFKTRDLD
FGNGEVRNCNIETDIPFKIYSSSNYYKLVTGDALDREQTPEYNVTIVATDRGKPPPLSSSRISITLYVADINDNAP
VFDQTSYVVHVAENNPPGASIAQVSASDEPDLGLNGHISYSIVASDLEPLAVSSYVSVSAQSGVVFQAQRAFDHEQL
RAFALTLQARDHGSPTLSANVSLRVLVGDRNDNAPRVLYPALGPDGSAFFDMVPRSAEPGYLVTKVVAVDADSGH
NAWLSYHVLQASEPGLFSLGLRTGEVRTARALGDRDAARQRLLVAVRDGGQPPLSATATLHLVFADNLQEILPDL
SDRPVLSDFQAELOFYLVVALALISVLFLLAVILAIALRLRRSLSPATWDCFHPGLCVKSGFVPPNYSEGTLPY
SYNLCIAHTGTKEFNFLKCSVPLHSNEDMVC SVSPGALIPPHGGEDLTSHPETLTSQAPPNTDWRF SQAQRPGTS
GSQNGDDTGTWPNNQFDTEMLQAMILASASEAADGSSTLGGGAGTMGLSARYGPQFTLQHVPDYRQNVYIPGSNA
TLTNAAGKRDGKAPAGGNGNKKKSGKKEKK

1917/6881
FIGURE 1764A

GCTGCGCAGACCTTGCCAGCACACCAGATTGCCAGCTCCGAGACCCGGGACTCCTCCTGTCTGGGCCGAATGC
TCTTTTAGCGCGGTAGAGTGCACCTTTCTCCAAGTGGAAAAGCGGGGACCCAGCGAGAACCCGAGCGAACGATGGG
AGGGAGCTGCGCGCAGAGGCGCCGGGCCGGCCCGCGGCAGGTACTATTTCTTTGCTGTCTGCCTTTGTTCTACCC
CACGCTGTGTGAGCCGATCCGCTACTCGATTCCGGAGGAGCTGGCCAAGGGCTCGGTGGTGGGGAACCTCGCTAA
GGATCTAGGGCTTAGTGTCTGGATGTGTCTGGCTCGCGAGCTGCGAGTGAGCGCGGAGAAGCTGCACCTTCAGCGT
AGACGCGCAGAGCGGGGACTTACTTGTGAAGGACCGAATAGACCGTGAGCAAATATGCAAAGAGAGAAGAAGATG
TGAGTTGCAATTGGAAGCTGTGGTGGAAAATCCTTTAAATATTTTTCATGTCAATTGTGGTGAATTGAGGATGTTAA
TGACCACGCCCCCTCAATTCCGGAAGATGAAATAAACTTAGAAATCAGTGAATCCGTCAGCCTGGGGATGGGAAC
AATTCTTGAGTCTGCAGAAGATCCTGATATTAGTATGAATTCGCTGAGCAAATACCAACTAAGTCCTAACGAGTA
TTTCTCATTGGTGGAGAAAGACAATCCTGATGGTGGCAAATATCCAGAATTAGTATTGCAGAAGACTCTGGACCG
AGAAACGCAGAGCGCTCACCACCTGGTACTGACCGCCTTAGATGGTGGGGACCCTCCCCGAAGCGGTACTGCTCA
GATAAGAATCCTGGTAATAGATGCCAATGACAACCCCCCAGTGTTTCAGCCAGGACGTGTACAGGGTTAGCCTTCG
GGAAGACGTGCCTCCAGGCACCTCCATCCTGAGAGTGAAGGCCACTGACCAGGACGAGGGGCATCAACTCAGAGAT
CACTTATTCTCTTTGGTGTGGCTGACAAAGCTCAGCACGTGTTCTCTCTGGATTACACTACAGGAAACATTCT
AACTCAGCAGCCTTTGGATTTTGAAGAAGTAGAAAGATATACGATAAACATAGAAGCAAAGACCGAGGATCTCT
CTCAACACGGTGTAAGTAATTGTAGAAGTTGTAGACGAAAACGACAACAGCCCAGAAATAATCATCAGTCACT
CTCTGATCAGATTATGGAGGATTCCCCTCCAGGAGTGGTTGTTGCCCTCTTCAAACACGGGACCAAGACTCAGG
GGAAAATGGGGAAGTCAGGTGTAGCTTAAGTAGAGGTGTTCCATTTAAGATTCAATTCTTCTTAATAATTACTA
CAAGCTAGTAACAGATGAGGCCCTGGATCGGGAGCAGACCCAGAGTACAACGTCAACATCGCAGCCACAGACAG
GGGCAAGCCTCCGTTATCCTCCAGCAAAACCATAACCCTGCACATTACTGACGTCAATGACAACGCGCCGGTTTT
CGGACAGTCAGCCTACCTGGTCCACGTGCCAGAAAACAACCAGCCGGGTGCCTCCATAGCGCAAGTCAGTGCCTC
TGACCCAGACTTCGGGCTCAACGGCCGTGTCTCCTACTCTCTCATTGCCAGCGACCTGGAGTCACGAACGCTGTC
GTCCTACGTGTCCGTGAGCGCGCAGAGCGGGGTGGTGTTCGCGCAGCGCGCCTTCGACCACGAGCAGCTGCGCAC
CTTCGAGCTCAGCTGCAGGCCCGCGACCAGGGCTCGCCCGCGCTCAGCGCCAATGTGAGCCTGCGCGTGTGGT
GGGCGACCGTAACGACAACGCACCGCGGGTGTGTACCCTGCGCTGGGTCCCGACGGCTCCGCGCTCTTCGACAC
AGTGCCGCGGGCCGCGCAGCCAGGCTACCTGGTGACCAAGGTGGTGGCCGTGGACGCGGACTCGGGGCACAATGC
CTGGCTGTCTACACGTGGTGCAGGCCAGTGAGCCCGGGCTCTTCAGCCTGGGGCTGCGAACAGGCGAGGTGCG
CATGGTGCCTGCTTTGGGTGACAAGGACTCGGTCCGCCAGCGCCTGCTAGTCGCTGTAAGAGATGGAGGACAGCC
ACCCCTTTTCAGCCACTGCCACGCTGCACCTGGTGTTCGAGATAGCTTGCAAGAGGTACTGCCGATTTTCAGCGA
CCATCCACACCCCTCTGACTCCCAGGCTGAGATGCAGTTTTACCTGGTGGTGGCCTTGCCCTTGATTTCTGTGCT
CTTCTCCTCGCGGTGATTCTAGCTATTGCTCTACGCCTGCGACAGTCTTTCAGCCCTACTGCAGGAGACTGCTT
TGAGTCAGTTCTCTGCTCCAAGTCCGGACCTGTGGGTCCCCCAACTACAGTGAGGGAACGTTGCCCTATGCCTA
TAATTTTTGTGTGCTGGGGATCAAATGAATCCAGAATTTAATTTTTTTCACATCTGTTGATCATTGTCCAGCCAC
ACAAGATAACCTCAACAAAGATAGCATGCTACTGGCTAGCATTTTAACTCCCAGCGTTGAAGCAGATAAGAAGAT
TCTTAAACAGCAAGCCCCGCCAACACGACTGGCGTTTCTCTCAGGCCCAGAGACCCGGCACCAGCGGCTCCCA
AAATGGCGATGACACCGGCACCTGGCCCAACAACAGTTTGACACAGAGATGCTGCAAGCCATGATCTTGGCGTC
CGCCAGTGAAGCTGCTGATGGGAGCTCCACCCTGGGAGGGGTGCCGGCACCATGGGATTGAGCGCCCGCTACGG
ACCCAGTTACCCCTGCAGCAGTGCCCGACTACCGCCAGAATGTCTACATCCAGGCAGCAATGCCACACTGAC
CAACGCAGCTGGCAAGCGGGATGGCAAGGCCCCAGCAGGTGGCAATGGCAACAAGAAGAAGTCGGGCAAGAAGGA
GAAGAAGTAACATGGAGGCCAGGCCAAGAGCCACAGGGCGGCCTCTCCCCAACCCAGCCAGCTTCTCCTTACCTG
CACCCAGGCCTCAGAGTTTTCAGGGCTAACCCCCAGAATACTGGTAGGGGCCAAGGCCATGCTCCCTTGGGAAAC
AGAAACAAGTGCCAGTCAGCACCTACCCCTTCCCCCCCAGGGGGTTGAATATGCAAAAGCAGTTCCGCTGGGAA
CCCCATCCAATCAACTGCTGTACCCATGGGGGTAGTGGGGTACTGTAGACACCAAGAACCATTGCCACACCC
CGTTTAGTTACAGCTGAACTCCTCCATCTTCCAAATCAATCAGGCCATCCATCCCATGCTCCCTCCTCCCCAC
CCCACTCCAACAGTTCTCTTTCCCGAGTAAGGTGGTGGGGTGTGAAAGTACCAAGTAACCTACAAGCCTCCTA
GTTCTGAAAAGTTGGAAGGGCATCATGACCTCTTGGCCTCTCCTTTGATTCTCAATCTTCCCCCAAAGCATGGTT
TGGTGCCAGCCCCTTACCTCCTTCCAGAGCCCAAGATCAATGCTCAAGTTTTGGAGGACATGATCACCATCCCC
ATGGTACTGATGCTTGCTGGATTTAGGGAGGGCATTTTGCTACCAAGCCTCTTCCCAACGCCCTGGGGACCAGTC

1918/6881
FIGURE 1764B

TTCTGTTTTGTTTTTCATTGTTTGACGTTTCCACTGCATGCCTTGACTTCCCCCACCTCCTCCTCAAACAAGAGA
CTCCACTGCATGTTCCAAGACAGTATGGGGTGGTAAGATAAGGAAGGGAAGTGTGTGGATGTGGATGGTGGGGGC
ATGGACAAAGCTTGACACATCAAGTTATCAAGGCCTTGGAGGAGGCTCTGTATGTCCTCAGGGGACTGACAACAT
CCTCCAGATTCCAGCCATAAACCAATAACTAGGCTGGACCCCTTCCCACTACATAATAGGGCTCAGCCCAGGCAGC
CAGCTTTGGGCTGAGCTAACAGGACCAATGGATTAAACTGGCATTTCAGTCCAAGGAAGCTCGAAGCAGGTTTAG
GACCAGGTCCCCCTTGAGAGGTGAGAGGGGCTCTGTGGGTGCTGGGTACTCCAGAGGTGCCACTGGTGGGAAGGGT
CAGCGGAGCCCCAGCAGGAAGGGTGGGCCAGCCAGGCCATTCTTAGTCCCTGGGTGGGGAGGCAGGGAGCTAGG
GCAGGGACCAAAATGAACAGAAAGTCTCAGCCCAGGATGGGGCTTCTTCAACAGGGCCCCCTGCCCTCCTGAAGCCT
CAGTCCTTTCACCTTGCCAGGTGCCGTTTTCTCTTCCGTGAAGGCCACTGCCAGGTCCCCAGTGCGCCCCCTAGTG
GCCATAGCCTGGTTAAAGTTCCCCAGTGCCTCCTTGTGCATAGACCTTCTTCTCCCACCCCTTCTGCCCTGGG
TCCCCGGCCATCCAGCGGGGCTGCCAGAGAACCCCAGACCTGCCCTTACAGTAGTGTAGCGCCCCCTCCCTCTTT
CGGCTGGTGTAGAAATAGCCAGTAGTGTAGTGCAGGTGTGCTTTTACGTGATGGCGGGTGGGCAGCGGGCGGCGGGC
TCCGCGCAGCCGTCTGTCCTTGATCTGCCCGCGGCGGCCCCGTGTTGTGTTTTGTGCTGTGTCCACGCGCTAAGGC
GACCCCTCCCCGTACTGACTTCTCCTATAAGCGCTTCTCTTCGCATAGTCACGTAGCTCCCACCCACCCCTCT
TCCTGTGTCTCACGCAAGTTTTATACTCTAATATTTATATGGCTTTTTTTCTTCGACAAAAAATAATAAACGT
TTCTTCTGAAAAGCTG

1919/6881
FIGURE 1765

MGGSCAQRRRAGPRQVLFP LLLPLFYPTLCEPIRYSIPEELAKGSVVG NLA KDLGLSVLDVSARELRVSAEKLHF
SVDAQSGDLLVKDRIDREQICKERRRCELQLEAVVENPLNIFHVIVVIEDVNDHAPQFRKDEINLEISESVSLGM
GTILES AEDPDISMNSLSKYQLSPNEYFSLVEKDNPDGGKYPELV LQKTL DRETQSAHHLVLTALDGGDPPRS GT
AQIRILVIDANDNPPVFSQDVYRVSLREDVPPGTSILRVKATDQDEGINSEITYSFFGVADKAQHVFSLDYTTGN
ILTQQPLDFEEVERYTINIEAKDRGSLSTRCKVIVEVVDENDNSPEIIITSLS DQIMEDSPPGVVVALFKTRDQD
SGENGEVRCSLSRGVPFKIHSSSNYYKLV TDEALDREQTPEYNVTIAATDRGKPPLSSSKTITLHITDVNDNAP
VFGQSAYLVHVPENNQPGASIAQVSASDPDFGLNGRVSYSLIASDLESRTLSSYVSVSAQSGVVFAQRAFDHEQL
RTFELTLQARDQGSPALSANVSLRVLVGDRNDNAPRVLYPALGPDGSALFDTVPRAAQP GYLVTKVVAVDADSGH
NAWLSYHV VQASEPGLFSLGLRTGEVRMVRALGDKDSVRQRLLVAVRDGGQPPLSATATLHLVFADSLQEVLPDF
SDHPTPSDSQAEMQFYLVVALALISVLFL LAVILAIALRLRQSFSPTAGDCFESVLC SKSGPVGPPNYSEGTLPY
AYNFCVPGDQMNPEFNFFTSVDHCPATQDNLNKDSMLLASILTPSVEADKKILKQQAPPNTDWRFSQAQRPGTSG
SQNGDDTGTWPNNQFDTEMLQAMILASASEAADGSSTLGGGAGTMGLSARYGFQFTLQHVPDYRQNVYIPGSNAT
LTNAAGKRDGKAPAGGNGNKKKSGKKEKK

1920/6881
FIGURE 1766A

ATGCTCCGCAAGGTGAGAAGCTGGACAGAAATCTGGCGGTGGGCTACCCTTTTGTTCCTCTTTTACCACCTGGGT
TACGTTTGTGGGCAGATCCGCTACCCGGTCCCAGAGGAGTCACAGGAAGGGACTTTTGTAGGGAATGTCGCTCAA
GATTTCTGCTGGATACGGACAGTCTGTGAGCTCGCAGGCTGCAGGTCGCTGGAGAGGTGAACCAAAGACACTTC
CGTGTGGATTTGGACAGCGGAGCCCTGCTCATCAAGAACCCAATCGACCGAGAGGCACTGTGTGGGCTCAGTGCC
AGCTGCATCGTGCCCTGGAGTTTGTACCGAAGGTCCTTTGGAAATGTACCGAGCAGAGGTAGAGATCGTAGAT
GTGAATGATCACGCCCCCGTTTTCCGCGGCAGCAGCTGGACTTGGAAATTGGGGAGGCAGCTCCTCCAGGACAG
CGTTTCCCGTTGGAAAAGGCTCAGGATGCAGATGTGGGGAGCAATTTCGATTAGCAGCTATAGGCTGAGCTCCAAT
GAACACTTTGCACTGGATGTGAAGAAGCGCAGCGACGGCAGCCTGGTCCCAGAGCTGCTCCTGGAGAAGCCTTTG
GATCGAGAGAAGCAATCGGACTACCGCCTGGTGCTGACTGCTGTGATGGAGGGAACCCGCCGAGATCTGGCACC
GCAGAGCTCCGGGTATCCGTGCTGGACGTAAACGACAACGCCCCAGCCTTCCAGCAATCCAGCTACAGGATTAGT
GTGTTGGAGAGCGCACCAGCGGGCATGGTGCTCATCCAGCTCAATGCCTCAGACCCGGACCTGGGTCCCAGTGGT
AACGTCACCTTTTATTTTCACTGGTTCATACCCCTGATCGTGTAAGAAAACCTCTTTAGCCTGCACCCCACTACTGGA
AAGCTTACTCTTTTGGGGCCCCCTAGACTTTGAGAGTGAGAATTACTATGAATTTGATGTGCGGGCTCGCGATGGG
GGTCTCCAGCCATGGAGCAACATTGCAGCCTTCGAGTGGATCTGCTGGACGTAAATGACAATGCCCCTTACATC
ACAGTGACCTCAGAGCTTGGAACCTCCCCGAGAGTGAGAACCTGGCACTGTGGTGGCACTTATCAGTGTGCAG
GATCCAGACTCAGGGTCAAACGGAGATGTGAGCCTCCGCATTCTTGACCATTGCCATTTGCCCTCAAGTCTGCC
TTCAGGAACCAAGTTCTCCCTGGTGACTGCTGGACCCTTGATCGAGAGGCCAAATCTAGCTATGACATCATGGTC
ACTGCTTCTGATGCTGGGAACCTCCTCTCAGTACCCACAGAACTATTTTCTCAATATTTTCACTGTGAATGAT
AATCCACCCTCTTTCTTTTCAAGGTCACATGAGGTGTTTGTTCCTGAGAACAATCGCCAGGGGACCTGCTTTGC
TCCCTTGACGCTCTGACCCAGACTCTGGCTTGAATGCGCTTATCTCTACTCACTCCTGGAGCCCAGGAATCGA
GATGTATCAGCTTCTCTTTTCTCTCTGAACCCCCAGACAGGAGCTGTTTATGCTACTCGATCCTTTGACTAT
GAGCAAACCCAGACACTGCAGTTTGGGTGCAGGCCCGGGATCGGGGCAACCCACCCCTTAGCAGCACTGTAACA
GTTTCGTCTATTTGTGCTGGACCTCAATGACAATGCTCCAGCTGTGCTCCGTCCTCGGGCCCGGCTGGTTCTTA
TGTCCCCAAGCACTGCCTCCATCAGTTGGTGCTGGCCACCTAATCACAAGGTGACTGCTGTGGACTTGGATTCA
GGTTACAATGCTTGGGTTTCTTATCAGCTCCTGGAGGCCCCAGATCCCAGCCTGTTTGCAGTCTCTCGATATGCT
GGGGAGGTGCGGACGGCTGTTCTTATCCCAGCTGACCTCCCACCACAGAAGCTGGTCATTGTGGTAAAGGATAGT
GGTAGTCCACCACTCTCTACCTCTGTTACTCTCTTAGTGCTCTTAGAGGAAGACACTCATCCAGTTGTCCAGAT
CTTCGAGAATCTTCAGCTCCAAGGAAGGAGAATCTCGTCTAACCTCTACTTGGCTGTGTCCCTAGTGGCAATT
TGCTTTGTCTCCTTTGGCTCATTCTGTGGCACTACTCTCTAAGTGTCTTCGTGGGGCAGCCTGTGGAGTCACATGC
TTTCTGCTGGCACCTGTGCTGTCTCACCAGATCTCGAAGGAGGGAGGGGCTTCCCCCTTCCAATGGGATCCTC
CGAATCCAGCTAGGGTCAGATGACCTATCAAGTTTGTGATGTGGGAGGCCACTCTCATGGCTGTACACCTTG
GCTTCTGCACCCACTCGGAGTGATAGCTTCATGATGGTGAAGTCACCCAGTGACCTATGGCAGGGGAGCCTGTT
CGCCCAAGCTGCCCACCTCTGATCTTCTCTATGGGCTAGAGCAAGCCCCGCCCAACACGGACTGGCGTTTCTCT
CAGGCCCAGAGACCCGGCACCAGCGGCTCCCAAAATGGCGATGACACCGGCACCTGGCCCAACAACAGTTTGAC
ACAGAGATGCTGCAAGCCATGATCTTGGCGTCCGCCAGTGAAGCTGCTGATGGGAGCTCCACCTGGGAGGGGGT
GCCGGCACCATGGGATTGAGCGCCCGCTACGGACCCAGTTACCCCTGCAGCACGTGCCCGACTACCGCCAGAAT
GTCTACATCCCAGGCAGCAATGCCACACTGACCAACGCAGCTGGCAAGCGGGATGGCAAGGCCCCAGCAGGTGGC
AATGGCAACAAGAAGAAGTCGGGCAAGAAGGAGAAGAAGTAACATGGAGGCCAGGCCAAGAGCCACAGGGCGGCC
TCTCCCCAACCAGCCCAGCTTCTCCTTACCTGCACCCAGGCCTCAGAGTTTCAGGGCTAACCCCCAGAATACTGG
TAGGGGCCAAGGCCATGCTCCCCTTGGGAAACAGAAACAAGTGCCAGTCAGCACCTACCCCTTCCCCCCCAGGG
GGTTGAATATGCAAAAGCAGTTCCGCTGGGAACCCCATCCAATCAACTGCTGTACCCATGGGGGTAGTGGGGTT
ACTGTAGACACCAAGAACCATTGCCACACCCCGTTTAGTTACAGCTGAATCCTCCATCTTCCAAATCAATCAG
GCCATCCATCCATGCTCCTCCTCCTCCCCACCCCACTCCAACAGTTCCTCTTTCCCGAGTAAGGTGGTTGGGGT
GTTGAAGTACCAAGTAACCTACAAGCCTCCTAGTTCTGAAAAGTTGGAAGGGCATCATGACCTCTTGGCCTCTCC
TTTGATTCTCAATCTTCCCCAAAGCATGGTTTGGTGCCAGCCCTTCACCTCCTTCCAGAGCCCAAGATCAATG
CTCAAGTTTGGAGGACATGATCACCATCCCCATGGTACTGATGCTTGTGGATTAGGGAGGGCATTTTGTCTAC
CAAGCCTCTTCCCAACGCCCTGGGGACCAGTCTTCTGTTTTGTTTTTCATTGTTTGACGTTTCCACTGCATGCTT
TGACTTCCCCACCTCCTCCTCAAACAAGAGACTCCACTGCATGTTCCAAGACAGTATGGGGTGGTAAGATAAGG

1921/6881
FIGURE 1766B

AAGGGAAGTGTGTGGATGTGGATGGTGGGGGCATGGACAAAGCTTGACACATCAAGTTATCAAGGCCTTGGAGGA
GGCTCTGTATGTCCTCAGGGGACTGACAACATCCTCCAGATTCCAGCCATAAACCAATAACTAGGCTGGACCCTT
CCCACTACATAATAGGGCTCAGCCCAGGCAGCCAGCTTTGGGCTGAGCTAACAGGACCAATGGATTAAACTGGCA
TTTCAGTCCAAGGAAGCTCGAAGCAGGTTTAGGACCAGGTCCCCTTGAGAGGTGAGAGGGGCTCTGTGGGTGCT
GGGTACTCCAGAGGTGCCACTGGTGGAAGGGTCAGCGGAGCCCCAGCAGGAAGGGTGGGCCAGCCAGGCCATTCT
TAGTCCCTGGGTGAGGGAGGCAGGGAGCTAGGGCAGGGACCAAATGAACAGAAAGTCTCAGCCCAGGATGGGGCT
TCTTCAACAGGGCCCCCTGCCCTCCTGAAGCCTCAGTCCTTACCTTGCCAGGTGCCGTTTCTCTTCCGTGAAGGC
CACTGCCCAGGTCCCCAGTGCGCCCCCTAGTGGCCATAGCCTGGTTAAAGTTCCCCAGTGCCTCCTTGTGCATAG
ACCTTCTTCTCCCACCCCCTTCTGCCCCTGGGTCCCCGGCCATCCAGCGGGGCTGCCAGAGAACCCAGACCTGC
CCTTACAGTAGTGTAGCGCCCCCTCCCTCTTTGGGCTGGTGTAGAATAGCCAGTAGTGTAGTGCAGGTGTGCTTTT
ACGTGATGGCGGGTGGGCAGCGGGCGGGCTCCGCGCAGCCGTCTGTCCTTGATCTGCCCAGCGGGCGGCCGTG
TTGTGTTTTGTGCTGTGTCCACGCGCTAAGGCGACCCCTCCCCGTACTGACTTCTCCTATAAGCGCTTCTCTT
CGCATAGTCACGTAGCTCCCACCCCACCTCTTCTGTGTCTCAGCAAGTTTTATACTCTAATATTTATATGGC
TTTTTTTCTTCGACAAAAAATAATAAACGTTTCTTCTGAAAAGCTG

1922/6881
FIGURE 1767

MLRKVRSWTEIWRWATLLFLFYHLGYVCGQIRYPVPEESQEGTFVGNVAQDFLLDTSLSARRLQVAGEVNQRHF
RVDLD SGALLIKNPIDREALCGLSASCIVPLEFVTEGPLEMYRAEVEIVDVNDHAPRFPRQQLDLEIGEAAPPGQ
RFPLEKAQDADVGSNSISSYRLSSNEHFALDVKKRSDGSLVPELLLEKPLDREKQSDYRLVLTAVDGGNPPRSGT
AELRVSVLDVNDNAPAFQSSYRISVLESAPAGMVLIQLNASDPDLGPGSNVTIFYFSGHTPDRVRNLFSLHPTTG
KLTL LGPLDFESENYEFDVRARDGGSPAMEQHCSLRVDLLDVNDNAPYITVTSELGTLPESAEPGTVVALISVQ
DPDSGSNGDVSLRIPDHLFPALKSAFRNQFSLVTAGPLDREAKSSYDIMVTASDAGNPPLSTHRTIFLNISDVND
NPPSFFQRSHEVFVPENNRPGDLLCSLAASDPDSGLNALISYSLLEPRNRDVSASSFISLNPQTGAVHATRSFDY
EQTQTLQFEVQARDRGNPPLSSTVTVRLFVLDLNDNAPAVLRPRARPGSLCPQALPPSVGAGHLITKVTAVDLDLDS
GYNAWVS YQLLEAPDPSLFAVSRYAGEVRTAVP IPADLPPQKLVIIVVKDSGSPPLSTSVTLLVSLEEDTHPVVPD
LRESSAPREGESRLTLYLAVSLVAICFVSFGSFVALLSKCLRGAACGVTCFPAGTCACLTRSRREGLPPSNGIL
RIQLGSDDPIKEFVDVGGHSHGCTPLASAPTRSDSFMMVKSPSAPMAGEPVRPSCPPSDLLYGLEQAPPNTDWRFS
QAQRPGTSGSQNGDDTGTWPNNQFDTEMLQAMILASASEAADGSSTLGGGAGTMGLSARYGPQFTLQHVPDYRQN
VYIPGSNATLTNAAGKRDGKAPAGGNGNKKKSGKKEKK

1923/6881
FIGURE 1768A

ATGGGGGCCCAAGACACTCCCACAGCTCGCTGGGAAATGGCAAGTGCTGTGCATGTTGTCCTTGTGCTGCTGGGGC
TGGGTGTCTGGGCAGCTTCGTTACTCAGTGGTGGAGGAGTCTGAGCCGGGGACGCTGGTGGGGAATGTTGCTCAG
GATCTGGGCTTAAAGATGACAGATCTGTTGAGCCGGCGGCTGCAATTGGGCTCTGAGGAGAATGGGCGCTATTTT
TCCCTGAGCTTGATGAGTGGTGCCCTGGCAGTGAATCAAAAGATTGACCGAGAAAGCCTATGTGGAGCCAGCACC
AGCTGCCTGCTGCCAGTGCAGGTGGTGACTGAACACCCCTGGAGCTAATCCGTGTAGAGGTAGAGATCCTGGAT
CTCAATGACAACTCTCCTAGCTTTGCCACCCCTGAGCGAGAGATGCGCATCTCAGAATCAGCAGCATCTGGGGCA
CGATTCCCAGTGGACAGTGGCCAGGATCCGGATGTGGGCACCAATACTGTGAGCTTTTACACTCTAAGCCCCAAC
AGCCACTTCTCTCTGAATGTGAAGACCCATAAAGATGGGAAGCCATTCCCAGAGCTGGTGCTAGAGCAGCAGCTG
GATCGTGAAGCCCAGGCAAGACATCAGCTGGTGCTTACTGCTGTGGATGGGGGGACCCAGCCCGCTCAGGGACC
ACCCTTATCTCTGTCTATCGTGCTGGACATCAATGATAATGCTCCAACCTTCCAATCCTCAGTTCTACGTGTGGGA
ATCCCAGAGAATGCACCCATTGGTACTCTGCTGCTCCGCCTCAATGCCACTGATCCAGACGAGGGCACCAACGGC
CAACTAGACTATTCTTTTGGAGACCACACATCTGAGGCAGTGCGGAACCTCTTTGGCCTAGACCCTAGCAGTGGG
GCAATCCATGTTGTTGGGTCCCATAGACTTTGAGGAGTCACGTTTCTATGAAATTCATGCAAGAGCCCGTGACCAG
GGACAGCCTGCCATGGAGGGCCACTGTGTGATTCAAGTGGATGTGGGGGATGTCAATGACAATGCCCCAGAGGTG
CTATTGGCCTCTTTGGCCAACCCCTGTCTTAGAGAGCACACCAGTGGGCACAGTAGTGGGGTTGTTTAATGTGCGA
GACCGGGACTCAGGTAGAAATGGTGAAGTGAAGCTTATCTCTCCGGACCTGCCATTTAGATTAAAGCCTTCT
GAGAACCCTACTCGCTGCTAACCAGCCAGCCTTTGGACCGGGAGGCCACATCCCCTATATCATCGAGCTGCTG
GCCAGCGATGCTGGTTACCTTCCCTACACAAACATCTCACCATCAGGCTCAACATTTAGATGTCAATGACAAT
GCACCCCGCTTCAACCAGCAGCTTTACACTGCTTACATCCTAGAAAACCGGCCTCCGGGCTCCCTTCTTTGCACT
GTGGCTGCCTCAGATCCAGACACTGGGGATAATGCCCGCCTCACCCTACTCCATTGTAGGAAATCAGGTTTCAGGGA
GCCCCAGCCTCCTCCTTTGTGTATGTCAACCCAGAGGATGGACGGATCTTTGCCAGCGTACCTTTGACTATGAA
TTGCTGCAGATGCTGCAGATTGTGGTGGGGGTTGAGACTCCGGCTCTCCCCATTGCATGCCAACACATCTCTG
CATGTGTTTGTCTAGACGAGAATGATAATGCCCCAGCTGTGCTGCACCCACGGCCAGACTGGGAACACTCAGCC
CCCCAGCGTCTCCCTCGCTCTGCTCCTCCTGGCTCCTTGGTACCAAGGTGACAGCCGTGGATGCTGATGCAGGC
CACAATGCGTGGCTCTCCTACTCACTGTTGCCACAGTCCACAGCCCCAGGACTGTTCTCTGTCTACACACACT
GGTGAGGTGCGCACAGCCCGGGCCTTACTGGAGGATGACTCTGACACCCAGCAGGTGGTGGTCTGGTGGAGGAC
AATGGTGACCCCTTCACTCTCCTCCACAGCCACAGTGTGCTGGTTCTGGAGGATGAGGACCCTGAGGAAATGCCC
AAATCCAGTGACTTCTCATAACCCCTCTGAGCGTTAGACCTTACCCTTTACCTCATTGTGGCTCTAGCGACC
GTCAGTCTCTTATCCCTAGTCACCTTCACCTTTCTGTGAGCGAAGTGCTTCAGGGAAACGCAGACGGGGACGGG
GGTGGAGGGCAGTGCTGCAGGCGCCAGGACTCACCTTCCCGGACTTCTATAAGCAGTCCAGCCCCAACCTGCAG
GTGAGCTCGGACGGCACGCTCAAGTACATGGAGGTGACGCTGCGGGCCACAGACTCGCAGAGCCACTGCTACAGG
ACGTGCTTTTACC GGCCCTCGGACGGCAGTGACTTCACTTTTCTAAGACCCCTCAGCGTTCAGCAGCCACAGCT
CTGGCGCTGGAGCCTGACGCCATCCGGTCCCGCTCTAATACGCTGCGGGAGCGGAGCCAGCAAGCCCCGCCAAC
ACGGACTGGCGTTTCTCTCAGGCCAGAGACCCGGCACAGCGGCTCCCAAAATGGCGATGACACCGGCACCTGG
CCCAACAACCAGTTTGACACAGAGATGCTGCAAGCCATGATCTTGGCGTCCGCCAGTGAAGCTGCTGATGGGAGC
TCCACCCTGGGAGGGGGTGGCGGCACCATGGGATTGAGCGCCCGCTACGGACCCAGTTACCCTGCAGCACGTG
CCCGACTACCGCCAGAATGTCTACATCCCAGGCAGCAATGCCACACTGACCAACGCAGCTGGCAAGCGGGATGGC
AAGGCCCCAGCAGGTGGCAATGGCAACAAGAAGAAGTCGGGCAAGAAGGAGAAGAAGTAACATGGAGGCCAGGCC
AAGAGCCACAGGGCGGCCCTCTCCCCAACAGCCAGCTTCTCCTTACCTGCACCCAGGCCCTCAGAGTTTCAGGGC
TAACCCCCAGAATACTGGTAGGGGCCAAGGCCATGCTCCCTTGGGAAACAGAAACAAGTGCCAGTCAGCACCT
ACCCCTTCCCCCCCAGGGGGTTGAATATGCAAAAGCAGTTCCGCTGGGAACCCCATCCAATCAACTGCTGTACC
CATGGGGGTAGTGGGGTTACTGTAGACACCAAGAACCATTGCCACACCCCGTTTAGTTACAGCTGAACCTCCTCC
ATCTTCAAATCAATCAGGCCCATCCATCCATGCCTCCCTCCTCCCCACCCCACTCCAACAGTTCTCTTTCCC
GAGTAAGGTGGTTGGGGTGTGAGTACCAAGTAACCTACAAGCCTCCTAGTTCTGAAAAGTTGGAAGGGCATCA
TGACCTCTTGGCCTCTCCTTTGATTCTCAATCTTCCCCAAAGCATGGTTTGGTGCCAGCCCTTACCTCCTTC
CAGAGCCCCAAGATCAATGCTCAAGTTTTGGAGGACATGATCACCATCCCCATGGTACTGATGCTTGCTGGATTTA
GGGAGGGCATTGTTGCTACCAAGCCTCTTCCCAACGCCCTGGGGACAGTCTTCTGTTTTGTTTTTCATTGTTTGA
CGTTTCCACTGCATGCCTTGACTTCCCCACCTCCTCCTCAAACAAGAGACTCCACTGCATGTTCCAAGACAGTA

1924/6881
FIGURE 1768B

TGGGGTGGTAAGATAAGGAAGGGAAGTGTGTGGATGTGGATGGTGGGGGCATGGACAAAGCTTGACACATCAAGT
TATCAAGGCCTTGGAGGAGGCTCTGTATGTCCTCAGGGGACTGACAACATCCTCCAGATTCCAGCCATAAACCAA
TAACTAGGCTGGACCCTTCCCACTACATAATAGGGCTCAGCCCAGGCAGCCAGCTTTGGGCTGAGCTAACAGGAC
CAATGGATTAAACTGGCATTTCAGTCCAAGGAAGCTCGAAGCAGGTTTAGGACCAGGTCCCCTTGAGAGGTCAGA
GGGGCCTCTGTGGGTGCTGGGTACTCCAGAGGTGCCACTGGTGGAAGGGTCAGCGGAGCCCCAGCAGGAAGGGTG
GGCCAGCCAGGCCATTCTTAGTCCCTGGGTGAGGAGGAGCTAGGGCAGGGACCAAATGAACAGAAAGTC
TCAGCCCAGGATGGGGCTTCTTCAACAGGGCCCCCTGCCCTCCTGAAGCCTCAGTCCTTCACCTTGCCAGGTGCCG
TTTCTCTTCCGTGAAGGCCACTGCCCAGGTCCCCAGTGCGCCCCCTAGTGGCCATAGCCTGGTTAAAGTTCCCCA
GTGCCTCCTTGTGCATAGACCTTCTTCTCCACCCCCCTTCTGCCCCCTGGGTCCCCGGCCATCCAGCGGGGCTGCC
AGAGAACCCCCAGACCTGCCCTTACAGTAGTGTAGCGCCCCCTCCCTCTTTCGGCTGGTGTAGAATAGCCAGTAGT
GTAGTGCGGTGTGCTTTTACGTGATGGCGGGTGGGCAGCGGGCGGGCTCCGCGCAGCCGTCTGTCCCTTGATC
TGCCCGCGGCGGGCCCGTGTGTGTTTTGTGCTGTGTCCACGCGCTAAGGCGACCCCCTCCCCGTACTGACTTCT
CCTATAAGCGCTTCTCTTCGCATAGTCACGTAGCTCCACCCCCACCCTCTTCCTGTGTCTCACGCAAGTTTTATA
CTCTAATATTTATATGGCTTTTTTTCTTCGACAAAAAATAATAAACGTTTCTTCTGAAAAGCTG

1925/6881
FIGURE 1769

MGPKTL PQLAGKWQVLCMLSLCCGWVSGQLRYSVVEESEPGTLVGNVAQDLGLKMTDLLSRRLQLGSEENG RYF
SLSLMSGALAVNQKIDRESLCGASTSCLLPVQVVTEHPLELIRVEVEILDLDNDNSPSFATPEREMRISESAA SGA
RFPLDSAQDPDVGTNTVSYFYLSPNSHFSLVNKTLDGKPFPELVLEQQLDREAQARHQLVLTAVDGGTPARSGT
TLISVIVLDINDNAPTFQSSVLRVGIPENAPIGTLLLRNLATDPDEGTNGQLDYSFGDHTSEAVRNLFGLDPSSG
AIHVLGPIDFEESRFYEIHARARDQGGPAMEGHCVIQVDVGDVNDNAPEVLLASLANPVLESTPVGTVVGLFNVR
DRDSGRNGEVSLDISPDLPFQIKPSENHYSLLTSQPLDREATSHYIIELLASDAGSPSLHKHLTIRLNI SDVNDN
APRFNQQLYTAYILENRPPGSLCTVAASDPDTGDNARLTYSIVGNQVQGAPASSFVYVNPEDGRIFAQRTFDYE
LLQMLQIVVGVRDSGSPPLHANTSLHVFVLDENDNAPAVLHPRPDWEHSAPQRLPRSAPPGSLVTKVTAVDADAG
HNAWLSYSLLPQSTAPGLFLVSTHTGEVRTARALLEDDSDTQQVVVLVRDNGDPSLSSTATVLLVLEDEDPEEMP
KSSDFLIHPPERSDLTLYLIVALATVSLLSLVTFTFLSAKCLQGNADGDGGGGQCCRRQDSPSPDFYKQSSPNLQ
VSSDGTLKYMEVTLRPTDSQSHCYRTCFSASDGSDFTFLRPLSVQQPTALALEPDAIRSRSNLRLERSQQAPPN
TDWRFSQAQRPGTSGSQNGDDTGTWPNNQFDTEMLQAMILASASEAADGSSTLGGGAGTMGLSARYGPFQFTLQHV
PDYRQNVYIPGSNATLTNAAGKRDGKAPAGGNGNKKKSGKKEKK

1926/6881
FIGURE 1770A

TTCATCTGTACCTTTCAAGTATTCAAATAGAAAAATATAAACAATGTAAATAAAATAGCAAAACAATGTAATATC
TCATAAAACTGCAATGGTAAAAGCATTATCTTATTGAAATTCACAATTTTTATTGAAAATATTATCGACATG
TAATTCAGTGGCATTTAGAAGAATAATTTAAAGCAACAACCTCTATAGAAAGCTTGTAATGATTAAGTAGTT
TAAACCAAATAAAACAATTTCTGAGTCAGTCATCTCCAGTAGGTCTATTTTAGTCTCAAGATAAAATTCATTCTG
GTGACAACTGAAGTTCTTAGTTATTTGTTAGTATATATTGGAGACATTTACAATAAAGCTTAGAGCACAAATGGGA
AATGAAAGTATCATGTTTTTTTTAAAGACCAAATGTATTGCAGAAATGTGAGTAATTTAATCCGATGCTACAATCT
GATCATTCTGATCTAATCTGATCATTAAATAACACTAAATAAAACCTTCATCTCACATTCTTTGGCTGTTTCTTT
TAAATATGGGTTTACGGATAAATCAAATAAATTCAAAACAAAGTAATAAGCAAATGATTTTTTTTCTCAGTAA
TCTAGTAGAGTATTACATTTAGAAGTAATCTGTATCTCAGTGCAGTAACATTTAGGACTGTAAGCGCCGCTGTT
CACCTACTGGAAGACAAATGCAACCGAAAACACTCAGATCTCACACCTCACGAAGACCCGCAGATGCCACAACT
AACTGCTGGACTGCAGCGAAACCCGACCCCTGTTTGGAGGCACTCCAGGTTTCCGGAGGATTGTCTATCTCCATAG
CTGCGGCAAGAACTAAATAAGACCCATTTATGCACAGTGAAGATTCTGAGAGGATTCTGCAGCAAAACAACAAT
GCCCGCTCCACAGAGTCGCCCCAGACGCGGCGAGCTGATCCTGCTGTGCGCGCTGCTGGGAACGCTGTGGGAAAT
CGGGAGGGGACAGATTGCTACTCTGTGCCAGAAGAGACGGACAAAGGCTCCTTCGTGGGTAATATCTCCAAGGA
CCTGGGGCTGGACCCCGGAAGCTGGCGAAGCACGGAGTCCGTATCGTCTCCAGAGGTAGGACGCAGCTCTTTGC
TCTGAACCCGCGCAGCGGCAGCTTGATCACCGCGGGCAGGATAGATCGGGAGGAGCTCTGCGCTCAGAGCCCGCG
GTGTCTGATAAATATTAACACCCTGGTTGAGGATAAAGGAAAACCTCTTTGGGGTAGAAATAGAAATAATTGATAT
TAACGATAATAACCCAAAATTCCAGGTGCAAGATCTAGAAGTAAAAATTAACGAAATCGCGGTTCTTGAGCACG
TTATCCACTCCCAGAAGCTGTTGACCCGGATGTGGGCGTGAACCTCCCTCCAGAGCTACCAGCTCAGCCCCAATCA
CCACTTCTCCCTGGACGTGCAGACTGGAGACAATGGAGCCATAAACCCAGAGCTGGTGCTGGAGCGCGCCCTGGA
CAGGGAGGAAGAGGCTGCTCACACCTGGTCTCACGGCCTCGGATGGCGGCAAGCCGCCTCGCTCTAGCACAGT
GCGCATCCACGTGACAGTGTTGGATACAAATGACAATGCCCGGTTTTTCTCACCCGATTTACCGAGTGAAAGT
CCTTGAGAACATGCCCCAGGCACGCGGCTGCTTACTGTAACAGCCAGCGACCCGGATGAGGGAATCAACGGAAA
AGTGGCATACAAATTCGGAAAATTAATGAAAAACAACTCCGTTATTCCAGCTTAATGAAAATACTGGGGAAAT
ATCAATAGCAAAAAGTCTAGATTATGAAGAATGTTCAATTTTATGAAATGGAATACAAGCCGAAGATGTGGGGGC
ACTTCTGGGGAGGACCAAATTGCTCATTTCGGTGGAAGATGTAATGACAATAGACCAGAAGTGATCATTACGTC
TTTGTTTAGCCCAGTGTTAGAAAATTCTCTCCCGGGACAGTAATTGCCTTCTTGAGTGTGCATGACCAAGACTC
TGGAAAGAATGGTCAAGTTGTCTGTTACACACGTGATAATTTACCTTTTAAATTAGAAAAGTCAATAGGTAATTA
TTATAGATTAGTGACAAGGAAATATTTGGACCGAGAAAATGTCTCTATCTACAATATCACAGTGATGGCCTCAGA
TCTAGGAACACCACCTCTGTCCACTGAAACTCAAATCGCTCTGCACGTGGCAGACATTAACGACAACCCTCCTAC
TTTCCCTCATGCCTCCTACTCAGCGTATATCCTAGAGAACAACCTGAGAGGAGCCTCCATCTTTTCTTGACTGC
ACACGACCCCGACAGCCAGGAGAATGCCAGGTCACCTACTCTGTGACCGAGGACACGCTGCAGGGGGCGCCCT
GTCTCTGTATATCTCCATCAACTCTGACACCGGTGTCTGTATGCGCTGCAATCTTTCGACTATGAGCAGATCCG
AGACCTGCAGCTACTGGTAACAGCCAGCGACAGCGGGGACCCGCCCTCAGCAGCAACATGTCACTGAGCCTGTT
CGTGCTGGACCAGAATGACAACGCGCCCGAGATCCTGTACCCCGCCCTCCCCACAGACGGTTCCACTGGCGTGGA
GCTGGCGCCCCGCTCCGCAGAGCGTGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACAGAGACTCGGGCCAGAA
CGCCTGGCTGTCTACCGCCTGCTCAAGGCCAGCGAGCCGGGACTCTTCTCGGTGGGTCTGCACACGGGCGAGGT
GCGCACGGCGGAGCCCTGCTGGACAGAGATGCGCTCAAGCAGAGCCTCGTGGTGGCCGTCCAGGACCATGGCCA
GCCCCCTCTCTCCGCCACTGTACGCTCACCGTAGCCGTGGCTGACAGCATCCCCGAAGTCTGACCGAGTTGGG
CAGTCTGAAGCCTTCGGTCGACCCGAACGATTCGAGCCTTACACTCTATCTCGTGGTGGCAGTGGCTGCCATCTC
CTGTGCTTCTCTCGCTTTGTGCTGTGCTTCTGGGGCTCAGGCTGAGGCGCTGGCACAAGTCACGCCTGCTCCA
GGATTCCGGTGGCAGATTGGTAGGCGTGCTGCCTCACATTTTGTGGGTGTTGAGGAGGTACAGGCTTTTCTGCA
GACCTATTTCCAGGAAGTCTCCCTCACCGCCGACTCGCGGAAGAGTCACCTGATCTTTCCCCAGCCCAACTACGC
AGACATGCTCATCAGTCAGGAGGGCTGTGAGAAAAATGATTCTTTGTTAACATCCGTAGATTTTTCATGAATATAA
GAATGAAGCTGATCATGGTCAGCAAGCCCCGCCAACACGGACTGGCGTTTCTCTCAGGCCAGAGACCCGGCAC
CAGCGGCTCCCAAATGGCGATGACACCGGCACCTGGCCCAACAACAGTTTGACACAGAGATGCTGCAAGCCAT
GATCTTGGCGTCCGCCAGTGAAGCTGCTGATGGGAGCTCCACCCTGGGAGGGGGTGCCGGCACCATGGGATTGAG
CGCCCGCTACGGACCCAGTTACCCCTGCAGCACGTGCCCGACTACCGCCAGAATGTCTACATCCCAGGCAGCAA

1927/6881
FIGURE 1770B

TGCCCACTGACCAACGCAGCTGGCAAGCGGGATGGCAAGGCCCCAGCAGGTGGCAATGGCAACAAGAAGAAGTC
GGGCAAGAAGGAGAAGAAGTAACATGGAGGCCAGGCCAAGAGCCACAGGGCGGCCTCTCCCCAACCAGCCCAGCT
TCTCCTTACCTGCACCCAGGCCTCAGAGTTTCAGGGCTAACCCCCAGAATACTGGTAGGGGGCCAAGGCCATGCTC
CCCTTGGGAAACAGAAACAAGTGCCAGTCAGCACCTACCCCTTCCCCCCCAGGGGGTTGAATATGCAAAAGCAG
TTCCGCTGGGAACCCCCATCCAATCAACTGCTGTACCCATGGGGGTAGTGGGGTTACTGTAGACACCAAGAACCA
TTTGCCACACCCCGTTTAGTTACAGCTGAACTCCTCCATCTTCCAAATCAATCAGGCCCATCCATCCCATGCCTC
CCTCCTCCCCACCCCACTCCAACAGTTCTCTTTCCCGAGTAAGGTGGTTGGGGTGTGAAGTACCAAGTAACCT
ACAAGCCTCCTAGTTCTGAAAAGTTGGAAGGGCATCATGACCTCTTGGCCTCTCCTTTGATTCTCAATCTTCCCC
CAAAGCATGGTTTGGTGCCAGCCCCCTTACCTCCTTCCAGAGCCCAAGATCAATGCTCAAGTTTGGAGGACATG
ATCACCATCCCCATGGTACTGATGCTTGGTGGATTTAGGGAGGGCATTTTGCTACCAAGCCTCTTCCCAACGCCC
TGGGGACCAGTCTTCTGTTTTGTTTTTTCATTGTTTGACGTTTCCACTGCATGCCTTGACTTCCCCACCTCCTCC
TCAAACAAGAGACTCCACTGCATGTTCCAAGACAGTATGGGGTGGTAAGATAAGGAAGGGAAAGTGTGTGGATGTG
GATGGTGGGGGCATGGACAAAGCTTGACACATCAAGTTATCAAGGCCTTGGAGGAGGCTCTGTATGTCCTCAGGG
GACTGACAACATCCTCCAGATTCCAGCCATAAACCAATAACTAGGCTGGACCCTTCCCACTACATAATAGGGCTC
AGCCCAGGCAGCCAGCTTTGGGCTGAGCTAACAGGACCAATGGATTAAACTGGCATTTTCAAGGAAGCTCG
AAGCAGGTTTAGGACCAGGTCCCCCTTGAGAGGTCAGAGGGGCCTCTGTGGGTGCTGGGTACTCCAGAGGTGCCAC
TGGTGGAAAGGGTCAGCGGAGCCCCAGCAGGAAGGGTGGGCCAGCCAGGCCATTCTTAGTCCCTGGGTGGGGAGG
CAGGGAGCTAGGGCAGGGACCAATGAACAGAAAGTCTCAGCCCAGGATGGGGCTTCTTCAACAGGGCCCCCTGCC
CTCCTGAAGCCTCAGTCCTTACCTTGCCAGGTGCCGTTTCTCTTCCGTGAAGGCCACTGCCAGGTCCCCAGTG
CGCCCCCTAGTGGCCATAGCCTGGTTAAAGTTCCCCAGTGCCTCCTTGTGCATAGACCTTCTTCTCCCACCCCT
TCTGCCCCCTGGGTCCCCGGCCATCCAGCGGGGCTGCCAGAGAACCCCAGACCTGCCCTTACAGTAGTGTAGCGCC
CCCTCCCTCTTTTCGGCTGGTGTAGAAATAGCCAGTAGTGTAGTGCAGGTGTGCTTTTACGTGATGGCGGTGGGCAG
CGGGCGGCGGGCTCCGCGCAGCCGTCTGTCTTGATCTGCCCGCGGCGGCCCGTGTGTGTTTTGTGCTGTGTCC
ACGCGCTAAGGCGACCCCTCCCCGTACTGACTTCTCCTATAAGCGCTTCTCTTCGCATAGTCACGTAGCTCCC
ACCCACCCCTCTTCTGTGTCTCACGCAAGTTTTATACTCTAATATTTATATGGCTTTTTTTCTTCGACAAAAA
ATAATAAACGTTTCTTCTGAAAAGCTG

1928/6881
FIGURE 1771

MAAPQSRPRRGELILLCALLGTLWEIGRGQIRYSVPEETDKGSFVGNISKDLGLDPRKLAKHGVRIVSRGRTQLF
ALNPRSGSLITAGRIDREELCAQSPRCLININTLVEDKGKLFGEIEIIDINDNNPKFQVEDLEVKINEIAVPGA
RYPLPEAVDPDVGVSLSQSYQLSPNHHFSLDVQTDGNGAINPELVLERALDREEEAAHHLVLTASDGGKPPRSST
VRIHVTVLDTNDNAPVFPHPIYRVKVLNMPGTRLLTVTASDPDEGINGKVAYKFRKINEKQTPLFQLNENTGE
ISIAKSLDYEECSFYEMEIQAEDVGALLGRTKLLISVEDVNDNRPEVIITSLFSPVLENSLPGTVIAFLSVHDQD
SGKNGQVVCYTRDNLFPKLEKSIGNYYRLVTRKYLDRENVSIYNITVMASDLGTPPLSTETQIALHVADINDNPP
TFPHASYSAYILENNLRGASIFSLTAHDPDSQENAQVTYSVTEDTLQGAPLSSYISINSDTGVLIALQSFDYEQI
RDLQLLVTASDSGDPPLSSNMSLSLFLVDQNDNAPEILYPALPTDGSTGVELAPRSAERGYLVTKVAVDRDSGQ
NAWLSYRLLKASEPGLFSVGLHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTLTVAVADSIPEVLTEL
GSLKPSVDPNDSSLTLYLVVAVAAISCVFLAFVAVLLGLRLRRWHKSRLQLQDSGGRLVGVPASHFVGVEEVQAF
QTYSQEVSLTADSRKSHLIFPQPNYADMLISQEGCEKNDSSLTSVDFHEYKNEADHGQQAPPNTDWRFSQAQRPG
TSGSQNGDDTGTWPNNQFDTEMLQAMILASASEAADGSSTLGGGAGTMGLSARYGPQFTLQHVPDYRQNVYIPGS
NATLTNAAGKRDGKAPAGGNGNKKKSGKKEKK

1929/6881
FIGURE 1772A

AGAATGGGCTCTAGGCGCCGCTGCTCACCAATCAGGGAATGGGAAGCTGCGCGCCATTGAGTCCCTCCCTCCCC
GCCTCTACCACACAAAGCGGAATGAGATGGATACTCACAGATCCTGACACTGGAGACTTAGAAGTATTTTCCTTC
GCTTTCTGATATATTTTGGATGTAGTCGGCCTAGGACTTCATAGATACATAAGCCGATTACAAACCAACCAGCTC
GAGAAAACCGCGGAATATCGGCTTAGAGCCTGCCATGGCGAATCGGCTACAGCGCGGGGACCGCAGTCGGCTGCTG
CTGCTGCTGTGCATTTTCTGGGGACGCTGCGGGGGTTCCGGGCCAGGCAGATCCGATATTCGGTGCCAGAAGAG
ACCGAAAAGGGCTCCTTCGTGGGCAATATCTCCAAGGACCTGGGGCTGGAGCCCCGGGAGCTGGCGAAGCGCGGA
GTCCGCATCGTCTCCAGAGGGAAGACACAGCTTTTCGTGTGAATCCGCGAAGCGGCAGCTTGATCACGGCAGGC
AGGATAGACCGGGAGGAGCTCTGTGAGACGGTGTCTCTCTGTTTTTAAATATGGAACCTCTCGTGAAGACACC
TTGAAGATTTACGGAGTGGAGGTGGAAATAATAGATATTAATGATAACGCCCCAGCTTCCAGGAGGACGAAGTG
GAGATAAAAGTCAGTGAGCACGCAATTCCTGGGGCGCGATTTGCTCTTCTTAATGCTAGGGATCCAGATGTGGGC
GTGAATCCCTCCAGAGCTACCAGCTCAGCCCTAATAATTACTTTTCTTGCAACTGCGGGGCAGAACGGATGGG
GCCAAGAATCCAGAGCTAGTACTGGAGGGAAGCCTGGACCGAGAGAAAGAGGCTGCTCACCTGCTCCTCTCACA
GCTTTAGATGGAGGCGATCCCATCCGAAAGGGCGCAGTTCCCATTCGTGTGGTGGTCTCTCGATGTAAATGATCAC
ATCCCAATGTTTACACAGTCCGTATATCGCGTGAGTGTTCAGAAAACATCAGCTCCGGAACCTCGGGTGTGATG
GTTAATGCAACGGATCCAGACGAGGGAATCAACGGGGAAGTAATGTATTCAATTCGGAACATGGAAAGCAAGGCT
TCTGAAATATTCCAATTGGATTACAACTGGAGAAGTTCAAGTACGGGGGTCTCTGGATTTTGAAAAATATAGA
TTCTATGAGATGGAAATTCAGGCCAAGATGGTGGAGGTCTCTTTACCACCACGACGATGTTGATCACTGTTGTG
GATGTGAATGATAACGCTCCAGAAATACTATCACCTCTTCTATTAATTCAATTCGGAAAACCTCTCCTCCAGGT
ACAGTGATTGCTCTTCTAAATGTGCAAGATCAAGATTCTGGAGAAAATGGTCAAGTCTCCTGTTTTATTCTTAAC
CACCTGCCTTTTAAATTAGAAAAGACTTATGGAAATTATTACAAATTGATAACAAGCAGAGTGCTGGACAGGGAG
TTGGTCCAGAGCTACAATATAACGTTGACAGCCACAGACCAGGGAAGCCCGCTTTGTCTGCAGAACTCATGTC
TGGCTGAATGTGGCAGATGACAACGATAACCCCTCCCGTTTTTCTCACTCCTCTTACTCTGCCTACATTCCCGAA
AACAACCCAGGGGTGCCTCCATCTTCTCAGTGACCGCCCTCGACCCGGACAGCAAACAGAATGCCCTGGTCACT
TACTCTCTGACGGATGACACTGTCCAGGGGTGCCTCTGTCTCTCTATGTCTCTATTAACCTCCAACACTGGTGT
CTCTATGCCCTACAATCCTTCGACTATGAGCAGTTTCGAGACTTAGAACTGAGAGTGATAGCACGTGACAGCGGG
GACCCGCCCCCTCAGCAGCAACGTGTGCTGAGCCTGTTCTGTCTGGACCAGAACGACAATGCGCCCCGAGATCCTG
TACCCTGCCCTCCCCACAGACGGCTCCACTGGCGTGGAGCTGGCGCCCCGCTCTGCGGAACCTGGCTACCTGGTG
ACCAAGGTGGTTGCGGTGGACAAAGATTACGGCCAGAACGCCTGGCTGTCTATCGCTGCTTAAGGCCAGCGAG
CCGGGACTCTTCGCGGTGGGGGAGCACACGGGCGAGCAAGCCCCGCCAACACGGACTGGCGTTTTCTCTCAGGCC
CAGAGACCCGGCACCAGCGGCTCCCAAAATGGCGATGACACCGGCACCTGGCCCAACAACAGTTTGACACAGAG
ATGCTGCAAGCCATGATCTTGCGCTCCGCCAGTGAAGCTGCTGATGGGAGCTCCACCCTGGGAGGGGGTGCCGGC
ACCATGGGATTGAGCGCCCGCTACGGACCCAGTTACCCCTGCAGCACGTGCCGACTACCGCCAGAATGTCTAC
ATCCAGGCAGCAATGCCACACTGACCAACGCAGCTGGCAAGCGGGATGGCAAGGCCCCAGCAGGTGGCAATGGC
AACAAGAAGAAGTCGGGCAAGAAGGAGAAGAAGTAACATGGAGGCCAGGCCAAGAGCCACAGGGCGGCCTCTCCC
CAACCAGCCCAGCTTCTCCTTACCTGCACCCAGGCCCTCAGAGTTTCAGGGCTAACCCCCAGAATACTGGTAGGGG
CCAAGGCCATGCTCCCCCTGGGAAACAGAAACAAGTGCCAGTCAGCACCTACCCCTTCCCCCCCAGGGGGTTGA
ATATGCAAAAGCAGTTCCGCTGGGAACCCCATCCAATCAACTGCTGTACCCATGGGGGTAGTGGGGTTACTGTA
GACACCAAGAACCATTGCCACACCCCGTTTAGTTACAGCTGAACTCCTCCATCTTCCAAATCAATCAGGCCCAT
CCATCCCATGCCTCCCTCCTCCCCACCCCACTCCAACAGTTCTCTTTCCCGAGTAAGGTGGTTGGGGTGTGAA
GTACCAAGTAACCTACAAGCCTCCTAGTTCTGAAAAGTTGGAAGGGCATCATGACCTCTTGGCCTCTCCTTTGAT
TCTCAATCTTCCCCCAAAGCATGGTTTGGTGCCAGCCCCCTCACCTCCTTCCAGAGCCCAAGATCAATGCTCAAG
TTTTGGAGGACATGATCACCATCCCCATGGTACTGATGCTTGCTGGATTTAGGGAGGGCATTITGCTACCAAGCC
TCTTCCCAACGCCCTGGGGACCACTCTCTGTTTTGTTTTTCATTGTTTGACGTTTCCACTGCATGCCTTGACTT
CCCCACCTCCTCCTCAAACAAGAGACTCCACTGCATGTTCCAAGACAGTATGGGGTGGTAAGATAAGGAAGGGA
AGTGTGTGGATGTGGATGGTGGGGGCATGGACAAAGCTTGACACATCAAGTTATCAAGGCCTTGAGAGGCTCT
GTATGTCCTCAGGGGACTGACAACATCCTCCAGATTCCAGCCATAAACCAATAACTAGGCTGGACCCCTCCCCT
ACATAATAGGGCTCAGCCCAGGCAGCCAGCTTTGGGCTGAGCTAACAGGACCAATGGATTAACTGGCATTTCAG
TCCAAGGAAGCTCGAAGCAGGTTTAGGACCAGGTCCCCCTTGAGAGGTGAGAGGGCCTCTGTGGGTGCTGGGTAC

1930/6881
FIGURE 1772B

TCCAGAGGTGCCACTGGTGGGAAGGGTCAGCGGAGCCCCAGCAGGAAGGGTGGGCCAGCCAGGCCATTCTTAGTCC
CTGGGTGTTGGGGAGGCAGGGAGCTAGGGCAGGGACCAAATGAACAGAAAGTCTCAGCCCAGGATGGGGCTTCTTCA
ACAGGGCCCCCTGCCCTCCTGAAGCCTCAGTCCTTCACCTTGCCAGGTGCCGTTTCTCTTCCGTGAAGGCCACTGC
CCAGGTCCCCAGTGCGCCCCCTAGTGGCCATAGCCTGGTTAAAGTTCCCCAGTGCCCTCCTTGTGCATAGACCTTC
TTCTCCCAACCCCTTCTGCCCCCTGGGTCCCCGGCCATCCAGCGGGGCTGCCAGAGAACCCAGACCTGCCCTTAC
AGTAGTGTAGCGCCCCCTCCCTCTTTCGGCTGGTGTAGAATAGCCAGTAGTGTAGTGCGGTGTGCTTTTACGTGA
TGGCGGGTGGGCAGCGGGCGGGGCTCCGCGCAGCCGTCTGTCTTGATCTGCCC GCGGCGGCCCGTGTGTGT
TTTGTGCTGTGTCCACGCGCTAAGGCGACCCCTCCCCCGTACTGACTTCTCCTATAAGCGCTTCTCTTCGCATA
GTCACGTAGCTCCCACCCACCCCTCTTCCTGTGTCTCACGCAAGTTTTATACTCTAATATTTATATGGCTTTTTT
TCTTCGACAAAAAATAATAAAACGTTTCTTCTGAAAAGCTG

1931/6881
FIGURE 1773

MANRLQRGDRSRLLLLLCIFLGTLRGFRARQIRYSVPEETEEKGSFVGNISKDLGLEPRELAKRGVRIVSRGKTQL
FAVNPRSGSLITAGRIDREELCETVSSCFLNMELLVEDTLKIYGVEVEIIDINDNAPSFQEDVEIKVSEHAIPG
ARFALPNARDPDVGVNSLQSYQLSPNNYFSLQLRGRTDGAKNPELVLEGSLDREKEAAHLLLLLTALDGGDPIRKG
AVPIRVVVLVDVNDHIPMFTQSVYRVSVPENISSGTRVLMVNATDPDEGINGEVMYSFRNMESKASEIFQLDSQTG
EVQVRGSLDFEKYRFYEMEIQQQDGGGLFTTTTMLITVVDVNDNAPEITITSSINSILENSPPGTVIALLLNVQDQ
DSGENGQVSCFIPNHLFPKLEKTYGNYYKLITSRVLDRELVQSYNITLTATDQGSPPLSAETHVWLVNADDNDNP
PVFPHSSYSAYIPENNPRGASIFSVTALDPDSKQNALVTYSLTDDTVQGVPLSSYVSINSNTGVLYALQSFDYEQ
FRDLELRVIARDSGDPPLSSNVSLSLFVLDQNDNAPEILYPALPTDGSTGVELAPRSAEPGYLVTKVVAVDKDSG
QNAWLSYRLLKASEPGLFAVGEHTGEQAPPNTDWRFSQAQRPGTSGSQNGDDTGTWPNNQFDTEMLQAMILASAS
EAADGSSTLGGGAGTMGLSARYGPQFTLQHVPDYRQNVYIPGSNATLTNAAGKRDGKAPAGGNGNKKKSGKKEKK

1932/6881
FIGURE 1774

CAGAAAGCCATGTCGGACTCGGCGCCCAGCGCCCAAGCGCTAACCCGCTGAAAGTTTCTCAGCGAAATCTCAGGG
ACGATCTGGACCCCGCTGAGAGGAACTGCTTTTGAGTGAGATGGTTCCAGAGGCCTGGAGGAGCGGACTGCAAGC
CCCGCCCAACACGGACTGGCGTTTCTCTCAGGCCAGAGACCCGGCACCAGCGGCTCCCAAAATGGCGATGACAC
CGGCACCTGGCCCAACAACAGTTTGACACAGAGATGCTGCAAGCCATGATCTTGGCGTCCGCCAGTGAAGCTGC
TGATGGGAGCTCCACCCTGGGAGGGGGTGCCGGCACCATTGGGATTGAGCGCCCGCTACGGACCCAGTTTACCCT
GCAGCACGTGCCCAGCTACCGCCAGAATGTCTACATCCCAGGCAGCAATGCCACACTGACCAACGCAGCTGGCAA
GCGGGATGGCAAGGCCCCAGCAGGTGGCAATGGCAACAAGAAGAAGTCGGGCAAGAAGGAGAAGAAGTAACATGG
AGGCCAGGCCAAGAGCCACAGGGCGGCCCTCTCCCAACCAGCCCAGCTTCTCCTTACCTGCACCCAGGCCTCAGA
GTTTCAGGGCTAACCCCCAGAATACTGGTAGGGGCCAAGGCCATGCTCCCCTTGGGAAACAGAAACAAGTGCCCA
GTCAGCACCTACCCCTTCCCCCCCAGGGGGTTGAATATGCAAAAGCAGTTCCGCTGGGAACCCCATCCAATCAA
CTGCTGTACCCATGGGGGTAGTGGGGTTACTGTAGACACCAAGAACCATTGTCACACCCCGTTTAGTTACAGCT
GAACTCCTCCATCTTCCAAATCAATCAGGCCCATCCATCCCATGCCTCCCTCCTCCCCACCCCACTCCAACAGTT
CCTCTTTCCCGAGTAAGGTGGTTGGGGTGTGAAGTACCAAGTAACCTACAAGCCTCCTAGTTCTGAAAAGTTGG
AAGGGCATCATGACCTCTTGGCCTCTCCTTTGATTCTCAATCTTCCCCCAAAGCATGGTTTGGTGCCAGCCCTT
CACCTCCTTCCAGAGCCCCAAGATCAATGCTCAAGTTTTGGAGGACATGATCACCATCCCCATGGTACTGATGCTT
GCTGGATTTAGGGAGGGCATTTTGCTACCAAGCCTCTTCCCAACGCCCTGGGGACCAGTCTTCTGTTTTGTTTTT
CATTGTGTGACGTTTCCACTGCATGCCTTGACTTCCCCACCTCCTCCTCAAAACAAGAGACTCCACTGCATGTTT
CAAGACAGTATGGGGTGGTAAGATAAGGAAGGGAAGTGTGTGGATGTGGATGGTGGGGGCATGGACAAAGCTTGA
CACATCAAGTTATCAAGGCCCTTGGAGGAGGCTCTGTATGTCTCAGGGGACTGACAACATCCTCCAGATTCCAGC
CATAAACCAATAACTAGGCTGGACCTTCCCCTACATAATAGGGCTCAGCCCAGGCAGCCAGCTTTGGGGCTGAG
CTAACAGGACCAATGGATTAACTGGCATTTCAGTCCAAGGAAGCTCGAAGCAGTTTAGGACCAGGTCCCCTTG
AGAGGTGAGAGGGGCTCTGTGGGTGCTGGGTACTCCAGAGGTGCCACTGGTGGGAAGGGTCAGCGGAGCCCCAGC
AGGAAGGGTGGGCCAGCCAGGCCATTCTTAGTCCCTGGGTGGGGAGGCAGGGAGCTAGGGCAGGGACCAATGA
ACAGAAAGTCTCAGCCCAGGATGGGGCTTCTTCAACAGGGCCCCCTGCCCTCCTGAAGCCTCAGTCCTTCACCTTG
CCAGGTGCCGTTTCTCTTCCGTGAAGGCCACTGCCAGGTCCCCAGTGCGCCCCCTAGTGGCCATAGCCTGGTTA
AAGTTCCCCAGTGCTCCTTGTGCATAGACCTTCTTCTCCACCCCTTCTGCCCCTGGGTCCCCGGCCATCCAG
CGGGGCTGCCAGAGAACCCAGACCTGCCCTTACAGTAGTGTAGCGCCCCCTCCCTCTTTCGGCTGGTGTAGAAT
AGCCAGTAGTGTAGTGCAGGTGTGCTTTTACGTGATGGCGGGTGGGCAGCGGGCGGGGCTCCGCGCAGCCGTCT
GTCCTTGATCTGCCCCGCGCGGCCCGTGTGTGTTTTGTGCTGTGTCCACGCGCTAAGGCGACCCCTCCCCCGT
ACTGACTTCTCCTATAAGCGCTTCTCTTCGCATAGTCACGTAGCTCCCACCCACCCCTCTTCTGTGTCTCACGC
AAGTTTTATACTCTAATATTTATATGGCTTTTTTCTTCGACAAAAAAATAATAAACGTTTCTTCTGAAAAGCT
G

1933/6881
FIGURE 1775

MVPEAWRSGQLQAPPNTDWRFSQAQRPGTSGSQNGDDTGTWPNNQFDTEMLQAMILASASEAADGSSTLGGGAGTM
GLSARYGPQFTLQHVPDYRQNVYIPGSNATLTNAAGKRDGKAPAGGNGNKKKSGKKEKK

1934/6881
FIGURE 1776

CAGAAAGCCATGTCGGA CTGGCGCC CAGCGCCCAAGCGCTAACCCGCTGAAAGTTTCTCAGCGAAATCTCAGGG
ACGATCTGGACCCCGCTGAGAGGAACTGCTTTTGAGTGAGATGTTCCAGAGGCCTGGAGGAGCGGACTGGTAAG
CACCGGGAGGGTAGTGAGGAGTTTGTCTTGTGCTTGGTGCCCTTGAACAAGGCTTCCACGGTCATTCACTATGAGAT
CCCGGAGGAAAGAGAGAAGGGTTTCGCTGTGGGCAACGTGGTCGCGAACCTTGGTTTGGATCTCGGTAGCCTCTC
AGCCCGCAGGTTCCGGGTGGTGTCTGGAGCTAGCCGAAGATTCTTTGAGGTGAACCGGGAGACCGGAGAGATGTT
TGTGAACGACCGTCTGGATCGAGAGGAGCTGTGTGGGACACTGCCCTCTTGCACTGTAACCTCTGGAGTTGGTAGT
GGAGAACCCGCTGGAGCTGTTT CAGCGTGGAAGTGGTGATCCAGGACATCAACGACAACAATCCTGCTTTCCCTAC
CCAGGAAATGAAATTGGAGATTAGCGAGGCCGTGGCTCCGGGGACGCGCTTTCCGCTCGAGAGCGCGCACGATCC
CGATGTGGGAAGCAACTCTTTTACAAACCTATGAGCTGAGCCGAAATGAATACTTTGCGCTTCGCGTGCAGACGCG
GGAGGACAGCACCAAGTACGCGGAGCTGGTGTGGAGCGCGCCCTGGACCGAGAACGGGAGCCTAGTCTCCAGTT
AGTGCTGACGGCGTTGGACGGAGGGACCCAGCTCTCTCCGCCAGCCTGCCTATTACATCAAGGTGCTGGACGC
GAATGACAATGCGCCTGTCTTCAACCAGTCCTTGTACCGGGCGCGCTCCTGGAGGATGCACCTCCGGCACGCG
CGTGGTACAAGTCTTGTCAACGGATCTGGATGAAGGCCCAACGGTGAAATTATTTACTCCTTCGGCAGCCACAA
CCGCGCCGGCGTGCGGCAACTATTCGCCTTAGACCTTGTAAACGGGATGCTGACAATCAAGGGTCGGCTGGACTT
CGAGGACACCAAACCTCCATGAGATTTACATCCAGGCCAAAGACAAGGGCGCCAATCCCGAAGGAGCACATTGCAA
AGTGTGGTGGAGGTTGTGGATGTGAATGACAACGCCCCGAGATCACAGTCACCTCCGTGTACAGCCAGTACC
CGAGGATGCCCCCTCTGGGGACTGTCATCGCTTTGCTCAGTGTGACTGACCTGGATGCTGGCGAGAACGGGCTGGT
GACCTGCGAAGTTCCACCGGGTCTCCCTTT CAGCCTTACTTCTTCCCTCAAGAATTACTTCACTTTGAAAACAG
TGCAGACCTGGATCGGGAGACTGTGCCAGAATAACAACCTCAGCATCACCGCCGAGACGCCGGAACCCCTTCCCT
CTCAGCCCTTACAATAGTGCCTGTCAAGTGTCCGACATCAATGACAACCTCCACAATCTTCTCAATCTTCCTA
CGACGTTTACATTGAAGAAAACAACCTCCCCGGGGCTCCAATACTAAACCTAAGTGTCTGGGACCCGACGCCCC
GCAGAATGCTCGGCTTTCTTTCTTTCTTCTTGGAGCAAGGAGCTGAAACCGGGCTAGTGGGTGCTATTT CACAAT
AAATCGTGACAATGGCATAGTGTCATCCTTAGTGCCCTTAGACTATGAGGATCGGCGGGAATTTGAATTAACAGC
TCATATCAGCGATGGGGGCACCCCGGTCCTAGCCACCAACATCAGCGTGAACATATTTGTCACTGATCGCAATGA
CAATGCCCCCAGGTCCTATATCCTCGGCCAGGTGGGAGCTCGGTGGAGATGCTGCCTCGAGGTACCTCAGCTGG
CCACCTAGTGTACGGGTGGTAGGCTGGGACGCGGATGCAGGGCACAATGCCTGGCTCTCCTACAGTCTCTTGGG
ATCCCTAACCAGAGCCTTTTTGCCATAGGGCTGCACACTGGTCAAATCAGTACTGCCCCTCCAGTCCAAGACAC
AGATTACCCAGGCAGACTCTCACGGTCTTGATCAAAGACAATGGGGAGCCTTCGCTCTCCACCACTGCTACCCCT
CACTGTGT CAGTAACCGAGGACTCTCCTGAAGCCCGAGCCGAGTTCCCTCTGGCTCTGCCCCCGGGAGCAGAA
AAAAAATCTCACCTTTTATCTACTTCTTTCTCTAATCCTGGTTTCTGTGGGGTTTGTGGTCACAGTGTTCCGGAGT
AATCATATTCAAAGTTTACAAGTGGAAGCAGTCTAGAGACCTATACCGAGCCCCGGTGAGCTCACTGTACCGAAC
ACCAGGGCCCTCCTTGCACGCGGACGCCGTGCGGGGAGGCCTGATGTCGCCGCACCTTTACCATCAGGTGTATCT
CACCACGGA CTCCCGCCGACGACCCGCTGCTGAAGAAACCTGGTGCAGCCAGTCCACTGGCCAGCCGCCAGAA
CACGCTGCGGAGCTGTGATCCGGTGTCTATAGGCAGGTGTTGGGTGCAGAGAGCGCCCTCCCGGACAGGTAAG
GTTTAGCAAGTCATGCTTGACCCTGTTAGTGCTTTTTTATTCTACATCATATTGAGGAAGGAATGGAGCTGTTT
TTTTAGTGATGAAGATGTTTTCTGGTGATGCATTACACTTTCAACTGGCCCTTCTAGATCAAAGTTAGTGCC
TTTGTGAGATGGTGGCCTGCCAGAGTGTGGTTTGTGGTCCCATTTCAGGGGGAAGATACTTGACTCATCTGTGGA
CCTAATTCACATCCTCAGC

1935/6881
FIGURE 1777

MVPEAWRSGLVSTGRVVGVLGALNKASTVIHYEIPEREKGFVGNVVALGLDLGSLSAARRFRVSGASRR
FFEVNRETGEMFVNDRLDREELCGTLPSCVTLELVVENPLELFSVEVVIQDINDNNPAFPTQEMKLEISEAVAP
GTRFPLESAHDPDVGSNSLQTYELSRNEYFALRVQTREDSTKYAELVLERALDREREP SLQLVLTALDGGTPALS
ASLP IHIKVL DANDNAPVFNQSLYRARVLEDAPSGTRVVQVLATDLDEGPNGEIIYSFGSHNRAGVRQLFALDLV
TGMLTIKGRLDFEDTKLHEIYIQAKDKGANPEGACHCKVLVEVVDVNDNAPEITVTSVYSPVPEDAPLGTVIALLS
VTDLDAGENGLVTCEVPPGLPFSLTSSLKNYFTLKTSADLDRETVPYNSITARDAGTPSLSALTIVRVQVSDI
NDNPPQSSQSSYDVYIEENNLPGAPIILNLSVWDPDAPQNARLSFFLLEQGAETGLVGRYFTINRDNGIVSSLVPL
DYEDRREFELTAHISDGGTPVLATNISVNIFVTDRNDNAPQVLYPRPGGSSVEMLPRGTSAGHLVSRVVGWDADA
GHNAWLSYSLLGSPNQSLFAIGLHTGQISTARPVQD TDSRQTLTVLIKDNGEPSLSTTATLT VSVTEDSPEARA
EFPSGSAPREQKNLTFYLLLSLILVSVGFVVTVFGV IIFKVYKWKQSRDLYRAPVSSLYRTPGPSLHADAVRGG
LMSPHLYHQVYLTTDSRRSDPLLKKPGAASPLASRQNTLRSCDPVFYRQVLGAESAPPGQVRF SKSCLTLLVLFY
SYIILRKEWSCFFSDEDVFLVMHSHFQLALPRSKLVPL

1936/6881
FIGURE 1778

CCTCAGTTTCCTTGTTTTGTAAAATAGTTGAACTAAATCTTGACCCTTTAATGCTTGTTTTGAAATCCAAGGCAAA
AAACAATTGCAAGCGCCCTTACTTCCGTGTTGCTTCATACTCCTCTTGCGCCTGCGCTGTCTCCTTGAGCAGAG
GCGGGGCCAACAAAGCCTGTTTTAGAAACCCTCCAGTCCTTAGCTCGTTTAGAACACAAGACTCCAAGCTTATTGG
AGGGCTATCTTGCTTACGGCTCCAAGCCGCTTTTTACGGCGTTTTTTCAGCTCGCCATTCACTTCGCTGTGAAGA
TGGCGTCGGGCAGCGGGGTAGGTGTTGTGTCTGAGGAGGAGGTTTTGCGGGGTGGGGAATGGTTTTTCAGACCTG
AATAGAGACAAACTCCTGCACCCGACTGGCTTCCCGATATCTCCTCGAGATCCCAGGGTTCAGGTTCAAGAACTC
CCAGTAATAGGCCTTGGCAGAGGGTCAGTAGAATCGCGGAGGTTTCTCGGGTTGGGGTCTTGAGGCTACCTCAG
TCTTCTCGTACAGTCCAAAGAGGCTTCGCTTTCAAAACGTCCTGTAGACACCTGGACCGCGAGGGCGCGGTTCCC
TGCTTCTCTAGGGGCCCAGACACGGCGACGGATCTTGACGCTTTTTCTCCCCACAGACAAAAAACTTGGAATTT
CGCCGAAAGTGGGACAAAGATGAATATGAGAACTCGCCGAGAAGAGGCTCACGGAAGAGAGAGAAAAGAAAGAT
GGAAAACAGTGCAGCCTGTCAAGCGAGAGCTTTTACGGCATAGGGACTACAAGGTGGACTTGGAATCCAAGCTT
GGGAAGACAATTGTCATTACCAAGACAACCC

1937/6881
FIGURE 1779

TCGATAGCCGGAAGTCATCCTTGCTGAGGCTGGGGCAACCACCGCAGGTCGAGACAGCAGGCGGGCTCAAGTGGAC
AGCCGGG**ATG**GCAGAGCGTGCGGCGCTGGAGGAGCTGGTGAAACTTCAGGGAGAGCGCGTGCGAGGCCTCAAGCA
GCAGAAGGCCAGCGCCGAGCTGATCGAGGAGGAGGTGGCGAAACTCCTGAAACTGAAGGCACAGCTGGGTCTCTGA
TGAAAGCAAACAGAAATTTGTGCTCAAAACCCCCAAGGGCACAAAGAGACTATAGTCCCCGGCAGATGGCAGTTCTG
CGAGAAGGTGTTTGACGTAATCATCCGTTGCTTCAAGCGCCACGGTGCAGAAGTCATTGATACACCTGTATTGTA
ACTAAAGGAAACACTGATGGGAAAGTATGGGGAAGACTCCAAGCTTATCTATGACCTGAAGGACCAGGGCGGGGA
GCTCCTGTCCCTTCGCTATGACCTCACTGTTCTTTTGCTCGGTATTTGGCAATGAATAAACTGACCAACATTAA
ACGCTACCACATAGCAAAGGTATATCGGCGGGATAACCCAGCCATGACCCGTGGCCGATACCGGGAATTCTACCA
GTGTGATTTTTGACATTGCTGGGAACTTTGATCCCATGATCCCTGATGCAGAGTGCCTGAAGATCATGTGCGAGAT
CCTGAGTTCACTTCAGATAGGCGACTTCCTGGTCAAGGTAAACGATCGACGCATTCTAGATGGGATGTTTGCTAT
CTGTGGTGTCTTGACAGCAAGTTCGTAACCATCTGCTCCTCAGTAGACAAGCTGGACAAGGTGTCCTGGGAAGA
GGTGAAGAATGAGATGGTGGGAGAGAAGGGCCTTGACCTGAGGTGGCTGACCGCATTGGGGACTATGTCCAGCA
ACATGGTGGGGTATCCCTGGTGGAAACAGCTGCTCCAGGATCCTAAACTATCCCAAACAAGCAGGCCTTGAGGG
CCTGGGAGACCTGAAGTTGCTCTTTGAGTACCTGACCCTATTTGGCATTGATGACAAAATCTCCTTTGACCTGAG
CCTTGCTCGAGGGCTGGATTACTACACTGGGGTGATCTATGAGGCAGTGCTGCTACAGACCCAGCCAGGCAGG
GGAAGAGCCCCCTGGGTGTGGGCAGTGTGGCTGCTGGAGGACGCTATGATGGGCTAGTGGGCATGTTGACCCCAA
AGGGCGCAAGGTGCCATGTGTGGGGCTCAGCATTGGGGTGGAGCGGATTTTCTCCATCGTGGAACAGAGACTAGA
GGCTTTGGAGGAGAAGATACGGACCACGGAGACACAGGTGCTTGTGGCATCTGCACAGAAGAAGCTGCTAGAGGA
AAGACTAAAGCTTGTCTCAGAACTGTGGGATGCTGGGATCAAGGCTGAGCTGCTGTACAAGAAGAACCCAAAGCT
ACTGAACCAGTTACAGTACTGTGAGGAGGCAGGCATCCCACTGGTGGCTATCATCGGCGAGCAGGAACCTCAAGGA
TGGGGTCATCAAGCTCCGTTCAGTGACGAGCAGGGAAGAGGTGGATGTCCGAAGAGAAGACCTTGTGGAGGAAAT
CAAAAGGAGAACAGGCCAGCCCCCTCTGCATCTGCT**TGA**ACTGAACAAACTATCAGAGGAAAGGAAGTGGGACTGGC
ACTATTTGAGGTTAAGACAAACTGCATATGTACTTCAATTGCTTTGCACTTTTCCGTTTCAGCGGAAGACCTGAA
GAGTGGTCAGAACAGAGCCTTTGATTTTTATTATGGTTATTTTATTGATTATTACTGGCAAAAACGGCCAGGTAC
AACACCTTTTTTCATACAAGGCCAGGAGGCTTAGTCCAGTCTGTGCTCCTGGGCTACAAGGACCCAGCCTGAGAT
GGTCCCATCTGCAGGGCCCCGCACCAGTTGGAGCAGATGCCTCCCCACCACCAATTGCCAAAGGTCCAATAAAAT
GCCTCAACCACGGAAAAAAAAAAAAAAAAAAAAA

1938/6881
FIGURE 1780

MAERAALEELVKLQGERVRGLKQQKASAELEEEVAKLLKLKAQLGPDESKQKFVLKTPKGTRDYSRQMAVREK
VFDVLIIRCFKRHGAVIDTPVFELKETLMGKYGEDSKLIYDLKDQGGELLSLRYDLTVPFARYLAMNKLTNIKRY
HIAKVYRRDNPAMTRGRYREFYQCDFDIAGNFDPMIPDAECLKIMCEILSSLQIGDFLVKVNDRRILDGMFAICG
VSDSKFRTICSSVDKLDKVSWEDEVKNEMVGEKGLAPEVADRIGDYVQQHGGVSLVEQLLQDPKLSQNKQALEGLG
DLKLLFEYLTTLFGIDDKISFDLSLARGLDYYTGVIYEAVLLQTPAQAGEEPLGVGSVAAGGRYDGLVGMFDPKGR
KVPCVGLSIGVERIFSIVEQRLEALEEKIRTTETQVLVASAQKKLEERLKLVSSELWDAGIKAELLYKKNPKLLN
QLQYCEEAGIPLVAIIGEQLKDGVIKLSVTSREEVDVRREDLVVEIKRRTGQPLCIC

1939/6881
FIGURE 1781

ACGCAAAGCAGTGTGGGTTGATTCTGAGGTGCACTGTGGGAAAGAGCTTGTGCTGCGGTGTTGCTGTTGGAGAC
TCGATTGTTGGTGACAGCGAAAGAACGATAACAAAATGCCGGAGCGAGATAGTGAGCCGTTCTCCAACCCTTTGG
CCCCGATGGCCACGATGTGGATGATCCTCACTCCTTCCACCAATCAAAACTCACCAATGAAGACTTCAGGAAAC
TTCTCATGACCCCCAGGGCTGCACCTACCTCTGCACCACCTTCTAAGTCACGTCACCATGAGATGCCAAGGGAGT
ACAATGAGGATGAAGACCCAGCTGCACGAAGGAGGAAAAAGAAAAGTTATTATGCCAAGCTACGCCAACAAGAAA
TTGAGAGAGAGAGAGAGCTAGCAGAGAAGTACCGGGATCGTGCCAAGGAACGGAGAGATGGAGTGAACAAAGATT
ATGAAGAAACCGAGCTTATCAGCACCCACAGCTAACTATAGGGCTGTTGGCCCCACTGCTGAGGCGGACAAATCAG
CTGCAGAGAAGAGAAGACAGTTGATCCAGGAGTCCAAATTCTTGGGTGGTGACATGGAACACACCCATTTGGTGA
AAGGCTTGGATTTTGTCTGTCTTCAAAAGGTACGAGCTGAGATTGCCAGCAAAGAGAAAAGAGGAAGAGGAACTGA
TGGAAGAGCCCCAGAAAGAAACCAAGAAAGATGAGGATCCTGAAAATAAAATTGAATTTAAACACGTCTGGGCC
GCAATGTTTACCGAATGCTTTTTTAAGAGCAAAGCATATGAGCGGAATGAGTTGTTCTGCGGGCCGCATGGCCT
ATGTGGTAGACCTGGATGATGAGTATGCTGACACAGATATCCCCACCACTCTTATCCGCAGCAAGGCTGATTGCC
CCACCATGGAGGCCAGACCACACTGACCACAAATGACATTGTCTATTAGCAAGCTGACCCAGATCCTTTCATACC
TGAGGCAGGGAACCCGTAACAAGAAGCTTAAGAAGAAGGATAAAGGGAAGCTGGAAGAGAAGAAACCTCCTGAGG
CTGACATGAATATTTTTGAAGACATTGGGGATTACGTACCCTCCACAACCAAGACACCTCGGGACAAGGAGCGGG
AGAGATATCGGGAACGGGAGCGTGATCGGGAAAGAGACAGAGACCGTGACCGAGAGCGAGAGCGAGAACGAGATC
GGGAACGAGAGCGAGAGCGGGACCGAGAGAGAGAAGAGGAAAAGAAGAGACACAGCTACTTTGAGAAGCCAAAAG
TAGATGATGAGCCCATGGACGTTGACAAAGGACCTGGGTCTACCAAGGAGTTGATCAAGTCCATCAATGAAAAGT
TTGCTGGGTCIGCTGGCTGGGAAGGCACAGAATCGCTGAAGAAGCCAGAAGACAAAAGCAGCTGGGAGATTTCT
TTGGCATGTCCAACAGTTATGCAGAGTGCTACCCAGCCACGATGGATGACATGGCTGTGGATAGTGATGAGGAGG
TGGATTATAGCAAAATGGACCAGGGTAACAAGAAGGGGCCCTTAGGCCGTTGGGACTTTGATACCCAGGAAGAAT
ACAGCGAGTATATGAACAACAAAGAAGCTTTGCCCAAGGCTGCATTCCAGTATGGTATCAAAATGTCTGAAGGGC
GGAAAACCAGGCGCTTCAAGGAAACCAATGACAAAGCAGAGCTTGATCGCCAGTGGAAGAAGATTAGTGCAATCA
TTGAGAAGAGGAAGAAGATGGAAGCTGATGGGGTTGAAGTCAAAGACCAAAATACTAA

1940/6881
FIGURE 1782

MPERDSEFFSNPLAPDGHVDVDDPHSFHQSKLTNEDFRKLLMTPRAAPTSAPPSKSRHHEMPREYNEDEDPAARRR
KKKSYYAKLRQQEIERERELAKEYRDRAKERRRDGVNKDYEETELISTTANYRAVGPTAEADKSAAEKRRQLIQES
KFLGGMEHHTLVKGLDFALLQKVRAEIASKEKEEEEELMEKPQKETKKDEDPENKIEFKTRLGRNVYRMLFKSKA
YERNEFLPLGRMAYVVDLDDEYADTDIPTTLIRSKADCPTMEAQTTLTNDIVISKLTQILSYLRQGTRNKKLKK
KDKGKLEEKKPPEADMNIFEDIGDYVPSTTKTPRDKERERYRERERDRERDRDRDRERERERDRERERERDRERE
EEKKRHSYFEKPKVDDEPMDVDKGPGSTKELIKSINEKFAGSAGWEGTESLKKPEDKKQLGDDFFGMSNSYAECYP
ATMDDMAVDSDEEVDYSKMDQGNKKGPLGRWDFDTQEEYSEYMNNKEALPKAAFQYGIKMSEGRKTRRFKETNDK
AELDRQWKKISAIIEKRKKMEADGVEVKRPKY

1941/6881
FIGURE 1783

GTGACCCCAGGCCCTGGTCACTCCATGCTTTGGAGGGTGCTTTTGTCAAAGAGGCCTCCTTTCCCTCACCCAGAG
CTGGATTTCCAAGAGGCTCCCATACCTAGCTGCCCTGGCAGACTCCCAGGGAGGAAAAACAGCGTGCCCTTGGCA
GCTGCCCCGAGGAAGGAGCCACAGGTGACAGGGAGAAGCCATTGCCATTCCCTGTCTGGCCCCCTTCAGCAAC
CCTGAACACTCTGCTCCAGCCAAGGTGGTGAGGGCAGCTGTTTCTAAACAGCGCAAAGGCAGCAAGGTTGGTGAC
TTTGAGATGCAATCAATTGGCCACACCTGGAGAGATAGCCACAAAGAGTGTTTCAGCCACAGTCCCAAGCCCT
CAGCCTACCCGTAAACTGCCACCCAAGAAGGACATGAAGGAACAGGAGAAAGGAGAAGGGAGTGATAGTAAGGAG
AGTCCAAAAACCAAATCAGATGAATCAGGGGAGGAAAAGAATGGAGATGAGGATTGCCAGCGAGGCGGGCAGAAG
AAGAAAGGAAACAAACACAAGTGGGTTCCATTACAAATAGACATGAAGCCTGAAGTGCCAGAGAGAAACTGGCT
TCACGCCCCACTCGCCACCCGAGCCTAGACACATACCTGCCAATCGCGGAGAGATCAAAGGGTCTGAGTCTGCC
ACCTACGTGCCCGTGGCCCCCCCCACCCAGCCTGGCAACCAGAGATCAAACCGGAGCCTGCCTGGCACGACCAG
GATGAGACATCGAGTGTGAAGAGTGATGGGGCTGGTGGGGCGCGGGCTTCCCTCCGTGGCCGTGGACGGGGGCGT
GGTCGCGGGCGGGGACGCGGGCCGGGGTGGCACTCGAACCCATTTTGACTACCAGTTTGGCTACCGAAAGTTTGAT
GGTGTGGAGGGGCTCGTACGCCCAAGTACATGAACAACATCACCTACTACTTTGACAATGTCAGCAGCACCCGAG
CTTTACAGTGTGGATCAGGAAGTCTCAAAGACTACATCAAGCGCCAGATTGAATACTACTTCAGCGTGGACAAT
TTAGAGCGAGACTTCTTCCGTGCGAAGGAAAATGGATGCTGATGGTTTCTACCCATCACCCTTATTGCTTCTTTC
CACCGAGTGCAGGCCCTTACCACTGACATTTCACTCATCTTTGCGGCCCTAAAGGACAGCAAGGTGGTGGAGATC
GTTGATGAGAAAGTTTCGTAGGAGGGAGGAACCAGAAAAGTGGCCTCTTCCCCCAATAGTGGATTATTACAGACT
GATTTCTCCAGCTTCTCAACTGCCCTGAATTTGTTCCCGTCAGCACTACCAAAAGGAGACAGAGTCGGCACCT
GGCTCTCTCGTGCAGTCACCCAGTGCCAACCAAAACAGAGGAGGTGAGCAACCTAAAGACACTACCCAAGGGC
CTGTCTGCCAGCCTGCCTGACCTGGATTCTGAGAACTGGATTGAAGTGAAGAAGAGGCCTCGGCCATCCCCAGCA
CGGCCCAAGAAGTCAGAGGAGTCCAGATTTTCCACCTGACCTCTCTGCCTCAGCAGCTGCCTTCCCAGCAGCTG
ATGTCCAAGGATCAGGATGAGCAAGAGGAACTGGATTTTCTGTTTGACGAGGAGATGGAGCAGATGGATGGGCGG
AAGAACACCTTCACTGCCTGGTCTGATGAGGAATCTGACTATGAGATTGATGACAGGGATGTCAACAAGATCCTC
ATTGTCACCCAGACACCACATTACATGCGCCGGCACCCAGGGGGGGACCGCACAGGCAACCACACCTCGCGTGCC
AAGATGAGCGCCGAAGTGGCCAAGGTCATTAATGATGGCCTCTTCTACTATGAGCAGGACCTGTGGGCTGAAAAG
TTTGAACCTGAGTATTCCCAGATCAAGCAAGAAGTCGAGAACCTCAAAAAGGTCAATATGATCAGCCGGGAGCAG
TTTGACACACTGACCCCTGAGCCCCCTGTGGATCCCAACCAGGAAGTTTCTCCTGGGGCCACCTCGGTTCCAGCAA
GTTCTACGGATGCCCTGGCCAACAAGTTGTTTGGTGCTCCTGAGCCCTCCACCATCGCCCGCTCTCTACCAACC
ACTGTCCCAGAGTCACCAAACCTACCGCAACACCAGGACCCCTCGCACTCCCCGGACACCACAGCTCAAAGACTCA
AGCCAGACATCACGGTTTTTACCCAGTGGTGAAAAGAAGGACGGACACTGGATGCCAAGATGCCTCGAAAAAGAAAG
ACAAGACACAGTTCAAACCCACCCCTTGGAGAGCCATGTGGGCTGGGTGATGGATTCCCGTGAGCACAGGCCCCGT
ACTGCTTCCATCAGTAAGATGGCCCCAGTGTGTGTTTCTGTTTCCCAAAGCAAGCTTTGAGAGCCACCTACCTA
TGACCAATGCTCTCTACTCCCTGCAGAGATGGCACAGACTGCAAATAGGCATGCTTTTGAAGAAAATATACAATT
GATCTTTGAACAACGAAGGGCGTGGGGTGGCCAGCTGCACACAGTTGAAAATCCGTGTATACTTTTGACTCTCC
AAAAGCCTACTGTTAACCAGAAGCCTTACCAATAACATATAGTCAATTAGCACATGTTTTGCATATTATATGTAT
TACATACTGTATTCTTACAATAAGCTAAATAA

1942/6881
FIGURE 1784

MKEQEKGEESDSKESPKTKSDESGEEKNGDEDCQGGGQKKKGKHKHWVPLQIDMKPEVPREKLASRPTRPPEPRH
IPANRGEIKGSESATYVPVAPPTPAWQPEIKPEPAWHDQDETSSVKSDGAGGARASFRGRGRGRGRGRGRGGT
RTHFDYQFGYRKFDGVEGPRTPKYMNNITYYFDNVSTELYSVDQELLDYIKRQIEYYFSVDNLERDFFLRKRM
DADGFLPITLIASFHRVQALTTDISLIFAALKDSKVVEIVDEKVRREEPEKWPLPPIVDYSQTDQSLLNCPEF
VPRQHYQKETESAPGSPRAVTPVPTKTEEVSNLKTLPKGLSASLPDLSENWIEVKKRPRPSPARPKKSEESRFS
HLTSLPQQLPSSQQLMSKDQDEQEELDFLFDEEMEQMDGRKNTFTAWSDEESDYEIDDRDVNKILIVTQTPHYMRR
HPGGDRTGNHTSRAKMSAELAKVINDGLFYEQDLWAEKFEPEYSQIKQEVENFKKVNMISSREQFDLTPEPPVD
PNQEVPPGPPRFQQVPTDALANKLFGAPEPSTIARSLPTTVFESPNYRNTRTPRTPRTPQLKDSSQTSRFYPVVK
EGRTLDKMPRKRKTRHSSNPPLSHVGVWMDSREHRPRTASISSPSEGTPTVGSYGCTPQSLPKFQHPHELL
KENGFTQHVYHKYRRRCLNERKRLGIGQSQEMNTLFRFWSFFLRDHFNKKMYEEFKQLALEDAKEGYRYGLECLF
RYYSYGLEKKFRLDIFKDFQEETVKDYEAGQLYGLEKFWAFLKYSKAKNLDIDPKLQEYLGKFRLEDVRVDP
GEEGNHKRHSVVAGGGGGEGGRKRCPSQSSSRPAAMISQPPTPPTGQPVREDAKWTSQHSNTQTLGK

1943/6881
FIGURE 1785

GGCACGAGGGAAGAGCTCCACCTTCTCTGGATGTGCCTGGGCTTGGACTGGCTAGAACTCTTCTCTGGACTGTT
GCATGTACAGTGCCTCCATCCTGGAGGCAAGAGAGTTGGGAGTGGCTCGAATCAGAGCCGTGCCCAAGATATCCC
TGCTGTTGCATCGTTTGAAGCTGACGTCTGTGTCTGTACACTGCTGCCACTGTTGTGTCTCGCTCTGCTTGCT
GTTGCCTCACGCCAGGCCCCGTCTGCGTGACACCTTTCATCCTACCCTTGGAAACCCCAAGGCCAAGTTGGTTC
AAACTGTTGGAGAACAGAGTTGGCCTGCATCTGGAACACACTTGTCTCAGCTTACCATCTCCTCACACCCCAGA
GTGGAAGGTGAACACCTGCAGCTGAGGCTTGGAAACGTTTCTTGTGTTGCCCTGAAAAATCTTTGAGACCTCAG
GGAGGCTCTGTCTCTCTTAAAAGGTGGAGAAAGATGCCATTCTCTCCCTAAGGTCTGGTGGAGTCTCCCCATCTT
GCATACCTTCTGCAAGCCATCTATCTCTGCTCACTCTCCAATTGACCCGCTGGGAACAAGGGATGAGGAGGAG
TTGGGGGCTGGGGGGAATCCTGCCAGTTGGTGAAGCCCTGTGGCAGGAAGGTATATGTGGACATAGAGTATACCT
GATTCTCTTTCTTCAGCCACTGACTGCTTGGGTTGGGCTGTGAATGATAATGGAATGGCTGGAGTCTGCTGTTGT
CAGAAGGCAGGGAGGGTGATGAAGGACTGACCCACATGGACTGGGATGTGTGTCGGTTATGGGCATGACTGCACG
TTCACCTCTCAGTGGGATCTGGGCAACATGGAGTTTATTGTCTGTTGCTTACTTACTGCAATGTCTTTGGCCCTC
CTTTTCAACTGGTTCCTCTGTTGGGCCCCAAAGGTTGGGAGTAGGAGACAGTATCCAGGCTGACAAGGGCTTGCC
CTTTACCTTGGGCACCTTGTTAATTTTTAGCCTGTGCCCTTCCCCACCTTTGCCCTCCAGTGGTTGGTATGTGG
GAAGCCCATCTCAGTTCCTGTGACTTCATGTCTCAAACCAAGGATGAGCGTCTGGTCTCTGCTATGATGGTGGTA
TCCGAGGCCTTTCCCTGCCAGTCTGGTGCCTGCCCCACATTGTACCGGACACTGGATTCTGGACCCCTTCTC
CTTTCTTTCTTTCTTCAGGTACGCAGCCCTGTACTGTATCCAGCACCACAGAAACCTCAGTGTTTTTCTCTCT
GCTGGTTTGGGGACAAGGAAGCCTTAGGGTATGGGGAAGGCTGTTATTACCTAGAGTTTACTCCAGGCCAGG
GGGCTGCCATCTTCTTCACAGACATCCCTGAAAGGAAGCCCTTTGGGGCAGGAGGTGAGGACTTCATCTCAAC
ATCGGCTGGTGGTTGGTAGGGGAGCTTTTTCTTTCTTTCTTTTTTTTTTTGTTTTTGTGTTTTGTTTTG
GTAAC**ATG**TTAGGAGTTAATGTTGCAAAGAGTAGTTTACATCTTCACTTTCTGAAGACACTTGAATTTAGGACCG
ATGTATCTGTGACAAGCATGCCAGAAGTGGCAGGGGCCATCAGGGCTAACCACTTCACACCTACCATCGTCCCAT
GGGGATCCAAGACCT**AG**AGATAAAAGCAACAGCCTGCCAGATCCCTCTGTTCATCCTATCCCTTCCAAGGTTGGTC
CATGCCAACATAACCTCTGGGCATCAGACATCAGCAGGTCTGTGTGCCTCAGCCCTGTTAAGGGGCAGGTTTCTC
TTTAGCCCTCTTCTGCACTTGGGAGCAAAGGCACTACCAGTAGAGAAGGGCCATCCAGCCGTGCCCCAGCCTGG
ACCCCTGGGGCTCAGATAGAGGTGCTGAGCCCTGTGTCAAAGTTGTTAAATGTTTTGTTTTGTTCCATTGTAG
CTCTTTTTTTTTTTTTTCCCTTTCCTGGTGATTGATTTTACAAAAGAAAGTAAGCTGCTTAGAAGGCCCTGGAAGG
GAAGTGAGGAGGAGGGACAAGGAAGATGACTAGTTACGGAGGGTGAGGGTTGTTTTTGGCAAAAAGCCTGGGTA
GAGTGATCTGAATTATCTGGCACCTCCTGAATGGAACCCAGAGTACCTCCTGTGTGGAAGGTCCTGGATTT
TCCCTAACACCCACCCTCTCCCCCTTCAGCCATGCTGATGGCAGAGAAGATAAGAAGTTGGAGCCCATTTCTCAC
TGGAGAGGAAAACCTTGTATCTGGCTTTGCGGAGAAGGTTCCACCTTACGCTCGTAGTACATTATCTTTACTATG
TGCTAGGATATCATATTTAAAAGGACAAAAAATGTAAATACTTGAATGAGCTTGTATTATAACATTAATATTA
TTGAGAGTATCTGCTTTCCAGGCTGAAGTGATTCATTATTCTAGTCCTGCTTTAGTCCTTTGTAATTTGTG
GTAATTATGCTTTTCTTTTAAATACAAAAAATGTATAAAAAATAAACACTTGAAAAGGCAAAAAAAAAAAAAA
AA

1944/6881
FIGURE 1786

MLGVNVAKSSLHLHFLKTLEFRTDVSVTSMPEVAGAIRANHFTPTIVPWGSKI

.

1945/6881
FIGURE 1787

GCGGTCTTATATAAGCCAGATCCGCAGGGGAGTCCGCAGAAGGGTTAAACAGGTCTTTGGGCTTCGGCGACCTCG
CCCGCGGCAGAAACCGGTAAGAAGACAGTGGGCTGCGCGTCTCATTTTCAGCCTTGCCCGGACTCTCCCAAAGCC
GGCGCCCAGTAGTGGCTCCAGAGCCCACAGGTGGCCCCCGGCAGTCTCTGGGGCGCATGGAGCGGCGTTAATAGG
GCTGGCGGCGCAGGCCAGTAGCCGCTCCAACATGAACCTCGTGGGCAGCTACGCACACCATCACCACCATCACCA
CCCGCACCTGCGCACCCCATGCTCCACGAACCTTCTCTTCGGTCCGGCCTCGCGCTGTCATCAGGAAAGGCC
CTACTTCCAGAGCTGGCTGCTGAGCCCGGCTGACGCTGCCCCGGACTTCCCTGCGGGCGGGCCGCCGCCCGCGGC
CGCTGCAGCCGCCACCGCCTATGGTCCTGACGCCAGGCCTGGGCAGAGCCCCGGGCGGCTGGAGGCGCTTGGCGG
CCGTCTTGGCCGGCGGAAAGGCTCAGGACCCAAGAAGGAGCGGAGACGCACTGAGAGCATTAAACAGCGCATTTCGC
GGAGTTGCGCGAGTGATCCCCAACGTGCCGGCCGACACCAAGCTCTCCAAGATCAAGACTCTGCGCCTAGCCAC
CAGCTACATCGCCTACCTGATGGACGTGCTGGCCAAGGATGCACAGTCTGGCGATCCCGAGGCCTTCAAGGCTGA
ACTCAAGAAGGCGGATGGCGGCCGTGAGAGCAAGCGGAAAAGGGAGCTGCAGCAGCACGAAGGTTTTCTCTCTGC
CCTGGGCCCAGTCGAGAAGAGGATTAAAGGACGCACCGGCTGGCCGCAGCAAGTCTGGGCGCTGGAGTTAAACCA
GTGAGCCCGAGGCCGCCGAGACTGGCCCAGGAGAGGAGGCAGCG
CGAACGCCAGGCTCTGGGCTCCGGCGACTGGTGCTACGCATCCCGCGGAGCTTCTGCTGAGCGCCGGCAGGTCTGT
CGGCTGCAACCACACACTTGGATCGCACGTGCAATGTCCTTTGATTTTTTTAATACATTAAAGAGAAAGAGAAAT
ATATATATATCCACCCCCAGCCCAACCGAGGGCGGCCCTTGGCGGCAACATGCAAGAAGGAGGGACTGTGCAACC
CAAGGGCTCAAAGACGCACTCTTCCACCCTTTTGGAGCGAATTTAGAACCTCAGCCCTATCTCCATTTCCTATC
TGGCTCTTTCTCTCTTGTCCCTCCATATGATCCGCCCCGACGCCGTCTTCTCTAATTAAATGCAATAAGGAATC
AATTCTTTTCTTGCCTGAGAAAGAGAACCAGACGCAGGAAGATGAAAGGCTGCCCTTTGTTCTTCGAATCGTGGT
GGTTTTATTTTATTTTCTTTTTGTGCTGCACTTCCTGTTTAGTTCCAAGGGAAACACTTCTCTCTTTCTCTG
TCTCTCTTTTTCTTCTTCTTTTCTTCTTCTTTTGTCTATCTAAATAAAAGCTTTCCTGTGTTGGAAAGTT
TTTATGTATTTAACTACCTACCATGCCTGTTGTGCTCAGGTGTTTGTTCATCCTGCCATCCCCAACCTTTTCT
ACCTCAAGTCTGTGTGACCACTCACAGCCCCCTCCCTTCGCCAAAGCAGTGTCTATGCTCTTGATTAATAAAAC
ATTTTCTGAAATCAAAAAAAAAA

1946/6881
FIGURE 1788

MNLVGSYAHHHHHHPHPAHPMLHEPFLFGPASRCHQERP YFQSWLLSPADAAPDFPAGGPPPAAAAAATAYGPD
ARPGQSPGRLEALGGRLGRRKGS GPKKERRRTE SINS AFAELRECIPNVPADTKLSKIKTLRLATS YIAYLMDVL
AKDAQSGDPEAFKAELKKADGGRESKRKRELQQHEGFPPALGFPVEKRIKGRTGWPQQVWALELNQ

1947/6881
FIGURE 1789

ATGCACTATTCTAAGGAATATAGGCAGATGTACAGAACTGAAATTCGAATGACAAGGATGGCAAGAAAAGCTGGC
AACTTCTATGTACCTGCAGAACCCAAATTGGAGTTTGTATCAGGATCAGAGGTATCAATGGTGATCAGATTCAT
AAGATCTATACTGTTGGAAAACGCTTCAAAGAAGCAAATAACTTTCTGTGGCCCTTCAAATTACCTTTCCACCA
GGCAGAGTGAAGAAAAAGACCACTTATTTGTAGAAGGTGGAAATGCTGGCAACAGGGAGGACCAGATCAACAGG
CTTATTAGAAGAATGAACTAA

1948/6881
FIGURE 1790

MHYSKEYRQMYRTEIRMTRMARKAGNFYVPAEPKLEFVIRIRGINGDQIHKIYTVGKRFKEANNEFLWPFKLPFPP
GRVKKKTTYFVEGGNAGNREDQINRLIRRMN

1949/6881
FIGURE 1791

GATCAGGGCCGAGTTGTCTCGGCGGCGCTGCCGAGGCCTCCACCCAGGACAGTCCCCCTCCCCGGGCCTCTCTCC
TCTTGCCCTACGAGTCCCCCTCTCCTCGTAGGCCTCTCGGATCTGATATCGTGGGGTGAGGTGAGCAGGCCCCGGGGA
GGGTGGTTACCGCTGAGGAGCTGCAGTCTCTGTCAAGATGATAGAGGTACTGACAACAAGTACTCTCAGAACT
GCTACACCAGCTGAATGCCCTGTTGGAACAGGAGTCTAGATGTCAGCCAAAGGTCTGTGGTTTGAGACTAATTGA
GTCTGCACACGATAATGGCCTCAGAATGACTGCAAGACTAAGGGACTTTGAAGTAAAAGATCTTCTTAGTCTAAC
TCAGTTCTTTGGCTTTGACACAGAGACATTTCTCTAGCTGTGAATTTACTGGACAGATTCTGTCTAAAATGAA
GGTACAGCCCAAGCACCTTGGGTGTGTTGGACTGAGCTGCTTTTATTTGGCTGTAAAATCAATAGAAGAGGAAAG
GAATGTCCCATTTGGCAACTGACTTGATCCGAATAAGTCAATATAGGTTTACGGTTTCAGACTTGATGAGAATGGA
AAAGATTGTATTGGAGAAGGTGTGTTGGAAAGTCAAAGCTACTACTGCCTTTCAATTTCTGCAACTGTATTATTC
ACTCCTTCAAGAGAACTTGCCACTTGAAAGGAGAAATAGCATTAATTTTGAAAGACTAGAAGCTCAACTGAAGGC
ATGTCATTGCAGGATCATATTTTCTAAAGCAAAGCCTTCTGTGTTGGCATTGTCTATCATTGCATTAGAGATCCA
AGCACAGAAGTGTTAGAGTTAACAGAAGGAATAGAATGTCTTCAGAAACATTCCAAGATAAATGGCAGAGATCT
GACCTTCTGGCAAGAGCTTGTATCCAAATGTTTAACTGAATATTCATCAAATAAGTGTTCCAAACCAAATGTTCA
GAAGTTGAAATGGATTGTTTCTGGGCGTACTGCACGGCAATTGAAGCATAGCTACTACAGAATAACTCACCTTCC
AACAATTCCTGAAATGGTCCCTTAACTGGATTATTACAGCACCAAAAACTTCTCTGAAGCCTTTCTCCACAACC
TTGTTCTATGGATTCCATAATGTTACAATGGATTAAAGCTATGAAGCCTCAAACATCACGAGATAAGCATGATG
GTCTCAGACTTGGGAAAACTGCCTAATATTATGCTGTAGTGGAATTATGTTTATGATTTGAATTCATCTGTGAAG
GCATTCAAATCAAAGCTAAAAGCCTAAATGTGAAATGCTAATGACAAGCCTGAGAAGGTAAACTATGAATCTTCA
TTTCTATCATTGATCTAACTTTAGATATTGGATCAATATATTTAGGTGGTATTGAAAATGCTATTGGAGGAGTCA
CACTAATACTATCAACTATCAGTCTTCCCACAGCTTCAATCACTGTCATTATTCTAATCCTACTCCTACTTAAAT
TTTAAGTTATGAGGTTTATGTGCAAAGCAACATTTCAAAATGTACTTTTAAGGCATAATAAGGGTTAACATTCT
AGG

1950/6881
FIGURE 1792

MIEVLTTTDSQKLLHQLNALLEQESRCQPKVCGLRLIESAHDNGLRMTARLRDFEVKDLLSLTQFFGFDTEFTSL
AVNLLDRFLSKMKVQPKHLGCVGLSCFYLA VKSIEEERNVPLATDLIRISQYRFTVSDLMRMEKIVLEKVCWKVK
ATTAFQFLQLYSSLQENLPLERRNSINFERLEAQLKACHCRIIFSKAKPSVLALSIIALEIQAKCVELTEGIE
CLQKHSKINGRDLTFWQELVSKCLTEYSSNKCSKPNVQKLKWIVSGRTARQLKHSYYRITHLPTIPEMVP

1951/6881
FIGURE 1793A

GTAGAGTTAAGGAAGGGCCTCTTCCTCTGTGAGAATTCAGCATTTTGTCAACCATCCAAAAATGTTGAGGGCATGC
TTTGCTTCCAGGGCAGACAGAGCAGCACAGTGAGCATGGGACACAGGATCCCTGACTTGCTGTGTGCCCTTAAAC
CAGCCACTACCTCTCTGACGTTCAAATTTAGCAATGGAAGGCAGCCTGCCCAACTGTTACCTGCCTGTATCAT
GAAAGCCTGCGGATGAGTGCAGAATACAGAACTGCAGCCATGACCACGCACGTCACCCTGGAAGATGCCCTGTC
CAACGTGGACCTGCTTGAAGAGCTTCCCCTCCCCGACCAGCAGCCATGCATCGAGCCTCCACCTTCCTCCATCAT
GTACCAGGCTAACTTTGACACAACTTTGAGGACAGGAATGCATTTGTACGGGCATTGCAAGGTACATTGAGCA
GGCTACAGTCCACTCCAGCATGAATGAGATGCTGGAGGAAGGACATGAGTATGCGGTATGCTGTACACCTGGCG
CAGCTGTTCCCGGGCCATTCCCAGGTGAAATGCAACGAGCAGCCCAACCGAGTAGAGATCTATGAGAAGACAGTA
GAGGTGCTGGAGCCGGAGGTACCAAGCTCATGAAGTTCATGTATTTTTCAGCGCAAGGCCATCGAGCGGTTCTGC
AGCGAGGTGAAGCGGCTGTGCCATGCCGAGCGCAGGAAGGACTTTGTCTCTGAGGCCTACCTCCTGACCCTTGGC
AAGTTCATCAACATGTTTGTGTCTGCTGGATGAGCTAAAGAACATGAAGTGCAGCGTCAAGAATGACCACTCTGCC
TACAAGAGGGCAGCACAGTTCCCTGCGGAAGATGGCAGATCCCCAGTCTATCCAGGAGTGCAGAACCTTTCCATG
TTCTTGCCCAACCACAACAGGATCACCCAGTGTCTCCACCAGCAACTTGAAGTGATCCCAGGCTATGAGGAGCTG
CTGGCTGACATTGTCAACATCTGTGTGGATTACTACGAGAACAAGATGTACCTGACTCCAGTGAGAAACATATG
CTCCTCAAGGTGATGGGCTTTGGCCTCTACCTAATGGATGGAATGTGAGTAACATTTACAACTGGATGCCAAG
AAGAGAAATTAATCTTAGCAAAATTGATAAATCTTTAAGCAGCTGCAGGTGGTGCCCCCTTTTCGGCGACATGCAG
ATAGAGCTGGCCAGATACATTAAGACCAGTGTCTACTATGAAGAGAACAAGTCCAAGTGGACGTGCACCCAGAGC
AGCATCAGCCCCAGTACAATATCTGCGAGCAGATGGTTCAGATCCGGGATGACCACATCCGCTTCATCTCCGAG
CTCGCTCGCTACAGCAACAGTGAGGTGGTGACGGGCTCAGGGCTGGACAGCCAGAAGTCAGACGAGGAGTATCGC
GAGCTCTTCGACCTAGCCCTGCGGGGTCTGCAGTCTCTATCCAAGTGGAGCGCCACGTCATGGAGGTGTACTCT
TGGAAGCTGGTTCATCCACAGACAAGTTCTGCAACAAGGACTGTCTGGCACCGCGGAGGAATATGAGAGAGCC
ACACGCTACAATTACACCAGTGAGGAAAAATTTGCCTTCGTTGAGGTGATCGCCATGATCAAAGGCCTGCAGGTG
CTCATGGGCAGGATGGAGAGCGTCTTCAACCAGGCCATCAGGAACACCATCTACGCGGCATTGCAGGACTTCGCC
CAGGTGACGCTGCGTGAGCCCCCTGCGGCAGGCGGTACGGAAGAAGAAGAATGTCTCATCAGCGTCTACAGGCA
ATTCGAAAGACCATCTGTGACTGGGAGGGAGGGCGAGAGCCCCCTAATGACCCATGCTTGAGAGGGGAGAAGGAC
CCCCAAGGTGGATTTGATATCAAGGTGCCCCGGCGTGCTGTGGGGCCATCCAGCACACAGCTGTACATGGTGC GG
ACCATGCTTGAATCACTCATTGCAGACAAAAGCGGCTCCAAGAAGACCCTGAGGAGCAGCCTGGATGGACCCATT
GTCTTCGCCATAGAGGACTTTTCAAAACAGTCCTTCTTCTTCAACATCTGCTCAACATCAGTGAAGCCCTGCAG
CAGTGTGTGACCTCTCCAGCTCTGGTTCCGAGAATTCTTCTGAGTTAACCATGGGCGGACGAATCCAGTTC
CCCATCGAGATGTCCATGCCCTGGATTCTAACGGACCATATCTGGAAACCAAAGAACCTTCCATGATGGAGTAT
GTCTCTACCTCTGGATCTGTACAACGACAGCGCCTACTATGCTCTGACCAAGTTTAAAAAGCAGTTCCTGTAC
GATGAGATAGAAGCTGAGGTGAACCTGTGTTTTGATCAGTTTGTCTACAAGCTGGCAGACCAGATCTTTGCTTAC
TACAAAGCCATGGCTGGCAGTGTCTGTGGATAAACGTTTTTCGAGCTGAGTGTAAGAATTATGGCGTCATCATT
CCGTATCCACCGTCCAATCGCTATGAAACACTGCTGAAGCAGAGACACGTCCAGCTGTTGGGTAGATCAATTGAC
TTGAACAGACTCATTACCCAGCGCATCTCTGCCGCCATGTATAAATCCTTGGACCAAGCTATCAGCCGCTTTGAG
AGTGAGGACCTGACCTCCATTGTGGAGCTGGAGTGGCTGCTGGAGATTAACCGGCTCACGCATCGGCTGCTCTGT
AAGCATATGACGCTGGACAGCTTCGATGCCATGTTCCGAGAGGCCAATCACAATGTGTCCGCCCCCTATGGCCGT
ATCACCTGTCATGTCTTCTGGGAACCTGAACTTTGACTTTCTCCCCAACTACTGCTACAATGGGTCCACTAACCGT
TTTGTGCGGACTGCCATTCCCTTTCACCCAAGAACCACAACGAGACAAACCTGCCAACGTCCAGCCTTATTACCTC
TATGGATCCAAGCCTCTCAACATTGCCTACAGCCACATCTACAGCTCCTACAGGAATTTCTGTGGGGCCACCTCAT
TTCAAGACTATCTGCAGACTCCTGGGTTATCAGGGCATCGCTGTGGTCATGGAGGAAGTGTAAAGATTGTGAAG
AGCTTGCTCCAAGGAACCATTTCTCCAGTATGTGAAAACACTGATAGAGGTGATGCCCAAGATATGCCGCTTGCCC
CGACATGAGTATGGCTCCCCAGGGATCCTGGAGTTCTTCCACCACCAGCTGAAGGACATCATTGAGTACGCAGAG
CTCAAAACAGACGTGTTCCAGAGCCTGAGGGAAGTGGGCAATGCCATCCTCTTCTGCCCTCCTCATAGAGCAAGCT
CTGTCTCAGGAGGAGGTCTGCGATTTGCTCCATGCCGCACCCTTCCAAAACATCTTGCTTAGAGTCTACATCAAA
GAGGGGGAGCGCCTGGAGGTCCGGATGAAACGTCTGGAAGCCAAGTATGCCCCGCTCCACCTGGTCCCTCTGATC
GAGCGGCTGGGGACCCCTCAGCAAAATCGCCATTGCTCGCGAGGGTGACCTCCTGACCAAGGAGCGGCTGTGCTGT
GGCCTGTCCATGTTTCGAGGTTCATCCTGACCCGCATTTCGGAGCTACCTGCAGGACCCCATCTGGCGGGGGCCACCG

1952/6881
FIGURE 1793B

CCCACCAATGGCGTCATGCACGTCGATGAGTGTGTGGAGTTCCACCGGCTGTGGAGCGCCATGCAGTTCGTGTAC
TGCATCCCTGTGGGAACCAACGAGTTCACAGCTGAGCAGTGTTTCGGCGATGGCTTGAAGTGGGCTGGTTGCTCC
ATCATTGTCCTGCTGGGCCAGCAGCGTCGCTTTGACCTGTTGACTTCTGTTACCACCTGCTAAAAGTGCAGAGG
CAGGACGGGAAGGATGAAATCATTAAGAATGTGCCCCCTGAAGAAGATGGCCGACCGGATCAGGAAGTATCAGATC
TTGAACAATGAGGTTTTTGGCATCCTGAACAAATACATGAAGTCCGTGGAGACAGACAGTTCCACTGTGGAGCAT
GTGCGCTGCTTCCAGCCACCCATCCACCAGTCCTTGGCCACCACTTGCTAAGCAGAAGATCCTGCAGACCCTTAT
CTGGAGGAGGAAGAGAAGCAGGAGAGAGAAAGCCACAGCCAGCCTGCCATAGGATCCAAGTGGACAACGTGTGGG
ATGGACCTGGAAACAAGCACCTCCCCAAACACATCACCCTCCCTAGGGCGGGGCCTGTGCATGCTCTCCCATGA
CATCTCCATGCTGGTTTTCTCCATAGCATAAATGAAAAAAAAAAAAAAAAAGTAAACAGGGCAGTGTGTGCTTTTT
CTTTTCTCCCCCTCAACTATATTAAGAACTCCTAGTTTCACCCTTTCTCCATCCCATCATCCCACCTATCTGTG
GTTGCTTCCCAAGACCT

1953/6881
FIGURE 1794

MKFMFYQRKAIERFCSEVKRLCHAERRKDFVSEAYLLTLGKFINMFAVLDELKNMKCSVKNDHSAYKRAAQFLRK
MADPQSIQESQNLSMFLANHNRTQCLHQQLEVIPGYEELLADIVNICVDYYENKMYLTPSEKHMLLKVMGFGLY
LMDGNVSNYKLDKAKKRINLSKIDKFFKQLQVVPLFGDMQIELARYIKTSAHYEENKSKWTCTQSSISPQYNICE
QMVQIRDDHIRFISELARYSNSEVVTGSGLDSSQSDDEYRELFDLALRGLQLLSKWSAHVMEVYSWKLVHPTDKF
CNKDCPGTAEYERATRYNYTSEEKFAFVEVIAMIKGLQVLMGRMESVFNQAIRNTIYAALQDFAQVTLREPLRQ
AVRKKKNVLISVLQAIRKTICDWEGGREPPNDPCLRGEKDPKGGFDIKVPRRAVGPSSQLYMVRTMLES LIADK
SGSKKTLRSSLDGPVLAIEDFHKQSFFFTHLLNISEALQQCCDLSQLWFREFFLELTMGRRIQFPIEMSPWIL
TDHILETKEPSMMEYVLYPLDLYNDSAYYALTKFKKQFLYDEIEAEVNLCFDQFVYKLADQIFAYYKAMAGSVLL
DKRFRAECKNYGVIIPYPPSNRYETLLKQRHVQLLGRSIDLNRLITQORISAAMYKSLDQAISRFESEDLT SIVEL
EWLLEINRLTHRLLCKHMTLDSFDAMFREANHNVSAPYGRITLHVFWELNFDLFPNYCYNGSTNRFVRTAIPFTQ
EPQRDKPANVQPYLYGSKPLNIAYSHIYSSYRNFGPPHFKTICRLLGYQGIADVMEELLKIVKSLLQGTILQY
VKTLIEVMPKICRLPRHEYGSPGILEFFHHQLKDIEYAEKTDVDFQSLREVGNAILFCLLIEQALSQEEVCDLL
HAAPFQNILPRVYIKEGERLEVRMKRLEAKYAPLHLVPLIERLGTPQQIAIAREGDLLTKERLCCGLSMFEVILT
RIRSYLQDPIWRGPPPTNGVMHVDECVEFHRLWSAMQFVYCI PVGTNEFTAEQCFGDGLNWAGCSIIVLLGQQR
FDLFDFCYHLLKVQRQDGKDEIIKNVPLKKMADRIRKYQILNNEVFAILNKYMKSVETDSSSTVEHVRCFQPPIHQ
SLATTC

1954/6881
FIGURE 1795

GCGGCCTCAGATGAATGCGGCTGTTAAGACCTGCAATAATCCAGAAATGGCTACTCTGATCTATGTTGATAAGGAA
AATGGAGAACCAGGCACCCGTGTGGTTGCTAAGGATGGGCTGAAGCTGGGGTCTGGACCTTCAATCAAAGCCTTA
GATGGGAGATCTCAAGTTTCAACACCACGTTTTGGCAAAACGTTTCGATGCCCCACCAGCCTTACCTAAAGCTACT
AGAAAGGCTTTGGGAACTGTCAACAGAGCTACAGAAAAGTCTGTAAAGACCAAGGGACCCCTCAAACAAAAACAG
CCAAGCTTTTCTGCCAAAAAGATGACTGAGAAGACTGTAAAGCAAAAAGCTCTGTTCCCTGCCTCAGATGATGCC
TATCCAGAAATAGAAAAATTCTTCCCTTCAATCCTCTAGACTTTGAGAGTTTTGACCTGCCTGAAGAGCACCAG
ATTGCGCACCTCCCCTTGAGTGGAGTGCCTCTCATGATCCTTGACGAGGAGAGAGCTTGAAAAGCTGTTTCAG
CTGGGCCCCCTTACCTGTGAAGATGCCCTCTCCACCATGGGAATCCAATCTGTTGCAGTCTCCTTCAAGCATT
CTGTCGACCCTGGATGTTGAATTGCCACCTGTTTGCTGTGACATAGATATTTAAATTTCTTAGTGCTTCAGAGTT
TGTGTGTATTTGTATTAATAAAGCATTCTTCAACAGAAAAAAAAAAAAAAAAAAAAA

1955/6881
FIGURE 1796

MATLIYVDKENGE PGTRV VAKDGLKLGSGPSIKALDGRSQVSTPRFGKTFDAPPALPKATRKALGTVNRATEKSV
KTKGPLKQKQPSFSAKKMTEKTVKAKSSVPASDDAYPEIEKFFPFNPLDFESFDLPEEHQIAHLPLSGVPLMILD
EERELEKLFQLGPPSPVKMPSPPWESNLLQSPSSILSTLDVELPPVCCDIDI

1956/6881
FIGURE 1797

ATGGCCCTGGAGTTTCTCCCTCAGACTAAGAACCATCCACCAGTAGCAGAAACTACATCCTCAGGGGGGGTTC
TTCGTGAATGCAAATGTCCCGGCACCTAAACGGTTCACATTACCGCAGGTGATTTCTGCAGCTGTAAC TAAGTTC
CATCCTCAGCAAGAATCAGAACCACCAGAGACAGAGCAGAGAGACACCATGCCCTCACTTGCGAGAGTTCAAATG
GCACTTTCTTGAAAAAGAAGATTGGGTGTTACAGCTTTCTGAGCAACAACGATACAAAGTGGATGCAATTCAT
CCATCGTCTCTGAAAAGTCTTCGACCATTGCATGAGATTGTAGAGGAAGACAGGCACAGGAAGACCAAACAGCGT
GTAGAGGATACGAAGATTGGCTACCCAAGTGTTCATCAGTACCCCATTCATCATCAACGGGTACAAACGAGTC
CTGGCCTTGCTGTGGAGACGGATTACACCTTCCCACTCGCTGAAAAGGTCAAGGCCTTCTTGGCTGATCCATCT
GCCTTTGGCTTTGATGTTTCAAGCAATGCTGGGTCAACCAACCACTCAGCACATTCCTGGACCTGGTCGTGCC
CAAGCTCCTCCACTGCATGATTCAGAGTTGAGATAG

1957/6881
FIGURE 1798A

GCAACTGGACAACAACCACATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGCTGCGCGATTTGGAGATCCTTAC
CCTCAACAACAACAACATCAGTCGCATCCTGGTCACCAGCTTCAACCACATGCCGAAGATCCGAACCTGCGCCT
CCACTCCAACCACCTGTACTGCGACTGCCACCTGGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGG
CCAGTTCACACTCTGCATGGCTCCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCAGAAGAAGGAGTACGT
GTGCCCAGCCCCCACTCGGAGCCCCCATCCTGCAATGCCAACTCCATCTCCTGCCCTTCGCCCTGCACGTGCAG
CAATAACATCGTGGACTGTGAGGAAAGGGCTTGATGGAGATTCTGCCAACCTGCCGGAGGGCATCGTCGAAAT
ACGCCTAGAACAGAACTCCATCAAAGCCATCCCTGCAGGAGCCTTCACCCAGTACAAGAACTGAAGCGAATAGA
CATCAGCAAGAATCAGATATCGGATATTGCTCCAGATGCCTTCAGGGCCTGAAATCACTCACATCGCTGGTCTCT
GTATGGGAACAAGATCACCGAGATTGTCAAGGGACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTCAA
TGCCAACAAGATCAACTGCCTGCGGGTGAACACGTTTCAGGACCTGCAGAACCTCAACTTGCTCTCCCTGTATGA
CAACAAGCTGCAGACCATCAGCAAGGGGCTCTTCGCCCCCTCTGCAGTCCATCCAGACACTCCACTTAGCCCCAAA
CCCATTGTGTGCGACTGCCACTTGAAGTGGCTGGCCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGC
CCGCTGCAGCAGCCCGCGCCGACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCGCTGCTCAGG
CTCCGAGGATTACCGCAGCAGGTTACGACGAGTGTTCATGGACCTCGTGTGCCCCGAGAAGTGTGCTGTGA
GGGCACGATTGTGGACTGCTCCAACCAGAAGCTGGTCCGCATCCCAAGCCACCTCCCTGAATATGTACCGACCT
GCGACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCATCTTCAAGAAGTTGCCAACCTGCGGAAAAT
AAATCTGAGTAACAATAAGATCAAGGAGGTGCGAGAGGGAGCTTTGATGGAGCAGCCAGCGTGCAGGAGCTGAT
GCTGACAGGGAACCAGCTGGAGACCGTGCACGGGCGCGTGTTCGCTGGCCTCAGTGGCCTCAAACCTTGATGCT
GAGGAGTAACTTGATCGGCTGTGTGAGTAATGACACCTTTGCCGGCCTGAGTTCGGTGAGACTGCTGTCCCTCTA
TGACAATCGGATCACCAACCATCACCCCTGGGGCCTTCACCACGCTTGTCTCCCTGTCCACCATAAACCTCCTGTC
CAACCCCTTCAACTGCAACTGCCACCTGGCCTGGCTCGGCAAGTGGTTGAGGAAGAGGCGGATCGTCAGTGGGAA
CCCTAGGTGCCAGAAGCCATTTTTCCTCAAGGAGATTCCCATCCAGGATGTGGCCATCCAGGACTTCACCTGTGA
TGGAACAGAGGAGAGTAGCTGCCAGCTGAGCCCGCGCTGCCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGCG
ATGCAGCAACAAGGGGCTCCGCGCCCTCCCAGAGGCATGCCCAAGGATGTGACCGAGCTGTACCTGGAAGGAAA
CCACCTAACAGCCGTGCCAGAGAGCTGTCCGCCCTCCGACACCTGACGCTTATTGACCTGAGCAACAACAGCAT
CAGCATGCTGACCAATTACACCTTCAGTAACATGTCTCACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAG
GTGCATCCCGCTCCACGCCTTCAACGGGCTGCGGTCCCTGCGAGTGCTAACCTCCATGGCAATGACATTTCCAG
CGTTCCTGAAGGCTCCTTCAACGACCTCACATCTCTTTCCCATCTGGCGCTGGGAACCAACCCACTCCACTGTGA
CTGCAGTCTTCGGTGGCTGTGCGAGTGGGTGAAGGCGGGGTACAAGGAGCCTGGCATGCCCCGCTGCAGTAGCCC
TGAGCCCATGGCTGACAGGCTCCTGCTCACCACCCCAACCCACCGCTTCAGTGCAAAGGGCCAGTGGACATCAA
CATTGTGGCCAAATGCAATGCCTGCCTCTCCAGCCCGTGCAAGAATAACGGGACATGCACCCAGGACCCCTGTGGA
GCTGTACCGCTGTGCCTGCCCCCTACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAA
CCCCTGTGAGCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTCAGCTGCTCCTGCCCTCTGGG
CTTTGAGGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAAAACAATGCCACCTGCGT
GGACGGGATCAACAACACTACGTGTGTATCTGTCCGCCTAACTACACAGGTGAGCTATGCGACGAGGTGATTGACCA
CTGTGTGCCTGAGCTGAACCTCTGTGAGCATGAGGCCAAGTGCATCCCCCTGGACAAAGGATTGAGCTGCGAGTG
TGTCCTGGCTACAGCGGGAAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCCAAGTGCCGCCACGGGGC
CCAGTGCCTGGACACAATCAATGGCTACACATGCACCTGCCCCAGGGCTTCAGTGGACCCCTTCTGTGAACACCC
CCCACCCATGGTCTACTGCGAGACCAGCCCATGCGACCAGTACGAGTGCCAGAACGGGGCCAGTGCATCGTGGT
GCAGCAGGAGCCACCTGCCGCTGCCACCAGGCTTCGCGGGCCCCAGATGCGAGAAGCTCATCACTGTCAACTT
CGTGGGCAAAGACTCCTACGTGGAAGTGGCCTCCGCCAAGGTCCGACCCAGGCCAACATCTCCCTGCAGGTGGC
CACTGACAAGGACAACGGCATCCTTCTCTACAAAGGAGACAATGACCCCTGGCACTGGAGCTGTACCAGGGCCA
CGTGC GGCTGGTCTATGACAGCCTGAGTTCCCTCCAACCACAGTGTACAGTGTGGAGACAGTGAATGATGGGCA
GTTTCACAGTGTGGAGCTGGTGACGCTAAACCAGACCCCTGAACCTAGTAGTGGAACAAGGAACTCCAAAGAGCCT
GGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAGCCCCCTCTACCTTGAGGCATCCCCACCTCCACCGG
CCTCTCTGCCTTGCGCCAGGGCACGGACCGGCCTCTAGGCGGCTTCACGGATGCATCCATGAGGTGCGCATCAA
CAACGAGCTGCAGGACTTCAAGGCCCTCCCACCACAGTCCCTGGGGGTGTCACCAGGCTGCAAGTCTGACCCGT
GTGCAAGCACGGCCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGC CGCCAGGCTGGACCGGCCC

1958/6881
FIGURE 1798B

ACTCTGCGATCAGGAGGCCCCGGGACCCCTGCCTCGGCCACAGATGCCACCATGGAAAATGTGTGGCAACTGGGAC
CTCATACATGTGCAAGTGTGCCGAGGGCTATGGAGGGGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCTG
CTCAGCCTTCAAGTGTCAACCATGGGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCGG
CTTTAGCGGCGAGCACTGCCAACAAGAGAATCCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCAGAA
AGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCCATCATGGAATGTCGTGGGGGCTGTGGGCCCCAGTGCTG
CCAGCCCACCCGCAGCAAGCGGCGGAAATACGTCTTCCAGTGACGACGGCTCCTCGTTTGTAGAAGAGGTGGA
GAGACACTTAGAGTGCGGCTGCCTCGCGTGTTCCTAAGCCCCCTGCCCGCCTGCCTGCCACCTCTCGGACTCCAGC
TTGATGGAGTTGGGACAGCCATGTGGGACCCCTGGTGATTCAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTA
AAGAAGAAGAGAATATTAAGTATATTGTAAAATAAACAAAAAATAGAACTTATTTTTATTATGGAAA

1959/6881
FIGURE 1799

GCCATGGGCGCGCGCCCGCCTGTTGTTACCGGTATTGTAAGAACAAGCCGTACCCAAAGTCTCGCTTCTGCCGA
GGTGTCCCTGATGCCAAGATTTCGCATTTTTGACCTGGGGCGGAAAAAGGCAAAAGTGGATGAGTTTCCACTTTGT
GGCCACATGGTGTTCAGATGAATATGAGCAGCTGTCTCTGAAGCCCTGGAGGCTGCCCCGAATTTGTGCCAATAAG
TACATGGTAAAAAGTTGTGGCAAAGATGGCTTCCATATCCGGGTGCGGCTCCACTCCTTCCACGTCATCCGCATC
AACAAGATGTTGTCCTGTGCTGGGGCTGACAGGCTCCAAACAGGCATGCGAGGTGCCTTTGGAAAGCCCCAGGGC
ACTTTGGCCAGGGTTTCACTGGCCAAGTTATCATGTCCATCCGCACCAAGCTGCAGAACAAAGGAGCATGTGATT
GAGGCCCCTGGGCAGGGCCAAGTTCAAGTTTCTGGCCGCCAGAAGATCCACATCTCAAAGAAGTGGGGCTTCACC
AAGTTCAATGCTGATGAATTTGAAGACATGGTGGCTGAAAAGCGGCTCATCCCAGATGGCTGTGGGGTCAAGTAC
ATCCCCAATCGTGGCCCTCTGGACAAGTGGCGGGCCCTGCACTCATGAGGGCTTCCAATGTGCTGCCCCCTCTT
AATACTCACCAATAAATTCTACTAACTCTCCAAAAAAAAAAAAAAAAAATAGAAAAAAAAAAAAAAAAATAGACCAA
AAAAAAAAAAAAAAAAA

1960/6881
FIGURE 1800

GGCACGAGGGTGAGACGCTGATGGGAGGATGGACGTACTGGTGTCTGAGTGCTCCGCGCGGCTGCTGCAGCAGGA
AGAAGAGATTAAATCTCTGACTGCTGAAATTGACCGGTTGAAAACTGTGGCTGTTTAGGAGCTTCTCCAAATTT
GGAGCAGTTACAAGAAGAAAATTTAAATTAAGTATCGACTGAATATTCTTCGAAAGAGTCTTCAGGCAGAAAG
GAACAAACCAACTAAAAATATGATTAACATTATTAGCCGCCTACAAGAGGTCTTTGGTCATGCAATTAAGGCTGC
ATATCCAGATTTGGAAAATCCTCCTCTGCTAGTGACACCAAGTCAGCAGGCCAAGTTTGGGGACTATCAGTGTA
TAGTGCTATGGGTATTTCTCAGATGCTCAAAACCAAGGAACAGAAAGTTAATCCAAGAGAAATTGCTGAAAACAT
TACCAAACACCTCCCAGACAATGAATGTATTGAAAAAGTTGAAATTGCTGGTCCTGGTTTTATTAATGTCCACTT
AAGAAAGGATTTTGTATCAGAACAATTGACCAGTCTTCTAGTGAATGGAGTTCAACTACCTGCTCTGGGAGAGAA
TAAAAAGGTTATAGTTGACTTTTCCTCCCCTAATATAGCTAAAGAGATGCATGTAGGCCACCTGAGGTCAACTAT
CATAGGAGAGAGTATAAGCCGCCTCTTTGAATTTGCAGGGTATGACGTGCTCAGGTTAAATCATGTAGGAGACTG
GGGGACCCAGTTTGGCATGCTCATCGCTCACCTGCAAGACAAATTTCCAGATTATCTAACAGTTTACCTCCTAT
TGGGGATCTTCAGGTCTTTTATAAGGAATCTAAGAAGAGGTTTGATACTGAGGAGGAATTTAAGAAGCGAGCATA
TCAGTGTGTAGTTCTGCTCCAGGGTAAAAACCCAGATATTACAAAAGCTTGGAAGCTTATCTGTGATGTCTCCCG
CCAAGAGTTAAATAAAATCTATGATGCATTGGACGTCTCTTTAATAGAGAGAGGGGAATCCTTCTATCAAGATAG
GATGAATGATATTGTAAAGGAATTTGAAGATAGAGGATTTGTGCAGGTGGATGATGGCAGAAAGATTGTATTTGT
CCCAGGGTGTTCCATACCATTAAACCATAGTAAAAATCAGATGGAGGTTATACCTATGATACATCTGACCTGGCTGC
TATTAAACAAAGACTATTTGAGGAAAAAGCAGATATGATTATCTATGTTGTGGACAATGGACAATCTGTGCACTT
CCAGACAATATTTGCTGCTGCTCAAATGATTGGTTGGTATGACCCTAAAAGTAACTCGAGTCTTCCATGCTGGATT
TGGTGTGGTGCTAGGGGAAGACAAGAAAAAGTTTAAACACGTTTCGGGTGAAACAGTGCGCCTCATGGATCTTCT
GGGAGAAGGACTAAACGATCCATGGACAAGTTGAAGGAAAAAGAAAGAGACAAGGTCTTAACTGCAGAGGAATT
GAAATGCTGCTCAGACATCCGTTGCATATGGCTGCATCAAATATGCTGACCTTTCCCATACCGGTTGAATGACTA
CATCTTCTCCTTTGACAAAATGCTAGATGACAGAGGAAATACAGCTGCTTACTTGTGTATGCCTTCACTAGAAT
CAGGTCTATTGCACGTCTGGCCAATATTGATGAAGAAATGCTCCAAAAGCTGCTCGAGAAACCAAGATTCTTTT
GGATCATGAGAAGGAATGAAACTAGGCCGGTGCATTTTACGGTTCCTGAGATTCTGCAAAAGATTTTAGATGA
CTTATTTCTCCACACTCTCTGTGATTATATATATGAGCTGGCAACTGCTTTCACAGAGTTCTATGATAGCTGCTA
CTGTGTGGAGAAAGATAGACAGACTGGAAAAATATTGAAGGTGAACATGTGGCGTATGCTGCTATGTGAAGCAGT
AGCTGCTGTGATGGCCAAGGGGTTTGATATCCTGGGAATAAAACCTGTCCAAAGGATGTAATCCTTCATAGGTTT
GAACACTGTGTGTTTTTACCAAAGTGGCCATTGGCACTGTTTGCTTTTTTACAATCATGTGGACACAAGCATAAG
TAAAGAAAATTTGTCAACCAAAAAAAAAAAAAAAAAAAAAA

1961/6881
FIGURE 1801

MDVLVSECSARLLQQEEEIKSLTAEIDRLKNCGLGASPNLEQLQEENLKLKYRLNILRKSLQAERNKPTKNMIN
IISRLQEVFGHAIKAAYPDLENPPLLVTSPQQAKFGDYQCNSAMGISQMLKTKEQKVNPREIAENITKHLPDNEC
IEKVEIAGPGFINVHLRKDFVSEQLTSLLVNGVQLPALGENKKVIVDFSSPNIAKEMHVGHRLRSTIIGESISRLF
EFAGYDVLRLNHVGDWGTQFGMLIAHLQDKFPDYLTVSPPIGDLQVFYKESKKRFDTEEEFKKRAYQCVLLQGK
NPDITKAWKLICDVSRLQELNKIYDALDVSLIERGESFYQDRMNDIVKEFEDRGFVQVDDGRKIVFVPGCSIPLTI
VKSDGGYTYDTSDLAAIKQRLFEEKADMIYVVDNGQSVHFQTIFAAAQMIGWYDPKVTRV FHAGFGVVLGEDKK
KFKTRSGETVRLMDLLGEGLKRSMDKLKEKERDKVLTAEELNAAQTSVAYGCIKYADLSHNRNDYIFSFDKMLD
DRGNTAAYLLYAFTRIRSIARLANIDEEMLQKAARETKILLDHEKEWKLGRCILRFPEILQKILDDFLHTLCDY
IYELATAFTEFYDSCYCVEKDRQTGKILKVNMMWRMLLCEAFAVMAKGF DILGIKPVQRM

1962/6881
FIGURE 1802

CAGTTCACAGTGTTTCATCAGGCGAGATACTTTTGGACCCACAAAGCCAGTTTTTTTGGGGGGATGCTCAGTGTCTA
CCTGCAGTGCCAAAGTTTTGCTTGAACAGCCCTCTTCTGCCGCGCCTCCCAGCTCCACCCCTATCAGTGGGTG
CTGGCTGCTTCTGCGTGAGGAGCTTCCTCTGATCACCTGTAGCATCTTTAGTGCCCTTCGTCCAGTCGGCCTGCAA
ATCCCATTTCCCAGAGAGGCTTGGGCAGGGCCCACTTGCCACTTGCCCTGTGCCCAGAGCGTTGGGGGCAGATG
GCAGCCAGGGGAAGAAGGGAGGTGGGGAAGGGCCGCCACCGCTTGAGGGTCCCCTCCCTTGAGAGGAGGCCCAT
GGCAGTTTTCTGAGTTCTTGATCCACTTTGGTTTAAACAACTTTTGTGAAGCTATGTGAGATTTGACTGCATTT
CAAAAGACAAAACACATGTTTTTTTCTGATTTGCTCTTTGCTTTTCAGCGACGCTTTTCAGATACTTTGTGAGTGT
CTACTCTGTGCTAGGTGCTGAGTAGACTGGGATGTGTGTGGCTCCATCCCTGGCTGGAAGAGCTTTGAGTCCTGT
CTGCTGACTTCACTGAAGGAGTTTTCTCTCTTGCTTCATTCTCTCCCTCCCGGGGGTTCAGCTGGGTAGGAGCAGACT
TGCCCTGCCTTCCTCTAGGCAGAAAGTTTTCTTGCAAATGAAAGAATCTGCCATTCTCTTTTGCTATGATGATGA
TGATTATTCTGACATGACCCGCGGGTACTGAAGCCACAGTCCTCTCTGTTCACTGTTCTCTCCTTGAGTCATATC
TATGGCCTGAGGACGTCTGTATCCAGCTCCTTTTCCTACAATGGTAGACACTTCCCCAGGCAGTGGGTGGGTGAG
GGTGGCCAGTCACTCTCCTAGCTGTCTTGCTGGGGACTTAGATTTACCCCATCCAGGACTGTGGTGCCTATTC
TGTGAGCGATTGATGGCGCATATGCAGAACTCCCCTGGAGTCATGGCTCTAGAAAGTGTCCAGGCCCATCGTGAC
AATGGTGCCAAGCACCGGGCTGGTGACCACTGCCTAAACACACACGCTCCTTTAATCCTTACGGCAAGCCTGTGA
GGCGGATAGGACCAGCCCTGATCTATAGTGAGAAAATTAAGGTTTCAGAGGGAGAAGGTCCAAATAGTGGCCAAGC
TGGGACTGAGATCTCGAGTTTGGGTTTGTGTTGGTTTTGTTGTTGTTGTTCTTTCCCTCGTGTCCATGACTTTTTCT
CTGCCATTAGCAGGGAAGTGTGCGGAGGGCTTCCAGGGAATCAAGTGACCCTCCCTCTGAATTTTCGGTGCCTCTT
CCCCCGCCCCCTTGCTCACACATTTTCTAGTGTACAGGCCAAATGGCAGCCCCAAAAGGTGGGCAGAGATTTTTT
TTTCTTCCCTCACCCCTGCTTATTAACACAATTGTGACAACCTACTTTACCTTACATCCCAGGGCAAACGGACAG
CTTGCGGTACCTCCAAAATTTGGA AAAACCCTGAGTCTAAGACCACCTCTTGATAAAAGAGGCCTTTGCTCACAT
GTTCTGCTCGGAATCTTTCTTTGCCATTGGTGGGTGTATGTCGTCCCAGCTGAGACTGCGGGAGAGCTGAGCTCC
AGCTTAAACCGCTTTTAAATGGCCCTTCCCTACTGGGGGATCGCTGGAGCCCATGCCAGGTTACGGTAGTCATTTT
AAACCTCTGCCACAAGGCCACGCCATAGAATCAATTTCCAAGTCAATGTTCTTGCCCTAAAATGTTTGCGCCCA
CTGAGGATTTTATTACCAGGTGGAAGATGGGGGAACATATGCCACGTTAAAGAGCAAGTGCTGAGTGTGCCAGGA
CTTGAGAAGGACCTTAGGCTGAGGAGTGGACAGTCTGGTATTTATTTGCTCTCCCAAGTACCCAGCACAGAGT
GGGAAAAAGAAGAACTGCTCCTGCCTTCCAGTAGCTGGCAACTTGACATCAAGAACA AAAACATTTCGTAGCTGG
ACCCCGCTCCTTTTATCGTGCCCAAGTCTTACATGTTGGCTTAAGCTGCCCCCTTGAGGGCGGTACCTTTCTCTT
TGGACTGTGACAGTGGACACCTAACAGCCTGAGCCATGTGTGGCTGTCTTATCCCCCAAGGGTTGTCCAGGCCCG
TTCTGCAGGGCTGTTGTGTAGACTGCAGACATCCATACCTCACCACAGACCAAAGATGACCTCGTGTGAGACTGT
GGGCTGATGAGAGGTAGAGCAGCATGCATCGAGGCCTGAGGGTGCAGGGCGCCCTCTCTTGGCCTGGAGGAATTG
CTCCTAACTAGAGTAAGTTTCCACGAGGGTCCCAGGCAGAGCTGCAGAGCTGGAACCGGAGGCTCCACAGTCCTT
GCCTGCTCATGGACCTCCTTCAGAGCACCTTTCTACAGACTGGACTGCCCAGCTCCGTGGGGTGGCATCTGGTTT
CTGGTGCTATTCTGCCAAGTTATCGAGCTCCTCCTCATGTTTCAACATTCCATCTTCCCGTTTCTATCCTCGACT
CCAAAGTAAGCCTTCTTAGCTCCAATCAGGGATGAGGGGCTCAACCTCTTCTGTCCTCAAAGAGGCCAAACGCAG
TGCCACAGTCGGTAGCCTTCACTTTTAGATGTCCTATTTCATGTAAAAAAGAAGGTGCCCCACCAGGCTTACATC
AGCAATAAGCAATTCTAATGCAACGATGGTGTCCACATTTTACCCAGTGTGTGCCATGTATGCCTTTGTGCCC
GTGTAATTATTGTTAGCGCCCTTCACTTAGAGGGGTGATGATAAACTGTGGCCACCTTGATTACAACCCACAT
TTCTTGCTTTGGGGAGCTTCCAAGTAACAGGCCATTTCTTACCTCCCTCCAGGAACAGTGGGCACTGCCACCAC
CTCGTGTCTGCTCATAGGATGACGCTGGAGATCCCCACACTTACTCTACCTCTTGGCAAATTGGCATTCCGGTG
GTGGTTTTTGTTCCTTTAACACATTAAATAAATGAGTATATAGGATGTGAGGGGAGGGGTGAGAACAACCTAGCT
GTAGCATGTGTAGGCTATATACTTTACCATTTGACTTCTTTCTTTTTTTTTTTTTTAAATAAAAAAAGTGCTTGA
CTGGTTTCAAGCTTCATCATG

1963/6881
FIGURE 1803

GGGGCCTGGTGTGATTCCGTCCTGCGCGGTTGTTCTCTGGAGCAGCGTTCTTTTATCTCCGTCCGCCTTCTCTCC
TACCTAAGTGCGTGCCGCCACCCGATGGGAAGATTTCGATGGACATGGACATGAGCCCCCTGAGGCCCCAGAACTAT
CTTTTCGGTTGTGAACTAAAGGCCGACAAAGATTATCACTTTAAGGTGGATAATGATGAAAATGAGCACCAGTTA
TCTTTAAGAACGGTCAGTTTAGGGGCTGGTGCAAAGGATGAGTTGCACATTGTTGAAGCAGAGGCAATGAATTAC
GAAGGCAGTCCAATTAAAGTAACACTGGCAACTTTGAAAATGTCTGTACAGCCAACGGTTTCCCTTGGGGGCTTT
GAAATAACACCACCAGTGGTCTTAAGGTTGAAGTGTGGTTTCAGGGCCAGTGCATATTAGTGGACAGCACTTAGTA
GCTGTGGAGGAAGATGCAGAGTCAGAAGATGAAGAGGAGGAGGATGTGAACTCTTAAGTATATCTGGAAAGCGG
TCTGCCCCCTGGAGGTGGTAGCAAGGTTCCACAGAAAAAAGTAAACTTGCTGCTGATGAAGATGATGACGATGAT
GATGAAGAGGATGATGATGAAGATGATGATGATGATGATGATTTTGATGATGAGGAAGCTGAAGAAAAAGCGCCAGTG
AAGAAATCTATACGAGATACTCCAGCCAAAAATGCACAAAAGTCAAATCAGAATGGAAAAGACTCAAAACCATCA
TCAACACCAAGATCAAAAGGACAAGAATCCTTCAAGAAACAGGAAAAAACTCCTAAACACCAAAAGGACCTAGT
TCTGTAGAAGACATTAAAGCAAAAATGCAAGCAAGTATAGAAAAAGGTGGTTCTCTTCCCAAAGTGGAAGCCAAA
TTCATCAATTATGTGAAGAATTGCTTCCGGATGACTGACCAAGAGGCTATTCAAGATCTCTGGCAGTGGAGGAAG
TCTCTTTTAAGAAAATAGTTTAAACAATTGTTAAAAAATTTTCCGTCTTATTTCATTTCTGTAACAGTTGATATC
TGGCTGTCCTTTTTATAATGCAGAGTGAGAACTTTCCCTACCGTGTTTGATAAATGTTGTCCAGGTTCTATTGCC
AAGAATGTGTTGTCCAAAATGCCTGTTTAGTTTTTAAAGATGGAATCCACCCTTGCTTGGTTTTAAAGTATGTA
TGGAATGTTATGATAGGACATAGTAGTAGCGGTGGTCAGACATGGAAATGGTGGGGAGACAAAAATACACATGTG
AAATAAACTCAGTATTTTAATAAAGTAAAAAAAAAAAAAAAAACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

1964/6881
FIGURE 1804

MEDSMDMDMSPLRPQNYLFGCELKADKDYHFKVDNDENEHQLSLRTVSLGAGAKDELHIVEAEAMNYEGSPIKVT
LATLKMSVQPTVSLGGFEITPPVVLRLKCGSGPVHISGQHLVAVEEDAEESEDEEEEDVKLLSISGKRSAPGGGSK
VPQKKVKLADEDDDDDDDEDDDEDDDDDDDFDDEEAEEKAPVKKSIRDTPAKNAQKSNQNGKDSKPSSTPRSKGQ
ESFKKQEKTPKTPKGPSSVEDIKAKMQASIEKGGSLPKVEAKFINYVKNCFRMTDQEAIQDLWQWRKSL

1965/6881
FIGURE 1805

GGGCGGCGCCCAATGGGCTGCGCGGAGCGTCACTTCCCGGCAGCGGGAGGCGAGTGGCGAGTGGCGAGTGGCGAG
TGTCAGGGGGGCGGCCGGCGGGGGCGGGGCGGCCGGAGGAGGCGTTGGCAGCGGGCTCGGACCCACGCGGCGCCG
CGGCCCGCCTGGCCTGCAGCGCTCCACCCCCGGCGGGCGGCACGATGCCCTTTGACTTCAGGAGGTTTGACATCT
ACAGGAAGGTGCCCAAGGACCTTACGCAGCCAACGTACACCGGGGGCCATTATCTCCATCTGCTGCTGCCTCTTCA
TCCTCTTCCTCTTCCTCTCGGAGCTCACCGGATTTATAACGACAGAAAGTTGTGAACGAGCTCTATGTCGATGACC
CAGACAAGGACAGCGGTGGCAAGATCGACGTCAGTCTGAACATCAGTTTACCCAATCTGCACTGCGAGTTGGTTG
GGCTTGACATTACAGGATGAGATGGGCAGGCACGAAGTGGGCCACATCGACAACCTCCATGAAGATCCCGCTGAACA
ATGGGGCAGGCTGCCGCTTCGAGGGGCGAGTTTCAGCATCAACAAGGTCCCCGGCAACTTCCACGTGTCCACACACA
GTGCCACAGCCCAGCCACAGAACCCAGACATGACGCATGTTCATCCACAAGCTCTCCTTTGGGGACACGCTACAGG
TCCAGAACATCCACGGAGCTTTCAATGCTCTCGGGGGAGCAGACAGACTCACCTCCAACCCCCCTGGCCTCCCACG
ACTACATCCTGAAGATTGTGCCACGCGTTTATGAGGACAAGAGTGGCAAGCAGCGGTACTCCTACCAGTACACGG
TGGCCAACAAGGAATACGTCGCCTACAGCCACACGGGCCGCATCATCCCTGCAATCTGGTTCCGCTACGACCTCA
GCCCCATCACGGTCAAGTACACAGAGAGACGGCAGCCGCTGTACAGATTTCATCACCACGATCTGTGCCATCATTG
GCGGGACCTTCACCGTCGCCGGCATCCTGGACTCATGCATCTTCACAGCCTCTGAGGCCTGGAAGAAGATCCAGC
TGGGCAAGATGCATTCAGCGCCACACCCAGCCTAATGGCCGAGGACCTGGGCATCGCCAGCCTTGCCCTCCAGTGC
CCTGTCTCCTTTGGCCCTCAATCTGGTCCCAAATCTGGCTGTGTCCCAAAGGGTGTGTGGGAAGTGGGGGGAAAG
TAGAGGATGGCTCGATGTTTTGCAGCTACCTCTTTTCCCGTGTTCTTTTTTAGACAAATTACACTGCCTGAAGT
TGCAGTTCCCCTTTCCCTGGGGAGCCCCAAGAACAGAGTCAGGCAAGGGGTGGGGAGTCCAGGGGAACATCCCAG
AATGCATATCGATCAGCTCTCAGCCAGGCTTCGACAATCTCGCAGCCCCCACTAGGTGGACACATTAATGATTTG
GTTTCTCCCCTGGGCAGCCAACCTGCCCCAGAGGCACCAGACCTGGGCTTTCAGCTTTGGGACCAGGCTGCCCAA
AGGTACTCCTTTATACACCCGGCACCTTCACGAAAGATGGTACTTCCCAAGCAAGCCCCTATGATTTGTCACTA
TAGATGGAAATGTGTGGCATGCACATGAGTTGAAATTCCTTTATGCATTTTTTTGAAGAAAAAAAAAAAAACAAC
TCTGAGGACATAGGGGATGTCAGTTTCCTATGGAAGAGACACCTCTGACCCGTTATTCTTATAATCAAAATCTGA
AGGGAAAAAATGTTTTAGTTCTTTCCCACTCGTTGGGTTCAACTAGATTAAAAGGCTGATTTTCAG

1966/6881
FIGURE 1806

MPFDFRRFDIYRKVPKDLTQPTYTGAIISICCLFILFLFLSELTGFFITTEVVNELYVDDPDKDSGGKIDVSLNI
SLPNLHCELVGLDIQDEMGRHEVGHIDNSMKIPLNNGAGCRFEGQFSINKVPGNFHVSTHSATAQPQNPDMTTHVI
HKLSFGDTLQVQNIHGAFNALGGADRLTSNPLASHDYILKIVPTVYEDKSGKQRYSYQYTVANKEYVAYSHTGRI
IPAIWFRYDLSPITVKYTERRQPLYRFITTICAIIGGTFTVAGILDSCIFTASEAWKKIQLGKMH

1967/6881
FIGURE 1807

ATGGCGTATCACGGCCTCACTGTGCCTCTCATTGTGATGAGCGTGTTCTGGGGCTTCGTCGGCTTCTTGGTGCCT
TGGTTCATCCCTAAGGGTCCTAACCGGGGAGTTATCATTACCATGTTGGTGACCTGTTTCAGTTTGCTGCTATCTC
TTAGCTAGTTTGAGCACAGGACATAATCACTTCCCAGGGGCCTGGGTGCACCGCTTTGGTTTCCAACCAAACCAT
GACTCCATGAGCGTGAACCAGGACTATTCTGCTCACCTTGTGTCTGCACACAGTAGGTGCTTAACAAACACCTGG
GGTATCTTCAAGTCCATTCCCTCATCTGACCCCTCACAGCAGCCCTCTGAGGAAGGCAGCCTGCACACTGGAGGAG
ACAGGTCTGCACTCAGCCATTCTGAAGACGGTAAAAGTGAGAGCCCTGGATGCCATGGGGGCAAGGACCATATCT
GTTCTGCTTTTTTCTGAAGTCCCTGACCCAATTTGTGCCCGGTACATTGAAGAAGCTCAGGACATGGCTATTATT
TCAATCAAGCTGAAATCTACTGAGCTGAGCTGGCCCAACCAGGAATTCAAGATAAGACAGTAG

1968/6881
FIGURE 1808A

GAAGCCGCCCATCCCGCCCCAAGTGGAGGAAGAGTATTACACCATCGCCGAATTCCAGACAACCATCCCAGACGG
CATCAGCTTCCAGGCAGGCCTGAAGGTCGAGGTGATCGAGAAAACTTGAGTGGCTGGTGGTACATTTCAGATTGA
AGATAAGGAAGGGTGGGCCCCGGCCACCTTCATTGACAAGTACAAGAAGACGAGCAACGCGTCGAGACCCAACTT
TCTGGCTCCCCTGCCCCACGAGGTGACCCAGCTCCGGCTGGGGGAAGCAGCAGCGCTGGAGAACAACACGGGCAG
CGAAGCCACGGGCCCCCTCCCGCCCCCTGCCTGACGCACCGCATGGTGTCATGGACTCGGGGTGCCATGGTCTAA
AGACTGGAAGGGCAGTAAGGATGTCCTGAGGAAGGCATCTTCAGACATGTCTGCGTCAGCAGGCTACGAGGAGAT
CTCAGACCCCGACATGGAGGAGAAGCCAGCCTCCCTCCGCGGAAAGAATCCATCATCAAGTCGGAGGGGGGAGCT
GCTGGAGCGGGAGCGGGAGCGGCAGAGGACGGAGCAGCTCCGGGGCCCCACTCCCAAGCCTCCGGGCGTGATTTT
GCCGATGATGCCAGCCAAACACATCCCTCCAGCCCGGGACAGCAGGAGGCCAGAGCCCAACCTGACAAAAGCAG
ACTGTTCCAGCTGAAAAATGACATGGGGCTGGAGTGTGGCCACAAGGTCTTGGCCAAGGAAGTGAAGAAGCCCAA
CCTCCGGCCCATCTCCAAATCCAAAAGTACCTGCCAGAGGAGAAGCCAGATGCCACTCCCCAGAATCCCTTCTT
GAAGTCCAGACCTCAGGTTAGGCCAAAACAGCTCCTTCCCCCAAAACGGAGCCACCTCAGGGCGAAGACCAAGT
CGACATCTGCAACCTCAGGAGTAAGCTCAGGCCTGCCAAGTCCCAAGACAAGTCTTGTGGATGGGGAGGGCCC
CCAGGCAGTAGGGGGCCAAGACGTGGCCTTCAGCCGAAGCTTCCTCCAGGAGAGGGGCTGGCCGCGCCAGGA
CAGGACGGGCAAACAGGATGGTCTCAGCCCAAAGAGATTTCTGTCAGAGCCCCTCCGAGGCCAGCCAAGACCAC
AGATCCTGTGTCTAAGAGCGTGCTGTCTCTCCAAGAGGCTCCCCAGCAGAGACCTGTGGTCCCACCCCGCAG
ACCACCTCCCCCAAGAAAACTCTCTGTCATCCAGGCCGCTCCAGAGGTCAGAGGTCCACAGTGTGAAGGCCA
CGAAAGCAGGGCAGCTCCCAACCCAGGCCGTGCTCTCTCGTCCCTCCAAAAGCCAAACCTTTTCTCTCAACTC
TTTGGGGGGCCAGGATGACACGCGAGGCAAAGGCAGCCTGGGGCCATGGGGGACCGGCAAGATTGGAGAAAACAG
GGAGAAAGCAGCTGCAGCCTCTGTCCCCAATGCCGACGGCCTGAAGGACTCTTTGTATGTGGCCGTGGCCGACTT
TGAAGGAGACAAAGACACCAGCAGCTTCCAGGAAGGGACAGTGTGTTGAAGTCCGGGAGAAGAACAGCAGTGGCTG
GTGGTCTGCCAGGTCTTGAGCGGAGCCCCCTTCTGGGAAGGGTGGATTCTTCCAATATCTCAGAAAGAAGCC
GTAGCCGACTCCCTTTCTGCCTAGAGGGCCCGCTGGTCTTGCTGGCTTTACCCACGTATTTAATACGCCTCTTA
ATTTATCATTCTCCACGCAGCTTCCAAGGCAGACAGACTCTGGGGTACTGTGACTTCTTGCTCCCATGGGTGGA
GAGTGAGTTTCGGACACCTCGGGCGCCCCCTGGGCCTGATCCCTCTATCACAGCATCACTGGAGGCTCAGAACCC
ACAGCCTTTGCTTTCTGTCCATGTGAGCATCCCTGCCTTAAGAGAACTCCTCCTGGCCAATGGCATTGCCACCCA
GCAGTGGGACCAAGACTCTCCAAGACCTCCAGGACTGGATCCCATTGCCTGGAGAAAACCTCCAGCAAGGGTCTCTC
ATGGCTTGACATGGCACAGTAAGGGGCAGCCAACCCAGTCCATGATGACTTTTGCTCCAATCTTTCATGTTTT
TAAAAGCCCAGTGGCTTTATTTACTCTCTCTAAATTTGCCTGCTACCAGAAGGAACCTTCATCCTGAAGAAATGCAT
TCCATTACCAGTTCCAGGGAAAGTGTCCCTTCCCCAAAGCCTCAGGCCCGTGGGCCTCTGAGGTTCCACTGGAT
GCGGCTCCCCCAGGAGTGGGCCTGGAGATCCGCTCAGCCGCCCTGCCTCCCACCTTCTATCTTGGGACCGTGGTC
AGCCCTGAAGGGTGGTTCCAGCCCCGCGTATGCTGCGCTTTGCTGCTGCAGGCTCCGGTCCCTCCAGGGCTTTTC
AATGAGAGTTCCACCCCAACTTGAGCATTTCATTTTTGCTTACCTAAAGCAAGAATCTCAAAGTTTGTGTTGAA
TAAGAGGCCCATTCACAAGTCGTGCCCTTGTGAGCACCCCTTTGCTGAGTGCCTCGTGGGTGCCAAACACTGTAC
TTGGCGCTTTGCATTTCATGCTTTGACCCTCACAACCTCCCTTTATAGATGAGGAAATTCACGCTCCATGTGCCCA
AGGACACACCAGCCAGGAGGAAGAGGGAAGAGGATTTGAGTCCAGGCCTGCCTGACTTCAGTGCCTGTGCCCTCC
CCTCTGTAAAAGACAAAACAGGCAGGGAAGAGATAGAAGCTGGCTAAGTGGTGGCCAAGTGGCTTCATTGTGAGG
GGGGTGAGGGGGCATTCTGTGGCTGCTCCACACCCACCATCCCTCCAGCCCACAGCAGCCTATACCAAAGGCTGC
CCTGGACTCAACAGCTGCATCTCCATGACAGGAGAATGCCAGGGTCCCTGGTGGTTGACACAGAGCCCTGTTCCCT
CTTCTAAGCTGTTGCCCCCTGGGGAATAGAGCTTATGGAGCAACGGGAGCTGAGGTGGCCTCGAGGGCCAGCCTG
GAGGGCTCTGAGCATAGCATGCAGCGGTCCCATAGGGAGGCAGGTAACCAAGGGCCAGGCAGAGCTGCTTCCTGT
GCCTCTCCGGCATTGTGTAATGTTTTTTCTTTTTTACGCACTGCCAAATCTGTTTTCTCCCTTGAAGAAACCCA
GGGCAGATGTGGTCACTGTCAAACCTGAGGTCTGGAGAGGCATGACTAAATCACTGCAGAAGCAAAATCAGGACC
CAGCATTCTTAGCTCCCAGCCCAGAGTAAGAGAGCAGAGCAGAACCCCTTCCATTCTACCCGACCGAGGCAGCC
CTGCCCTGCCCTGCCCGCCCCCTCCCCACCTGCCCTGCCCCAGAGATCTCCAGTTCACAGTGTTCATCAGGCGA
GATACTTTTGGACCCACAAAGCCAGTTTTTTGGGGGGATGCTCAGTGTCTACCTGCAGTGCCAAAGTTTTGCTTG
AACAGCCCTCTTCTGCCGCGCTCCAGCTCCACCCCTATCACGTGGGTGCTGGCTGCTTCTGCGTGAGGAGCT
TCTCTGATCACCTGTAGCATCTTTAGTGCCTTCGTCCAGTCGGCCTGCAAATCCCATTTCCAGAGAGGCTTGG

1969/6881
FIGURE 1808B

GCAGGGCCCACTTGCCACTTGGCCCTGTGCCCAGAGCGTTGGGGGCAGATGGCAGCCAGGGGAAGAAGGGAGGTG
GGGAAGGGCCGCCACCGCTTGAGGGTCCCCCTCCCTTGAGAGGAGGCCCATGGCAGTTTTCTGAGTTCTTGATC
CACTTTGGTTTAAACAACCTTTGTGAAGCTATGTGAGATTTGACTGCATTTCAAAGACAAAACACATGTTTTTT
TCTGATTTGCTCTTTGCCTTTCAGCGACGCTTTCAGATACTTTGTGAGTGTCTACTCTGTGCTAGGTGCTGAGTA
GACTGGGATGTGTGTGGCTCCATCCCTGGCTGGAAGAGCTTTGAGTCCTGTCTGCTGACTTCACTGAAGGAGTTT
CTCTCTTGCTTCATTCCCTCCCTCCCGGGGGTCAGCTGGGTAGGAGCAGACTTGCCCTGCCTTCCCTCTAGGCAGAA
AGTTTTCTTGCAAATGAAAGAATCTGCCATTCTCTTTTGCTATGATGATGATGATTATTCTGACATGACCCGCGG
GTACTGAAGCCACAGTCCTCTCTGTTCACTGTTCTCTCTTGAGTCATATCTATGGCCTGAGGACGTCTGTATCC
AGCTCCTTTTTCTACAATGGTAGACACTTCCCCAGGCAGTGGGTGGGTGAGGGTGGCCAGTCACTCTCCTAGCTG
TCCTTGCTGGGGACTTAGATTTACCCCATCCAGGACTGTGGTGCCTATTCTGTGAGCGATTGATGGCGCATATG
CAGAACTCCCCCTGGAGTCATGGCTCTAGAAAGTGTCCAGGCCCATCGTGACAATGGTGCCAAGCACCAGGGCTGGT
GACCAGTGCCATAACACACACGCTCCTTTAATCCTTACGGCAAGCCTGTGAGGCGGATAGGACCAGCCCTGATCT
ATAGTGAGAAAAATTAAGTTTCAAGGGAGAAGGTCCAAATAGTGCCAAGCTGGGACTGAGATCTCGAGTTTGGG
TTTGTTTGGTTTTTGTGTGTGTGTCTTTCCCTCGTGTCATGACTTTTCTCTGCCATTAGCAGGGAAGTGTGCG
GAGGGCTTCCAGGGAATCAAGTGACCCTCCCTCTGAATTTGCGTGCCTCTTCCCCCGCCCCCTTGCTCACACATT
TCAGTAGGTACAGGCCAAATGGCAGCCCCAAAGGTGGGCAGAGATTTTTTTTTTCTTCCCCTCACCCCTGCTTAT
TAACACAATTGTGACAACACTTTACCTTACATCCAGGGCAAACGGACAGCTTGCGGTACCTCCAAAAATTTGG
AAAACCCTGAGTCTAAGACCACCTCTTGATAAAAGAGGCCTTTGCTCACATGTTCTGCTCGGAATCTTCTTTGC
CATTGGTGGGTGTATGTCGTCCCAGCTGAGACTGCGGGAGAGCTGAGCTCCAGCTTAAACCGCTTTAATGGCCC
TTCCCTACTGGGGGATCGCTGGAGCCCATGCCAGGTTACGGTAGTCATTTTAAACCTCTGCCACAAGGCCACGCC
ATAGAATCAATTTCCAAGTCAATGTTCTTGCCCTAAAATGTTTGCGCCCACTGAGGATTTTATTACCAGGTGGA
AGATGGGGGAACATATGCCACGTTAAAGAGCAAGTGCTGAGTGTGCCAGGACTTGAGAAGGACCTTAGGCTGAGG
AGTGACAGTCTGGTATTTATTTGCTCTTCCCAAGTACCCAGCACAGAGTGGGAAAAAGAAGAACTGCTCCTG
CCTTCCAGTAGCTGGCAACTTGACATCAAGAACAAAAACATTCGTAGCTGGACCCCGCTCCTTTTATCGTGCCCCA
AGTCTTACATGTTGGCTTAAGCTGCCCCCTTGAGAGCCGTACCTTTCTCTTTGGACTGTGACAGTGGACACCTAA
CAGCCTGAGCCATGTGTGGCTGTCTTATCCCCCAAGGGTTGTCCAGGCCCGTTCTGCAGGGCTGTTGTGTAGACT
GCAGACATCCATACCTCACCACAGACCAAAGATGACCTCGTGTGAGACTGTGGGCTGATGAGAGGTAGAGCAGCA
TGCATCGAGGCCTGAGGGTGCAGGGCGCCCTCTCTTGCCCTGGAGGAATTGCTCCTAACTAGAGTAAGTTTCCAC
GAGGGTCCCAGGCAGAGCTGCAGAGCTGGAACCGGAGGCTCCACAGTCCTTGCCCTGCTCATGGACCTCCTTCAGA
GCACCTTTCTACAGACTGGACTGCCCAGCTCCGTGGGGTGGCATCTGGTTTCTGGTGCTATTCTGCCAAGTTATC
GAGCTCCTCCTCATGTTTCAACATTCCAICTTCCCGTTTCTATCCTCGACTCCAAAGTAAGCCTTCTTAGCTCCA
ATCAGGGATGAGGGGCTCAACCTCTTCTGTCTCAAAGAGGCCAAACGCAGTGCCACAGTCGGTAGCCTTCACTT
TTAGATGTCCTATTTCATGTAAAAAAGAAGGTGCCCCACCAGGCTTACATCAGCAATAAGCAATTCTAATGCAAC
GATGGTGTCCACATTTTACCCAGTGTGTGCCCATGTATGCCTTTGTGCCCCGTGTAATTATTGTTAGCGCCCCCTT
TCACTTAGAGGGGTGATGATAAACTGTGGCCACCTTGATTACAACCCACATTTCTGCTTTGGGGAGCTTCCAAG
TAACAGGCCATTTCTTACCTCCCTCCAGGAACAGTGGGCACTGCCACCACCTCGTGTCTGCTCATAGGATGACG
CTGGAGATCCCCACACTTACTCTACCCTCTTGGCAAATTGGCATTCCGGTGGTGGTTTTTGTTCCTTTAACACA
TTAAATAAATGAGTATATAGGATGTGAGGGGAGGGGTGAGAACAACTAGCTGTAGCATGTGTAGGCTATATACTT
TACCATTGACTTCTTTCTTTTTTTTTTTTTTAAATAAAAAAAGTGCTTGACTGGTTTCAAGCTTCATCATG

1970/6881
FIGURE 1809

MDSGLPWSKDWKGSKDVLRLKASSDMSASAGYEEISDPDMEEKPSLPPRKESI IKSEGELLERERERERQRTEQLRGP
TPKPPGVILEMMPAKHIPPARDSRRPEPKPDKSRLFQLKNDMGLECGHKVLAKEVKKPNLRPISKSKTDLPEEKP
DATPQNPFLKSREPVRPKPAPSPKTEPPQGEDQVDICNLRSKLRPAKSQDKSLLDGEGPQAVGGQDVAFSRSFLP
GEGPGRAQDRTGKQDGLSPKEISCRAPPRPAKTTPVSKSVPVPLQEAPQQRPVVPPRRPPPPKKTSSSSRPLPE
VRGPQCEGHESRAAPTTPGRALLVPPKAKPFLSNSLGGQDDTRGKGS LGPWGTGKIGENREKAAAASVPNADGLKD
SLYVAVADFE GDKDTSSFQEGTVFEVREKNSSGWWFCQVLSGAPSWEGWIPSNYLRKKP

1971/6881
FIGURE 1810

TTGGCTGATTGCAATTCTGGCCCAACTCAACCCTCTCTTTGGACCGCAATTGAAAAATGAAACCATCTGGTATCT
GAAGTATCATTGGCCTTGAGGAAGAAGACATGCTCTACAGTGCTCAGTCTTTGAGGTCACGAGAAGAGAATGCCT
TCTAGATGCAAAATCACCTCCAAACCAGACCACTTTTCTTGACTTGCCGTGTTTTGGCCATTAGCTGCCTTAAACG
TTAACAGCACATTTGAATGCCTTATTCTACAATGCAGCGTGTTTTCTTTGCCTTTTTTGCACTTTGGTGAATTA
CGTGCTCCATAACCTGAACTGTGCCGACTCCACAAAACGATTATGTACTCTTCTGAGATAGAAGATGCTGTTCT
TCTGAGAGATACGTTACTCTCTCCTTGGAATCTGTGGATTTGAAGATGGCTCCTGCCTTCTCACGTGGGAATCAG
TGAAGTGTTTAGAAACTGCTGCAAGACAAACAAGACTCCAGTGGGGTGGTCAGTAGGAGAGCACGTTGAGAGGGA
AGAGCCATCTCAACAGAATCGCACCAAACATACTTTCAGGATGAATTTCTTCTTTCTGCCATCTTTTGAATAA
ATATTTTCCTCCTTTCTATGGA

1972/6881
FIGURE 1811

GTCCCCAACATGGCGGCTCCCCAAGACGTCCACGTCCGGATCTGTAACCAAGAGATTGTCAAATTTGACCTGGAG
GTGAAGGCGCTTATTCAGGATATCCGTGATTGTTTCAGGACCCCTTAAGTGCTCTTACTGAACTGAATACTAAAGTA
AAAGAGAAATTTCAACAGTTGCGTCACAGAATACAGCCAGTTCTCTATCAAAGGGCATTATTTGGACTGCTTCC
ACATTTTTTTTTTAAGCTAACTTATTCCTGACAGACTTTTCTTCAACTCAGCATGACTTCAACTCTCCAACCTACA
CCTGTTACCTTCAGTGACCTGGAGCAGTTGGCTAAAGAGCAAGACAAAGAATCAGAGAAACAACCTTCTACTCCAG
GAAGTGGAGAATCACAAAAAGCAGATGCTCAGCAATCAGGCCTCATGGAGGAAAGCTAATCTCACCTGCAAAATT
GCAATCGACAATCTAGAGAAAGCAGAACTTCTTCAGGGAGGAGATCTCTTAAGGCAAAGGAAAACCAACAAAGAG
AGCCTGGCCCAGACATCCAGTACCATCACTGAGAGCCTCATGGGGATCAGCAGGATGATGGCCCAGCAGGTCCAG
CAGAGCGAGGAGGCCATGCAGTCTCTAGTCACTTCTTCACGAACGATCCTGGATGCAAATGAAGAATTTAAGTCC
ATGTCGGGCACCATCCAGCTGGGCCGGAAGCTTATCACAAAATACAATCGCCGGGAGCTGACGGACAAGCTTCTC
ATCTTCCTTGCGCTAGCCCTGTTTCTTGCTACGGTCCTCTATATTGTGAAAAGCGGCTCTTTCCATTTTTGTGA
GATCCCAAAGGTGCCAGTTCTGGCCCTTTTCAGCTCCTGTTTCAGGATCTGTCCTGGTTCTGAGCTCTAGGCTGC
TAAGCTGAGCCACACACCCCTCCGTTTGCACCAAGTTGCCTGCAGGTTGGATGGAACACAGTGCCCCACTTTTCTG
CAAGTAGCTGGCTTGTAAGGGTGAACAGAGCCATGGGAGGAAGGTCTGGCATTGGGATGCCGCCCTGGGGACAT
ACGAACCGCCTCCTTCCACCATTGTGCACTATGGGAGGCCGCTGCTGCGTGGAGCACTTAAAGTCCAGCCTCCAG
GACCGGATGCCCTCCTGTCTCCCGCTCCCATCGTGCCCTTAAATGCCAGATCTGGTGGAGGGAAGAGAGAAGAG
GTAGGAAGAAAGGTGATGAAAACCTCCTGGTCATTCTTGAATAAA

1973/6881
FIGURE 1812

GAGGAGGAGGGAAAAGGCGAGCAAAAAGGAAGAGTGGGAGGAGGAGGGGAAGCGGCGAAGGAGGAAGAGGAGGAG
GAGGAAGAGGGGAGCACAAAGGATCCAGGTCTCCCGACGGGAGGTAAATACCAAGAACCATGTGTGCCGAGCGGC
TGGGCCAGTTCATGACCCTGGCTTTGGTGTGGCCACCTTTGACCCGGCGCGGGGGACCGACGCCACCAACCCAC
CCGAGGGTCCCCAAGACAGGAGCTCCAGCAGAAAGGCCGCCTGTCCCTGCAGAATACAGCGGAGATCCAGCACT
GTTTGGTCAACGCTGGCGATGTGGGGTGTGGCGTGTGTTGAATGTTTCGAGAACAACCTCTTGTGAGATTCGGGGCT
TACATGGGATTTGCATGACTTTTCTGCACAACGCTGGAAAATTTGATGCCAGGGCAAGTCATTTCATCAAAGACG
CCTTGAAATGTAAGGCCACGCTCTGCGGCACAGGTTTCGGCTGCATAAGCCGGAAGTGCCCGGCCATCAGGGAAA
TGGTGTCCAGTTGCAGCGGGAATGCTACCTCAAGCACGACCTGTGCGCGGCTGCCAGGAGAACACCCGGGTGA
TAGTGGAGATGATCCATTTCAAGGACTTGCTGCTGCACGAACCCTACGTGGACCTCGTGAACCTTGCTGCTGACCT
GTGGGGAGGAGGTGAAGGAGGCCATCACCCACAGCGTGCAGGTTTCAGTGTGAGCAGAACTGGGGAAGCCTGTGCT
CCATCTTGAGCTTCTGCACCTCGGCCATCCAGAAGCCTCCCACGGCGCCCCCGAGCGCCAGCCCCAGGTGGACA
GAACCAAGCTCTCCAGGGCCACCACGGGGAAGCAGGACATCACCTCCCAGAGCCCAGCAGTAGGGAGACTGGCC
GAGGTGCCAAGGGTGAGCGAGGTAGCAAGAGCCACCCAAACGCCCATGCCCCAGGCAGAGTCGGGGGCCTTGGGG
CTCAGGGACCTTCCGGAAGCAGCGAGTGGGAAGACGAACAGTCTGAGTATTCTGATATCCGGAGGTTGAAATGAAA
GGCCTGGCCACGAAATCTTTCTCCACGCCGTCCATTTTCTTATCTATGGACATTCCAAAACATTTACCATTAGA
GAGGGGGGATGTACACGCAGGATTCTGTGGGGACTGTGGACTTCATCGAGGTGTGTGTTTCGCGGAACGGACAGG
TGAGATGGAGACCCCTGGGGCCGTGGGGTCTCAGGGGTGCCTGGTGAATTCTGCACTTACACGTACTCAAGGGAG
CGCGCCCGCGTTATCCTCGTACCTTTGTCTTCTTTCCATCTGTGGAGTCAGTGGGTGTGCGCCGCTCTGTTGTGG
GGGAGGTGAACCAGGGAGGGGACAGGGCAAGGCAGGGCCCCCAGAGCTGGGCCACACAGTGGGTGCTGGGCCTCGC
CCCGAAGCTTCTGGTGCAGCAGCCTCTGGTGTGTCTCCGCGGAAGTCAGGGCGGCTGGATTCCAGGACAGGAGT
GAATGTAAAAATAAATATCGCTTAGAATGCAGGAGAAGGGTGGAGAGGAGGCAGGGGCCGAGGGGGTGCTTGGTG
CCAAACTGAAATTCAGTTTCTTGTGTGGGGCCTTGCGGTTTCAGAGCTCTTGGCGAGGGTGGAGGGAGGAGTGTCA
TTTCTATGTGTAATTTCTGAGCCATTGTACTGTCTGGGCTGGGGGGGACACTGTCCAAGGGAGTGGCCCCATGA
GTTTATATTTTAACCACTGCTTCAAATCTCGATTTCACTTTTTTTATTTATCCAGTTATATCTACATATCTGTCA
TCTAAATAAATGGCTTTCAAACAAAGCAACTGGGTCATTAATAACCAGCTCAAAGGGGGTTAAAAAAAAAAAAAAC
CAGCCCATCCTTTGAGGCTGATTTTTCTTTTTTTTAAAGTTCTATTTTAAAAGCTATCAAACAGCGACATAGCCAT
ACATCTGACTGCCTGACATGGACTCCTGCCCACTTGGGGGAAACCTTATACCCAGAGGAAAATACACACCTGGGG
AGTACATTTGACAAATTTCCCTTAGGATTTCTGTTATCTCACCTTGACCTCAGCCAAGATTGGTAAAGCTGCGTC
CTGGCGATTCCAGGAGACCCAGCTGGAAACCTGGCTTCTCCATGTGAGGGGATGGGAAAGGAAAGAAGAGAATGA
AGACTACTTAGTAATTCCCATCAGGAAATGCTGACCTTTTACATAAAATCAAGGAGACTGCTGAAAATCTCTAAG
GGACAGGATTTTCCAGATCCTAATTGGAAATTTAGCAATAAGGAGAGGAGTCCAAGGGGACAAATAAAGGCAGAG
AGAGAGAGAGAGAGAGGGAGAGGAAGAAAAGAGAGAGAGAAAAGAGCCTCGTGCC

1974/6881
FIGURE 1813

MCAERLGQFMTLALVLATFDPARGTDATNPPEGPDQRSSQQKGRLSLQNTAEIQHCLVNAGDVGCGVFECFENNS
CEIRGLHGICMTFLHNAGKFDAQGKSF IKDALKCKAHALRHRFGCISRKCPAIREMVSQLQRECYLKHDLCAAAQ
ENTRVIVEMIHFKDLLLHEPYVDLVNLLLTGEEVKEAITHSVQVQCEQNWGSILCSILSFCTSAIQKPPTAPPER
QPQVDRTKLSRAHHGEAGHHLPEPSSRETGRGAKGERGSKSHPNAHARGRVGGLGAQGPGSGSSEWEDEQSEYSDI
RR

1975/6881
FIGURE 1814

GCGGCGCCAGGACTGACTGCGCCGTGGAGGCTGCTGCAGTGTTGTGAGTTGGAAGCTGGGGAGCTCGGCATGGCG
GTCCCCGCTGCAGCCATGGGGCCCTCGGCGTTGGGCCAGAGCGGCCCCGGCTCGATGGCCCCGTGGTGCTCAGTG
AGCAGCGGCCCCGTGCGCTACGTGCTTGGGATGCAGGAGCTGTTCCGGGGCCACAGCAAGACGCGCGAGTTCTCTG
GCGCACAGCGCCAAGGTGCACTCGGTGGCCTGGAGTTGCGACGGGCGTCGCCTAGCCTCGGGGTCTTCGACAAG
ACGGCCAGCGTCTTCTTGCTGGAGAAGGACCGGTTGGTCAAAGAAAACAATTATCGGGGACATGGGGATAGTGTG
GACCAGCTTTGTTGGCATCCAAGTAATCCTGACCTATTTGTTACGGCGTCTGGAGATAAAACCATTCGCATCTGG
GATGTGAGGACTACAAAATGCATTGCCACTGTGAACACTAAAGGGGAGAACATTAATATCTGCTGGAGTCCTGAT
GGGCAGACCATTGCTGTAGGCAACAAGGATGATGTGGTGACCTTTATTGATGCCAAGACACACCGTTCCAAAGCA
GAAGAGCAGTTCAAGTTCGAGGTCAACGAAATCTCCTGGAACAATGACAATAATATGTTCTTCCTGACAAATGGC
AATGGTTGTATCAACATCCTCAGCTACCCAGAACTGAAGCCTGTGCAGTCCATCAACGCCCATCCTTCCAACCTGC
ATCTGTATCAAGTTTGACCCCATGGGGAAGTACTTTGCCACAGGAAGTGCAGATGCTTTGGTCAGCCTCTGGGAT
GTGGATGAGTTAGTGTGTGTTTCGGTGCTTTTCCAGGCTGGATTGGCCTGTAAGAACCCTCAGTTTCAGCCATGAT
GGGAAAATGCTGGCGTCAGCATCGGAAGATCATTTTTATTGACATTGCTGAAGTGGAGACAGGGGACAAACTATGG
GAGGTACAGTGTGAGTCTCCGACCTTACAGTGGCGTGGCACCCCAAAAGGCCTCTGCTGGCATTTCCTGTGAT
GACAAAGACGGCAAATATGACAGCAGCCGGAAGCCGGAAGTGTGAAGCTGTTTGGGCTTCCTAATGATTCTTGA

GAGGAGGTTGTAGGGAGAGGAGGCCCGGCAGAGGTCTTCCTTCATGTGGTTAGTTTGGTCTGTTCTCTCGGAGT
TGGTGGGCACCCTAAATATTTGTAAGTTGGTATAAATTGTAAACGTCTCTGGTCAGGCTGCGCATTTTCGTTCTTT
TGCTTTGICTGTGTATTAGCTCTTTCCATTCTTTGCCCCAGCATGAGTTAACTCGCGTGGACTCTGCAGTGCGA
GTAGTGACCCAGCATACCTTGTCCTCTGGACCTCCTGTCTTCTCTGCTTCTGGGTGCATGGTAGACTTTGTGGC
ATTTGATACAACCTTGACAATACCTAGTTTGGAGGGAGGGGAATGGAAGGGCATGGAAGTTTTTTTTAAATAATTA
AAAATATATACATATAATTTGAGAATTGAGCATTTAATAAACTGACTTTTGTATTATGAAAAAAAAAAAAAA
AA

1976/6881
FIGURE 1815

MAVPAAAMGPSALGQSGPGSMAPWCSVSSGSPRYVLGMQELFRGHSKTREFLAHSKVVHSAVWSCDGRRLASGSF
DKTASVFILLEKDRLVKENNYRGHGDSVDQLCWHPSPNDLFVTASGDKTIRIWDVVRTTKCIATVNTKGENINICWS
PDGQTIAVGNKDDVVTFIDAKTHRSKAEQFKFEVNEISWNNDNNMFFLTNGNGCINILSYPELKPVQSINAHPS
NCICIKFDPMGKYFATGSADALVSLWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIAEVETGDK
LWEVQCESPTFTVAWHPKRPLLAFCDDKDGKYDSSREAGTVKLFGLPND

1977/6881
FIGURE 1816

ATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTGTGGAAATTTGAGACCAGCAAGTACT
ATGTGACTATCACTGATGCTCCAGGACACAGAGACTTCATCAAAAACATGATTACAGGGACATCTCAGGCTGACT
GTGCTGTCCCGATTGTTGCTGCTGGTGTGGTGAATTTGAAGCTGGTATCTCTAAGAATGGGCAGACCCGAGAGC
ATGCCCTTCTGGCTTACACACTGGGTGTGAAACAATAATTGTTGGTGTAAACAAAATGGAAGTCAGCACTTACA
TTAAGAAAATTGGCTACAACCCCGACACAGTAGCATTGTGCCAATTTCTGGTTGGAATGGTAACAACATGCTGG
AGCCAAGTGCTAACATGCCTTGGTTCAAGGGATGGAAAGTCACCCGTAAGGATGGCAATGCCAGTGGAACCATGC
TGCTTGAGGCTCTGGACTGCATCCTACCACCAACTCGTCCAAGTGGCAAGCCGGCCAAATAAGCGCGTGGCTATG
CCCCATGTAATTGGATTGTCCACACGGCTACATATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGC
CGTTCTGGTAAAAAGCTGGAAGATGGCCCTAAATTCTTGAAGTCCGGTGATGCTGCCATTGTTGATATGGTTCCT
GGCAAGCCCATGTGTGCTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTGCTGTTTCGTGATATGAGACAC
ACAGTTGCGGTGGGTGTCATCAAAGCAGTGGACAAGAAGGCTGCTGGAGCTGGCAAGGTCACCAACTCTGCCCAG
AAAGCTCAGATGGCTAAATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGGGAAGAACGGTC
TCAGAACTGTTTGTTCATTGGCCATTTAAGTTTAGTAGTAAAAGACTGGTACTTTTTTAATGGAAACAACCTTGA
CCAAAAATTTGTCACAGAATTTTGAGACCCATTAAAAAAGTTTAATGAG

1978/6881
FIGURE 1817

GGGTCAGAACACTGGCGGCCGATCCCAACGAGGCTCCCTGGAGCCCGACGCAGAGCAGCGCCCTGGCCGGGCCAA
GCAGGAGCCGGCATCATGGATTCCCTCAAAGTAGTGCTGGAGGGGCCAGCACCTTGGGGCTTCGGGCTGCAAGGG
GGCAAGGACTTCAATGTGCCCCCTCTCCATTTCCCGGCTCACTCCTGGGGGCAAAGCGGCGCAGGCCGGAGTGGCC
GTGGGTGACTGGGTGCTGAGCATCGATGGCGAGAATGCGGGTAGCCTCACACACATCGAAGCTCAGAACAAGATC
CGGGCCTGCGGGGAGCGCCTCAGCCTGGGCCTCAGCAGGGCCCAGCCGGTTCAGAGCAAACCGCAGAAGGTACGA
GGCTGGCCGGGACATCCGGGCGGTGGGCGGTGTGGGCTTGGACGGCCAGGCCTGCTCGCCCTCCTGGCACATTCT
CGGTACCCCAATCCCTGGCCGGGAGTGGAGGGCAGAAACCGGAGCTAAGGCGGGTCTAGGGCCCTGGAGTTGAGC
CAGGGGCTGCTGCACGGTCCTGGCACCACGCATGTCCGCCTGTCTGTCCGCCTGTCTGTCCGCCTGCTGCCTCCC
GCCGCCGGCGCTGCGTGCTCGCCCGCACTCGGTGAGCCCTCGGTCCTGCGTGGACTGAGATCGCCACTCCCAAAT
GGGCCCCTTGAAACCTGAGTCGTCCTCTCCCCGTAGCCTCCAAATAGATGTAGGGGGTGGGGTGGGGGTGGGGGG
CTGGAGCTGCCGCTGTCTCTGCTGCAGGCGCCC

1979/6881
FIGURE 1818

AATGGAGGAGTCGGAACCCGAACGGAAGCGGGCTCGCACCGACGAGGTGCCTGCCGGAGGAAGCCGCTCCGAGGC
GGAAGATGAGGACGACGAGGACTACGTGCCCTATGTGCCGTTACGGCAGCGCCGGCAGCTACTGCTCCAGAAGCT
GCTGCAGCGAAGACGCAAGGGAGCTGCGGAGGAAGAGCAGCAGGACAGCGGTAGTGAACCCCGGGGAGATGAGGA
CGACATCCCGCTAGGCCCTCAGTCCAACGTCAGCCTCCTGGATCAGCACCAGCACCTTAAAGAGAAGGCTGAAGC
GCGCAAAGAGTCTGCCAAGGAGAAGCAGCTGAAGGAAGAAGAGAAGATCCTGGAGAGTGTTGCCGAGGGCCGAGC
ATTGATGTCAGTGAAGGAGATGGCTAAGGGCATTACGTATGATGACCCCATCAAAACCAGCTGGACTCCACCCCG
TTATGTTCTGAGCATGTCTGAAGAGCGACATGAGCGCGTGCGGAAGAAATACCACATCCTGGTGGAGGGGAGACGG
TATCCCACCACCCATCAAGAGCTTCAAGGAAATGAAGTTTCTGTCAGCCATCCTGAGAGGCCCTGAAGAAGAAAGG
CATTCAACCACCCAACACCCATTAGATCCAGGGCATCCCCACCATTCTATCTGGCCGTGACATGATAGGCATCGC
TTTCACGGGTTTCAGGCAAGACACTGGTGTTTACGTTGCCCGTCATCATGTTCTGCCTGGAACAAGAGAAGAGGTT
ACCCTTCTCAAAAGCGCGAGGGGCCCTATGGACTCATCATCTGCCCTCGCGGGAGCTGGCCCCGGCAGACCCATGG
CATCCTGGAGTACTACTGCCGCTGCTGCAGGAGGACAGCTCACCCTCCTGCGCTGCGCCCTCTGCATTGGGGG
CATGTCCGTGAAAGAGCAGATGGAGACCATCCGACACGGTGTACACATGATGGTGGCCACCCCGGGGCGCCTCAT
GGATTTGCTGCAGAAGAAGATGGTCAGCCTAGACATCTGTGCTACCTGGCCCTGGACGAGGCTGACCGCATGAT
CGACATGGGCTTCGAGGGTGACATCCGTACCATCTTCTCCTACTTCAAGGGCCAGCGACAGACCCTGCTCTTCAG
TGCCACCATGCCGAAGAAGATTGAGAACTTTGCTAAGAGTGCCCTTGTAAGCCTGTGACCATCAATGTGGGGCG
CGCTGGGGCTGCCAGCCTGGATGTCATCCAGGAGGTAGAATATGTGAAGGAGGAGGCCAAGATGGTGTACCTGCT
CGAGTGCTGCAGAAGACACCCCGCCTGTACTCATCTTGCAGAGAAGAAGGCAGACGTGGACGCCATCCACGA
GTACCTGCTGCTCAAGGGGGTTGAGGCCGTAGCCATCCATGGGGGGCAAAGACCAGGAGGAACGGACTAAGGCCAT
CGAGGCATTCCGGGAGGGCAAGAAGGATGTCCTAGTAGCCACAGACGTTGCCTCCAAGGGCCTGGACTTCCCTGC
CATCCAGCACGTATCAATTATGACATGCCAGAGGAGATTGAGAACTATGTACACCGGATTGGCCGCACCGGGCG
CTCGGGAAACACAGGCATCGCCACTACCTTCATCAACAAAGCGTGTGATGAGTCAGTGCTGATGGACCTCAAAGC
GCTGCTGCTAGAAGCCAAGCAGAAGGTGCCGCCCGTGCTGCAGGTGCTGCATTGCGGGGATGAGTCCATGCTGGA
CATTGGAGGAGAGCGCGGCTGTGCCTTCTGCGGGGGCCTGGGTTCATCGGATCACTGACTGCCCCAAACTCGAGGC
TATGCAGACCAAGCAGGTCAGCAACATCGGTGCAAGGACTACCTGGCCCACAGCTCCATGGACTTCTGAGCCGA
CAGTCTTCCCTTCTCTCCAAGAGGCCTCAGTCCCCAAGACTGCCACCAGTCTACACATACAGCAGCCCCCTGGAC
AGAATCAGCATTTTCACTCAGCTGAGCTGGCCTGGGATGGGCCAGGCTGGTCCTGGCTGCCTGTTCCCTGTGCTCTTCAG
AATTACTGTTTTTGTTCCTTTTACCCAGCTGCCATTAAAGCCCCAAACCTCTAGCCC

1980/6881
FIGURE 1819

GCAAGATGGCTGTGGAGCTGGGCGTGCTGCTCGTCCGGCCCCGGCCCGGAACCGGGCTGGGTAGAGTGATGCGGA
CCCTCCTGCTGGTGCTGTGGCTGGCGACGCGCGGAAGCGCGCTCTACTTTCACATCGGAGAGACGGAGAAGAAGT
GCTTTATTGAGGAGATCCCGGACGAGACCATGGTCATAGGAAACTACCGGACGCAGCTGTATGACAAGCAGCGGG
AGGAGTACCAGCCGGCCACCCGGGGCTTGGCATGTTTGTGGAGGTGAAGGACCCAGAGGACAAGGTCATCCTGG
CCCGGCAGTATGGCTCCGAGGGCAGGTTCACTTTCACTTCCCATACCCCCTGGTGAGCACCAGATCTGTCTTCACT
CCAATTCCACCAAGTTCTCCCTCTTTGCTGGAGGCATGCTGAGAGTTCACCTGGACATCCAGGTAGGTGAACATG
CCAATGACTATGCAGAAATTGCTGCTAAAGACAAGTTGAGTGAGTTGCAGCTACGAGTGCGACAGCTGGTGGAAC
AAGTGGAGCAGATCCAGAAAGAGCAGAACTACCAGCGGTGGCGAGAGGAGCGCTTCCGGCAGACCAGTGAGAGCA
CCAACCAGCGGGTGCTGTGGTGGTCCATTCTGCAGACCTCATCCTCGTGGCCATCGGTGTCTGGCAGATGCGGC
ACCTCAAGAGCTTCTTTGAAGCCAAGAAGCTTGTGTAGCTGTCCCAGGCGTCACAACCCATCCTCCCAGGCTGGG
GGAGGGGAATGGGCAGGCAAGCCAGTCTTCTGTCTTCCCTTT

1981/6881
FIGURE 1820

GCCTCCGCCCCCGCCGCGGACCCTCCGCGGTACACCTTGCACCCAGCGTCTCCCTCTACAAGACGGCCCCGGCCCT
TTGGTGCGCCCCCGCCCGCTGACAGCGCCCCGAGCAGAATGGACAGCCGCTCCGACCGCTGGTCCCAGATGCCA
GCAAGCAGCGGCTGATGGAGAACACAGAGGACTGGCGGCCGCGGCCGGGACAGGCCAGTCGCGTTCCCTCCGCA
TCCTTGCCACCTCACAGGCACCGAGTTCATGCAAGACCCGGATGAGGAGCACCTGAAGAAATCAAGCCAGGTGC
CCAGGACAGAAGCCCCAGCCCCAGCCTCATCTACACCCAGGAGCCCTGGCCTGGCCCTACCGCCCCAGCCCTA
CCAGCCGCCCCGCTGGGCTGTGGACCCTGCGTTTGCCGAGCGCTATGCCCCGACAAAACGAGCACAGTGCTGA
CCCGGCACAGCCAGCCGGCCACGCCCACGCCGCTGCAGAGCCGCACCTCCATTGTGCAGGCAGCTGCCGGAGGGG
TGCCAGGAGGGGGCAGCAACAACGGCAAGACTCCCGTGTGTCAACAGTGCCACAAGGTCATCCGGGGCCGCTACC
TGGTGGCGCTGGGCCACGCGTACCACCCGGAGGAGTTTGTGTGTAGCCAGTGTGGGAAGGTCCTGGAAGAGGGTG
GCTTCTTTGAGGAGAAGGGCGCCATCTTCTGCCCACCATGCTATGACGTGCGCTATGCACCCAGCTGTGCCAAGT
GCAAGAAGAAGATTACAGGCGAGATCATGCACGCCCTGAAGATGACCTGGCACGTGCACTGCTTTACCTGTGCTG
CCTGCAAGACGCCCATCCGGAACAGGGCCTTCTACATGGAGGAGGGCGTGCCCTATTGCGAGCGAGACTATGAGA
AGATGTTTGGCACGAAATGCCATGGCTGTGACTTCAAGATCGACGCTGGGGACCGCTTCTTGAGGGCCCTGGGCT
TCAGCTGGCATGACACCTGCTTCGTCTGTGCGATATGTCAGATCAACCTGGAAGGAAAGACCTTCTACTCCAAGA
AGGACAGGCCTCTCTGCAAGAGCCATGCCTTCTCTCATGTGTGAGCCCCCTTCTGCCCACAGCTGCCGCGGTGGCC
CCTAGCCTGAGGGGCCTGGAGTCGTGGCCCTGCATTTCTGGGTAGGGCTGGCAATGGTTGCCTTAACCCCTGGCTC
CTGGCCCGAGCCTGGGGCTCCCTGGGCCCTGCCCCACCCACCTTATCCTCCCACCCCACTCCCTCCACCACCACA
GCACACCGGTGCTGGCCACACCAGCCCCCTTTCACCTCCAGTGCCACAATAAACCTGTACCCAGCTG

1982/6881
FIGURE 1821

AGGTGGAGCAAGATGGCTGTGGAGCTGGGCGTGCTGCTCGTCCGGCCCCGGCCCCGGAACCGGGCTGGGTAGAGTG
ATGCGGACCCTCCTGCTGGTGCTGTGGCTGGCGACGCGCGGAAGCGCGCTCTACTTTACATCGGAGAGACGGAG
AAGAAGTGCTTTATTGAGGAGATCCCGGACGAGACCATGGTCATAGGAAACTACCGGACGCAGCTGTATGACAAG
CAGCGGGAGGAGTACCAGCCGGCCACCCCGGGGCTTGGCATGTTTGTGGAGGTGAAGGACCCAGAGGACAAGGTC
ATCCTGGCCCCGGCAGTATGGCTCCGAGGGCAGGTTCACTTTCACTTCCCATACCCCTGGTGAGCACCAGATCTGT
CTTCACTCCAATTCCACCAAGTTCTCCCTCTTTGCTGGAGGCATGCTGAGAGTTCACCTGGACATCCAGGTAGGT
GAACATGCCAATGACTATGCAGAAATTGCTGCTAAAGACAAGTTGAGTGAGTTGCAGCTACGAGTGCGACAGCTG
GTGGAACAAGTGGAGCAGATCCAGAAAGAGCAGAACTACCAGCGGTGGCGAGAGGAGCGCTTCCGGCAGACCACT
GAGAGCACCAACCAGCGGGTGCTGTGGTGGTCCATTCTGCAGACCCTCATCCTCGTGGCCATCGGTGTCTGGCAG
ATGCGGCACCTCAAGAGCTTCTTTGAAGCCAAGAAGCTTGTGTAGCTGTCCCAGGCGTCACAACCCATCCTCCCA
GGCTGGGGGAGAAAGGACCTCCTGGAAGTGACTTCTTCTGTGTCAGGAGGACTGGTTTCCAGCCATACCTGTTCTGG
AAGGGAGAGGGGGCTGGAGGCACCCACAGGCACAAGCTGAAGGCAGCAGCTTGGCTAATACTGAGCAGGTAGTGGG
GCAAATTCCTGCCCTCTCTCTCTGGCCTCTGGGCCGTTTGGTAGTAATCACCCAGGGGCTGGTAAAGCCCCCTCCT
CTTGGCACCTCAGAATCACAGTGTTACTGATCAGGGATGTGAGGCTGCTGTTGGGGGTGGGGGAGGGGAATGGG
CAGGCAAGCCAGTCTTCTGTCTTCCTTTGCTAACTTAGGGTTTTGAGCAGGTTGGGGTATGGTGCCTGTCATACC
CACCTGCCACCCTGGGAACCTCACTGTTCTCTCTTTCAGCCTAGACCTGCTGATCCAGGGTGTGTGTGAGTTGAG
GGTGGGTGGAGGGGTTTGCAGTGTGGGAATGTGGCCCTGCAGTTGACCTGAGCTGCTTCACATGGTTGTCCATT
TGGGGCTTAAAGAACTGGGACCAGACCAAGTAGAGGCCTTGGTGCTGGTTGGGGTGGGGCCTGCAGAGTCTTAGT
TACTGATTTCATTTTCAATAAATGTAGGTTTGTTACATGAGTTTCCCAATAAAAAAAAAAATG

1983/6881
FIGURE 1822

MRTLLLVWLATRGSAFYFHIGETEKKCFIEEIPDETMVIGNYRTQLYDKQREEYQPATPGLGMFVEVKDPEDKV
ILARQYGSEGRFTFTSHTPGEHQICLHSNSTKFSLFAGGMLRVHLDIQVGEHANDYAEIAAKDKLSELQLRVRQL
VEQVEQIQKEQNYQRWREERFRQTSESTNQRVLWWSILQTLILVAIGVWQMRHLKSFFEAKKLIV

1984/6881
FIGURE 1823

AATGGAGGAGTCGGAACCCGAACGGAAGCGGGCTCGCACCGACGAGGTGCCTGCCGGAGGAAGCCGCTCCGAGGC
GGAAGATGAGGACGACGAGGACTACGTGCCCTATGTGCCGTTACGGCAGCGCCGGCAGCTACTGCTCCAGAAAGCT
GCTGCAGCGAAGACGCAAGGGAGCTGCGGAGGAAGAGCAGCAGGACAGCGGTAGTGAACCCCGGGGAGATGAGGA
CGACATCCCGCTAGGCCCTCAGTCCAACGTCAGCCTCCTGGATCAGCACCAGCACCTTAAAGAGAAGGCTGAAGC
GCGCAAAGAGTCTGCCAAGGAGAAGCAGCTGAAGGAAGAAGAGAAGATCCTGGAGAGTGTTGCCGAGGGCCGAGC
ATTGATGTCAGTGAAGGAGATGGCTAAGGGCATTACGTATGATGACCCCATCAAAACCAGCTGGACTCCACCCCG
TTATGTTCTGAGCATGTCTGAAGAGCGACATGAGCGCGTGCGGAAGAAATACCACATCCTGGTGGAGGGGAGACGG
TATCCCACCACCCATCAAGAGCTTCAAGGAAATGAAGTTTCTGTCAGCCATCCTGAGAGGCCTGAAGAAGAAAGG
CATTCAACACCCAAACACCCATTAGATCCAGGGCATCCCCACCATTCTATCTGGCCGTGACATGATAGGCATCGC
TTTCACGGGTTTCAGGCAAGACACTGGTGTTTACGTTGCCCGTCATCATGTTCTGCCTGGAACAAGAGAAGAGGTT
ACCCTTCTCAAAGCGCGAGGGGCCCTATGGACTCATCATCTGCCCTCGCGGGAGCTGGCCCCGGCAGACCCATGG
CATCCTGGAGTACTACTGCCGCTGCTGCAGGAGGACAGCTCACCCTCCTGCGCTGCGCCCTCTGCATTGGGGG
CATGTCCGTGAAAGAGCAGATGGAGACCATCCGACACGGTGACACATGATGGTGGCCACCCCGGGGCGCCTCAT
GGATTTGCTGCAGAAGAAGATGGTCAGCCTAGACATCTGTCGCTACCTGGCCCTGGACGAGGCTGACCGCATGAT
CGACATGGGCTTCGAGGGTGACATCCGTACCATCTTCTCCTACTTCAAGGGCCAGCGACAGACCCTGCTCTTCAG
TGCCACCATGCCGAAGAAGATTGAGAACTTTGCTAAGAGTGCCCTTGTAAGCCTGTGACCATCAATGTGGGGCG
CGCTGGGGCTGCCAGCCTGGATGTCATCCAGGAGGTAGAATATGTGAAGGAGGAGGCCAAGATGGTGTACCTGCT
CGAGTGCCCTGCAGAAGACACCCCGCCTGTACTCATCTTTGCAGAGAAGAAGGCAGACGTGGACGCCATCCACGA
GTACCTGCTGCTCAAGGGGGTTGAGGCCGTAGCCATCCATGGGGGCAAAGACCAGGAGGAACGGACTAAGGCCAT
CGAGGCATTCCGGGAGGGCAAGAAGGATGTCCTAGTAGCCACAGACGTTGCCTCCAAGGGCCTGGACTTCCCTGC
CATCCAGCACGTCAATTAAGACATGCCAGAGGAGATTGAGAACTATGTACACCGGATTGGCCGCACCGGGCG
CTCGGGAAACACAGGCATCGCCACTACCTTCATCAACAAAGCGTGTGATGAGTCAGTGCTGATGGACCTCAAAGC
GCTGCTGCTAGAAGCCAAGCAGAAGGTGCCGCCCGTGCTGCAGGTGCTGCATTGCGGGGATGAGTCCATGCTGGA
CATTGGAGGAGAGCGCGGCTGTGCCTTCTGCGGGGGCCTGGGTTCATCGGATCACTGACTGCCCCAAACTCGAGGC
TATGCAGACCAAGCAGGTCAGCAACATCGGTGCAAGGACTACCTGGCCCACAGCTCCATGGACTTCTGAGCCGA
CAGTCTTCCCTTCTCTCCAAGAGGCCTCAGTCCCCAAGACTGCCACCAGTCTACACATACAGCAGCCCCCTGGAC
AGAATCAGCATTTTCACTCAGCTGAGCTGGCCTGGAATGGGCCAGGCTGGTCTGGCTGCCTGTTCCCTGTGCTCTTCAG
AATTACTGTTTTTGTTCCTTTTACCCAGCTGCCATTAAAGCCCCAAACCTCTAGCCC

1985/6881
FIGURE 1824

CCCAACGAGGCTCCCTGGAGCCCGACGCAGAGCAGCGCCCTGGCCGGGCCAAGCAGGAGCCGGCATCATGGATTCTTTCAAAGTAGTGCTGGAGGGGCCAGCACCTTGGGGCTTCCGGCTGCAAGGGGGCAAGGACTTCAATGTGCCCCCTCTCCATTTCCCGGCTCACTCCTGGGGGCAAAGCGGGCGCAGGCCGGAGTGGCCGTGGGTGACTGGGTGCTGAGCATCGATGGCGAGAAATGCGGGTAGCCTCACACACATCGAAGCTCAGAACAAAGATCCGGGCCTGCGGGGAGCGCCTCAGCCTGGGCCTCAGCAGGGCCCAGCCGGTTTCAAGCAAACCGCAGAAAGGCCTCCGCCCCCGCCGCGGACCCCTCCGCGGTACACCTTTGCACCCAGCGTCTCCCTCAACAAGACGGCCCCGGCCCTTTGGGGCGCCCCCGCCCGCTGACAGCGCCCCGCAGCAGAAATGGACAGCCGCTCCGACCGCTGGTCCCAGATGCCAGCAAGCAGCGGCTGATGGAGAACACAGAGGACTGGCGGGCCGCGGCCGGGGACAGGCCAGTGCAGTTCCCTTCCGCATCCTTGCCACCTCACAGGCACCGAGTTCATGCAAGACCCGGATGAGGAGCACCTGAAGAAATCAAGCCAGGTGCCAGGACAGAAGCCCCAGCCCCAGCCCTCATCTACACCCAGGAGCCCTGGCCTGGCCCTACCGCCCCAGCCCTACCAGCCGCGCCCGCCCTGGGCTGTGGACCCTGCGTTTGCCGAGCGCTATGCCCCGGACAAAACGAGCACAGTGCTGACCCGGCACAGCCAGCCGGCCACGCCCCACGCCGCTGCAGAGCCGCACCTCCATTGTGCAGGCAGCTGCCGGAGGGGTGCCAGGAGGGGGCAGCAACAACGGCAA GACTCCCGTGTGTACACAGTGCCACAAGGTCATCCGGGGCCGCTACCTGGTGGCGCTGGGCCACGCGTACCACCCGGAGGAGTTTGTGTGTAGCCAGTGTGGGAAGGTCTTGAAGAGGGTGGCTTCTTTGAGGAGAAGGGCGCCATCTTCTGCCCACCATGCTATGACGTGCGCTATGCACCCAGCTGTGCCAAGTGCAAGAAGAAGATTACAGGCGAGATCATGCACGCCCTGAAGATGACCTGGCACGTGCACTGCTTTACCTGTGCTGCCTGCAAGACGCCCATCCGGAACAGGGCCTTCTACATGGAGGAGGGCGTGCCCTATTGCGAGCGAGACTATGAGAAGATGTTTGGCACGAAATGCCATGGCTGTGACTTCAAGATCGACGCTGGGGACCGCTTCTGGAGGCCCTGGGCTTCAGCTGGCATGACACCTGCTTCGTCTGTGCGATATGTCAGATCAACCTGGAAGGAAAGACCTTCTACTCCAAGAAGGACAGGCCTCTCTGCAAGAGCCATGCTTCTCTCATGTGTGACCCCCTTCTGCCCACAGCTGCCGCGGTGGCCCCCTAGCCTGAGGGGCCTGGAGTCGTGGCCCTGCATTTCTGGGTAGGGCTGGCAATGGTTGCCTTAACCTGGCTCCTGGCCCCGAGCCTGGGGCTCCCTGGGCCCTGCCCCACCCACCTTATCCTCCACCCCACTCCCTCCACCACCACAGCACACCGGTGCTGGCCACACCAGCCCCCTTTCACCTCCAGTGCCACAATAAACCTGTACCCAGCTG

1986/6881
FIGURE 1825

MDSFKVVLEGPAPWGFR LQGGKDFNVPLSISRLTPGGKAAQAGVAVGDWVLSIDGENAGSLTHIEAQNKIRACGE
RLSLGLSRAQPVQSKPQKASAPAADPPRYTFAPSVSLNKTARPF GAPP PADSAPQQNGQPLRPLVPDASKQRLME
NTEDWRPRPGTGQSRSFRI LAHLTGTEFMQDPDEEHLKKSSQVPRTEAPAPASSTPQEPWPGPTAPSP T SRPFWA
VDP AFAERYAPDKTSTVLTRHSQPATPTPLQSR TSIVQAAAGGVPGGGSNNGKTPVCHQCHKVIRGRYLVALGHA
YHPEEFVCSQCGKVLEEGGF FEEKGAIFCPCYDVRYAPSCAKCKKKITGEIMHALKMTWHVHCFTCAACKTPIR
NRAFYMEEGVFPYCERDYEKMFGTKCHGCD FKIDAGDRFLEALGF SWHDTCFVCAICQINLEGKTFYSKKDRPLCK
SHAFSHV

1987/6881
FIGURE 1826

GGGGGCGCGCGCCCCGCGCCTCCAGCCCAGCGCTCGGAGCCGCTTTTCGCTGCCACTGTCTGCTCCCCGGGGCCGC
CGCCGCTCCCCCGCAGGCCCGGGGCTCTGTCCGCTGGGCCCCGCGCTGCTCGCCCCGGGCCAGGAGAACGAGCT
CGAGGAGGATGCCTGGGCCCGGTGCAAGGTTCCCCCTCTCACCCGCAGCTGTGGAGAGGAGGAAGCGGAAC TAGA
GATGCCCATCTGGAGTGAGTGCAGGACCAGGTCCCGCGCGGCCCGGGTGAGGCACGCCCCGCGCGCCCGCCGGCG
CCATGGGAAGGAGCGGGCGCCGCTGCTGTCCCCCGCCGGCGCGCGCACGACTTGAGACCTGCCACGGGCAGCCCC
CGGCCGCGGGTCCCCGAGTGACGCTGGCGGCACCTGAGAGTGTGGCGCGGGCCCGGGGCCACGCAGCGGAGCCCA
GTGTCCAGTGAAGCGTCTGAGGACCCGCCGCCGTGCCGCCGCCATGGTGATGTCCCAGGGCACCTACACGTTCC
TCACGTGCTTCGCCGGCTTCTGGCTCATCTGGGGTCTCATCGTCTGCTCTGCTGCTTCTGCAGCTTCCTGCGCC
GCCGCTCAAACGGCGCCAGGAGGAGCGACTGCGCGAGCAGAACCTGCGCGCCCTAGAGCTGGAGCCCCCTCGAAC
TCGAGGGCAGTCTGGCCGGGAGTCCCCCGGGCCTGGCGCCGCCGCAGCCACCACACCCGTAGCCGCCTGGAGG
CGCCGGCTCACGCGCACTCGCATCCGCACGTGCACGTGCACCCGCTGCTGCACCACGGGCCCCGCGCAGCCGCACG
CGCACGCGCACCCACACCCGCACCAACACGCGCTCCCGCACCCGCCGCTACGCACCTGTCGGTGCCGCCACGGC
CCTGGAGCTACCCGCGCCAAGCGGAATCGGACATGTCCAAACCACCGTGTTACGAAGAGGCGGTGCTGATGGCAG
AGCCGCCCGCCGCCCTATAGCGAGGTGCTCACGGACACGCGCGGCCTCTACCGCAAGATCGTCACGCCCTTCCTGA
GTGCGCCGCGACAGCGCGGAGAAGCAGGAGCAGCCGCTCCCAGCTACAAGCCGCTCTTCCTGGACCGGGGCTACA
CCTCGGCGCTGCACCTGCCCAGCGCCCCCTCGGCCCGCGCCGCCCTGCCCAGCCCTCTGCCTGCAGGCCGACCGTG
GCCGCCGGGTCTTCCCCAGCTGGACCGACTCAGAGCTCAGCAGCCGCGAGCCCCCTGGAGCACGGAGCTTGGCGTC
TGCCGGTCTCCATCCCCTTGTTGCGGGAGGACTACAGCCGTATAGAGGGGCGCCCGGCGCCCCGGGCCCCACCGGC
GGACTCCTGGCCTGACTGCGGGGCTTTTTAAATGCTTCCCTGGACTGCGGGGAGGGGCGGGGGGAGGGAGGGATT
TCTTATCCCGTTTGTTACATTTGAGGATAATAAAGGTGTGTGATCTGGTTTGGTGAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAA

1988/6881
FIGURE 1827

MVMSQGTYTFLTCTFAGFWLIWGLIVLLCCFCNFLRRRLKRRQEERLREQNLRALALEPLELEGLAGSPPGLAPP
QPPPHRSRLEAPAHASHPHVHVHPLLHHGPAQPHAHAPHPHHHALPHPPPTHLSVPPRPWSYPRQAESDMSKP
PCYEEAVLMAEPPPPYSEVLTDTRGLYRKIVTFPLSRSDSAEKQEPPPSYKPLFLDRGYTSALHLPAPRPAPP
CPALCLQADRGRRVFPSWTDSELSSREPLEHGAWRLPVSIPPLFGRTTAV

1989/6881
FIGURE 1828

CTATTGATCTGGACTCCTGGATAGGCAGCTGGACCAACGGACGGACGCCATGAGGGCTCTGCTGCTCCTGGGGTT
CCTGCTGGTGAGCTTGGAGTCAACACTTTCGATTCCACCTTGGGAAGCCCCAAGGAGCATAAGTACAAAGCTGA
AGAGCACACAGTCGTTCTCACTGTCACCGGGGAGCCCTGCCACTTCCCTTCCAGTACCACCGGCAGCTGTACCA
CAAATGTACCCACAAGGGCCGGCCAGGCCCTCAGCCCTGGTGTGCTACCACCCCCAACTTTGATCAGGACCAGCG
ATGGGGATACTGTTTGGAGCCCCAAGAAAGTGAAGACCCTGCAGCAAACACAGCCCCCTGCCAGAAAGGAGGGAC
CTGTGTGAACATGCCAAGCGGCCCCCACTGTCTCTGTCCACAACACCTCACTGGAAACCACTGCCAGAAAGAGAA
GTGCTTTGAGCCTCAGCTTCTCCGGTTTTTCCACAAGAATGAGATATGGTATAGAACTGAGCAAGCAGCTGTGGC
CAGATGCCAGTGCAAGGGTCCTGATGCCCACTGCCAGCGGCTGGCCAGGCCAGGCCTGCCGCACCAACCCGTGCCT
CCATGGGGGTGCTGCCTAGAGGTGGAGGGCCACCGCCTGTGCCACTGCCCGGTGGGCTACACCGGACCCTTCTG
CGACGTGGACACCAAGGCAAGCTGCTATGATGGCCGCGGGCTCAGCTACCGCGGCCTGGCCAGGACCACGCTCTC
GGGTGCGCCCTGTGAGCCGTGGGCCTCGGAGGGCCACCTACCGGAACGTGACTGCCGAGCAAGCGCGGAACCTGGGG
ACTGGGCGGGCCACGCTTCTGCCGGAACCCGGACAACGACATCCGCCCCGTGGTGCTTCGTGCTGAACCGCGACCG
GCTGAGCTGGGAGTACTGCGACCTGGCACAGTGCCAGACCCCAACCCAGGCGGCGCCTCCGACCCCGGTGTCCCC
TAGGCTTCATGTCCCACTCATGCCGCGCAGCCGGCACCGCCGAAGCCTCAGCCCACGACCCGGACCCCGCCTCA
GTCCAGACCCCGGGAGCCTTGCCGGCGAAGCGGGAGCAGCCGCCTTCCCTGACCAGGAACGGCCCACTGAGCTG
CGGGCAGCGGCTCCGCAAGAGTCTGTCTTCGATGACCCGCGTCGTTGGCGGGCTGGTGGCGCTACGCGGGGCGCA
CCCCTACATCGCCGCGCTGTACTGGGGCCACAGTTTCTGCGCCGGCAGCCTCATCGCCCCCTGCTGGGTGCTGAC
GGCCGCTCACTGCCTGCAGGACCGGCCCGCACCCGAGGATCTGACGGTGGTGTCTCGGCCAGGAACGCCGTAACCA
CAGCTGTGAGCCGTGCCAGACGTTGGCCGTGCGCTCCTACCGCTTGACAGAGGCCTTCTCGCCCCGTGAGCTACCA
GCACGACCTGGCTCTGTTGCGCCTTCAGGAGGATGCGGACGGCAGCTGCGCGCTCCTGTGCGCTTACGTTACGCC
GGTGTGCCTGCCAAGCGGCGCCGCGGACCCCTCCGAGACCACGCTCTGCCAGGTGGCCGGCTGGGGCCACCAGTT
CGAGGGGGCGGAGGAATATGCCAGCTTCTGCGAGGAGCGCAGGTACCGTTCCTCTCCCTGGAGCGCTGCTCAGC
CCCGGACGTGCACGGATCCTCCATCCTCCCCGGCATGCTCTGCGCAGGGTTCCTCGAGGGCGGCACCGATGCGTG
CCAGGGTGATTCCGGAGGCCCGCTGGTGTGTGAGGACCAAGCTGCAGAGCGCCGGCTCACCTGCAAGGCATCAT
CAGCTGGGGATCGGGCTGTGGTGACCGCAACAAGCCAGGCGTCTACACCGATGTGGCCTACTACCTGGCCTGGAT
CCGGGAGCACACCGTTTCCTGATTGCTCAGGGACTCATCTTTCCCTCCTTGGTGATTCCGCAGTGAGAGAGTGGC
TGGGGCATGGAAGGCAAGATTGTGTCCATTCCCCAGTGCGGCCAGCTCCGCGCCAGGATGGCGAGGAACTCAA
TAAAGTGCTTTGAAAATGCTGAG

1990/6881
FIGURE 1829

MRALLLLGFLLVSLSTLSIPPWEAPKEHKYKAEHHTVVLTVTGEPCHFQYHRQLYHKCTHKGRPGPQPCAT
TPNFDQDQRWGYCLEPKKVKDHCSKHSPCQKGGTCVNMPSGPHCLCPQHLTGNHCQKEKCFEPQLLRFFHKNEIW
YRTEQAAVARCQCKGPDHQCRLASQACRTNPLHGGRCLEVEGHRLCHCPVGYTGPFCDVDTKASCYDGRGLSY
RGLARTTILSGAPCQPWASEATYRNVTAEQARNWGLGGHAFCRNPDNDIRPWCFVLNRDRLSWEYCDLAQCQTPTQ
AAPPTPVSPRLHVPLMPAQPAAPPKPQPTTRTPPQSQTGALPAKREQPPSLTRNGPLSCGQRLRKSLSMTRVVG
GLVALRGAPYIAALYWGHSCAGSLIAPCWVLTAAHCLQDRPAPEDLTVVLGQERRNHSCEPCQTLAVRSYRLH
EAFSPVSYQHDLALLRLQEDADGSCALLSPYVQPVCLPSGAARPSETTLCQVAGWGHQFEGAEYASFLQEAQVP
FLSLERCSAPDVHGSSILPGMLCAGFLEGGTDACQGDSSGGPLVCEDQAAERRLTQGIISWGS CGDRNKPGVYT
DVAYYLA WIREHTVS

1991/6881
FIGURE 1830

ATGGCGGCGGAAGGCTGGATTGCGTTGGGGCTGGGGCCGGCGGTGCCTGGGAAGGCCTGGGCTTCTCGGCCCC
GGCCCTGGCCCCACTACACCTCTCTTTCTTCTTTTGTGTTGGGGTCTGTGACTGCGGATATAACTGACGGCAAC
AGTGAACATCTCAAGCGGGAGCATTGCTCATTAAAGCCCTACCAAGGGGTCGGTTCCAGCTCTATGCCCTCTGG
GACTTCCAGGGCAGCACTATGCTCACGAGCCAGTACGTACGTCTGACCCCTGACGAGCGCAGCAAAGAGGGCTCT
ATCTGGAACCACCAGCCGTGCTTCCCTCAAAGACTGGGAAATGCACGTCCACTTCAAAGTCCACGGCACAGGGAAG
AAGAACCTCCATGGAGACGGCATCGCCTTGTGGTACACCCGGGACCGCCTCGTGCCAGGGCCTGTGTTTGGAAGC
AAAGATAACTTCCACGGCTTAGCCATCTTCTGGACACCTACCCCAATGATGAGACCACTGAGCGCGTGTTCCTCG
TACATCTCGGTGATGGTGAACAATGGCTCCCTGTCTACGACCACAGCAAGGATGGGCGCTGGACCGAGCTGGCG
GGCTGCACGGCTGACTTCCGCAACCGCGATCACGACACCTTCTGGCTGTGCGCTACTCCCGGGGCCGTCTGACG
GTGATGACCGACCTGGAGGACAAGAACGAGTGGAAGAACTGCATTGACATCACGGGAGTGCGCCTGCCACCGGC
TACTACTTCGGGGCCTCCGCCGGCACCGGCGACCTGTCTGACAATCATGACATCATCTCCATGAAGCTGTTCCAG
CTGATGGTGGAGCACACGCCCCGACGAGGAGAGCATCGACTGGACCAAGATCGAGCCCAGCGTCAACTTCTCTCAAG
TCGCCCCAAGACAACGTGGACGACCCACGGGGAACCTCCGCAGCGGGCCCCTGACGGGGTGGCGGGTGTTCCTG
CTGCTGCTGTGCGCTCTCTGGGCATCGTTGTCTGCGCCGTGGTGGGGCCGTGGTGTTCAGAAGCGGCAGGAG
CGGAACAAGCGCTTCTACTGAGTGGCGCCTCCGGCGGGGCCTGTCCCTGGGCCCAGGAGCCAATGTGAACTTTTT
TTTTTACCGGGATTATAAAAGAACAACAAGATGACCTTATTTCTTAAGTGTTCAAATAAATGATTAAAGTATTT
TCATACATTTTGCTTCTTGCCAGCAGGGACAGGTGGCAGAGCCGAGGCTTAGGGTCTGGCACCCCCACAGCTG
GAGACGGAGGCTCTCCTGGGGCTGGTGTCTCAGGAGCAGGGGTCTGTGTCTACAGATGGGCTGTGGCCCTGCAG
GCAGCTGTTGAACACTGGAGGGTCCCCCGACCACACTGGGGTGGGCTCCTGAGGAC

1992/6881
FIGURE 1831

MAAEGWIWRWGWGRRCLGRPGLLGPGPGPTTPLFLLLLLLGSVTADITDGNSEHLKREHSLIKPYQGVGSSSMPLW
DFQGSTMLTSQYVRLTPDERSKEGSIWNHQPCFLKDWEMHVHF'KVHGTGKKNLHGDGIALWYTRDRLVPGPVFGS
KDNFHGLAIFLDIYPNDETERVFPYISVMVNNGSLSYDHSDGRWTELAGCTADFRNRDHDFTFLAVRYSRGRIT
VMTDLEDKNEWKNCIDITGVRLPTGYFFGASAGTGDLSDNHDIISMKLFQLMVEHTPDEESIDWTKIEPSVNFLK
SPKDNVDDPTGNFRSGPLTGWRVFLLLLCALLGIVVCAVVGAVVFQKRQERNKRFY

1993/6881
FIGURE 1832

GGCACGAGGGCTTGCTCCGGCCGGCACCCCTAGGCCGGCCCGCCGCCAGCTGTGCGCCGACATGGAACCCTTGGCCA
GCAACATCCAGGTCCTGCTGCAGGCGGCCGAGTTCTTGGAGCGCCGTGAGAGAGAGGCCGAGCATGGTTATGCGT
CCCTGTGCCCCGCATCGCAGTCCAGGCCCCATCCACAGGAGGAAGAAGCGACCCCCCAGGCTCCTGGCGCGCAGG
ACAGCGGGCGGTTCAGTGCACAATGAACTGGAGAAGCGCAGGAGGGCCCAGTTGAAGCGGTGCCTGGAGCGGCTGA
AGCAGCAGATGCCCCCTGGGGGCCGACTGTGCCCCGTACACCACGCTGAGCCTGCTGCGCCGTGCCAGGATGCACA
TCCAGAAGCTGGAGGATCAGGAGCAGCGGGCCCGACAGCTCAAGGAGAGGCTGCGCAGCAAGCAGCAGAGCCTGC
AGCGGCAGCTGGAGCAGCTCCGGGGGCTGGCAGGGGCGGCCGAGCGGGAGCGGCTGCGGGCGGACAGTCTGGACT
CCTCAGGCCTCTCCTCTGAGCGCTCAGACTCAGACCAAGAGGAGCTGGAGGTGGATGTGGAGAGCCTGGTGTGTTG
GGGGTGAGGCCGAGCTGCTGCGGGGCTTCGTGCGCCGCCAGGAGCACAGCTACTCGCACGGCGGCGGCGCCTGGC
TATGATGTTCTCACCAGGGCGGGCCTCTGCCCTCTACTCGTGCCAGGCCCACTTGCCAGGCAGGAGCCCTCCC
CAAGCCTTCAGGGCTGCTCGGAGTCACCTGTTGGAATGGACTAAAAGGACCCTTGTGTGGGAACAGGTGCTCCCC
AAACACCCTGCTGCTGGCTGCCAGGCAGGCCCTCTGGAAGGGAAGGGGCAGGACTCATCAGGACCTCCCTGGACC
CCTGCAGGGCAGGCAGCTTGGGCCGAGCCCAAGCATTGCGCTCTGCTGCCCCCAAGGGGACAGGAAGCCTCTTG
GGCCTCTTCCCTTCCTGGACAAGGCCCCCTGCCTTTGCCTCACATAAACTGTACAGTATTTTCATTAAAAGCCTC
TTTCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

1994/6881
FIGURE 1833

MEPLASNIQVLLQAAEFLERREREAEHGYASLCPHRSPGPIHRRKKRPPQAPGAQDSGRSVHNELEKRRRAQLKR
CLERLKQQMPLGADCARYTTLSLLRRARMHIQKLEDQEQRARQLKERLRSKQOSLQRQLEQLRGLAGAAERERLR
ADSLDSSGLSSERSDSQEELEVDES LVFGGEALLRGFVAGQEHSYSHGGGAWL

1996/6881
FIGURE 1835

MVKYFLGQSVLRSSWDQVFAAFWQRYPNPYSKHVLTEDIVHREVTPDQKLISRLLTKTNRMPRWAERLFPANVA
HSVYVLEDSIVDPQNQTMTTFTWNINHARLMVVEERCVCVNSDMSGWTEIRREAWVSSSLFGVSRVQEFGLAR
FKSNVTKTMKGFYILAKLQGEAPSKTLVETAKEAKEKAKETALAATEKAKDLASKAATKKQQQQQFV

1997/6881
FIGURE 1836

CCGAGGAGCGCTCGGGCTGTCTGCGGACCCTGCCGCGTGCAGGGGTCGCGGCCGGCTGGAGCTGGGAGTGAGGCG
GCGGAGGAGCCAGGTGAGGAGGAGCCAGGAAGGCAGTTGGTGGAAGTCCAGCTTGGGTCCCTGAGAGCTGTGAG
AAGGAG**ATG**CGGCTGCTGCTGGCCCTGTTGGGGTCTCTGCTGAGTGTGCCTGGGCCTCCAGTCTTGTCCCTGGAG
GCCTCTGAGGAAGTGGAGCTTGAGCCCTGCCTGGCTCCCAGCCTGGAGCAGCAAGAGCAGGAGCTGACAGTAGCC
CTTGGGCAGCCTGTGCGGCTGTGCTGTGGGCGGGCTGAGCGTGGTGGCCACTGGTACAAGGAGGGCAGTCGCCTG
GCACCTGCTGGCCGTGTACGGGGCTGGAGGGGCCGCTAGAGATTGCCAGCTTCCTACCTGAGGATGCTGGCCGC
TACCTCTGCCTGGCAGGAGCTCCATGATCGTCCTGCAGAATCTCACCTTGATTACAGGTGACTCCTTGACCTCC
AGCAACGATGATGAGGACCCCAAGTCCCATAGGGACCTCTCGAATAGGCACAGTTACCCCCAGCAAGCACCCCTAC
TGGACACACCCCCAGCGCATGGAGAAGAACTGCATGCAGTACCTGCGGGGAACACCGTCAAGTTCCGCTGTCCA
GCTGCAGGCAACCCACGCCACCATCCGCTGGCTTAAGGATGGACAGGCCTTTCATGGGGAGAACCGCATTGGA
GGCATTTCGGCTGCGCCATCAGCACTGGAGTCTCGTGATGGAGAGCGTGGTGCCCTCGGACCGCGGCACATACACC
TGCCTGGTAGAGAACGCTGTGGGCAGCATCCGCTATAACTACCTGCTAGATGTGCTGGAGCGGTCCCCGCACCGG
CCCATCCTGCAGGCCGGGCTCCCGGCCAACACCACAGCCGTGGTGGGCAGCGACGTGGAGCTGCTGTGCAAGGTG
TACAGCGATGCCCAGCCCCACATCCAGTGGCTGAAGCACATCGTCATCAACGGCAGCAGCTTCGGAGCCGACGGT
TTCCTTATGTGCAAGTCTTAAAGACTGCAGACATCAATAGCTCAGAGGTGGAGGTCTGTACCTGCGGAACGTG
TCAGCCGAGGACGCAGGCGAGTACACCTGCCTCGCAGGCAATTCCATCGGCCTCTCCTACCAGTCTGCCTGGCTC
ACGGTGCTGCCAGAGGAGGACCCACATGGACCGCAGCAGCGCCCGAGGCCAGGTATACGGACATCATCCTGTAC
GCGTCGGGCTCCCTGGCCTTGCTGTGCTCCTGCTGCTGGCCGGGCTGTATCGAGGGCAGGCGCTCCACGGCCGG
CACCCCGCCCGCCCGCCACTGTGCAGAAGCTCTCCGCTTCCCTCTGGCCCGACAGTTCTCCTGGAGTCAGGC
TCTTCCGGCAAGTCAAGCTCATCCCTGGTACGAGGCGTGCCTCTCTCCTCCAGCGGCCCGCCTTGCTCGCCGGC
CTCGTGAGTCTAGATCTACCTCTCGACCCACTATGGGAGTTCCCCCGGGACAGGCTGGTGCTTGGGAAGCCCCCTA
GGCGAGGGCTGCTTTGGCCAGGTAGTACGTGCAGAGGCCTTTGGCATGGACCCTGCCCGGCCTGACCAAGCCAGC
ACTGTGGCCGTCAAGATGCTCAAAGACAACGCCTCTGACAAGGACCTGGCCGACCTGGTCTCGGAGATGGAGGTG
ATGAAGCTGATCGGCCGACACAAGAATCATCAACCTGCTTGGTGTCTGCACCCAGGAAGGGCCCCCTGTACGTG
ATCGTGGAGTGCGCCGCCAAGGGAACCTGCGGGAGTTCTGCGGGCCCCGGCGCCCCCAGGCCCGACCTCAGC
CCCGACGGTCTCTCGGAGCAGTGAGGGGCCGCTCTCCTTCCCAGTCCTGGTCTCCTGCGCCTACCAGGTGGCCCGA
GGCATGCAGTATCTGGAGTCCCGGAAGTGTATCCACCGGGACCTGGCTGCCCGCAATGTGCTGGTGAAGTGAAGGAC
AATGTGATGAAGATTGCTGACTTTGGGCTGGCCCGCGGCGTCCACCACATTGACTACTATAAGAAAACCAGCAAC
GGCCGCCTGCCTGTGAAGTGGATGGCGCCGAGGCCTTGTTTGACCGGGTGTACACACACCAGAGTGACGTGTGG
TCTTTTGGGATCCTGCTATGGGAGATCTTACCCTCGGGGGCTCCCCGTATCCTGGCATCCCGGTGGAGGAGCTG
TTCTCGCTGCTGCGGGAGGGACATCGGATGGACCGACCCACACTGCCCCCAGAGCTGTACGGGCTGATGCGT
GAGTGCTGGCAGCAGCGCCCTCCCAGAGGCCTACCTTCAAGCAGCTGGTGGAGGCGCTGGACAAGGTCTGTGCTG
GCCGTCTCTGAGGAGTACCTCGACCTCCGCTGACCTTCGGACCCCTATTCCCCCTCTGGTGGGGACGCCAGCAGC
ACCTGCTCCTCCAGCGATTCTGTCTTACGCCACGACCCCTGCCATTGGGATCCAGCTCCTTCCCCCTTCGGGTCT
GGGTGCGAGACA**TGAG**CAAGGCTCAAGGCTGTGCAGGCACATAGGCTGGTGGCCTTGGGCCTTGGGGCTCAGCCA
CAGCCTGACACAGTGTCTGACCTTGATAGCATGGGGCCCCCTGGCCAGAGTTGCTGTGCCGTGTCCAAGGGCCGT
GCCCTTGCCCTTGGAGCTGCCGTGCCTGTGCTCTGATGGCCAAATGTCAGGGTTCTGCTCGGCTTCTTGGACCA
TGGCGCTTAGTCCCCATCCCGGGTTTGGCTGAGCCTGGCTGGAGAGCTGCTATGCTAAACCTCCTGCCTCCCAAT
ACCAGCAGGAGGTTCTGGGCCTCTGAACCCCTTTCCCCACACCTCCCCCTGCTGCTGCTGCCCCAGCGTCTTGA
CGGGAGCATTGGCCCCCTGAGCCAGAGAAGCTGGAAGCCTGCCGAAAACAGGAGCAAATGGCGTTTTATAAATTA
TTTTTTTGAATAAA

1998/6881
FIGURE 1837

MRLLLALLGVLLSVPGPPVLSLEASEEVELEPCCLAPSLEQQEQELTVALGQPVRLLCCGRAERGHHWYKEGSRLAP
AGRVRGWRGRLEIASFLPEDAGRYLCLARGSMIVLQNLTLITGDSLTSSNDDDEPKSHRDLSNRHSYPQQAPYWT
HPQRMKKLHAVPAGNTVKFRCPAAGNPTPTIRWLKDGQAFHGENRIGGIRLRHQHWSLVMESVVPDRGTYTCL
VENAVGSIRYNYLLDVLEERSPHRPILQAGLPANTTAVVGSDEVLLCKVYSDAQPHIQWLKHIVINGSSFGADGFP
YVQVLKTADINSSEVEVLVLRNVSAEDAGEYTCLAGNSIGLSYQSAWLTVLPEEDPTWTAAAPPEARYPDIIILYAS
GSLALAVLLLLAGLYRGQALHGRHPRPPATVQKLSRFPLARQFSLESGSSGKSSSSLVRGVRLSSSGPALLAGLV
SLDLPLDPLWEFPRDRLVLGKPLGEGCFGQVVRAEAFGMDPARPDQASTVAVKMLKDNASDKDLADLVSEMEVMK
LIGRHKNIINLLGVCTQEGPLYVIVECAAKGNLREFLRARRPPGDLSPDGPRSSEGPLSFPVLVSCAYQVARGM
QYLESRKCIHRDLAARNVLVTEEDNVMKIADFGLARGVHHIDYYKTSNGRLPVKWMAPALFDRVYTHQSDVWSF
GILLWEIFTLGGSPYPGIPVEELFSLREGHRMDRPPHCPPELYGLMRECWAAPSQRPTFKQLVEALDKVLLAV
SEYLDLRLTFGPYSPSGGDASSTCSSSDSVFSDHPLPLGSSSFPGSGVQT

1999/6881
FIGURE 1838

CCGAGGAGCGCTCGGGCTGTCTGCGGACCCTGCCGCGTGACAGGGTTCGCGGCCGGCTGGAGCTGGGAGTGAGGCG
GCGGAGGAGCCAGGTGAGGAGGAGCCAGGAAGGCAGTTGGTGGGAAGTCCAGCTTGGGTCCCTGAGAGCTGTGAG
AAGGAGATGCGGCTGCTGCTGGCCCTGTTGGGGTCTCTGCTGAGTGTGCCTGGGCCTCCAGTCTTGTCCCTGGAG
GCCTCTGAGGAAGTGGAGCTTGAGCCCTGCCTGGCTCCCAGCCTGGAGCAGCAAGAGCAGGAGCTGACAGTAGCC
CTTGGGCAGCCTGTGCGGCTGTGCTGTGGGCGGGCTGAGCGTGGTGGCCACTGGTACAAGGAGGGCAGTCGCCTG
GCACCTGCTGGCCGTGTACGGGGCTGGAGGGGCCCGCTAGAGATTGCCAGCTTCCTACCTGAGGATGCTGGCCGC
TACCTCTGCCTGGCACGAGGCTCCATGATCGTCTGACAGTCTCACCTTGATTACAGGTGACTCCTTGACCTCC
AGCAACGATGATGAGGACCCCAAGTCCCATAGGGACCTCTCGAATAGGCACAGTTACCCCCAGCAAGCACCCCTAC
TGGACACACCCCCAGCGCATGGAGAAGAACTGCATGCAGTACCTGCGGGGAACACCGTCAAGTTCCGCTGTCCA
GCTGCAGGCAACCCACGCCCACCATCCGCTGGCTTAAGGATGGACAGGCCTTTCATGGGGAGAACCGCATTGGA
GGCATTTCGGCTGCGCCATCAGCACTGGAGTCTCGTGATGGAGAGCGTGGTGCCCTCGGACCGCGGCACATACACC
TGCCTGGTAGAGAACGCTGTGGGCAGCATCCGCTATAACTACCTGCTAGATGTGCTGGAGCGGTCCCCGCACCGG
CCCATCCTGCAGGCCGGGCTCCCGGCCAACACCACAGCCGTGGTGGGCAGCGACGTGGAGCTGCTGTGCAAGGTG
TACAGCGATGCCCAGCCCCACATCCAGTGGCTGAAGCACATCGTCATCAACGGCAGCAGCTTCGGAGCCGACGGT
TTCCCTATGTGCAAGTCTTAAAGACTGCAGACATCAATAGCTCAGAGGTGGAGGTCTGTACCTGCGGAACGTG
TCAGCCGAGGACGCAGGCGAGTACACCTGCCTCGCAGGCAATTCCATCGGCCTCTCCTACCAGTCTGCCTGGCTC
ACGGTGCTGCCAGGTACTGGGCGCATCCCCACCTCACATGTGACAGCCTGACTCCAGCAGGCAGAACCAAGTCT
CCCACCTTTCAGTCTTCCCTGGAGTCAGGCTCTTCCGGCAAGTCAAGCTCATCCCTGGTACGAGGCGTGCGTCTC
TCCTCCAGCGGCCCGCCTTGCTCGCCGGCCTCGTGAGTCTAGATCTACCTCTCGACCCACTATGGGAGTTCCCC
CGGGACAGGCTGGTGTCTGGGAAGCCCCTAGGCGAGGGCTGCTTTGGCCAGGTAGTACGTGCAGAGGCCTTTGGC
ATGGACCCTGCCGGCCTGACCAAGCCAGCACTGTGGCCGTCAAGATGCTCAAAGACAACGCCTCTGACAAGGAC
CTGGCCGACCTGGTCTCGGAGATGGAGGTGATGAAGCTGATCGGCCGACACAAGAACATCATCAACCTGCTTGGT
GTCTGCACCCAGGAAGGGCCCCCTGTACGTGATCGTGGAGTGCGCCGCCAAGGGAAACCTGCGGGAGTCTCTGCGG
GCCCCGCGCCCCCAGGCCCGACCTCAGCCCCGACGGTCTCGGAGCAGTGAGGGGCCGCTCTCCTTCCCAGTC
CTGGTCTCCTGCGCCTACCAGGTGGCCCGAGGCATGCAGTATCTGGAGTCCCGGAAGTGTATCCACCGGGACCTG
GCTGCCCCGAATGTGCTGGTGAAGTGAAGACAATGTGATGAAGATTGCTGACTTTGGGCTGGCCCCGCGCGTCCAC
CACATTGACTACTATAAGAAAACCAGCAACGGCCGCTGCCTGTGAAGTGGATGGCGCCCCAGGCCTTGTTTGAC
CGGGTGTACACACACCAGAGTGACGTGTGGTCTTTTGGGATCCTGCTATGGGAGATCTTACCCCTCGGGGGCTCC
CCGTATCCTGGCATCCCGGTGGAGGAGCTGTTCTCGCTGCTGCGGGAGGGACATCGGATGGACCGACCCCCACAC
TGCCCCCAGAGCTGTACGGGCTGATGCGTGAGTGCTGGCACGCAGCGCCCTCCAGAGGCCTACCTTCAAGCAG
CTGGTGGAGGCGCTGGACAAGGTCTGTGGCCGTCTCTGAGGAGTACCTCGACCTCCGCCTGACCTTCGGACCC
TATTCCCCCTCTGGTGGGGACGCCAGCAGCACCTGCTCCTCCAGCGATTCTGTCTTCAGCCACGACCCCCCTGCCA
TTGGGATCCAGCTCCTTCCCTTCGGGTCTGGGGTGCAGACATGAGCAAGGCTCAAGGCTGTGCAGGCACATAGG
CTGGTGGCCTTGGGCCCTTGGGGCTCAGCCACAGCCTGACACAGTGCTCGACCTTGATAGCATGGGGCCCCCTGGCC
CAGAGTTGCTGTGCCGTGTCCAAGGGCCGTGCCCTTGCCCTTGGAGCTGCCGTGCCTGTGTCTGTGATGGCCCCAA
TGTCAGGGTTCTGCTCGGCTTCTTGGACCATGGCGCTTAGTCCCCATCCCGGGTTTGGCTGAGCCTGGCTGGAGA
GCTGCTATGCTAAACCTCCTGCCTCCCAATACCAGCAGGAGGTTCTGGGCCTCTGAACCCCTTTCCCCACACCT
CCCCCTGCTGCTGCTGCCCCAGCGTCTTGACGGGAGCATTGGCCCCCTGAGCCCAGAGAAGCTGGAAGCCTGCCGA
AAACAGGAGCAAATGGCGTTTTATAAATTATTTTTTTGAAATAAA

2000/6881
FIGURE 1839

MRLLLALLGVLLSVPGPPVLSLEASEEVELEPCLAPSLEQQEQELTVALGQPVRLCCGRAERGHHWYKEGSRLAP
AGRVRGWRGRLEIASFLPEDAGRYLCLARGSMIVLQNLTLITGDSLSSNDDDEDPKSHRDLNHRHSYPQQAPYWT
HPQRMEKKLHAVPAGNTVKFRCPAAGNPTPTIRWLKDGQAFHGENRIGGIRLRHQHWSLVMESVVPSDRGTYTCL
VENAVGSIRYNYLLDVLEERSPHRPILQAGLPANTTAVVGSDVELLCKVYSDAQPHIQWLKHIVINGSSFGADGFP
YVQVLKTADINSSEVEVLYLRNVSAEDAGEYTCLAGNSIGLSYQSAWLTVLPGTGRIPHLTCDSLTPAGRTKSPT
LQFSLESGSSGKSSSSLVRGVRLSSSGPALLAGLVSLDLPLDPLWEFFPRDRLVLGKPLGEGCFGQVVRAEAFGMD
PARPDQASTVAVKMLKDNASDKDLADLVSEMEVMKLI GRHKNI INLLGVCTQEGPLYVIVECAAKGNLREFLRAR
RPPGPDLSPDGPRSSEGPLSFVVLVSCAYQVARGMQYLESRKCIHRDLAARNVLVTEDNVMKIADFGLARGVHHI
DYYKKTSNGRLPVKWMAPEALFDRVYTHQSDVWSFGILLWEIFTLGGSPYPGIPVEELFSLREGHRMDRPPHCP
PELYGLMRECWHHAAPSQRPTFKQLVEALDKVLLAVSEEYLDLRLTFGPYSPSGGDASSTCSSSDSVF SHDFLPLG
SSSFPGSGVQT

2001/6881
FIGURE 1840

GGCACCGCGCGGGACGGAGCTTGGCTGTTGGTCGGTGGGTTCCTGCGGCGGCGGCCAAGGAGGAGGAGACACA
GTTGGAGCAGCTCCGIGGGCTGACTGGGGCGAGGCCTCAGCAGCGCGAGCTTGAGTGCGGCCGAGCCTGCGGCGC
CTTCCCTGCGGGTGGGGACGAGCGGGCCCCGCGGCGTCATCGGCGGCGAGGAGCCGCCGCGCCTCGGCCTAGCA
TGTCGGAAGCGGGCGAGGAGCAGCCCATGGAGACGACGGGCGCCACCGAGAACGGACATGAGGCCGTCCCCGAAG
GCGAGTCGCGGCGCGGGCTGGCACGGGCGCCGCGGCGGGGGCTGGAGGCGCGACCGCGGCGCCCCGAGCGGGA
ATCAGAACGGCGCGCGAGGGCGACCAGATCAACGCCAGCAAGAACGAGGAGGACGCGGGAAAAATGTTGTTGGTG
GCCTGAGCTGGGATACTAGCAAAAAAGATTTAAAAGACTATTTTACTAAATTTGGAGAGGTCGTTGACTGTACAA
TAAAAATGGATCCCAACACTGGACGGTCAAGAGGGTTTGGGTTTATCCTGTTCAAAGATGCAGCCAGTGTGGAGA
AGGTCCTAGACCAGAAGGAGCACAGGCTGGATGGCCGTGTCATTGACCCTAAAAAGGCCATGGCTATGAAGAAGG
ACCCGGTGAAGAAAATCTTCGTTGGGGTCTGAATCCTGAAGCCACTGAGGAAAAGATCAGGGAGTACTTTGGCG
AGTTTGGGGAGATTGAGGCCATTGAATTGCCAATGGATCCAAAGTTGAACAAAAGACGAGGTTTGTGTTTATCA
CCTTTAAGAAGAAGAACCCGTGAAGAAGTTCTGGAGAAAAAGTTCCATACTGTCAGTGGAAGCAAGTGTGAGA
TCAAGGTGGCCAGCCCAAAGAAGTCTATCAGCAGCAGCAGTATGGCTCTGGGGGCCGTGGAACCGCAACCGAG
GGAACCGAGGCAGCGGAGGTGGTGGTGGAGGTGAGGTCAGGGTAGTACAACTACGGCAAGAGCCAGCGACGTG
GTGGCCATCAGAATAACTACAAGCCATACTGAGGCGGCAGCAGGAGCGACCAACTGATCGCACACATGCTTTGTT
TGGATATGGAGTGAACACAATTATGTACCAATTTAACTTGGCAAATTTCTATTGCCTGTCCCATGTGCATCTT
ATTTAAAATTTCCCCATGGAAATCACTCTCCTGTTGACTATTTCCAGAGCTCTAGGTGTTTAGGCAGCGTGTGG
TGCTGAGAGGCCATAGCGCCATCATGGGCTGATTTTTATTACCAGGTCCCCAGAAGCAGGTGGGAGGCTCTGC
TTCCTGCTGCCGCTCTGCAGCCTGGACCTGTGGACCCTGGTTGTAAAGAGTAAATTGTATCTTAGGAAACAGTG
TCACCTTTTTTTTACCTTTTAAATTTTATATTATTTGCGTCATACATTTCTGTAAACGGAAGTGTTAATTTTACTG
TACTTTTTTGGTACCTTTTGGGAATCTAATGTATTGTAAGGTATTTTACACGTGTCCTGATTTTGCCACAACCTGG
ATATTGAAGCTATCCAAGCTTTTGAATAAAATTTAAAAACCCCCAAGCCTGGGTGAGTGTGGG

2002/6881
FIGURE 1841

GGCACCGCGCGGGACGGAGCTTGGCTGTTGGTCGGTGGGTTCCTCGTGC GGCGGGCGGCCAAGGAGGAGGAGACACA
GTTGGAGCAGCTCCGTGGGCTGACTGGGGCGAGGCCTCAGCAGCGCGAGCTTGAGTGGCGCCGAGCCTGCGGGCGC
CTTCCCTGCGGGTGGGGACGAGCGGGCCCCGCGGCGTCATCGGCGGCGAGGAGCCGCCCGCCTCGGCCTAGCA
TGTCGGAAGCGGGCGAGGAGCAGCCCATGGAGACGACGGGCGCCACCGAGAACGGACATGAGGCCGTCCCCGAAG
GCGAGTCGCCGGCCGGGGCTGGCACGGGCGCCGCGGGGGGCTGGAGGCGCGACCGCGGCGCCCCGAGCGGGA
ATCAGAACGGCGCCGAGGGCGACAGATCAACGCCAGCAAGAACGAGGAGGACGCGGGAAAAATGTTTCGTTGGTG
GCCTGAGCTGGGATACTAGCAAAAAAGATTTAAAAGACTATTTTACTAAATTTGGAGAGGTCGTTGACTGTACAA
TAAAAATGGATCCCAACACTGGACGGTCAAGAGGGTTTGGGTTTATCCTGTTCAAAGATGCAGCCAGTGTGGAGA
AGGTCCTAGACCAGAAGGAGCACAGGCTGGATGGCCGTGTCATTGACCCTAAAAAGGCCATGGCTATGAAGAAGG
ACCCGGTGAAGAAAATCTTCGTTGGGGGTCTGAATCCTGAAGCCACTGAGGAAAAGATCAGGGAGTACTTTGGCG
AGTTTGGGGAGATTGAGGCCATTGAATTGCCAATGGATCCAAAGTTGAACAAAAGACGAGGTTTTGTGTTTATCA
CCTTTAAAGAAGAAGAACCCGTGAAGAAGGTTCTGGAGAAAAAGTTCCATACTGTCA GTGGAAGCCAGTGTGAGA
TCAAGGTGGCCAGCCCAAAGAAGTCTATCAGCAGCAGCAGTATGGCTCTGGGGGCCGTGGAAACCGCAACCGAG
GGAACCGAGGCAGCGGAGGTGGTGGTGGAGGTGGAGGTGAGGTTAGTACAAACTACGGCAAGAGCCAGCGACGTG
GTGGCCATCAGAATAACTACAAGCCATACTGAGGCGGCAGCAGGAGCGACCAACTGATCGCACACATGCTTTGTT
TGGATATGGAGTGAACACAATTATGTACCAAATTTAACTTGGCAAACCTTTCTATTGCCTGTCCCATGTGCATCTT
ATTTAAAATTTCCCCCATGGAAATCACTCTCCTGTTGACTATTTCCAGAGCTCTAGGTGTTTAGGCAGCGTGTGG
TGTCTGAGAGGCCATAGCGCCATCATGGGCTGATTTTTATTACCAGGTCCCCCAGAAGCAGGTGGGAGGCTCTGC
TTCTGCTGCCGCTCTGCAGCCTGGACCTGTGGACCCTGGTTGTAAAGAGTAAATTGTATCTTAGGAAACAGTG
TCACCTTTTTTTTACCTTTTTAATTTTATATTATTTGCGTCATACATTTCTGTAAACGGAAGTGTTAATTTTACTG
TACTTTTTTGGTACCTTTTTGGGAATCTAATGTATTGTAAGGTATTTTACACGTGTCCTGATTTT GCCACAACCTGG
ATATTGAAGCTATCCAAGCTTTTGAAATAAAATTTAAAAACCCCAAGCCTGGGTGAGTGTGGG

2003/6881
FIGURE 1842

GAAATGTCCTTACGATGATCATTTAGAGGTTTATTTTGAACAACCTGGCAATTCCACGAATGATGGAATAAACATA
TGAAGTAGAAGGACTGGAACCTCCAGAAAAAGTACTTTAAGTTACCTACAGGTGATCCTAGTCAGGTATGAATTG
ATAAGAAATGCCTGCACCTTCCCTCCTTCCTATCTTTCCCTTGCCTACAGAAAATTAAAAGGCAAAACAATGGAC
ATCTACATATTCTTCATTTCAGATCAACCAGTGGCTAGCATTGTCACCTTTTGCAGTTTCTTTCTCTTTCCATAA
GTACTTTCTTCTCTGAATCATTGAAAGCAAATGAAAACAGTAGCCTAAAGTGTGAGTTTCAACCAGAAAATAAC
AGCTCTGATTTCTCATGGCTCACACTCTTCTGAAACGACTCGGGTAGAGGCTGAGGAAGGCCGTGTTGTTTGTCT
ACCTGGGACTAGTGGGATGAGAGACTGAGAAAAGAAATAAGACACGGAGACAAAGTACAGAGAAAGAACAGCGGG
CCCAGGAGACCGGCACTCAGCATACGGAGGACCAGCACTGGCACC GGCTCTGAGTTCCCTCAGTTTATTGATT
CCATTTTCAGTGTCTCAGCAAGAGGAATGCGGTAGGAGAGCAGGGTGTGAGCAAGAAAACCTGTGAGCCTTTCT
TTCGCTGCTGCGGCCGAGCCATGAGCATGCTCGGGCTCAGAAGAGGCTCGCCTCTAGTGTCTCCTCGCTGTGGC
AAGAAGAAGGTCTGGTTAGACCCAGTGAGACCAATGAAATCGCCAATGCCAACTCCCGTCAGCAGATCCGGAAG
CTCATCAAAGACGGGCTGATCATCCGCAAGCCTGTGACGGTCCATTCCCGGGCTCGATGCCGGAACACCTTG
GCCCCGCGGAAGGGCAGGCACGTGGCCATAGGTGAGCAGAAGGTACAGCCAATGCCGAATGCCAGAGAAGGTC
ACATGGATGAGGAGAATGACGATTTTGCGCCGGCTGCTCAGAAGATACCGTGAATCTAAGAAGATCGATCGCCAC
ACGTATCACAGCCTGTACCTGAAGGTGAAGGGGAATGTGTTCAAAGACAAGCGGATTCTCATGGAACACATCCAC
AAGCTGAAGGCAGACAAGGCCCCGAAGAAGCTCCTGGCTGACCAGGCTGAGGCCCCGAGGTCTAAGACCAAGGAA
GCAGGCAAGTGCCCTGAAGAGCGCTCCAGGCCAAGAAGGAGGAGTTCATCAAGACTTTATCCAAGGAGGAAGAG
ACCAAGAAATAAAAGCTCCCCCTTTGTCTGTACATACTGGCCTCTGTGATTACATAGATCAGCCATGAAAATAAA
ACAAGCCTTAA

2004/6881
FIGURE 1843

GGCACGAGGCGCCCATCCTGGGAAGGGGCCCGAGTGTGAGAGAGAGACTCCCCACGCCCATCCTGGAAAGGAG
CCCGGAGTGTGAGCTGAGTGGTCCGAGCTATACCTGTGGACATTGGTTTCTCCATTGAAGAGCTGGAGGACCTTT
ACATGGTGTTTAAGGCCAAGCACCTGGCTAGCCAGTACTGGGGGTGCAGCCGCACAATGGCCGGCCGTCGGGACC
CCAGCCTGCCCTACCTGGAGCAGTACCGGATTGATGCCAGCCAGTTCGGGGAACCTCTTTGCCAGCCTGACACCCT
GGGCCTGTGGCTCCACACACCTCTGCTGGCAGGGCGCATGTTTTCAGGCTCCTGGACGAAAACAAGGACTCGCTGA
TCAACTTCAAGGAGTTCGTGACAGGGATGAGCGGGATGTACCACGGGTACCTGACAGAGAAGCTCAAGGTGCTCT
ACAAGCTACACCTTCCCCCAGCTCTGAGCCCAGAGGAAGCCGAGTCAGCCCTGGAGGCGGGCCATTATTTTCACAG
AGGACAGCTCCTCAGAAGAAGCACTACCACAGGAAGAGCAAGAAGGAAGTGGAAAGTGAGGAGAGAGGAGAGGAGA
AGGGGACCAGCTCTCCGGACTATCGGCACTACCTTTCGAATGTGGGCCAAGGAGAAAGAGGCTCAGAAGGAGACGA
TTAAGGATCTTCCCAAGATGAACCAGGAGCAGTTTCATTGAGCTGTGCAAGACGCTTTACAACATGTTTCAGTGAAG
ACCCCATGGAGCAGGACCTGTACCACGCCATCGCCACCGTGGCCAGCCTCCTGCTCCGCATCGGAGAGGTGGGGA
AGAAGTTCTCAGCCCGCACAGGCAGGAAGCCCAGGGACTGTGCCACTGAGGAGGACGAGCCACCAGCACCCGAAC
TGCATCAGGACGCAGCCAGGGAGCTTCAGCCCCCAGCTGCAGGAGACCCCCAAGCCAAAGCAGGCGGAGACACAC
ACCTCGGAACAGCCCCACAGGAGAGCCAGGTGGTGGTGGAGGGGGGCAGCGCGAGGGACAGGGCTCACCCCTCCC
AGCTGCTGTCTGACGATGAAACCAAAGACGACATGTCCATGTCTCTCTACTCGGTGGTCAGCACGGGGCTCCCTGC
AATGTGAAGACCTTGACAGCAGACCGGTGCTGGTGGGCGGGGAGGCCTGCAGCCCCACAGCGCGCATCGGCGGCA
CCGTGACACCGACTGGTGCATCTCCTTTGAGCAGATCCTGGCCCTCCATCCTGACGGAGTCCGTGCTGGTGAACCT
TCTTTGAGAAGAGAGTGGACATTGGACTCAAGATCAAGGACCAAAAGAAAGTGGAGAGACAGTTTCAGCACCCGCCA
GTGACCATGAGCAGCCTGGAGTTTCCGGCTTGATGCCTGCAGCTGTGAGGCCTGGCCCAAGGTGTCATCAGTGGGG
CTGGCCTCATCTCCTCCTGCCTTTCTCCTCCCTTATCAGTTTCTCTTTAAAGGTGTGCCCTCCTGCTCTCCCAGGA
GCAGTGAGTTGTGAGTGGAAAGAAGGCTGGTGCAGACCCAGCTGCCTTAGACAGATTCCCTGGGCCTGCATCTCC
TGGCGCCGGCTGCTTCTGGGCCCAGGAAGAGGCTGTGGCTCCACCTTCTTACACCTGGTGGGAGCCCGCCTCG
CACCAGCTGCACCTGCCTAGCATTAGAGGCTCTCAGATCTGCCCTTGCTTGCTTCATACCTCTGTGCTCCACACT
GCGGCCAGGCCAGCTGAGTCCCTCCATCCGTGGATGCTTTCTGCAGCTATGTGGTATGGGGGTTCATTCTGCCT
CTTGTCACCAGGTTGGGGGGCATGTGCTTGTGGGCACCAAGTGATGGAACCTCAGGTGCTCTCCGGGAGCCT
GAACCTCCTGACTGAGGAACATGGGCAGAACATGTTTATTGCACAGAGTGGGCGCTGCGCACAGGCGTGGCTGTA
CACGTGCTCTCAGCTCATCATCTTTCCAGTAACCTTTAAAAAAACATCCCTCAGGTCTGATATATTTCTCTGGA
TTCATTTCACTTGGCTAGAAATTACACTGTGCTCAATGCCTTAATAAATCCCTGAAAGAAATAAAAAACCACTGTG
TGCAATGCCTTGCTGTGGCCCCCAACCACTGCTTAGGCCTCCCAACTTCTCCCCAGGCCAAGTATGGGGCCCTGG
CTGTGTTCTGGAAGTTCAAGACACTTAGTCCTCCACAGTGGGTGGAAGAGTGCAAGGTCTGCCAGGTTCAGATGGA
GACGCAGAACCTGCTGGTGCAAGCTGGGCAGGTCTGACCAACCTGCATCAGGGGATGCCCTGAGCTCCACAGGT
CTTCATGGGCAGGGGTTGTGGGTCCCTGGTGAAGGAAGTGATCCTCAGGCCTGGGCTGTAGCAAGCTGTCTGCCC
TTGGGTTCAAGAACCAGACTGTGGAGCCAAAGGTGACCGCAGGGGGCCCCAGGGCTGGAGCCACAAGGATACCTT
CACTTTGCATGAGGAGCTGAAACTGACCAGTGTCAGTGTTAGCCCCCACATGGGGCTGCTCTTGCTTCTACTAA
AAGATACAGCAGTTACCCCTTATCCACAGGGGATACAGTGGATATCTAAAACCAGACCCCAAGTGGATGTCTAA
AACCACAGATAATAACAAACCTTATACATACTGTTTTTCTCTATGCATACATACCTGTGATTAAGTTTATGAATT
AGGCACCTTAAGAGATTGACAACAATAACTAATAATAAAATGTAACGGTTTACTGTAAAAA

2005/6881
FIGURE 1844

MAGRDRPSLPYLEQYRIDASQFRELFASTPWACGSHTPLLAGRMFRLLDENKDSLINFKEFVTGMSGMYHGYLE
EKLKVLKYLHLPPALSPPEEAESAEEAHHYFTEDSSSEEALPQEEQEGSGSEERGEKGTSSPDYRHYLRMWAKEK
EAQKETIKDLPKMNQEQFIELCKTLYNMFSEDPMEQDLYHAIATVASLLLRIGEVGKKFSARTGRKPRDCATEED
EPPAPELHQDAARELQPPAAGDPQAKAGDTHLGTAPQESQVVVEGGSGEGQGPSQLLSDDETKDDMSMSSYSV
VSTGSLQCEDLADDTVLVGGEACSP TARIGGTVD TDWCISFEQILASILTESVLVNFFEKRVDIGLKIKDQKKVE
RQFSTASDHEQPGVSG

2006/6881
FIGURE 1845

GCGCGGCGGCTGCGACCGGGACGGCCCGTTTTCCGCCAGCTCGCCGCTCGCTATGGCGTCGCTCACCGTGAAGGC
CTACCTTCTGGGCAAGGAGGACGCGGCGCGGAGATTGCGCGCTTCAGCTTCTGCTGCAGCCCCGAGCCTGAGGC
GGAAGCCGAGGCTGCGGCGGGTCCGGGACCCTGCGAGCGGCTGCTGAGCCGGGTGGCCGCCCTGTTCCCCGCGCT
GCGGCCTGGCGGCTTCCAGGCGCACTACCGCGATGAGGACGGGGACTTGGTTGCCTTTTCCAGTGACGAGGAATT
GACAATGGCCATGTCCTACGTGAAGGATGACATCTTCCGAATCTACATTAAAGAGAAAAAGAGTGCCGGCGGGA
CCACCGCCCAACCGTGTGCTCAGGAGGCGCCCCGCAACATGGTGCACCCCAATGTGATCTGCGATGGCTGCAATGG
GCCTGTGGTAGGAACCCGCTACAAGTGCAGCGTCTGCCCAGACTACGACTTGTGTAGCGTCTGCGAGGGAAAGGG
CTTGACCGGGGGCACACCAAGCTCGCATTCGCCAGCCCCCTTCGGGCACCTGTCTGAGGGCTTCTCGCACAGCCG
CTGGCTCCGGAAGGTGAAACACGGACACTTCGGGTGGCCAGGATGGGAAATGGGTCCACCAGGAAACTGGAGCCC
ACGTCCTCCTCGTGCAGGGGAGGCCCGCCCTGGCCCCACGGCAGAATCAGCTTCTGGTCCATCGGAGGATCCGAG
TGTGAATTTCTGAAGAACGTTGGGGAGAGTGTGGCAGCTGCCCTTAGCCCTCTGGGCATTGAAGTTGATATCGA
TGTGGAGCACGGAGGGGAAAAGAAGCCGCCTGACCCCCGTCTCTCCAGAGAGTTCCAGCACAGAGGAGAAGAGCAG
CTCACAGCCAAGCAGCTGCTGCTCTGACCCAGCAAGCCGGGTGGGAATGTTGAGGGCGCCACGCAGTCTCTGGC
GGAGCAGATGAGGAAGATCGCCTTGAGTCCGAGGGGCGCCCTGAGGAACAGATGGAGTCGGATAACTGTTTCAGG
AGGAGATGATGACTGGACCCATCTGTCTTCAAAAGAAGTGGACCCGTCTACAGGTGAACTCCAGTCCCTACAGAT
GCCAGAATCCGAAGGGCCAAGCTCTCTGGACCCCTCCCAGGAGGGACCCACAGGGCTGAAGGAAGCTGCCTTGTA
CCCACATCTCCCGCCAGAGGCTGACCCGCGGCTGATTGAGTCCCTCTCCAGATGCTGTCCATGGGCTTCTCTGA
TGAAGGCGGCTGGCTCACCAGGCTCCTGCAGACCAAGAACTATGACATCGGAGCGGCTCTGGACACCATCCAGTA
TTCAAAGCATCCCCCGCGTTGTGACCACTTTTTGCCACCTCTTCTGCGTGCCCTCTTCTGTCTCATAGTTGTG
TTAAGCTTGCGTAGAATTGCAGGTCTCTGTACGGGCCAGTTTCTCTGCCTTCTTCCAGGATCAGGGGTTAGGGTG
CAAGAAGCCATTTAGGGCAGCAAAACAAGTGACATGAAGGGAGGGTCCCTGTGTGTGTGTGTGCTGATGTTTCCT
GGGTGCCCTGGCTCCTTGAGCAGGGCTGGGCCTGCGAGACCCAAGGCTCACTGCAGCGCGCTCCTGACCCCTCC
CTGCAGGGGCTACGTTAGCAGCCCAGCACATAGCTTGCCATATGGCTTTCACCTTCTCTTTTGTTTTAAATGACT
CATAGGTCCCTGACATTTAGTTGATTATTTCTGCTACAGACCTGGTACACTCTGATTTTAGATAAAGTAAGCCT
AGGTGTTGTCAGCAGGCAGGCTGGGGAGGCCAGTGTGTGGGCTTCTGCTGGGACTGAGAAGGCTCACGAAGGG
CATCCGCAATGTTGGTTTCACTGAGAGCTGCCTCCTGGTCTCTTCACCACTGTAGTTCTCTCATTTCCAAACCAT
CAGCTGCTTTTAAAATAAGATCTCTTTGTAGCCATCCTGTAAATTTGTAAACAATCTAATTAAATGGCATCAGC
ACTTTAACCAAT

2007/6881
FIGURE 1846

TGCAGCCTCGGCCCCGCGGGCGCCCGCCGCGCACCCGAGGAGATGAGGGCTCCGCAATGGCACCTTCCTGACGCTG
CTGCTCTTCTGCTGTGCGCCTTCCTCTCGCTGTCTGGTACGCGGCACTCAGCGGCCAGAAAGGCGACGTTGTG
GACGTTTACCAGCGGGAGTTCCCTGGCGCTGCGCGATCGGTTGCACGCAGCTGAGCAGGAGAGCCTCAAGCGCTCC
AAGGAGCTCAACCTGGTGCTGGACGAGATCAAGAGGGCCGTGTCAGAAAGGCAGGCGCTGCGAGACGGAGACGGC
AATCGCACCTGGGGCCGCCTAACAGAGGACCCCGATTGAAGCCGTGGAACGGCTCACACCGGCACGTGCTGCAC
CTGCCCACCGTCTTCCATCACCTGCCACACCTGCTGGCCAAGGAGAGCAGTCTGCAGCCCGCGGTGCGCGTGGGC
CAGGGCCGCAACCGGAGTGTCGGTGGTGATGGGCATCCCGAGCGTGCGGCGCGAGGTGCACTCGTACCTGACTGAC
ACTCTGCACTCGCTCATCTCCGAGCTGAGCCCGCAGGAGAAGGAGGACTCGGTTCATCGTGGTGCTGATCGCCGAG
ACTGACTCACAGTACACTTCGGCAGTGACAGAGAACATCAAGGCCTTGTTCCCCACGGAGATCCATTCTGGGCTC
CTGGAGGTATCTCACCTCCCCCACTTCTACCTGACTTCTCCCGCTCCGAGAGTCCCTTTGGGGACCCCAAG
GAGAGAGTCAGGTGGAGGACCAACAGAACCTCGATTACTGCTTCCTCATGATGTACGCGCAGTCCAAAGGCATC
TACTACGTGCAGCTGGAGGATGACATCGTGGCCAAGCCCACTACCTGAGCACCATGAAGAACTTTGCACTGCAG
CAGCCTTCAGAGGACTGGATGATCCTGGAGTTCTCCAGCTGGGCTTCATTGGTAAGATGTTCAAGTCGCTGGAC
CTGAGCCTGATTGTAGAGTTCACTTCTCATGTTCTACCGGGACAAGCCCATCGACTGGCTCCTGGACCATATTCTG
TGGGTGAAAGTCTGCAACCCCGAGAAGGATGCGAAGCACTGTGACCGGCAGAAAGCCAACCTGCGGATCCGCTTC
AAACCGTCCCTCTTCCAGCACGTGGGCACCTCACTCCTCGCTGGCTGGCAAGATCCAGAACTGAAGGACAAAGAC
TTTGAAAGCAGGCGCTGCGGAAGGAGCAIGTGAACCCGCCAGCAGAGGTGAGCACGAGCCTGAAGACATACCAG
CACTTCACCCTGGAGAAAGCCTACCTGCGCGAGGACTTCTTCTGGGCCCTTCAACCCTGCGCGGGGGGACTTCATC
CGCTTCCGCTTCTTCCAACCTCTAAGACTGGAGCGGTTCTTCTTCCGAGTGGGAACATCGAGCACCCGGAGGAC
AAGCTCTTCAACACGTCTGTGGAGGTGCTGCCCTTCGACAACCTCAGTCAGACAAGGAGGCCCTGCAGGAGGGC
CGCACCGCCACCCTCCGGTACCCTCGGAGCCCCGACGGCTACCTCCAGATCGGCTCCTTCTACAAGGGAGTGGCA
GAGGGAGAGGTGGACCCAGCCTTCGGCCCTCTGGAAGCACTGCGCCTCTCGATCCAGACGGACTCCCCTGTGTGG
GTGATTCTGAGCGAGATCTTCCTGAAAAAGGCCGACTAAGCTGCGGGCTTCTGAGGGTACCCTGTGGCCAGCCCT
GAAGCCACATTTCTGGGGGTGTCGTCACTGCCGTCCCCGGAGGGCCAGATACGGCCCCGCCCAAAGGGTTCTGC
CTGGCGTCGGGCTTGGGCCGCGCTGGGGTCCGCCGCTGGCCCCGAGGCCCTAGGAGCTGGTGCTGCCCCGCCCCG
CCGGGCCGCGGAGGAGGCAGGCGGCCCCACACTGTGCCTGAGGCCCGGAACCGTTTCGCACCCGGCCTGCCCCAG
TCAGGCCGTTTTAGAAAGAGCTTTTACTTGGGCGCCCGCCGTCTCTGGCGGAACACTGGAATGCATATACTACTT
TATGTGCTGTGTTTTTTTATTCTTGATACATTTGATTTTTTTCACGTAAGTCCACATATACTTCTATAAGAGCGTG
ACTTGTAAATAAAGGGTTAATGAAG

2008/6881
FIGURE 1847

MRLRNGTFLTLTLFCLCAFLSLSWYAALSGQKGDVVDVYQREFLALRDRLHAAEQESLKRSKELNLVLDEIKRAV
SERQALRDGDGNRTWGRLTEDPRLKPWNGSHRHVLHLPTVFHHLPHLLAKESSLQPAVRVGQGRITGVSVVMGIPS
VRREVHSYLTDTLHSLISELSPQEKEDSVIVVLI AETDSQYTSAVTENIKALFPT EIHSGLL EVISPSPHFYPDF
SRLRESFGDPKERVWRWKQNLDYCFLLMYAQSKGIYYVQLEDDIVAKPNYLSTMKNFALQQPSEDWMILEFSQL
GFIGKMFKSLDLSLIVEFILMFYRDKPIDWLLDHILWVKVCNPEKDAKHCDRQKANLRIRFKPSL FQHVGTHSSL
AGKIQKLKDKDFGKQALRKEHVNPPAEVSTSLKTYQHFTLEKAYLREDDFFWAFTPAAGDFIRFRFFQPLRLERFF
FRSGNIEHPEDKLFNTSVEVLFFDNPQSDKEALQEGRTATLRYPRSPDGYLQIGSFYKGVAEGEVDPAFGPLEAL
RLSIQTDSPVWVILSEIFLKKAD

2009/6881
FIGURE 1848

TTTTCAGAGACTCGCCTGGCAGAGGCCTGGAGCGTCCTGCTGCGTGGACTGTGGGCACCGAGCCACCAGGAGGTT
GTTGATCTCATTCTTGCTCACTGGTCCCTGCCAGACTGGTGGTGCCTCTCTACTGTGCGGCAGCCCCACCTCTGT
GCTGCCCCATCCACCTACAGCCCTCATGCCTGGGCCCAGCTGGAGGTTCTGACAGGGGCCCCCTGGGGTGGCATG
CGGACCCTTCAGGGTGGCCCAGGCGCAGCACAGGTCTCCAGAGACACAGGCACCAGGGCGTTTCAGAGCTAGTCCC
CTCGCTGCTGTTGACTGTCCTTGAGCAGCCCCAGGGCCGGTTTCTCAACCTCATTGTGCTACCTGAGCAATGAAG
TGAGGTGGGCTCCTGGAAGTGCAGCAGCCACCCCCCGGGGCCATCGTGAGGCTAAGAATCCAGTGCAGGGTGAGC
AACCAGCGACCGCTACAAGGACAGTGAAGAGCTAGCACCAGGACCTTGGGTAGCCACCCGCTGGAGGGAGCGTG
TGCTGCAAAAAGCAAGAGTGGGCTTTGGAGGCCAACGGATGGAGCGGATTAGTCTGAGGCTGTTCCAGCCCTTG
CTTAGGATCCACCTACCTAGGTCTGGAATCGTATTTCCACTTCAGATGCCTTCTCAGAGGATAAAATAACCCCC
GGTGGGGGAGAGTACTGGAAGAGGGCTAATTCCCCTGGTTTTCTCCCCATGAGCATTAGTGTCAAGTGAATTTTA
GAGTGACCCAGCTATGTCACGTGTGGCAGGCACAAGAACAGATGTCAATGAGCTATTGCAGAGGTGGACACCCA
GATGTGTGCGCTGGCACACTGGAGGGGCCCGTAGGGTGGCTCTAGACCGCCCCCTCGTGACGGCTTGCTTACCAC
CTGCAGGCGACGTTGTGGACGTTTACCAGCGGGAGTTTCTGGCGCTGCGCGATCGGTTGCACGCAGCTGAGCAGG
AGAGCCTCAAGCGCTCCAAGGAGCTCAACCTGGTGCTGGACGAGATCAAGAGGGCCGTGTGAGAAAGGCAGGCGC
TGCGAGACGGGAGACGGCAATCGCACCTGGGGCCGCTAACAGAGGACCCCGATTGAAGCCGTGGAACGGCTCAC
ACCGGCACGTGCTGCACCTGCCCACCGTCTTCCATCACCTGCCACACCTGCTGGCCAAGGAGAGCAGTCTGCAGC
CCGCGGTGCGCGTGGGCCAGGGCCGCACCGGAGTGTGCGGTGGTGATGGGCATCCCGAGCGTGCGGCGCGAGGTGC
ACTCGTACCTGACTGACACTCTGCACTCGCTCATCTCCGAGCTGAGCCCGCAGGAGAAGGAGGACTCGGTCTATCG
TGGTGCTGATCGCCGAGACTGACTCACAGTACACTTCGGCAGTGACAGAGAACATCAAGGCCTTGTTCCCCACGG
AGATCCATTCTGGGCTCCTGGAGGTCTCTCACCTCCCCCACTTCTACCCTGACTTCTCCCGCCTCCGAGAGT
CCTTTGGGGACCCCAAGGAGAGAGTCAAGGTGGAGGACCAAACAGAACCTCGATTACTGCTTCTCTCATGATGTACG
CGCAGTCCAAAGGCATCTACTACGTGCAGCTGGAGGATGACATCGTGCCCAAGCCCACTACCTGAGCACCATGA
AGAAGTTTGCACTGCAGCAGCCTTCAGAGGACTGGATGATCCTGGAGTTCTCCAGCTGGGCTTCATTGGTAAGA
TGTTCAAGTCGCTGGACCTGAGCCTGATTGTAGAGTTTATTCTCATGTTCTACCGGGACAAGCCCATCGACTGGC
TCCTGGACCATATTCTGTGGGTGAAAGTCTGCAACCCCCGAGAAGGATGCGAAGCACTGTGACCGGCAGAAAGCCA
ACCTGCGGATCCGCTTCAAACCGTCCCTCTTCCAGCACGTGGGCACTCACTCCTCGCTGGCTGGCAAGATCCAGA
AACTGAAGGACAAAGACTTTGGAAAGCAGGCGCTGCGGAAGGAGCATGTGAACCCGCCAGCAGAGGTGAGCACGA
GCCTGAAGACATAACCAGCACTTCAACCTGGAGAAAGCCTACCTGCGCGAGGACTTCTTCTGGGCCTTCAACCCCTG
CCGCGGGGACTTTCATCCGCTTCCGCTTCTTCCAACCTCTAAGACTGGAGCGGTTCTTCTTCCGAGTGGGAAACA
TCGAGCACCCGGAGGACAAGCTTCAACACGTCTGTGGAGGTGCTGCCCTTCGACAACCCTCAGTCAGACAAGG
AGGCCCTGCAGGAGGGCCGCACCGCCACCCTCCGGTACCCTCGGAGCCCCGACGGCTACCTCCAGATCGGCTCCT
TCTACAAGGGAGTGGCAGAGGGAGAGGTGGACCCAGCCTTCGGCCCTCTGGAAGCACTGCGCCTCTCGATCCAGA
CGGACTCCCCTGTGTGGGTGATTCTGAGCGAGATCTTCTGAAAAAGGCCGACTAAGCTGCGGGCTTCTGAGGGT
ACCCTGTGGCCAGCCCTGAAGCCACATTTCTGGGGGTGTGCTCACTGCCGTCCCCGGAGGGCCAGATACGGCCC
CGCCCAAAGGGTTCTGCCTGGCGTGGGGCTGGGGCCGGCCTGGGGTCCGCGCTGGCCCGGAGGCCCTAGGAGCT
GGTGCTGCCCCCGCCCGGGCCGCGGAGGAGGCAGGCGGCCCCCACACTGTGCTGAGGCCCCGAACCGTTTCG
CACCCGGCCTGCCCCAGTCAGGCCGTTTTTGAAGAGCTTTTACTTGGGCGCCCGCCGTCTCTGGCGCGAACACTG
GAATGCATATACTACTTTATGTGCTGTGTTTTTTTATTCTTGATACATTTGATTTTTTTCACGTAAGTCCACATAT
ACTTCTATAAGAGCGTGACTTGTAATAAAGGGTTAATGAAG

2010/6881
FIGURE 1849

MSRVAGTRTDVNELLQRWTPRCVRWHTGGARRVALDRPLVTACLPPAGDVVDVYQREFLALRDRLHAAEQESLKR
SKELNLVLDEIKRAVSERQALRDGDGNRTWGRLTEDPRLKPWNGSHRHVLHLPTVFHHLPHLLAKESSLQPAVRV
GQGRITGVSVVMGIPSVRREVHSYLTDTLHSLISELSPQEKEDSVIVVLIETDSQYTSAVTENIKALFFTEIHSG
LLEVISPSPHFYPPDFSRLRESFGDPKERVVRWRTKQNLDYCFLLMYAQSKGIYYVQLEDDIVAKPNYLSTMKNFAL
QQPSEDWMILEFSQLGFIGKMFKSLDLSLIVEFILMFYRDKPIDWLLDHILWVKVCNPEKDAKHCDRQKANLRIR
FKPSLFQHVGTSSLAGKIQKLKDKDFGKQALRKEHVNPPAEVSTSLKTYQHFTLEKAYLREDDFFWAFTPAAGDF
IRFRFFQPLRLERFFFRSGNIEHPEDKLFNTSVEVLPPDNPOSDKEALQEGRTATLRYPRSPDGYLQIGSFYKGV
AEGEVDPAFGPLEALRLSIQTDSPVWVILSEIFLKKAD

2011/6881
FIGURE 1850

TTTTTTTTTTTCGTCTTAGCCACGCAGAAGTCGCGTGTCTAGTTTGTTCGACGCCGGACCGCGTAAGAGACGATG

ATGTTGGGCACGGAAGGTGGAGAGGGATTTCGTGGTGAAGGTCCGGGGCTTGCCCTGGTCTTGCTCGGCCGATGAA
GTGCAGAGGTTTTTTTCTGACTGCAAAATTCAAAATGGGGCTCAAGGTATTTCGTTTCATCTACACCAGAGAAGGC
AGACCAAGTGGCGAGGCTTTTGTGAACTTGAATCAGAAGATGAAGTCAAATTGGCCCTGAAAAAGACAGAGAA
ACTATGGGACACAGATATGTTGAAGTATTCAAGTCAAACAACGTTGAAATGGATTGGGTGTTGAAGCATACTGGT
CCAAATAGTCCTGACACGGCCAATGATGGCTTTGTACGGCTTAGAGGACTTCCCTTTGGATGTAGCAAGGAAGAA
ATTGTTTCAGTTCTTCTCAGGGTTGGAAATCGTGCCAAATGGGATAACATTGCCGGTGGACTTCCAGGGGAGGAGT
ACGGGGGAGGCCTTCGTGCAGTTTGCTTTCACAGGAAATAGCTGAAAAGGCTCTAAAGAAACACAAGGAAAGAATA
GGGCACAGGTATATTGAAATCTTTAAGAGCAGTAGAGCTGAAGTTAGAACTCATTATGATCCACCACGAAAGCTT
ATGGCCATGCAGCGGCCAGGTCCTTATGACAGACCTGGGGCTGGTAGAGGGTATAACAGCATTGGCAGAGGAGCT
GGCTTTGAGAGGATGAGGCGTGCTTATGGTGGAGGCTATGGAGGCTATGATGATTACAATGGCTATAATGAT
GGCTATGGATTTGGGTCAGATAGATTGGAAGAGACCTCAATTACTGTTTTTTCAGGAATGTCTGATCACAGATAC
GGGGATGGTGGCTCTACTTTCCAGAGCACAAACAGGACACTGTGTACACATGCGGGGATTACCTTACAGAGCTACT
GAGAATGACATTTATAATTTTTTTTACCAGCTCAACCCTGTGAGAGTACACATTGAAATTGGTCTCTGATGGCAGA
GTAAGTGGTGAAGCAGATGTCGAGTTCGCAACTCATGAAGATGCTGTGGCAGCTATGTCAAAAGACAAAAGCAAAT
ATGCAACACAGATATGTAGAATCTTCTTGAATTCTACAGCAGGAGCAAGCGGTGGTGTCTTACGAACACAGATAT
GTAGAATCTTCTTGAATTCTACAGCAGGAGCAAGCGGTGGTGTCTTATGGTAGCCAAATGATGGGAGGCATGGGC
TTGTCAAACAGTCCAGCTACGGGGGGCCAGCCAGCCAGCAGCTGAGTGGGGGTTACGGAGGCGGCTACGGTGGC
CAGAGCAGCATGAGTGGATACGACCAAGTTTTTACAGGAAAACCTCAGTGATTTTCAATCAAACATTGCATAGGTA
ACCAAGGAGCAGTGAACAGCAGCTACTACAGTAGTGGAAGCCGTGCATCTATGGGCGTGAACGGAATGGGAGGGT
TGTCTAGCATGTCCAGTATGAGTGGTGGATGGGGAATGTAATTGATCGATCCTGATCACTGACTCTTGGTCAACC
TTTTTTTTTTTTTTTTTTCTTTAAGAAAACCTCAGTTTAACAGTTTCTGCAATACAAGCTTGTGATTTATGCTT
ACTCTAAGTGGAAATCAGGATTGTTATGAAGACTTAAGGCCAGTATTTTTGAATACAATACTCATCTAGGATGT
AACAGTGAAGCTGAGTAACTATAACTGTAAACTTAAGTCCAGCTTTTCTCAAGTTAGTTATAGGATGTACTT
AAGCAGTAAGCGTATTTAGGTAAAAGCAGTTGAATTATGTTAAATGTTGCCCTTTGCCACGTTAAATTGAACACT
GTTTTGGATGCATGTTGAAAGACATGCTTTTATTTTTTTTGTAAAACAATATAGGAGCTGTGTCTACTATTAAAA
GTGAAACATTTTGGCATGTTTGTAAATTCTAGTTTCATTTAATAACCTGTAAGGCACGTAAGTTTAAGCTTTTTT
TTTTTTTAAGTTAATGGGAAAAATTTGAGACGCAATACCAATACTTAGGATTTTGGTCTTGGTGTGTTGTATGAAA
TTCTGAGGCCTTGATTTAAATCTTTCATTGTATTGTGATTCCTTTTAGGTATATTGCGCTAAGTGAAACTTGTC
AAATAAATCCTCCTTTTAAAAACTGC

2012/6881
FIGURE 1851

MMLGTEGGEGFVVKVRGLPWSCSADEVQRFFSDCKIQNGAQGIRFIYTREGRPSGEAFVELESEDEVKLALKKDR
ETMGHRYVEVFKSNNVEMDWVLKHTGPNSPDTANDGFVRLRGLPFGCSKEEIVQFFSGLIIVPNGITLPVDFQGR
STGEAFVQFASQEIAEKALKKKKERIGHRYIEIFKSSRAEVRTHYDPPRKLMMQRPQPYDRPGAGRGYNSIGRG
AGFERMRRGAYGGGYGGYDDYNGYNDGYGFGSDRFGDLNYCFSGMSDHRYGDGGSTFQSTTGHCVHMRGLPYRA
TENDIYNFFSPLNPVRVHIEIGPDGRVTGEADVEFATHEDAVAAMSKDKANMQHRYVELFLNSTAGASGGAYEHR
YVELFLNSTAGASGGAYGSQMMGGMGLSNQSSYGGFPASQQLSGGYGGGYGGQSSMSGYDQVLQENSSDFQSNIA

2013/6881
FIGURE 1852

CTGCAAGGCGGCGGCAGGAGAGGTTGTGGTGCTAGTTTCTCTAAGCCATCCAGTGCCATCCTCGTCGCTGCAGCG
ACACCGCTCTCGCCGCCGCCATGACTGAGCAGATGACCCCTTCGTGGCACCCCTCAAGGGCCACAACGGCTGGGTAA
CCCAGATCGCTACTACCCCGCAGTTCCCGGACATGATCCTCTCCGCCTCTCGAGATAAGACCATCATCATGTGGA
AACTGACCAGGGATGAGACCAACTATGGAATTCCACAGCGTGCTCTGCGGGGTCCTCCCACTTTGTTAGTGATG
TGGTTATCTCCTCAGATGGCCAGTTTGCCCTCTCAGGCTCCTGGGATGGAACCCTGCGCCTCTGGGATCTCACAA
CGGGCACCACCACGAGGCGATTTGTGGGCCATACCAAGGATGTGCTGAGTGTGGCCTTCTCCTCTGACAACCGGC
AGATTGTCTCTGGATCTCGAGATAAAACCATCAAGCTATGGAATACCCCTGGGTGTGTGCAAATACACTGTCCAGG
ATGAGAGCCACTCAGAGTGGGTGTCTTGTGTCCGCTTCTCGCCCAACAGCAGCAACCCTATCATCGTCTCCTGTG
GCTGGGACAAGCTGGTCAAGGTATGGAACCTGGCTAACTGCAAGCTGAAGACCAACCACATTGGCCACACAGGCT
ATCTGAACACGGTGACTGTCTCTCCAGATGGATCCCTCTGTGCTTCTGGAGGCAAGGATGGCCAGGCCATGTTAT
GGGATCTCAACGAAGGCAAACACCTTTACACGCTAGATGGTGGGGACATCATCAACGCCCTGTGCTTCAGCCCTA
ACCGCTACTGGCTGTGTGCTGCCACAGGCCCCAGCATCAAGATCTGGGATTTAGAGGGAAAGATCATTGTAGATG
AACTGAAGCAAGAAGTTATCAGTACCAGCAGCAAGGCAGAACCACCCAGTGCACTTCCCTGGCCTGGTCTGCTG
ATGGCCAGACTCTGTTTGCTGGCTACACGGACAACCTGGTGCGAGTGTGGCAGGTGACCATTGGCACACGCTAGA
AGTTTATGGCAGAGCTTTACAAATA

2014/6881
FIGURE 1853

MTEQMTLRGTLKGHNGWVTQIATTPQFPDMILSASRDKTIIMWKLTRDETNYGIPQRALRGHSHFVSDVVISSDG
QFALSGSWDGTLLRLWDLTTGTTTTRRFVGHTKDVLSVAFSSDNRQIVSGSRDKTIKLWNTLGVCKYTVQDESHSEW
VSCVRFSPNSSNPIIVSCGWDKLVKVWNLANCKLKTNHIGHTGYLNTVTVSPDGSLCASGGKDGQAMLWDLNEGK
HLYTLDGGDIINALCFSPNRYWLCAATGPSIKIWDLEGKIIIVDELKQEVISTSSKAEPQCTSLAWSADGQTLFA
GYTDNLVRVWQVTIGTR

2015/6881
FIGURE 1854

GCGGAGCCACGGAGCCACGGAGGAGCCACGGAGGAGCCCGAGCGTCCGAACGGGCAGACCCCTCGAGCCGC
GAAGGAGCCCGAGAAGCAGCCACG**ATG**TGCGGAATCTTTGCCTACATGAAGTACAGAGTCCCCGGACGAGGAAG
GAGATCTTCGAAACCCTCATCAAGGGCCTGCAGCGGCTGGAGTACAGAGGCTACGACTCGGCAGGTGTGGCGATC
GATGGGAATAATCACGAAGTCAAAGAAAGACACATTACAGCTGGTCAAGAAAAGGGGAAAGTCAAGGCTCTCGAT
GAAGAACTTTACAAACAAGACAGCATGGACTTAAAAGTGGAGTTTGAGACACACTTCGGCATTGCCACACGCGC
TGGGCCACCCACGGGGTCCCCAGTGTGTCAACAGCCACCCTCAGCGCTCAGACAAAGGCAACGAATTTGTTGTC
ATCCACAATGGGATCATCACAATTACAAAGATCTGAGGAAATTTCTGGAAAGCAAAGGCTACGAGTTTGAGTCA
GAAACAGATACAGAGACCATCGCCAAGCTGATTAAATATGTGTTTCGACAAACAGAGAACTGAGGACATTACGTTT
TCAACGTTGGTTCGAGAGAGTCATTACGAGTTGGAAGGTGCATTTCGCGCTGGTTTTCAAGAGTGTCCACTACCCA
GGAGAAGCCGTTGCCACACGGAGAGGCAGCCCCCTGCTCATCGGAGTCCGGAGCAAATACAAGCTCTCCACAGAA
CAGATCCCTATCTTATACAGGACGTGCACTCTGGAGAATGTGAAGAATATCTGTAAGACACGGATGAAGAGGCTG
GACAGCTCCGCTGCCTGCATGCTGTGGGCGACAAGGCCGTTGAATTCTTCTTTGCTTCTGATGCAAGCGCTATC
ATAGAGCACACCAACCGGGTTCATCTTCCTGGAGGACGATGACATCGCCGAGTGGCTGATGGGAACTCTCCATT
CACCGGGTCAAGCGCTCGGCCAGTGATGACCCATCTCGAGCCATCCAGACCTTGACAGTGGAACTGCAGCAAATC
ATGAAAGGTAACCTTCAGTGCGTTTATGCAGAAGGAGATCTTCGAACAGCCAGAATCAGTTTTCAATACTATGAGA
GGTCGGGTGAATTTTGAAACCAACACAGTGCTCCTGGGTGGCTTGAAGGACCACTTGAAGGAGATTCGACGATGC
CGACGGCTCATCGTGATTGGCTGTGGAACCAGCTACCACGCTGCCGTGGCTACGCGGCAAGTTTTGGAGGAACTG
ACTGAGCTTCTGTGATGGTTGAAGTTGCTAGTGATTTTTCTGGACAGGAACACACCTGTGTTTCAGGGATGACGTT
TGCTTTTTTCATCAGCCAGTCAGGCGAGACCGCGGACACCCTCCTGGCGCTGCGCTACTGTAAGGACCGCGGCGCT
CTCACCGTGGGCGTACCAACACCGTGGGCAGCTCCATCTCTCGCGAGACCGACTGCGGCGTCCACATCAACGCA
GGGCCGGAGATCGGCGTGGCCAGCACCAAGGCTTATACCAGTCAGTTTCATCTCTCTGGTGATGTTTGGTTTGATG
ATGCTGAAGACCGAATTTCACTACAAAACAGGAGGCAAGAGATCATCCGTGGCTTGAGATCTTTACCTGAGCTG
ATCAAGGAAGTGCTGTCTCTGGAGGAGAAGATCCACGACTTGGCCCTGGAGCTCTACACGCAGAGATCGCTGCTG
GTGATGGGGCGGGGCTACAACTATGCCACCTGCCTGGAAGGAGCCCTGAAAATTAAAGAGATAACCTACATGCAC
TCAGAAGGCATCCTGGCTGGGGAGCTGAAGCACGGGCCCTGGCACTGATTGACAAGCAGATGCCCGTCATCATG
GTCATTATGAAGGATCCTTGCTTCGCCAAATGCCAGAACGCCCTGCAGCAAGTCACGGCCCGCCAGGGTCGCCCC
ATTATACTGTGCTCCAAGGACGATACTGAAAGTTCCAAGTTTGCGTATAAGACAATTGAGCTGCCCCACACTGTG
GACTGCCTCCAGGGCATCCTGAGCGTGATTCCGCTGCAGCTGCTGTCCTTCCACCTGGCTGTTCTCCGAGGATAT
GACGTTGACTTCCCCAGAAATCTGGCCAAGTCTGTAAGTGTGGAAT**GA**GGCTGAGACCGTGACAAGACCATCACC
ACCTTTCATCTGATTCCAGACCTGTCCCAACAGCAGGGATGCTACATGGGAAGAGAAGTGAGCATCCCACATGTT
CTGCGTGCTCCTGTAGAGCTTGACAGCTTCCACGTGCCTTCTACCCAAGTGCTTTTGCTTACAGCAGATACTGTT
TCTCTGTGCTCCTGAAGTCGCCAGAGGAGAAGGGAATCATTGTTTACACATGGGGATCAGAGCAGACTTCTCCACT
ACTGTGCAATAGAGATACAGCTCTCTTCAGAGTAAGTGTGAACCTTTTATAACCAACACTAGAGTTAGTTTTTAA
AGACAAGATATTTATAATGACGACTGTATAGCTTTTAAAGTTATTTTTCTAGTATGTGGCTTTCTGTAGCCGTGGT
AACGGCCAAACTGTTTCATCCTAGCTACCCATGCTCTGTGTCCAGGCTTGCTCCTGGCAGGTGGCATTTCATCTCAG
ATGTGAGCACAAGGCATTGGCCCTCTGGACTCCTTTCTCCTTTTCTTTCTCTCTAGGCTGCTCCTGAATCCTGT
TCTCTGACATCCGTGGAGCCCTCCTGCATCCACCTATGCCTCCTATAAGTCCAGTTGAAATCTCAGCCTCCTTC
AACATTTTCTTCTCGTGTGTGGCCACATCCCTCCACTTCTCCAAGTCTGTTTAACTGATCAGGCTCTTTTT
AAGCCCTGGCAGCATTTTGGTCCCTGCTCCTTGCCCATAGTAAAACAGCTTGAAATATCCCATGCAAGAGAGTAG
TTTCAAGTGGGCGACTCTGCTCTCTATTTAAAAGCGTGACAATCAAAGTACTATGCAATTTTAGGACAATAAA
GAACATACAGTTCC

2016/6881
FIGURE 1855

MCGIFAYMNYRVPRTRKEIFETLIKGLQRLEYRGYDSAGVAIDGNNHEVKERHIQLVKKRGKVKALDEELYKQDS
MDLKVEFETHFGIAHTRWATHGVPSAVNSHPQRSKGNFVVIHNGIITNYKDLRKFLSKGYEFESETDTETIA
KLIKYVFDNRETEDITFSTLVERVIQQLEGAFALVFKSVHYPGEAVATRRGSPLLIGVRSKYKLSTEQIPILYRT
CTLENVKNICKTRMKRLDSSACLHAVGDKAVEFFFASDASAIIEHTNRVIFLEDDDIAAVADGKLSIHRVKRSAS
DDPSRAIQTLQMELOQIMKGNFSAFMQKEIFEQPESEVNTMRGRVNFETNTVLLGGLKDHLKEIRRCRRLIVIGC
GTSYHAAVATROVLEELTELPVMVELASDFLDNRNTPVFRDDVCFFISQSGETADTLLALRYCKDRGALTGVGTNT
VGSSISRETDCGVHINAGPEIGVASTKAYTSQFISLVMFGLMMSEDRISLQNRQEIIRGLRSLPELIKEVLSLE
EKIHDLALELYTQSRLLVMGRGYNYATCLEGALKIKEITYMHSEGILAGELKHGPLALIDKQMPVIMVIMKDPCF
AKCQNALQQVTARQGRPIILCSKDDTESSKFAYKTIELPHTVDCLQGILSVIPLQLLSFHLAVLRGYDVDFPRNL
AKSVTVE

2017/6881
FIGURE 1856

ATGGAGAACCGAGGAAGAGAAACAGGTTTTGTGGAAGACAAGCACAAGTCCACGCCTAGGTGTATGGGAAGTGAG
GTCCTCATGGGGCATAGCTACAGAGATCCCTTTTTTGGAGGGATGACTCGAGATGAAGATGATGATGAGGAAGAA
GAGGAAGAAGGGGGCTCATGGGGCTGTGGGAACCCAAGCTTCAGCCCAGGAGGAGGGATACGTTTCCACGATAAC
TTCGGCTTTGATGACCTAGTACAAGATTTCAATAGCATCTTCAGCAATATGGGGGCCTGGACCTTGCCTTCCCAT
CCTCCTGAACTTCCAGGTTCTGAGTCAGAGACACCTGGTGAGAGACTGCGGGAGGGACAGGCACCTTCGAGAATCA
ATGCTTAAGTATCCAGATAGTCACCAGCCCAGGATCTTTGAGGGGGTCTTGGAGAGTGATGCAAGAAGAGCGTCT
TGGCCCGGTTCTACAGCCCCAGCCCAGATCTACTTCAAGAGCATCTCTGTGACCAAAATCACTAAGCCAGATGGG
ATAGTGGAGGAGCGCTGGACTGTGGTGGACACCCTGGATGATGCCTTCTCCATCCTGGACTTATTCCTAGGATGC
TGGTTCCGGTCCCGGTAG

2018/6881
FIGURE 1857

ATGGCCCCCACAGTGTGGAGAGTGGACGGACAGACAGAAGCAGTGTGTGCAGCCTTGCCTCTCATCAGAGTCACT
GGGAGCAGGATTTCTTTGACCTCGCTGAGTACACTGCGGACGTTGACGGAGTTGGCACTCTACGACTTCTAGAT
GCAGTTAAGACTTGTGGCCTTATCAACTCTGTGAAGTTCTACCAAGCCTCAACAAGTGAACTTTATGGGAAAGTG
CAGGAAATACCCAGAAAGGAGACCACCCCTTTCTATCCCCGGTCACCCTATGGTGAGAACATGCGTGCACACCGG
AGCACATGTGTGGCGTTATCTGTGGGTGTGGGGGGGGCAGCAAACTCTATGCCTATTGGATTGTGGTGAAC TTC
CGTGAGGCGTATAATCTCTTTGCAGTGAACGGCATTCTCTTCAATCATGAGAGTCCCAGAAGAGGAGATCAGTTG
AAGATTTCCGTCTTTCGATGA

2019/6881
FIGURE 1858

CTGATGGCATCTTCTAAGCTGAAATGAATGAGTTTCTTACTCAGGAGCTGGCTGAAGATGGCTACTCTGGAGTTG
AGATGCGAGTTACACCAACCAGGACAGAAATCATTGTCTTAGCCACCAGAACACAGAATGTTCTTGGTGAGAAGG
GCCGGCGGATTTCGGGAACTGACTGCTGTAGTTCAGAAGAGGTTTGGCTCTCCAGGCAGAGTCTCTGCCTTACAAA
CTCCTAGGAGGGCTTGCTGTGCGGAGGGCCTGCTATGGTGTGTGCGGTTTCATCATGGAAACTGGGGCCAAAGGC
TGTGAGGTCGTGGTGTCTGGGAACTCTGAGGACAGAGAGCTAAATCCATGAAGTTTGTGGA

2020/6881
FIGURE 1859A

CCGACCAACACCAACACCCAGCTCCGACGCAGCTCCTCTGCGCCCTTGCCGCCCTCCGAGCCACAGCTTTCCTCC
CGCTCCTGCCCCCGGCCCGTCCGCGTCTCCGCGCTCGCAGCGGCCCTCGGGAGGGCCCAGGTAGCGAGCAGCGACC
TCGCGAGCCTTCCGCACTCCCGCCCGGTTCCCCGGCCGTCCGCCTATCCTTGCCCCCTCCGCTTTCCTCCGCGCC
GGCCCCCTCGCTTATGCCTCGGCGCTGAGCCGCTCTCCCGATTGCCCGCCGACATGAGCTGCAACGGAGGCTCC
CACCCGCGGATCAACACTCTGGGCCGCATGATCCGCGCCGAGTCTGGCCCGGACCTGCGCTACGAGGTGACCAGC
GGCGGCGGGGGCACCAGCAGGATGTACTATTCTCGGCGCGGCGTGATCACCGACCAGAACTCGGACGGCTACTGT
CAAACCGGCACGATGTCCAGGCACCAGAACCAGAACACCATCCAGGAGCTGCTGCAGAACTGCTCCGACTGCTTG
ATGCGAGCAGAGCTCATCGTGACGCTGAATTGAAGTATGGAGATGGAATACAACCTGACTCGGAGTCGAGAATTG
GATGAGTGTGTTTGGCCAGGCCAATGACCAAATGGAAATCCTCGACAGCTTGATCAGAGAGATGCGGCAGATGGGC
CAGCCCTGTGATGCTTACCAGAAAAGGCTTCTTCAGCTCCAAGAGCAAATGCGAGCCCTTTATAAAGCCATCAGT
GTCCCTCGAGTCCGACGGGCCAGCTCCAAGGGTGGTGGAGGCTACACTTGTGAGAGTGGCTCTGGCTGGGATGAG
TTCACCAAACATGTACCAGTGAATGTTGGGGTGGATGAGGCAGCAAAGGGCGGAGATGGACATGGTGGCCCTGG
GGTGTGGACCTGGCCTCAGTGGAGCAGCACATTAACAGCCACCGGGGCATCCACAACCTCCATCGGCGACTATCGC
TGGCAGCTGGACAAAATCAAAGCCGACCTGCGCGAGAAATCTGCGATCTACCAGTTGGAGGAGGAGTATGAAAAC
CTGCTGAAAGCGTCCTTTGAGAGGATGGATCACCTGCGACAGCTGCAGAACATCATTCAGGCCACGTCCAGGGAG
ATCATGTGGATCAATGACTGCGAGGAGGAGGAGCTGCTGTACGACTGGAGCGACAAGAACACCAACATCGCTCAG
AAACAGGAGGCCTTCTCCATACGCATGAGTCAACTGGAAGTTAAAGAAAAAGAGCTCAATAAGCTGAAACAAGAA
AGTGACCAACTTGTCTCAATCAGCATCCAGCTTCAGACAAAATTGAGGCCTATATGGACACTCTGCAGACGCAG
TGGAGTTGGATTCTTCAGATCACCAAGTGCATTGATGTTTCATCTGAAAAAATGCTGCCTACTTTCAGTTTTTTG
AAGAGGCGCAGTCTACTGAAGCATACCTGAAGGGGCTCCAGGACTCCATCAGGAAGAAGTACCCCTGCGACAAGA
ACATGCCCTGACAGCAGCTGCTGGAACAGATCAAGGAGCTGGAGAAAGAACGAGAGAAAATCCTTGAATACAAGC
GTCAGGTGCAGAACTTGGTAAACAAGTCTAAGAAGATTGTACAGCTGAAGCCTCGTAACCCAGACTACAGAAGCA
ATAAACCATTATTCTCAGAGCTCTCTGTGACTACAAACAAGATCAGAAAATCGTGCATAAGGGGGATGAGTGTA
TCCTGAAGGACAACAACGAGCGCAGCAAGTGGTACGTGACGGGCCCCGGGAGGCGTTGACATGCTTGTTCCTCTG
TGGGGCTGATCATCCCTCCTCCGAACCCACTGGCCGTGGACCTCTCTTGCAAGATTGAGCAGTACTACGAAGCCA
TCTTGGCTCTGTGGAACAGCTCTACATCAACATGAAGAGCCTGGTGTCTTGGCACTACTGCATGATTGACATAG
AGAAGATCAGGGCCATGACAATCGCCAAGCTGAAAACAATGCGGCAGGAAGATTACATGAAGACGATAGCCGACC
TTGAGTTACATTACCAAGAGTTCATCAGAAATAGCCAAGGCTCAGAGATGTTTGGAGATGATGACAAGCGGAAAA
TACAGTCTCAGTTCACCGATGCCCAGAAGCATTACCAGACCCTGGTCATTGAGCTCCCTGGCTATCCCCAGCACC
AGACAGTGACCACAACCTGAAATCACTCATCATGGAACCTGCCAAGATGTCAACCATAATAAAGTAATTGAAACCA
ACAGAGAAAATGACAAGCAAGAAACATGGATGCTGATGGAGCTGCAGAAAGATTGCGAGGCAGATAGAGCACTGCG
AGGGCAGGATGACTCTCAAAAACCTCCCTCTAGCAGACCAGGGATCTTCTCACCACATCAGAGTAAAATTAACG
AGCTTAAGAGTGTGCAGAAATGATTCACAAGCAATTGCTGAGGTTCTCAACCAGCTTAAAGATATGCTTGCCAACT
TCAGAGGTTCTGAAAAGTACTGCTATTTACAGAATGAAGTATTTGGACTATTTAGAAACTGGAAAATATCAATG
GTGTTACAGATGGCTACTTAAATAGCTTATGCACAGTAAGGGCACTGCTCCAGGCTATTCTCCAAACAGAAGACA
TGTTAAAGGTTTATGAAGCCAGGCTCACTGAGGAGGAAAATGTCTGCCTGGACCTGGATAAAGTGGAAGCTTACC
GCTGTGGACTGAAGAAAATAAAAAATGACTTGAACCTGAAGAAGTCGTTGTTGGCCACTATGAAGACAGAAGTAC
AGAAAGCCAGCAGATCCACTCTCAGACTTCACAGCAGTATCCACTTTATGATCTGGACTTGGGCAAGTTCGGTG
AAAAAGTCACACAGCTGACAGACCGCTGGCAAAGGATAGATAAACAGATCGACTTTAGGTTATGGGACCTGGAGA
AACAAATCAAGCAATTGAGGAATTATCGTGATAACTATCAGGCTTTCTGCAAGTGGCTCTATGATGCTAAACGCC
GCCAGGATTCTTAGAATCCATGAAATTTGGAGATTCCAACACAGTCATGCGGTTTTTGAATGAGCAGAAGAACT
TGCACAGTGAAATATCTGGCAAACGAGACAAATCAGAGGAAGTACAAAAAATTGCTGAACCTTTGCGCCAATTCAA
TTAAGGATTATGAGCTCCAGCTGGCCTCATAACCTCAGGACTGGAACTCTGCTGAACATACCTATCAAGAGGA
CCATGATTACAGTCCCTTCTGGGGTGATTCTGCAAGAGGCTGCAGATGTTTCATGCTCGGTACATTGAACTACTTA
CAAGATCTGGAGACTATTACAGGTTCTTAAGTGAGATGCTGAAGAGTTTGAAGATCTGAAGCTGAAAAATACCA
AGATCGAAGTTTTGGAAGAGGAGCTCAGACTGGCCCGAGATGCCAACTCGGAAAACCTGTAATAAGAACAAATTC
TGGATCAGAACCTGCAGAAATACCAGGCAGAGTGTTCCAGTTCAAAGCGAAGCTTGCGAGCCTGGAGGAGCTGA
AGAGACAGGCTGAGCTGGATGGGAAGTCGGCTAAGCAAAATCTAGACAAGTGCTACGGCCAAATAAAGAAGTCA

2021/6881
FIGURE 1859B

ATGAGAAGATCACCCGACTGACTTATGAGATTGAAGATGAAAAGAGAAGAAGAAAATCTGTGGAAGACAGATTG
ACCAACAGAAGAATGACTATGACCAACTGCAGAAAGCAAGGCAATGTGAAAAGGAGAACCTTGGTTGGCAGAAAT
TAGAGTCTGAGAAAGCCATCAAGGAGAAGGAGTACGAGATTGAAAGGTTGAGGGTTCTACTGCAGGAAGAAGGCA
CCCCGAAGAGAGAATATGAAAATGAGCTGGCAAAGGTAAGAAACCACTATAATGAGGAGATGAGTAATTTAAGGA
ACAAGTATGAAACAGAGATTAACATTACGAAGACCACCATCAAGGAGATATCCATGCAAAAAGAGGATGATTCCA
AAAATCTTAGAAACCAGCTTGATAGACTTTCAAGGGAAAATCGAGATCTGAAGGATGAAATTGTCAGGCTCAATG
ACAGCATCTTGCAAGGCACTGAGCAGCGAAGGCGAGCTGAAGAAAACGCCCTTCAGCAAAAAGGCCTGTGGCTCTG
AGATAATGCAGAAGAAGCAGCATCTGGAGATAGAAGTGAAGCAGGTCATGCAGCAGCGCTCTGAGGACAATGCC
GGCACAAGCAGTCCCTGGAGGAGGCTGCCAAGACCATTGAGGACAAAAATAAGGAGATCGAGAGACTCAAAGCTG
AGTTTCAGGAGGAGGCCAAGCGCCGCTGGGAATATGAAAATGAACTGAGTAAGGTAAGAAACAATTATGATGAGG
AGATCATTAGCTTAAAAAATCAGTTTGAGACCGAGATCAACATCACCAAGACCACCATCCACCAGCTCACCATGC
AGAAGGAAGAGGATACCAAGTGGCTACCGGGCTCAGATAGACAATCTCACCCGAGAAAACAGGAGCTTATCTGAAG
AAATAAAGAGGGCTGAAGAACACTCTAACCAGACCACAGAGAATCTCAGGAGGGTGAAGAAGACATCCAACAGC
AAAAGGCCACTGGCTCTGAGGTGTCTCAGAGGAAACAGCAGCTGGAGGTTGAGCTGAGACAAGTCACTCAGATGC
GAACAGAGGAGAGCGTAAGATATAAGCAATCTCTTGATGATGCTGCCAAAACCATCCAGGATAAAAAACAAGGAGA
TAGAAAAGGTTAAACAACCTGATCGACAAAAGAAACAAATGACCGGAAATGCCTGGAAGATGAAAACGCGAGATTAC
AAAGGGTCCAGTATGACCTGCAGAAAGCAAAACAGTAGTGCGACGGAGACAATAAAACAACTGAAGGTTTCAGGAGC
AAGAAGTGCACGCTGAGGATCGACTATGAAAGGGTTTCCAGGAGAGGACTGTGAAGGACCAGGATATCACGC
GGTTCCAGAATCTCTGAAAGAGCTGCAGCTGCAGAAGCAGAAGGTGGAAGAGGAGCTGAATCGGCTGAAGAGGA
CCGCGTCAGAAGACTCCTGCAAGAGGAAGAAGCTGGAGGAAGAGCTGGAAGGCATGAGGAGGTCGCTGAAGGAGC
AAGCCATCAAAATCACCAACCTGACCCAGCAGCTGGAGCAGGCATCCATTGTTAAGAAGAGGAGTGAGGATGACC
TCCGGCAGCAGAGGGACGTGCTGGATGGCCACCTGAGGGAAAAGCAGAGGACCCAGGAAGAGCTGAGGAGGCTCT
CTTCTGAGGTCGAGGCCCTGAGGCGGCAGTTACTCCAGGAACAGGAAAGTGTCAAACAAGCTCATTGAGGAATG
AGCATTTCCAGAAGGCGATAGAAGATAAAAGCAGAAGCTTAAATGAAAGCAAAATAGAAATTGAGAGGCTGCAGT
CTCTCACAGAGAACCTGACCAAGGAGCACTTGATGTTAGAAGAAGAACTGCGGAACCTGAGGCTGGAGTACGATG
ACCTGAGGAGAGGACGAAGCGAAGCGGACAGTGATAAAATGCAACCATCTTGGAACCTAAGGAGCCAGCTGCAGA
TCAGCAACAACCGGACCCTGGAAGTGCAGGGGCTGATTAATGATTTACAGAGAGAGAGGGAAAATTTGAGACAGG
AAATTGAGAAATTCCAAAAGCAGGCTTTAGAGGCATCTAATAGGATTCAGGAATCAAAGAATCAGTGTACTCAGG
TGGTACAGGAAAGAGAGAGCCTTCTGGTGAAGTCAAAAGTCTGAGCAAGACAAGGCAAGGCTGCAGAGGCTGG
AGGATGAGCTGAATCGTGCAAAATCAACTCTAGAGGCAGAAACCAGGGTGAAACAGCGCCTGGAGTGTGAGAAAC
AGCAAATTCAGAATGACCTGAATCAGTGGAAGACTCAATATTCCCGCAAGGAGGAGGCTATTAGGAAGATAGAAT
CGGAAAGAGAAAAGAGTGAGAGAGAGAAGAACAGTCTTAGGAGTGAGATCGAAAGACTCCAAGCAGAGATCAAGA
GAATTGAAGAGAGGTGCAGGCGTAAGCTGGAGGATTCTACCAGGGAGACACAGTCACAGTTAGAAACAGAACGCT
CCCGATATCAGAGGGAGATTGATAAACTCAGACAGCGCCATATGGGTCCCATCGAGAGACCCAGACTGAGTGTG
AGTGGACCGTTGACACCTCCAAGCTGGTGTGTTGATGGGCTGAGGAAGAAGGTGACAGCAATGCAGCTCTATGAGT
GTCAGCTGATCGACAAAACAACCTTGGACAAACTATTGAAGGGGAAGAAGTCAGTGGAAGAAGTTGCTTCTGAAA
TCCAGCCATTCTTCGGGGTGCAGGATCTATCGCTGGAGCATCTGCTTCTCCTAAGGAAAAATACTCTTTGGTAG
AGGCCAAGAGAAAAGAAATTAATCAGCCCAGAATCCACAGTCATGCTTCTGGAGGCCAGGCAGCTACAGGTGGTA
TAATTGATCCCCATCGGAATGAGAAGCTGACTGTCGACAGTGCCATAGCTCGGGACCTCATTGACTTCGATGACC
GTCAGCAGATATATGCAGCAGAAAAAGCTATCACTGGTTTTGATGATCCATTTTCAGGCAAGACAGTATCTGTTT
CAGAAGCCATCAAGAAAAATTTGATTGATAGAGAAACCGGAATGCGCCTGCTGGAAGCCCAGATTGCTTCAGGGG
GTGTAGTAGACCCTGTGAACAGTGTCTTTTTGCCAAAAGATGTGCGCTTGGCCCGGGGGCTGATTGATAGAGATT
TGTATCGATCCCTGAATGATCCCCGAGATAGTCAGAAAAACTTTGTGGATCCAGTCACCAAAAAGAAGGTCAGTT
ACGTGCAGCTGAAGGAACGGTGCAGAATCGAACCACATACTGGTCTGCTCTTGCTTTCAGTACAGAAGAGAAGCA
TGTCTTCCAAGGAATCAGACAACCTGTGACCGTCACTGAGCTAGTAGATTCTGGTATATTGAGACCGTCCACTG
TCAATGAACTGGAATCTGGTCAGATTCTTATGACGAGGTTGGTGAGAGAATTAAGGACTTCCTCCAGGGTTCAA
GCTGCATAGCAGGCATATACAATGAGACCACAAAACAGAAGCTTGGCATTATGAGGCCATGAAAATTGGCTTAG
TCCGACCTGGTACTGCTCTGGAGTTGCTGGAAGCCCAAGCAGCTACTGGCTTTATAGTGGATCCTGTTAGCAACT

2022/6881
FIGURE 1859C

TGAGGTTACCACTGGAGGAAGCCTACAAGAGAGGTCTGGTGGGCATTGAGTTCAAAGAGAAGCTCCTGTCTGCAG
AACGAGCTGTCACTGGGTATAATGATCCTGAAACAGGAAAACATCATCTCTTTGTTCCAAGCCATGAATAAGGAAC
TCATCGAAAAGGGCCACGGTATTTCGCTTATTAGAAGCACAGATCGCAACCGGGGGGATCATTGACCCAAAGGAGA
GCCATCGTTTACCACTTGACATAGCATATAAGAGGGGCTATTTCAATGAGGAACTCAGTGAGATTCTCTCAGATC
CAAGTGATGATACCAAAGGATTTTTTGACCCCAACACTGAAGAAAATCTTACCTATCTGCAACTAAAAAGAAAGAT
GCATTAAGGATGAGGAAACAGGGCTCTGTCTTCTGCCTCTGAAAGAAAAGAAGAAACAGGTGCAGACATCACAAA
AGAATACCTCAGGAAGCGTAGAGTGGTCATAGTTGACCCAGAAACCAATAAAGAAATGTCTGTTCAAGGAGGCCT
ACAAGAAGGGCCTAATTGATTATGAAACCTTCAAAGAACTGTGTGAGCAGGAATGTGAATGGGAAGAAATAACCA
TCACGGGATCAGATGGCTCCACCAGGGTGGTCCTGGTAGATAGAAAGACAGGCAGTCAGTATGATATTCAAGATG
CTATTGACAAGGGCCTTGTTGACAGGAAGTTCTTTGATCAGTACCGATCCGGCAGCCTCAGCCTCACTCAATTTG
CTGACATGATCTCCTTGAAAAATGGTGTGCGCACCCAGCAGCAGCATGGGCAGTGGTGTGACGATGATGTTTTTA
GCAGCTCCCGACATGAATCAGTAAGTAAGATTTCCACCATATCCAGCGTCAGGAATTTAACCATAAGGAGCAGCT
CTTTTTTCAGACACCCCTGGAAGAATCGAGCCCCATTGCAGCCATCTTTGACACAGAAAACCTGGAGAAAATCTCCA
TTACAGAAGGTATAGAGCGGGGCATCGTTGACAGCATCACGGGTGAGAGGCTTCTGGAGGCTCAGGCCTGCACAG
GTGGCATCATCCACCCAACCACGGGCCAGAAGCTGTCACTTCAGGACGCAGTCTCCAGGGTGTGATTGACCAAG
ACATGGCCACCAGGCTGAAGCCTGCTCAGAAAGCCTTCATAGGCTTCGAGGGTGTGAAGGGAAAGAAGATGT
CAGCAGCAGAGGCAGTGAAAGAAAAATGGCTCCCGTATGAGGCTGGCCAGCGCTTCTGAGATTCCAGTACCTCA
CGGGAGGTCTTGTTGACCCGGAAGTGCATGGGAGGATAAGCACCGAAGAAGCCATCCGGAAGGGGTTCATAGATG
GCCGCGCCGCACAGAGGCTGCAAGACACCAGCAGCTATGCCAAAATCCTGACCTGCCCCAAAACCAAATTAATAA
TATCCTATAAGGATGCCATAAATCGCTCCATGGTAGAAGATATCACTGGGCTGCGCCTTCTGGAAGCCGCCTCCG
TGTCGTCCAAGGGCTTACCCAGCCCTTACAACATGTCTTCGGCTCCGGGGTCCCGCTCCGGCTCCCGCTCGGGAT
CTCGCTCCGGATCTCGCTCCGGGTCCCGCAGTGGGTCCCGGAGAGGAAGCTTTGACGCCACAGGGAATTCTTCCT
ACTCTTATTCCTACTCATTTAGCAGTAGTTCATTGGGCACTAGTAGTCAGTTGGGAGTGGTTGCTATACCTTGA
CTTCATTTATATGAATTTCCACTTTATTAAATAATAGAAAAGAAAATCCCGGTGCTTGCAGTAGAGTGATAGGAC
ATTCTATGCTTACAGAAAATATAGCCATGATTGAAATCAAATAGTAAAGGCTGTTCTGGCTTTTTATCTTCTTAG
CTCATCTTAAATAAGCAGTACACTTGGATGCAGTGCCTCTGAAGTGCTAATCAGTTGTAACAATAGCACAAATCG
AACTTAGGATTTGTTTCTTCTTCTGTGTTTCGATTTTTGATCAATTCTTTAATTTTGAAGCCTATAATACAG
TTTTCTATTCTTGGAGATAAAAATTAAATGGATCACTGATATTTTAGTCATTCTGCTTCTCATCTAAATATTTCC
ATATTCTGTATTAGGAGAAAATTACCCTCCCAGCACCAGCCCCCTCTCAAACCCCAACCCAAAACCAAGCATT
TTGGAATGAGTCTCCTTTAGTTTCAGAGTGTGGATTGTATAACCCATATACTCTTCGATGTACTTGTGTTGGTTTG
GTATTAATTTGACTGTGCATGACAGCGGAATCTTTTCTTTGGTCAAAGTTTCTGTTTATTTTGCTTGTTCATAT
TCGATGTACTTTAAGGTGTCTTTATGAAGTTTGCTATTCTGGCAATAAACTTTTAGACTTTT

2023/6881
FIGURE 1860

GTCA TGTTC TCGCGCCCTGGTGTGGACACTGCCAGCGGCTGCAGCCGACTTGGAATGACCTGGGAGACAAATAC
AACAGCATGGAAGATGCCAAAGTCTATGTGGCTAAAGTGGACTGCACGGCCCACTCCGACGTGTGCTCCGCCAG
GGGTGCGAGGATACCCACCTTAAAGCTTTTCAAGCCAGGCCAAGAAGCTGTGAAGTACCAGGGTCCCTCGGGAC
TTCCAGACACTGGAAAAGTGGATGCTGCAGACACTGAACGAGGAGCCAGTGACACCAGAGCCGGAAGTGGAAACG
CCAGTGCCCCCGAGCTCAAGCAAGGGCTGTATGAGCTCTCAGCAAGCAACTTTGAGCTGCACGTTGCACAAGGC
GACCACTTTATCAAGTTCCTTCGCTCCGTGGTGTGGTCACTGCAAAGCCCTGGCTCCAACCTGGGAGCAGCTGGCT
CTGGGCCTTGAACATTCCGAAACTGTCAAGATTGGCAAGGTTGATTGTACACAGCACTATGAACTCTGCTCCGGA
AACCAGGTTCTGCTGCTATCCCACTCTTCTCTGGTTCGAGATGGGAAAAAGGTGGATCAGTACAAGGGAAGCGG
GATTTGGAGTCACTGAGGGAGTACGTGGAGTCGCAGCTGCAGCGCACAGAGACTGGAGCGACGGAGACCGTCACG
CCCTCAGAGGCCCCGGTGTGCTGGCAGCTGAGCCCCAGGCTGACAAGGGCACTGTGTTGGCACTCACTGAAAATAAC
TTCGATGACACCATTGCAGAAGGAATAACCTTCATCAAGTTTTATGCTCCATGGTGTGGTCATTGTAAGACTCTG
GCTCCTACTTGGGAGGAACTCTCTAAAAAGGAATTCCCTGGTCTGGCGGGGTCAAGATCGCCGAAGTAGACTGC
ACTGCTGAACGGAATATCTGCAGCAAGTATTCGGTACGAGGCTACCCACGTTATTGCTTTTCCGAGGAGGGAAG
AAAGTCAGTGAGCACAGTGGAGGCAGAGACCTTGACTCGTTACACCGCTTTGTCCTGAGCCAAGCGAAAAGACGAA
CTTTAGGAACACAGTTGGAGGTCACCTCTCCTGCCCAGCTCCCGCACCCCTGCGTTTAGGAGTTTCACTCCACAGA
GGCCACTGGGTTCACAGTGGTGGCTGTTTCAAGAAAGCAGAACTAAGCGTGAGGTATCTTCTTTGTGTGTGTG
TTTTCCAAGCCAACACACTCTACAGATTCTTTATTAAGTTAAGTTTCTCTAAGTAAATGTGTAAGTCACTGATGAC
TGTGTAAACATTTTCACTGGCGATATATCCCTTTGACCTTCTCTTGATGAAATTTACATGGTTTTCTTTGAGAC
TAAATAGCGTTGAGGGAATGAAATTGCTGGACTATTTGTGGCTCCTGAGTTGAGTGATTTTGGTGAAAGAAAG
CACATCCAAAGCATAGTTTACCTGCCACGAGTTCTGGAAAAGGTGGCCTTGTGGCAGTATTGACGTTCCCTCTGAT
CTTAAGGTCACAGTTGACTCAATACTGTGTTGGTCCGTAGCATGGAGCAGATTGAAATGCAAAAACCCACACCTC
TGGAAGATACCTTCACGGCCGCTGCTGGAGCTTCTGTTGCTGTGAATACTTCTCTCAGTGTGAGAGGTTAGCCGT
GATGAAAGCAGCGTTACTTCTGACCGTGCCTGAGTAAGAGAATGCTGATGCCATAACTTTATGTGTGATACTTG
TCAAATCAGTTACTGTTTCAAGGGGATCCTTCTGTTTCTCACGGGGTGAAACATGTCTTTAGTTCCCTCATGTTAACA
CGAAGCCCAGAGCCCATGAACTGTTGGATGTCTTCCTTAGAAAGGTTAGGCATGGAAAATTCCACGAGGCTCA
TTCTCAGTATCTCATTAAGTCAATTGAAAGATTCCAGTTGTATTTGTCACCTGGGGTGACAAGACCAGACAGGCTT
TCCCAGGCCTGGGTATCCAGGGAGGCTCTGCAGCCCTGCTGAAGGGCCCTAACTAGAGTTCTAGAGTTTCTGATT
CTGTTTCTCAGTAGTCCCTTTTAGAGGCTTGCTATACTTGGTCTGCTTCAAGGAGGTCGACCTTCTAATGTATGAA
GAATGGGATGCATTTGATCTCAAGACCAAAGACAGATGTCAGTGGGCTGCTCTGGCCCTGGTGTGCACGGCTGTG
GCAGCTGTTGATGCCAGTGTCTCTAAGTCACTGCTGTCTGTTGATTAAACACCTCTATCTCCCTTGGGAATAAG
CACATACAGGCTTAAGCTCTAAGATAGATAGGTGTTTGTCTTTTACCATCGAGCTACTTCCATAATAACCACT
TTGCATCCAACACTCTTACCCACCTCCCATACGCAAGGGGATGTGGATACTTGGCCCAAAGTAACTGGTGGTAG
GAATCTTAGAAACAAGACCACTTATACTGTCTGTCTGAGGCAGAAGATAACAGCAGCATCTCGACCAGCCTCTGC
CTTAAAGGAAATCTTTATTAATCACGTATGGTTCACAGATAATTCTTTTTTTAAAAAACCACCTCCTAGAGA
AGCACAAGTGTCAAGAGTCTTGTACACACAACCTCAGCTTTGCATCACGAGTCTTGTATTCCAAGAAAATCAAAG
TGGTACAATTTGTTTGTGTTTACACTATGATACTTTCTAAATAAACTCTTTTTTTTT

2024/6881
FIGURE 1861

ATGGACAGGACTGTCATT CAGAAATACCACACTGTGAATGGCCACAGCTGTGAAGTTAGGAAAAGCCCTGTCAAAG
CAAGAGATGGTTAGTGCTTCATCCAGCCAAAGAGGTCGAAGTGGTTCIGGAACTTTGCTGGTGGTCTTAGAAGT
GGTTTCAGTGGGAATAACAAC TTTGGTCGTGGAGGAACTTCCGTGGTCGTGGGGCCTTTGGTGGCAGCCGTGGT
GGTGGTGGATATGATGGCAGTGGGGATGGCTATAATGGATATGGTAACGATTGA

2025/6881
FIGURE 1862

ATGAAGGCCAACTACAGCGCAGAGGAGCGCTTTCTCCTGCTGGGTTTCTCCGACTGGCCTTCCCTGCAGCCGGTC
CTCTTCGCCCTTGTCTCCTGTGCTACCTCCTGACCTTGACGGGCAACTCGGCGCTGGTGCTGCTGGCGGTGCGC
GACCCGCGCCTGCACACGCCCATGTACTACTTCCTCTGCCACCTGGCCTTGGTAGACGCGGGCTTCACTACTAGC
GTGGTGCCGCCGCTGCTGGCCAACCTGCGCGGACCAGCGCTCTGGCTGCCGCGCAGCCACTGCACGGCCCAGCTG
TGCGCATCGCTGGCTCTGGGTTTCGGCCGAATGCGTCCTCCTGGCGGTGATGGCTCTGGACCGCGCGGCCGAGTG
TGCCGCCCGCTGCGCTATGCGGGGCTCGTCTCCCCGCGCCTATGTCGCACGCTGGCCAGCGCCTCCTGGCTAAGC
GGCCTCACCAACTCGGTTGCGCAAACCGCGCTCCTGGCTGAGCGGCCGCTGTGCGCGCCCCGCTGCTGGACCAC
TTCATCTGTGAGCTGCCGGCGTTGCTCAAGCTGGCCTGCGGAGGCGACGGAGACACTACCGAGAACCAGATGTTT
GCCGCCCGCTGGTCATCCTGCTGCTGCCGTTTGCCGTCATCCTGGCCTCCTACGGTGCCGTGGCCCGAGCTGTC
TGTTGCATGCGGTTTACGCGGAGGCCGGAGGAGGGCGGTGGGCACGTGTGGGTCCCACCTGACAGCCGCTGTCCTG
TTCTACGGCTCGGCCATCTACACCTACCTGCAGCCCGCGCAGCGCTACAACAGGCACGGGGCAAGTTCGTATCG
CTCTTCTACACCGTGGTCACACCTGCTCTCAACCCGCTCATCTACACCCTCAGGAATAAGAAAGTGAAGGGGGCA
GCGAGGAGGCTGCTGCGGAGTCTGGGGAGAGGCCAGGCTGGGCAGTGA

2026/6881
FIGURE 1863

ACTTCTGGGGCAGCCGTGAGCAGCGGGCACACGGGCAGCCACGAAAGCAGCAGCGAGGGTGGTGCAAACACCTCA
TAACTACACCGAATCCAGTAGCGCCTGGCGCCCCCGGCGCGCAAGGCCGCTCTACTCCGCCTCATCTTTGTCCC
AAGTCCTTTTACAGCCTGCCTTCCTCAAACGGCCCGATGCGCCCCCGTCTTTGCCGGAGTAAGCAGACCGCCAGC
AGCCGGCCCCGAGGTCAGTCGACCCCTCTCTGGATGCAGGTGCGCCGGGAAAACCCGGAGCGGAGCATCCCTCGGGC
CGGGAAACGCCCTCGGCGCGCACCCACTGGCGCGCATGCTCAGTCCGCGCGGCGGCTGCGAGTAGGAAGCTCCGC
GCGGCGGCGGGGCGGCGACGGCGACTGGCGGGTGGGAGTGGAGGCACCGGCTGGCGGGCGGGGTACAGGGACG
GGGCAGGGGCTCCCGCTCCAGGTTCTTGAAGCACTTCCGACCGGAAGCCCGGCGGAGAAGCGAGCTAACC
AGAGCCAACAACGAGCGCGGAGAGGGCAGCGGACTGAGCGGAGCCGCCCGGCCAGAGCGGGCTCGGAGCCCGGGT
TCCGCCGCTCGGGACCCGGCTAGGCGGCGGGCGGGGCGGCGCATGTTCCACTGCATCCCCCTGTGGCGGTGCAACC
GTCATGTGGAGAGCATCGACAAGCGCCACTGCTCGCTGGTCTACGTCCCCGAGGAGATCTACCGCTATGCCCGGA
GCCTGGAGGAGCTGCTGCTGGACGCCAACCAGCTCCGCGAGCTGCCCGAGCAATTTTCCAGCTAGTCAAATTAC
GAAAGCTTGGACTTAGTGATAATGAAATTCAGCGGCTCCCTCCAGAAATAGCAAATTCATGCAGCTGGTGGAAAC
TAGATGTGTCTCGAAATGAGATTCTGAAATTCAGAAAGCATTTTCTGTAAAGCACTGCAGGTAGCTGACT
TCAGCGGAAACCCACTGACTAGGTTGCCAGAAAGCTTCTGAAATTACAGAATTTAACATGTCTTTCTGTAAATG
ACATCTCACTACAGTCTCTACCTGAAATATTGGCAATCTTTATAACCTGGCTTCACTGGAAGTGAAGAGAAATC
TTCTTACATATCTTCTGACTCTCTTACCCAGCTGCGAAGACTAGAAGAACTTGATTTAGGAAACAATGAAATAT
ATAATTTGAATCAATTGGAGCCCTCTTACATCTTAAAGATCTCTGGTTGGATGGAAATCAACTGTCAGAATTACC
TCAGGAAATAGGAAATCTGAAGAACCTGCTGTGTTTTAGATGTCTCTGAAAACAGGTTGGAAAGACTTCTTGAAAG
AATCAGTGGCCTGACTTCATTAAACGGATTTAGTCATTTCCAGAACTTATTAGAAACGATTCCGGATGGCATTGG
AAAATAAGAAACTGTCAATCTTGAAGGTGGATCAGAATAGACTCACACAGTTGCCTGAAGCAGTTGGGGAAATG
TGAAAGTCTCACTGAGTTAGTTCTTACAGAAATCAGCTCCTGACCCTGCCTAAAAGCATTGGAAACTAAAGAA
GTTGAGCAACTTGAATGCAGACAGAAATAAATTAGTGTCTTACCAAAGAGGTATGTGCTTTTAGAGAAATCAC
ATGATAATAATTATGAAGAAATAATAATAATACATAAGGGATCAAAAATGTCAAATGCTTTGAAAAGACGCATGT
GTTGTTTTTTAAAGGTGTGAACTCTAAATCTGTGAGTATAGAGCCAACCTGGAGGAATTATGTCAAAGAATGATCA
TCAGTAACATTAAGGAGAGTTGGAAAAGGTGAATTTATAGGATTTTAAATGGGAGAAAGAAAGAGATTGACATTT
TGGGTTTGATATACAGAGAATGGTGACACCATTGGCAGAAATTGATAATTTGGGAGTTTGACAGAGGAAGTGGAT
GCCTTTGGGTTTGATTTTGAATTTAATGTGAAATTAAGCTCCATCCCATAGCAATTGGAATTATAAAAATTGA
TCTTGATGCAACCATATTTCTGGGCAGAGATTTACATTGGGCCATGCTCATGTCTTGATGAGGTTGAACAACT
GTTCAAAAGGCATACACATAGAGGAAGGTGAATGGGAAGCTAAAGCCAGCTTCCTAGGACTTTTTTTTTGGTTA
GTAGTCTAAGCACGAGAAAAATGAGACATCACCATCTGTTGTGGAGAGTAGCTGTATGGACTGAGAGGCATTTAAA
TTCTGGCAAGGGAGGTGGAAATGCTGACAATGAGGAGGAAGCTTATAGTGGGTCAAACAAGGAGGTGTCTAGTGT
GTTGTTTTAAAAGAAGGCTTACAATTAGCCAGGCGTGGTGGCGGGCGCCTGTAGTCCAGCTACTCGGGAGGCTG
AGGCAAGAGAATTGCCTGAACCCGGGAGGCTAAGGTTGCAGTGAGCCGAGACCACGCCACTGCACTCCAGCCCGG
GTGACAGAGCGAGACTCTATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAATG

2027/6881
FIGURE 1864

MFHCIPLWRCNRHVESIDKRHCSLVYVP EEIYRYARSLEELLLDANQLRELPEQFFQLVKLRKLGLSDNEIQRLP
PEIANFMQLVELDVS RNEIPEIPESISFCKALQVADFSGNPLTRLPE SFPELQNL TCLSVNDISLQSLPENIGNL
YNLASLELR ENLLTYLPDSL TQLRRLEELDLGNNEIYNLNQLEPSYI

2028/6881
FIGURE 1865A

CGGTGCTGGAGAAGTTTGCGCTGCGGTTTCGTGAGCGCAGGGTGCGGGCCCCGCCGGCCGCTGCGCGCCCGCTGCC
ATGGCTTTCCGCAGGAGGACGAAAAGTTACCCGCTCTTCAGCCAGGAGTTCGTTCATCCACAACCATGCGGACATC
GGCTTCTGCGCTGGTGCTCTGCGTCCTCATCGGGCTTATGTTTCGAGGTCACAGCCAAGACTGCCTTTCTATTATT
TTACCTCAGTATAACATTAGCGTGCCTACAGCAGACAGTGAGACCGTGCACTACCACTATGGCCCTAAGGACCTG
GTCACAATCTTGTCTACATCTTCATCACCATCATCTTGCATGCTGTGGTTCAGGAGTACATTTTAGATAAAAATC
AGCAAACGGCTTCATCTCTCCAAAGTCAAACACAGCAAGTTCAATGAATCTGGACAGCTGGTCGTCTTTCATTTT
ACCTCGGTGATTTGGTGCTTCTACGTGGTGGTGACGGAAGGATACTTAACAAACCCAAGAAGCCTCTGGGAAGAC
TACCCGCATGTGCACCTCCCCCTCCAGGTGAAGTTTTTCTACCTATGCCAGCTGGCCTACTGGCTGCACGCACTT
CCTGAGCTATACTTCCAGAAGGTACGGAAGGAGGAAATTTCCCCGCCAGCTCCAGTATATTTGCCTGTACCTGGTG
CATATAGCTGGAGCATACCTCTTAAACCTGAGCCGCTGGGCCTGATCTTGCTGCTGCTGCAGTACTCAACTGAG
TTCTCTTCCACACGGCTAGACTCTTCTACTTTGCAGATGAAAACAACGAGAACTGTTTCAGTGCCTGGGCTGCT
GTTTTTGGGGTTACCCGCCTCTTCATCCTCACCTTGCCGTGCTGGCCATTGGCTTTGGACTGGCTCGCATGGAA
AACCAGGCATTTGATCCCCGAGAAAGGGAACCTTCAACACTTTGTTTTGCAGGCTCTGCGTGCTGCTGCTGGTGTGT
GCCGCCAGGCCTGGCTCATGTGGCGCTTCATCCACTCCAGCTGCGGCACTGGCGGGAATACTGGAATGAGCAG
AGTGCAAAGCGGAGAGTCCCAGCCACACCCAGACTACCAGCCAGGCTCATCAAGAGGGAATCTGGTTACCATGAA
AATGGAGTGGTGAAGGCAGAGAACGGAACCTCCCCACGGACTAAGAACTCAAGTCTCCCTAAGGCCAAAGTGCT
AAGAACAGGAATCCTCTTGGTGGGGGCCGAGCAGGGGGCAAGGAGCCAGGCCCTCCCTGCCTCCTCCTTCTT
GCCTGTGATGCTCCGTCTCAAACAGCCGAAACCTGTCTTGCAATGGGGGGAGGGGGCGTTTCGCTTTCTTCTTCT
TTGGCTTCCTCTTATTCTTCCACAAACCATTTCTCAATAAAGCCAAAAATCTTTCTTTCTCCCCCTCAGGCCAC
CTCCTGTCTCTACTCCTGTCTGTGCTGGCTTTTCTGGAACGCCAGGCGCCCATGGCTGGCACCTTTCTGCTTGC
TCTGTCTCTTGCCTTATGGCTGCTGCTTTTTCTTTTTTACTTCTATTTTACCTTATCTTGCAATTTTTCTGTCT
GATTTTTACAATGGGAGGGGAGCTAAGATTGCAGTCTGTCTTTCGGTCCCCCAGGGCCTGCCGGTCAGAAGCCT
GGGGCTGGTAGGCCCTTGGTGGTCTCATGTGGATGGGCAAGAAGAGAGCGGCCATCTCGGATCATAATCTCCTT
GGTGCTGATTAAGTACGAGATATATGATTCCAGTCTGTCATGTACCATCTTGAGGCACAGCAGCCACTGCTCGT
TGTAATGCCAAGGCATTTGGCTTTGGGACGTGACAACCTCAATCCAGAAGGATGGTGTGAACTCGGTTGGGTCCC
GTGACTCGAGCTCTACCAGTGGCTGGCCGCGGATTGGAAGCCAGCCTGCTGTGCTCTGTGGGGGGGGACACGT
CTTCCCACTGCTTAGAGCGAGAGCAGAGCAAACCTGCGCAGCAGGCACCTCCAGAAAGGTAATGGTGGCAGAACCC
ACAGTGGAGTCGACCTAGGCCTTTCTCCAGCAGTCCCAGTCCGCTATTGCTTTTTTTCAGCCATTACAAGCATTCAA
AACCAAACCAAACAGCAGTTTCATATACCTGCCCTGAGATAGGCTGGTCTCACCTCCAGAGCCAGCCAGCCCCGTC
AGGGGCCAAACTTACTACCTTGACTTCATCTCTAGCTGCAGAAACACTAAGTCTCAAGGGCTTCAGCCCCATGCT
GGTCCCTTGGTGTTCAGGGAGGGTCACTTGGACCGCTGTTTCATCTGGCCGCCCTTGTGAGTGTCTTTTGAATT
GTCGTTTTTTTGGAGCACAACCTACAGCATTTTAGACTGCATGAAACCATGACTGACTGAGAGTCACTCTCTGGGTAG
ATGATAGGCGCTTTTCTGGCCCCCTTCCCTCACAGATTCTTTCCCTCCCTCCACCTGAAGAGAAGGCCTCCAAG
TCCTTTTGGTGCCTTGTGAGGACTTTTAGAAGGGCGTTCAGCTTTAAAAAGCCGGTCTTAATTACGGCCGGACG
CAGTAGCTTACGCCTGTTATCCAGCACTTTGGGAGGTCGAGGTGGGCAGATCACCTGAGGTTAGGAGTTCAAGA
CCAGCCTGGCCAACATGGTGAACCCCATCTCTACTAAAAATACAAAAAATTAGGTGTAGTGGCAGGCACCTGTA
ATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCTAGAAGGCGGAGGTTGCAGTGAGCGGAGATT
GTACCATGGCACTCCAGCCTGGACAACAAGAGCGAAATCTGTCTAAAAAACAAGTCCCAATTAAGAACCCTC
CGAACTCTGTTTTGAGGCAAAGGGGAGTAGTTCTTGGTAGGTGCAGGAATAGTAGTGTCAATTTGGAATACTGGTC
ATCTTTCTGACATCACAGTAGAAACCAAACCTTGGATTTAGATTCAAAAGGGGGGAAATGGGTCTTTTCATCAAG
GCAACTCCCCCTTCTCAAGTCACTTACATCATAGATAAATTTAGCTTCCAGTAACTGAGGGATTTGTTTCTTA
ACGCCATTGGAGGCCTTCATCCCTCTCTACGATAAGGTTGCAGAAATGGGAAGAGCTACCCGTGGTTGCTTTTGA
TTACCCTTAGGAAGTGAGACAGTGTTTTTGAAAATATGTATTTCCCCCATTTCTCCCTCTCCTTCCCTGACACTT
CTCTGGGCTGCACAGCAGAAACGTTGGTAAAAGGGCAGTTTGGTTTCAACACAGCAGACCTGATATGGGATCCCT
TAGCCACTTTAGTCAAAACAGCCCTGACAGAGTCTATAATTGAGTTTCAGGCCCCCCACCTTGCTAATAACTGCAA
ATCGCATGTTTCAGCCAGCAGCCTCCTAAGCCCACCTTCCCTCCCCCATTTAGAGAACACCCATCCTAGGTGCTCTCC
AGGCTGTGTCAATTGGCAGGGCTTCACATGCAGGAGGCCTCTCTCAGGTGAGTCCAGGTTAAACTGTTGAGTTGTG
GCTTCAACAGATATGTATGGCATGCTGGGATGTGCCAGGTGCCTGCGTTGTGCCAGTTGCTGGAGAGGTAGTGTG

2029/6881
FIGURE 1865B

AGCAGAGCAGCTGAAATCTTGCCATCAAGCAACCCTCATTCTCATGCTGTAGGTTTCCATTGCTCTGTCCCAGG
ACACTTGCGTGCCAGAGACGCCACAACCTTCATGTCCCTGTCTCTTGCAAGCTCCCCGTGCTGCCAGTACTTCATG
CCTTGGATGTGGTCCCACCAGCCCAGTGGCCGGGGTTCAGCTTAGGCTCTGCTTCCAGTGGACGGGTGTGCTAAG
GGTTTATTTTATGTAAAAAACAACCAAAAAACCCCTGAGACCATGAGTGGGGCTGGCATCTTGCCA
GCCTGGGCTTCAGGGATGTTTGGGGGGGGTGGTTAGAGGGTAGTTGTAGGGTACTTTGTACCCCCCTCCCCCTG
CCACCCTCCCTGGCACGTTTATTTACAGCAGAGCCAAGTCTGTGGCAGGTTGACACAGACTGTGTTGCCAGAGC
TGAAATAATTCCACTTCATCCTATGAGCGTGTGGGGCTAGCTTGTCTAATTTTGGCCACTTTGGCTGTTTTCTT
CAGTTTTATGCATTCTCTCCTGCCCCAAGTGCCAAGCCATTTGTGAAGGCTCTGCCAGACACCTCCAAGCTTGA
GAGCTCAGCACCATGCACCAAGAGCAGGAGAAAAGACGTAAACCTACCCAGCAACTGTGGCCTCTCGACAGCCC
TGGCTAACTAACTTACATTTGTGGGGAAGCCAACAGACACAGCAGGAGGAGAGGGAGGTGGCGCTGGTGGACCAA
GGATCTGTGCTACCCGCTCCCCCTCCTTGGAGGTGCAGTGATGATGGGAGTTATTTTACCATCCGGGCGCTGATA
GCTGCACTATTAATAAATGTCATGTGTTCTTTTGAAGGTAGGGGATGGTTCGGGTGAGAGGGGAGCAGGCTGA
GCCGGCGGGGATCTGCTGTCCTCCCTTTTGTAGTCAGTTCTAATCCCATGTGTGTCTGGGCCACCAGACCGAAAT
GGTTGCTGAGAACTTGTCTGTTTCATGTCCCAAGGCATAACTTCCCAACATTTAAGAAACCCCAATAGACACCTC
TGCCCTGGCCACGTTTACAGATCCTTCTCTTGACCGGAAACCCCTGGGACCCTAAGAACCCCTGAAGCTTGGGGTG
GGTGTGTGCTTCTGGGGTCTCTTTTGGGACCTCCTTTGTGCTAGTACCCCTTCTTTTTTCTAAGCAGCTAATAAGAG
GTTGGGTGAAAGAGTGCATCTCCTCCCAGGATTCCACAACAAAATCTTATCTTCCATGGATGCTTTAATTGGAA
GTGGGTGGCCGACCCCTTGTGCCTAGAAAAGGCCTTCGCTTGGGTTTCTTTGTATGCTTCAGCCTTCCTAGTT
GGTTTTTCTAGGCCTGGTGTGAGAGGTAGGGAAGTCTGCACATAACTAATCTTTTGTCTAAGGGCCTATGGCAC
AAGTGCACAAACTTCAATTCTTGATGTTCTAAGCTCTCTCCTCTAACAGAGGGAGTGCTGAAAGCTTTTGTAGTCA
AGACAATGGAGTGCTCTTCTCCTCCTACTCTGCCTTCCGAGCTTATGGTTCCTTTTCTCAGGAGAGGATTTTCAG
GATTATTGGAGGATTAGGTCAATTGTCAGATGACTGGAACCTAAATAGGATCTCTCTCCAGCTCAAGGTTGTCC
CAGTGAGGAAGACTTTACCAACTTCTCACTCTACCCCACTACTCACATGAGTGTAGCTCCACCTTGCAAAGGCT
GAAGACCAGTTCTCCCCAGTGAAAGCTGCCTCATTCTTTTATGGAGTTCCTGGAGTGGCAGAGCTATAAAGACG
AGCATTGGGATTTGCAGTCTCCATGTAGCCTTTTCGTGCTTGGCAACCCCTGTAGACTTTTTGTCCCAAGCAGATT
GCGTGCGTGCGCTGTGTGTGAGAATAAGTGCCTTACTTTGTGTGTGGTTTTCAACTTGTACTCCGTGGCCAGC
CCCCAGTTGCCAGGGCTCGACGGCAGCCAAGGACACCATACTCAGTATAGTTATATATAAAGGGACACGGATT
GTGACAGTTTACCCCATTTGTTTTCTAACCCCGCTGCCAGGATTAGGGTCTGTGGTGTGTTCTGTTTTGTTTTT
GGTTTCTCCCTTGTGTGCTGTTCTCTTCTGGCCAGCTGGGTGGCTGTGGAAGTCTGTGAGGTGGCCCAACCACAA
GCATACCTATTAAGAGAAGCCCAGAGCTTCCAGCCCCCACTTCGAAAACCTCTCCTCTGGCCCCACATAGCAAAC
CCTTCTCCGTTATTTTCCCCACCCCAAGATTTTTTTTAAAGGCCCACTTGCCGTAACCTCTTTTGGTCTATTTT
GCTTCCCATTCAGCCCAAAGTTTATATGATAAAGGTGTTTACTTTTACTTCCAGTCTCCAAGTGCTAACACATA
AACACATACATGTCTGACTGTTGCAGAACTGTTTCAGACTCCTAATTCAGTGTACCTTGTTTTAGTCGCAGCAAC
CCTCTCCCTACCCCTTGCCCGCCACGTTTTTCTCACTCTTCCGGGTGTGCAATAACTCTCCAGCCAGTGGT
CCTTTCACAGCCTTTCTGTCCCTTAAACACCTGCAACTGGGGGAGAAATGGGACCCATGGGAGGGGGAGTCGT
CATCCCTTACACAAGAAATAGCCACTTTCCTTTTGTGTGCTATTCTTGTGATCCTGGGTGGGTTTCTGTGGCACTC
TTTTAGAACATGTAGCATCATCTTAGAGGTCTATTTTTTAAAAAATGTGTTGAAGAGGAAAAACCATTCTCACGA
TGGGGCTTAAGTCATTGTCCAGGAATAAGATTGGCGTGGTGGCCATGACATCACCGTCACTCTGCCTAAAAGCAC
TCTAGAGCTACTTGTTCACGTGGAGAGGAAGGATATTTTGCAGAACACAGCCGAGGTGGAGAGCCCTGTTTAC
CTGATAGGGTCTAGCTGTGACAGTAAATATAATACCGCTGTTTCTTGGGTACAGATTTGAGTGTTTCATGTGATG
AGACTGTAAACCTCATTTTTTCGTTTCTCTGTTTAAAAAACATCTGAAGGATGAACCTAAGGCTGCTGGTGCCTT
GAGCAACTGATAATGCAAAATGTGGACAAAGTGTCTGTTTTCTACTCTAGCCTGTTTCATATGGACCAAATTTCAAC
AAGGAACCTCAAGGAAAATTTGTACCTGCCGTATTTATGCTTTTCATGTAAAAAGGGTTGGGGGGAGGGGTGTCTT
TTTGCTTTTGGTGAACCTTTTTTCAAATCATTTTTTCCACTGTTTCTGTCTGGTTTTTAAACAAATTACAGTTTT
GTATGGATTTTTTAAATGTACATTTTGAACAAATGATCAAATATTTTCTGAAATAACAATAAAGGCAGAAAAAT

T

FIGURE 1866

CGGCACGAGGCGACTTTGGTGGAGGTAGTTCTTTGGCAGCGGGGATGCGCGGGTACCGTGTTGCTGGACGATGTGG
AGCTGCGGGGAGGCTCAGAGAGATTACCTGGACTTCTTGGACGACGAGGAAGACCAGGGAATTTATCAGAGCAAAG
TTCGGGAGCTGATCAGTGACAACCAATACCGGCTGATTGTCAATGTGAATGACCTGCGCAGGAAAAACGAGAAGA
GGGCTAACCGGCTTCTGAACAATGCCTTTGAGGAGCTGGTTGCCTTCCAGCGGGCCTTAAAGGATTTTGTGGCCT
CCATTGATGCTACCTATGCCAAGCAGTATGAGGAGTTCTACGTAGGACTGGAAGGCAGCTTTGGCTCCAAGCAG
TCTCCCCGCGGACTCTTACCTCCTGCTTCCTCAGCTGTGTGGTCTGTGTGGAGGGCATTGTCTACTAAATGTTCTC
TAGTTCGTCCCAAAGTCGTCCGCAGTGTCCACTACTGTCTGCTACTAAGAAGACCATAGAGCGACGTTATTCTG
ATCTCACCACCCTGGTGGCCTTTCCCTCCAGCTCTGTCTATCCTACCAAGGATGAGGAGAACAAATCCCCTTGAGA
CAGAATATGGCCTTTCTGTCTACAAGGATCACCAGACCATCACCATCCAGGAGATGCCGGAGAAGGCCCCAGCCG
GCCAGCTCCCCCGCTCTGTGGACGTCATTCTGGATGATGACTTGGTGGATAAAGCGAAGCCTGGTGACCGGGTTT
AGGTGGTGGGAACCTACCGTTGCCTTCCCTGGAAAGAAGGGAGGCTACACCTCTGGGACCTTCAGGACTGTCCTGA
TTGCCTGTAATGTTAAGCAGATGAGCAAGGATGCTCAGCCCTCTTTCTCTGCTGAGGATATAGCCAAGATCAAGA
AGTTCAGTAAAACCCGATCCAAGGATATCTTTGACCAGCTGGCCAAGTCATTGGCCCCAAGTATCCATGGGCATG
ACTATGTCAAGAAAGCAATCCTCTGCTTGCTCTTGGGAGGGGTGGAACGAGACCTAGAAAATGGCAGCCACATCC
GTGGGGACATCAATATTCTTCTAATAGGAGACCCATCCGTTGCCAAGTCTCAGCTTCTGCGGTATGTGCTTTGCA
CTGCACCCCGAGCTATCCCCACCACTGGCCGGGGCTCCTCTGGAGTGGGTCTGACGGCTGCTGTACCACAGACC
AGGAAACAGGAGAGCGCCGTCTGGAAGCAGGGGCCATGGTCTGGCTGACCGAGGCGTGGTTTGCATTGATGAAT
TTGACAAAATGTCTGACATGGATCGCACAGCCATCCATGAAGTGATGGAGCAGGGTCGAGTGACCATTGCCAAGG
CTGGCATCCATGCTCGGCTGAATGCCCCGTGCAGTGTTTTGGCAGCTGCCAACCTGTCTACGGCAGGTATGACC
AGTATAAGACTCCAATGGAGAACATTGGGCTACAGGACTCACTGCTGTCTACGATTTGACTTGCTCTTCATCATGC
TGGATCAGATGGATCCTGAGCAGGATCGGGAGATCTCAGACCATGTCCTTCGGATGCACCGTTACAGAGCACCTG
GGGAGCAGGATGGCGATGCTATGCCCTTGGGTAGTGCTGTGGATATCCTGGCCACAGATGATCCCAACTTTAGCC
AGGAAGATCAGCAGGACACCCAGATTTATGAGAAGCATGACAACCTTCTACATGGGACCAAGAAGAAAAAGGAGA
AGATGGTGAGTGACGATTTCATGAAGAAGTACATCCATGTGGCCAAAATCATCAAGCCTGTCTGACACAGGAGT
CGGCCACCTACATTGCAGAAAGATATTACAGCCTGCGCAGCCAGGATAGCATGAGCTCAGACACCGCCAGGACAT
CTCCAGTTACAGCCCGAACACTGGAAACTCTGATTGACTGGCCACAGCCCATGCGAAGGCCCGCATGAGCAAGA
CTGTGGACCTGCAGGATGCAGAGGAAGCTGTGGAGTTGGTCCAGTATGCTTACTTTAAGAAGGTTCTGGAGAAGG
AGAAGAAACGTAAGAAGCGAAGTGAGGATGAATCAGAGACAGAAGATGAAGAGGAGAAAAGCCAAGAGGACCAGG
AGCAGAAGAGGAAGAGAAGGAAGACTCGCCAGCCAGATGCCAAAGATGGGGATTATACGACCCCTATGACTTCA
GTGACACAGAGGAGGAAATGCCTCAAGTACACACTCCAAAGACGGCAGACTCACAGGAGACCAAGGAATCCCAGA
AAGTGGAGTTGAGTGAATCCAGGTTGAAGGCATTCAAGGTGGCCCTCTTGATGTGTTCCGGGAAGCTCATGCGC
AGTCAATCGGCATGAATCGCCTCACAGAATCCATCAACCGGGACAGCGAAGAGCCCTTCTCTTCAGTTGAGATCC
AGGCTGCTCTGAGCAAGATGCAGGATGACAATCAGGTCATGGTGTCTGAGGGCATCATCTTCTCTCATCTGAGGAG
GCCTCGTCTCTGAACCTTGGGTTGTGCCGAGAGAGTTTGTCTGTGTTTCCACCCCTCTCCCTGACCCAAGTCTTT
GCCTCTACTCCCTTAACAGTGTTGAATTCAACTGAAGGCAGGAAATGTTGGTGATGAAGCTGAGTTCAGGACTCG
GTGGACCCTTTGGGAATGGGTCTATGAAAGCTGCCATGGGGTGAGGAAAGAGGAGACAGTGGGAGAGGACAATGAC
TATTGCATCTTCATTGCAAAAGCACTGGCTCATCCGCCCTACTTCCCATCCCACACAAACCAATTGTAAATAAC
ATATGACTTCTGAGTACTTTTGGGGGCACAACCTGTTTTCTGTTTGCTGTTTTTTTTTGTGTTTTTTTTTCTCCAG
AGCACTTTGGTCTAGACTAGGCTTTGGGTGGTTCCAATTGGTGGAGAGAAGCTCTGAGGCACGTCATGCAGGTCA
AGAAAGCTTTCTTTGCAGTAGCACCAGTTAAGGTGAATATGTATTGTATCACAAAAACAAACCAATATCCAGATG
AATATCCGAGATGTTGAATAAACTTAGCCATTTCTGTACAAAAAAGGGGGGGCCCGGTAAAC

2031/6881
FIGURE 1867

MAGTVVLDDELREAQRDYLDLDFLDDEEDQGIYQSKVRELISDNQYRLIVNVNDLRRKNEKRANRLLNNAFEELVA
FQALKDFVASIDATYAKQYEEFYVGLGSEFGSKHVSPRTLTSCLSCVVCVEGIVTKCSLVRPKVVRVSVHYCPA
TKKTIERRYSDLTTLVAFPSSSVYPTKDEENNPLETEYGLSVYKDHQTITITIQEMPEKAPAGQLPRSDVILDDDL
VDKAKPGDRVQVVGTYRCLPGKKGGYTSGTFRTVLIACNVKQMSKDAQPSFSAEDIAKIKKFSKTRSKDIFDQLA
KSLAPSIHGHYVKKAILCLLLGGVERDLENGSHIRGDINILLIGDPSVAKSOLLRYVLCTAPRAIPTTGRGSSG
VGLTAAVTDDQETGERRLEAGAMVLADRGVVCIDEFDKMSDMDRTAIHEVMEQGRVTIAKAGIHARLNARCSVLA
AANPVYGRYDQYKTPMENIGLQDSLRSRFDLLFIMLDQMDPEQDREISDHVLRMHRYRAPGEQDGDAMPLGSAVD
ILATDDPNFSQEDQODTQIYEKHDNLLHGTTKKKKEKMSAAMKYYIHVAKIIPVLTQESATYIAEEYSRLRSQ
DSMSSDTARTSPVTARTLETILRLATAHAKARMSKTVDLQDAEEAVELVQYAYFKKVLEKEKKRKRSEDESETE
DEEEKSQEDQEQKRKRKTRQPDAGDSYDPYDFSDTEEMPQVHTPKTADSQETKESQKVELSESRLKAFKVA
LLDVFREAHQAQSIGMNRLTESINRDSEEPFSSVEIQAALSKMQDDNQVMVSEGIIFLI

2032/6881
FIGURE 1868

ATGACTGCATCCAACCTCGCAGGTGCGCCAGAACTACCACCAGGACTCAGAGGCCGCCATCAACCGCCAGATCAAC
CTGGAGCTCTACGCCTCCTACTTTAACCTCTCCATGTCTTACTACTTTGACCGTGATGATGCGGCTTTGAAGAAC
TTTGCCAAATACTTTCTTCACCAATCTCATGAGGAGAGGGAGCATGCTGAGAACTGATGAACTGCAGAACCAA
CAAGAGTGTGCATTACATTTGGAAAAAATGTGAATCAGTCACTACTGGAAGTGCACAACTGGCCACTGACAAA
AATGACCCCCATTTGTGTGACTTCATTGAGACACATTACCTGAATGAGCAGAATTGGGTGAACGTGACCAACTTG
CACAAGATGGGAGCACCCGAATCTGGCTTGGCAGAATATCTCTTTGACAAGCACACCCTGGGAGAAAGAGGGAGC
ACTGGAATGTTTAATTCGGACAATGCCAATACAAGTTTACAGAGAAGAGAGAACTTTCCATTGGGTTTTGAAGGT
TCTGCTGATTTTCAATGGGCAGAGGTGGAGGAACAGTCTGAGCAGAGAGAACATCATAAACAAAGGAGTGAATGT
GAGAAAGGCTTCAGGTCCCATCAGAGTACTGGCTTCACCTTGACTGTAGAAGATTTAGTTGAAGCAGTATTCAA
AGTGTAGAACTTGTCAAGCTACCTATCCAGTCCTCTTGTCTTCTGAAACAGTGGTTACCTGCTCTGGAAAACCTT
CTCTCTCCATCCTCCAAAGCTCCTGGGGTACAGCTTTATCAGCGCACCTATCACACTGATTCTGGTCTCCAAAA
CTCTTCTTGCTGAAAACAGCATACAAAATACTTTCCCTCTTCAAAGCCCAATACAACACTGGAAAAGCAATGGAG
AAGAAAGTACTCAGTATCTTTTCCCCACTAAAAGTTGTACTGCAATGCTTGAACACAACCTGGAGGAGCCCTAGGT
TTATCAAAAGTATCTGCCATTTCTAAAAGAATGTGTTTCCAAGGCATCCAGAAAGAGCTCTTTCCAAGTGCACCA
AATTCATTTGCTTTCCACACCCTGTCCCGACAAGGGGTGCTGCAGAAGCACAAAGCCAGCCAGATGCATTGA

2033/6881

FIGURE 1869

MTASNSQVRQNYHQDSEAAINRQINLELYASYFNLSMSYYFDRDDAALKNFAKYFLHQSHEEREHAEKLMKLQNO
QECALHLEKNVNQSLLELHKLATDKNDPHLCDFIETHYLNQNWVNVTNLHKMGAPESGLAEYLFDKHTLGERGS
TGMFNSDNANTSLQRRENFPPLGFEGSADFQWAEVEEQSEQREHHKQRSECEKGFRSHQSTGFTLTVEDLVEAVFK
SVELVKLPIQSSCLLKQWLPALLENLLSPSSKAPGVQLYQRTYHTDSGLQKLFLLKTAYKILSLFKAQYNTGKAME
KKVLSIFSPLKVVLQCLNTTGGALGLSKVSAISKRMCFQGIQKELFPTAPNSICFPHFVPTRGAEEAQSQPD

2034/6881
FIGURE 1870

CGGACGCGTGGGCGGTTTCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGCCCTCGCCTCCTGCAGCCGCATCG
CCCGCCGAGCCACAGCCACGATGATCGCGGGCTCCCTTCTCCTGCTTGATTCTTAGCACCACCACAGCTCAGC
CAGAACAGAAGGCCTCGAATCTCATTGGCACATACCGCCATGTTGACCGTGCCACCGGCCAGGTGCTAACCTGTG
ACAAGTGTCCAGCAGGAACCTATGTCTCTGAGCATTGTACCAACACAAGCCTGCGCGTCTGCAGCAGTTGCCCTG
TGGGGACCTTTACCAGGCATGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAATGA
TTGAGAAATTACCTTGTGCTGCCTTGACTGACCGAGAAATGCACTTGCCACCTGGCATGTTCCAGTCTAACGCTA
CCTGTGCCCCCATACGGTGTGTCTGTGGGTGGGGTGTGCGGAAGAAAGGGACAGAGACTGAGGATGTGCGGT
GTAAGCAGTGTGCTCGGGGTACCTTCTCAGATGTGCCTTCTAGTGTGATGAAATGCAAAGCATAACAGACTGTC
TGAGTCAGAACCTGGTGGTGATCAAGCCGGGGACCAAGGAGACAGACAACGTCTGTGGCACACTCCCGTCCTTCT
CCAGCTCCACCTCACCTTCCCCCTGGCACAGCCATCTTTCACGCCCTGAGCACATGGAAACCCATGAAGTCCCTT
CCTCCACTTATGTTCCCAAAGGCATGAAGTCAACAGAATCCAAGTCTTCTGCCTCTGTTAGACCAAAGGTACTGA
GTAGCATCCAGGAAGGGACAGTCCCTGACAACACAAGCTCAGCAAGGGGGAAGGAAGACGTGAACAAGACCCCTCC
CAAACCTTCAGGTAGTCAACCACCAGCAAGGCCCCACCACAGACACATCCTGAAGCTGCTGCCGTCCATGGAGG
CCACTGGGGGCGAGAAGTCCAGCACGCCCATCAAGGGCCCCAAGAGGGGACATCCTAGACAGAACCTACACAAGC
ATTTTGACATCAATGAGCATTGCGCCTGGATGATTGTGCTTTTCTGCTGCTGGTGTCTGTGGTATTGTGGTGT
GCAGTATCCGGAAGGCTCGAGGACTCTGAAAAGGGGGCCCCGGCAGGATCCAGTGCCATTGTGGAAAAGGCAG
GGCTGAAGAAATCCATGACTCCAACCCAGAACCAGGGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCGATA
TCCTGAAGCTTGTAGCAGCCCAAGTGGGAAGCCAGTGGAAGATATCTATCAGTTTCTTTGCAATGCCAGTGAGA
GGGAGGTTGCTGCTTTCTCCAATGGGTACACAGCCGACCACGAGCGGGCCTACGCAGCTCTGCAGCACTGGACCA
TCCGGGGCCCCGAGGCCAGCCTCGCCCAGCTAATTAGCGCCCTGCGCCAGCACCGGAGAAACGATGTTGTGGAGA
AGATTGCTGGGCTGATGGAAGACACCACCCAGCTGGAACTGACAACTAGCTCTCCCGATGAGCCCCAGCCCGC
TTAGCCCGAGCCCCATCCCCAGCCCCAACGCGAAACTTGAGAATTCGCTCTCCTGACGGTGGAGCCTTCCCCAC
AGGACAAGAACAAGGGCTTCTTCGTGGATGAGTCGGAGCCCCCTTCTCGCTGTGACTCTACATCCAGCGGCTCCT
CCGCGCTGAGCAGGAACGGTTCCTTTATTACCAAGAAAAGAAGGACACAGTGTGCGGCAGGTACGCCTGGACC
CCTGTGACTTGCAGCCTATCTTTGATGACATGCTCCACTTTCTAAATCCTGAGGAGCTGCGGGTGATTGAAGAGA
TTCCCCAGGCTGAGGACAACTAGACCGGCTATTGCAAAATTATTGGAGTCAAGAGCCAGGAAGCCAGCCAGACCC
TCCTGGACTCTGTTTATAGCCATCTTCCTGACCTGCTGTAGAACATAGGGATACTGCATTCTGGAAATTACTCAA
TTTAGTGGCAGGGTGGTTTTTTAATTTTCTTCTGTTTCTGATTTTTGTTGTTTGGGGTGTGTGTGTGTGTTGTG
TGTGTGTGTGTGTGTGTGTGTGTGTTTAAACAGAGAATATGGCCAGTGCTTGAGTTCTTTCTCCTTCTCTCT
CTCTCTTTTTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTTATAAGCCTTTGCCAGGTGTAAGTGTGTGAAATA
CCCACCACTAAAGTTTTTTAAGTTCCATATTTTCTCCATTTTGCCTTCTTAATGATTTTTCAAGATTATTCTGTGC
ACTTTAAATTTACTTAACTTACCATAAATGCAGTGTGACTTTTCCACACACTGGATTGTGAGGCTCTTAACTTC
TTAAAAGTATAATGGCATCTTGTGAATCCTATAAGCAGTCTTTATGTCTCTTAACATTACACCTACTTTTTTAAA
AACAAATATTATTACTATTTTTATTATTGTTTGTCTTTATAAATTTTCTTAAAGATTAAGAAAATTTAAGACCC
CATTGAGTTACTGTAATGCAATTCAACTTTGAGTTATCTTTTAAATATGTCTTGTATAGTTTATATTATGGCTG
AAACTTGACCACACTATTGCTGATTGTATGGTTTTTACCTGGACACCGTGTAGAATGCTTGATTACTTGTACTCT
TCTTATGCTAATATGCTCTGGGCTGGAGAAATGAAATCCTCAAGCCATCAGGATTGCTATTTAAGTGGCTTGAC
AACTGGGGCCACCAAAGAACTTGAAGTTTACCTTTTAGGATTTGAGCTGTTCTGGAACACATTGCTGCACCTTTGGA
AAGTCAAAATCAAGTGCCAGTGGCGCCCTTTCCATAGAGAATTTGCCAGCTTTGCTTTAAAAGATGTCTTGTTT
TTTATATACATAATCAATAGGTCCAATCTGCTCTCAAGGCCTTGGTCTGGTGGGATTCCTTACCAATTACT
TTAATTTAAAAATGGCTGCAACTGTAAGAACCCTTGTCTGATATATTGCAACTATGCTCCCATTTACAAATGTAC
CTTCTAATGCTCAGTTGCCAGGTTCCAATGCAAAGGTGGCGTGGACTCCCTTTGTGTGGGTGGGGTTTGTGGGTA
GTGGTGAAGGACCGATATCAGAAAAATGCCTTCAAGTGTACTAATTTATTAATAAACATTAGGTGTTTGTAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

2035/6881
FIGURE 1871

MGTSPPSSSTALASCSRIARRATATMIAGSLLLLLGFLSTTTAQPEQKASNLIQTYRHVD RATGQVLTCDKCPAGTY
VSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQPCPWPMIEKLP CAALTDRECTCPPGMFQSNATCAPHTVC
PVGWGVRRKGTETEDVRCKQCARGTFSDVPSSVMKCKAYTDCLSQLVVIKPGTKETDNVCGTLP SFSSSTSPSP
GTAIFPRPEHMETHEVPSSTYVPKGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPLNLQV VNH
QQGPHHRHILKLLPSMEATGGEKSSTPIKGPKRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVVI VVCSIRKSSR
TLKKGPRQDPSAIVEKAGLKKSMTPTONREKWIYYCNGHGIDILKLVA AQVGSQWKDIYQFLCNASEREVA AFSN
GYTADHERAYAALQHW TIRGPEASLAQLISALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSP SPLSPSP IPS
PNAKLENSALLTVEPSPQDKNKGFFVDESEPLLRC DSTSSGSSALSRNGSFITKEKKD TVLRQVR LDP CDLQPIF
DDMLHFLNPEELRVIEEIPQAEDKLDRLFEIIGVKSQEASQTLLDSVYSHLPDLL

2036/6881
FIGURE 1872

GCGCGGCACTTCCGCTGGCCGCTGGCTCGCTGGCCGCTCCTGGAGGCGGCGGGAGCGCAGGGGGCGCGCGGC
CCGGGGACTCGCATCCCCGGTTCCCCCTCCACCCACGCGGCCCTGGACC**ATGG**ACGCCAGATGGTGGGCAGTGG
TGGTGCTGGCTGCGTTCCCCCTCCCTAGGGGCAGGTGGGGAGACTCCCGAAGCCCCTCCGGAGTCATGGACCCAGC
TATGGTTCTTCCGATTTGTGGTGAATGCTGCTGGCTATGCCAGCTTTATGGTACCTGGCTACCTCCTGGTGCAGT
ACTTCAGGCGGAAGAACTACCTGGAGACCGGTAGGGGGCCTCTGCTTTCCCCTGGTGAAAGCTTGTGTGTTTGGCA
ATGAGCCCAAGGCCCTCTGATGAGGTTCCCCCTGGCGCCCCGAACAGAGGCGGCAGAGACCACCCCGATGTGGCAGG
CCCTGAAGCTGCTCTTCTGTGCCACAGGGCTCCAGGTGTCTTATCTGA**CTT**GGGGTGTGCTGCAGGAAAGAGTGA
TGACCCGCAGCTATGGGGCCACAGCCACATCACCGGGTGAGCGCTTTACGGACTCGCAGTTCCCTGGTGCTAATGA
ACCGAGTGCTGGCACTGATTGTGGCTGGCCCTCTCCTGTGTTCTCTGCAAGCAGCCCCGGCATGGGGCACCCATGT
ACCGGTACTCCTTTGCCAGCCTGTCCAATGTGCTTAGCAGCTGGTGCCAATACGAAGCTCTTAAGTTCGTCAGCT
TCCCCACCCAGGTGCTGGCCAAGGCCTCTAAGGTGATCCCTGTCTGCTGATGGGAAAGCTTGTGTCTCGGCGCA
GCTACGAACACTGGGAGTACCTGACAGCCACCCTCATCTCCATTGGGGTCAGCATGTTTCTGCTATCCAGCGGAC
CAGAGCCCCGCAGCTCCCCAGCCACCACACTCTCAGGCCTCATCTTACTGGCAGGTTATATTGCTTTTGACAGCT
TCACCTCAA**ACT**GGCAGGATGCCCTGTTTGCCTATAAGATGTCATCGGTGCAGATGATGTTTGGGGTCAATTTCT
TCTCCTGCCTCTTCACAGTGGGCTCACTGCTAGAACAGGGGGCCCTACTGGAGGGAACCCGCTTCATGGGGCGAC
ACAGTGAGTTTGCTGCCCATGCCCTGCTACTCTCCATCTGCTCCGCATGTGGCCAGCTCTTCATCTTTTACACCA
TTGGGCAGTTTGGGGCTGCCGTCTTCACCATCATCATGACCCTCCGCCAGGCCTTTGCCATCCTTCTTTCCTGCC
TTCTCTATGGCCACACTGTCACCTGTGGTGGGAGGGCTGGGGGTGGCTGTGGTCTTTGCTGCCCTCCTGCTCAGAG
TCTACGCGCGGGGCGGTCTAAAGCAACGGGGAAAGAAGGCTGTGCCTGTTGAGTCTCCTGTGCAGAAGGTT**TGAG**
GGTGAAAGGGCCTGAGGGGTGAAGTGAATAGGACCCTCCACCATCCCCTTCTGCTGTAACCTCTGAGGGAGC
TGGCTGAAAGGGCAAAATGCAGGTGTTTTCTCAGTATCACAGACCAGCTCTGCAGCAGGGGATTGGGGAGCCCAG
GAGGCAGCCTTCCCTTTTGCCTTAAGTCACCCATCTTCCAGTAAGCAGTTTATTCTGAGCCCCGGGGGTAGACAG
TCCTCAGTGAGGGGTTTTGGGGAGTTTGGGGTCAAGAGAGCATAGGTAGGTTCCAGTTACTCTTCCCACAAGTTC
CCTTAAGTCTTGCCCTAGCTGTGCTCTGCCACCTTCCAGACTCACTCCCCTCTGCAAATACCTGCATTTCTTACC
CTGGTGAGAAAAGCACAAAGCGGTGTAGGCTCCAATGCTGCTTTCCAGGAGGGTGAAGATGGTGCTGTGCTGAGG
AAAGGGGATGCAGAGCCCTGCCAGCACCACCACCTCCTATGCTCCTGGATCCCTAGGCTCTGTTCCATGAGCCT
GTTGCAGGTTTTGGTACTTTAGAAATGTAACTTTTTGGCTCTTATAATTTTATTTTATTAAATTAAATTACTGCA

2037/6881
FIGURE 1873

MDARWWAVVVLAAPSLGAGGETPEAPPESWTQLWFFRFVVNAAGYASFMVPGYLLVQYFRRKNYLETGRGLCFP
LVKACVFGNEPKASDEVPLAPRTEAAETTPMWQALKLLFCATGLQVSYLTWGV LQERVMTRSYGATATSPGERFT
DSQFLVLMNRVLALIVAGLSCVLCKQPRHGAPMYRYSFASLSNVLSWCQYEALKFVSFPTQVLAKASKVIPVML
MGKLVSRRSYEHWEYLTATLISIGVSMFLLSSGPEPRSSPATTLSGLILLAGYIAFDSFTSNWQDALFAYKMSSV
QMMFGVNFFSCLFTVGSLLLEQGALLEGTRFMGRHSEFAAHALLSICSACGQLFIFYTIGQFGAAVFTIIMTLRQ
AFAILLSCLLYGHTVTVVGGLGVAVVFAALLLRVYARGRLKQRGKKAVPVESPQKV

2038/6881
FIGURE 1874

CTCCGGCGCAGTGTGGGACTGTCTGGGTATCGGAAAAGCAAGCCTACGTTGCTCACTATTACGTATAATCCTTTT
CTTTTCAAGATGCTGAGGAAGTGCACCATGGAGAGGAGGAGGTGGAGACTTTTGCCTTTACGGCAGAAAATTGCC
CAACTCATGTCCCTCATCATCAATACCTTCTATTCCAACAAGGAGATTTTCCTTCGGGAGTTGATCTCTAATGCT
TCTGATGCCTTGGACAAGATTTCGCTATGAGAGCCTGACAGACCCTTCGAAGTTGGACAGTGGTAAAGAGCTGAAA
ATTGACATCATCCCCAACCTCAGGAACGTACCCTGACTTTGGTAGACACAGGCATTGGCATGACCAAAGCTGAT
CTCATAAATAAATTTGGGAACCATTGCCAAGTCTGGTACTAAAGCATTTCATGGAGGCTCTTCAGGCTGGTGCAGAC
ATCTCCATGATTGGGCAGTTTGGTGTGGCTTTTATTCTGCCTACTTGGTGGCAGAGAAAGTGGTTGTGATCACA
AAGCACAACGATGATGAACAGTATGCTTGGGAGTCTTCTGCTGGAGGTTTCCTTCACTGTGCGTGCTGACCATGGT
GAGCCCATTGGCAGGGGTACCAAAGTGATCCTCCATCTTAAAGAAGATCAGACAGAGTACCTAGAAGAGAGGCGG
GTCAAAGAAGTAGTGAAAGCATTCTCAGTTCATAGGCTATCCCATCACCTTTATTTGGAGAAGGAACGAGAG
AAGGAAATTAGTGATGATGAGGCAGAGGAAGAGAAAGGTGAGAAAGAAGAGGAAGATAAAGATGATGAAGAAAA
CCCAAGATCGAAGATGTGGGTTTCAGATGAGGAGGATGACAGCGGTAAGGATAAGAAGAAGAAAACTAAGAAGATC
AAAGAGAAATACATTGATCAGGAAGAACTAAACAAGACCAAGCCTATTTGGACCAGAAACCCTGATGACATCACC
CAAGAGGAGTATGGAGAATTCTACAAGAGCCTCACTAATGACTGGGAAGACCACTTGGCAGTCAAGCACTTTTCT
GTAGAAGGTGAGTTGGAATTCAGGGCATTGCTATTTATTCTCGTCGGGCTCCCTTTGACCTTTTTTGAGAACAAG
AAGAAAAAGAACAACATCAAACCTCTATGTCCGCCGTGTGTTTCATCATGGACAGCTGTGATGAGTTGATAACGAG
TATCTCAATTTTATCCGTGGTGTGGTTGACTCTGAGGATCTGCCCCGTAACATCTCCCGAGAAATGCTCCAGCAG
AGCAAAATCTTGAAAGTCATTCGCAAAAACATTGTTAAGAAGTGCCTTGAGCTCTTCTCTGAGCTGGCAGAAGAC
AAGGAGAATTACAAGAAATTTCTATGAGGCATTCTCTAAAAATCTCAAGCTTGGAATCCACGAAGACTCCACTAAC
CGCCGCCGCTGTCTGAGCTGCTGCGCTATCATACCTCCAGTCTGGAGATGAGATGACATCTCTGTCAGAGTAT
GTTTCTCGCATGAAGGAGACACAGAAGTCCATCTATTACATCACTGGTGAGAGCAAAGAGCAGGTGGCCAACCTCA
GCTTTTGTGGAGCGAGTGCAGGAAACGGGGCTTCGAGGTGGTATATATGACCGAGCCATTGACGAGTACTGTGTG
CAGCAGCTCAAGGAATTTGATGGGAAGAGCCTGGTCTCAGTTACCAAGGAGGGTCTGGAGCTGCCTGAGGATGAG
GAGGAGAAGAAGAAGATGGAAGAGAGCAAGGCAAAGTTTGAGAACCTCTGCAAGCTCATGAAAGAAATCTTAGAT
AAGAAGGTTGAGAAGGTGACAATCTCCAATAGACTTGTGTCTTCACCTTGCTGCATTGTGACCAGCACCTACGGC
TGGACAGCCAATATGGAGCGGATCATGAAAGCCCAGGCACCTTCGGGACAACTCCACCATGGGCTATATGATGGCC
AAAAAGCACCTGGAGATCAACCCTGACCACCCCATTTGTGGAGACGCTGCGGCAGAAGGCTGAGGCCGACAAGAAT
GATAAGGCAGTTAAGGACCTGGTGGTGTGCTGCTGTTTGAACCGCCCTGCTATCTTCTGGCTTTTCCCTTGAGGAT
CCCCAGACCCACTCCAACCGCATCTATCGCATGATCAAGCTAGGTCTAGGTATTGATGAAGATGAAGTGGCAGCA
GAGGAACCCAATGCTGCAGTTCCTGATGAGATCCCCCTCTCGAGGGCGATGAGGATGCGTCTCGCATGGAAGAA
GTCGATTAGGTTAGGAGTTTCATAGTTGGAAAACCTTGTGCCCTTGATAGTGTCCTTCATGGGCTCCCACTGCAGCC
TCGAGTGCCCTGTCCACCTGGCTCCCCCTGCTGGTGTCTAGTGTTTTTTTCCCTCTCCTGTCCTGTGTTGAA
GGCAGTAACTAAGGGTGTCAAGCCCCATTCCCTCTCTACTCTTGACAGCAGGATTGGATGTTGTGATTGTGGT
TTATTTTATTTTCTTCATTTTGTCTGAAATTAAAGTATGCAAAATAAAGAATATGCCGTTTTAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAA

2039/6881
FIGURE 1875

MPEEVHHGEEVEVTFQAEIAQLMSLIINTFYSNKEIFLRELISNASDALDKIRYESLTDPSKLD SGKELKIDI
IPNPQERTLTTLVDTGIGMTKADLINNLGTIAKSGTKAFMEALQAGADISMIGQFGVGFYSAYLVAEKVVVITKHN
DDEQYAWESSAGGSFTVRADHGEP IGRGTKVILHLKEDQTEYLEERRVKEVVKKHSQFIGYPITLYLEKEREKEI
SDDEAEEEEKGEKEEEDKDDEEKP KIEDVGSDEEDDSGDKKKKTKKIKEKYIDQEELNKT KPIWTRNPDDITQEE
YGEFYKSLTNDWEDHLAVKHFSVEGQLEFRALLFIPRRAPFDLFENKKKKNNIKLYVRRVFIMDSCDELIPEYLN
FIRGVVDSEDLPLNISREMLQQSKILKVIRKNIVKKCLELFS ELAEDKENYKKFYEA FSKNLKLG IHEDSTNRRR
LSELLRYHTSQSGDEMTSLSEYVSRMKETQKSIYYITGESKEQVANS AFVERVRKRGFEVVYMT EPIDEYCVQQL
KEFDGKSLVSVTKEGLELPEDEEEKKKMEESKAKFENLCKLMKEILDKKVEKVTISNRLVSSPCCIVTSTYGWTA
NMERIMKAQALRDNSTMGYMAKKHLEINPDHP IVETLRQKAEADKNDKAVKDLVLLFETALLSSGFSLEDPQT
HSNRIYRMIKLG LGIDED EVA AEEPNA AVPDEIPPLEGDEDASRMEEVD

2040/6881
FIGURE 1876

GGGCTGCGCTCTCCAGCTGTGGCTATGGCCCCAGCCCCGAGATGAGGAGGGAGAGAACTAGGGGCCCCGAGGCCT
GGGAATTTCCGTCCCCACCAAGTCCGGATGCTCACTCCAAAGTCTCAGCAGGCCCTGAGGGAGGGAGCTGTCA
GCCAGGGAAAACCGAGAACACCATCACCATGACAACCAGTCACCAGCCTCAGGACAGATACAAAGCTGTCTGGCT
TATCTTCTTCATGCTGGGTCTGGGAACGCTGCTCCCGTGGAATTTTTTCATGACGGCCACTCAGTATTTACAAA
CCGCCTGGACATGTCCCAGAATGTGTCCTTGGTCACTGCTGAACTGAGCAAGGACGCCCAGGCGTCAGCCGCCCC
TGCAGCACCCCTTGCTGAGCGGAACCTCTCTCAGTGCCATCTTCAACAATGTCATGACCCTATGTGCCATGCTGCC
CCTGCTGTTATTACCTACCTCAACTCCTTCCTGCATCAGAGGATCCCCAGTCCGTACGGATCCTGGGCAGCCT
GGTGGCCATCCTGCTGGTGTCTGATCACTGCCATCCTGGTGAAGGTGCAGCTGGATGCTCTGCCCTTCTTTGT
CATCACCATGATCAAGATCGTGCTCATTAAATTCATTTGGTGCCATCCTGCAGGGCAGCCTGTTTGGTCTGGCTGG
CCTTCTGCCTGCCAGCTACACGGCCCCCATCATGAGTGGCCAGGGCCTAGCAGGCTTCTTTGCCTCCGTGGCCAT
GATCTGCGCTATTGCCAGTGGCTCGGAGCTATCAGAAAGTGCCCTTCGGCTACTTTATCACAGCCTGTGCTGTTAT
CATTTTGACCATCATCTGTTACCTGGGCCTGCCCCGCCTGGAATTCACCGCTACTACCAGCAGCTCAAGCTTGA
AGGACCCGGGGAGCAGGAGACCAAGTTGGACCTCATTAGCAAAGGAGAGGAGCCAAGAGCAGGCAAAGAGGAATC
TGGAGTTTTCAGTCTCCAACCTCTCAGCCCACCAATGAAAGCCACTCTATCAAAGCCATCCTGAAAAATATCTCAGT
CCTGGCTTTCTCTGTCTGCTTCATCTTCACTATCACCATTGGGATGTTTCCAGCCGTGACTGTTGAGGTCAAGTC
CAGCATCGCAGGCAGCAGCACCTGGGAACGTTACTTCATTCTGTGTCCTGTTTCTTGACTTTCAATATCTTTGA
CTGGTTGGGCGGAGCCTCACAGCTGTATTATGTGGCCTGGGAAGGACAGCCGCTGGCTGCCAAGCCTGGTGCT
GGCCCGGCTGGTGTTTGTGCCACTGCTGCTGCTGTGCAACATTAAGCCCCGCCGCTACCTGACTGTGGTCTTCGA
GCACGATGCCTGGTTTCATCTTCTTCATGGCTGCCTTTGCCTTCTCCAACGGCTACCTCGCCAGCCTCTGCATGTG
CTTCGGGCCCAAGAAAGTGAAGCCAGCTGAGGCAGAGACCGCAGGAGCCATCATGGCCTTCTTCCTGTGTCTGGG
TCTGGCACTGGGGGCTGTTTTCTCCTTCTGTTCCGGGCAATTGTGTGACAAAGGATGGACAGAAGGACTGCCTG
CCTCCCTCCCTGTCTGCCCTCCTGCCCCCTTCTTCTGCCAGGGGTGATCCTGAGTGGTCTGGCGGTTTTTTCTTCT
AACTGACTTCTGCTTTCCACGGCGTGTGCTGGGCCCCGATCTCCAGGCCCTGGGGAGGGAGCCTCTGGACGGACA
GTGGGGACATTGTGGGTTTGGGGCTCAGAGTCGAGGGACGGGGTGTAGCCTCGGCATTTGCTTGAGTTTCTCCAC
TCTTGGCTCTGACTGATCCCTGCTTGTGCAGGCCAGTGGAGGCTCTTGGGCTTGAGAACACGTGTGTCTCTGTG
TATGTGTCTGTGTGTCTGCGTCCGTGTCTGTGCAGACTGTCTGCCTGTCTGGGGTGGCTAGGAGCTGGGTCTGAC
CGTTGTATGTTTTGACCTGATATACTCCATTCTCCCTGCGCCTCCTCCTGTGTCTCTCCATGTCCCCCTCC
CAACTCCCCATGCCCAGTTCTTACCCATCATGCACCCTGTACAGTTGCCACGTTACTGCCTTTTTTAAAAATATA
TTTGACAGAAACCAGGTGCCTTCAGAGGCTCTCTGATTTAAATAAACCTTCTTGTTTTTTT

2041/6881
FIGURE 1877

CACATGCTGCACGCGCATCTCGCCCCAGGGGCACTGCCTGGAAGATTTCAGGAGCCTGGGCGGCCTTCGCTTACT
CTCACCTGCTTCTGAGTTGCCAGGAGACCACTGGCAGATGTCCCGGCGAAGAGAAGAGACACATTGTTGGAAGA
AGCAGCCCATGACAGCTCCCCCTTCTGGGACTCGCCCTCATCCTCTTCTGCTCCCCCTTCTGGGGTGCAGCCTA
AAAGGACCTATGTCCTCACACCATTGAAACCACTAGTTCTGTCCCCCAGGAGACCTGGTTGTGTGTGTGTGAGT
GGTTGACCTTCCCTCCATCCCCCTGGTCCTTCCCTTCCCTTCCCGAGGCACAGAGAGACAGGGCAGGATCCACGTGC
CCATTGTGGAGGCAGAGAAAAGAGAAAGTGTTTTATATACGGTACTTATTTAATATCCCTTTTTAATTAGAAATT
AAAACAGTTAATTTAATTAAAGAGTAGGGTTTTTTTTTCAGTATCTTGGTTAATATTTAATTTCAACTATTTATG
AGATGTATCTTTTGCTCTCTCTTGCTCTCTTATTTGTACCGGTTTTTGTATATTTGAACAGATATTTAATTTTGC
TAACACTCAGCTCTGCCCTCCCCGATCCCCTGGCTCCCCAGCACACATTCCTTTGAAATAAGGTTTCAATATACA
TCTACATACTATATATATATTTGGCAACTTGTATTTGTGTGTATATATATATATATA

2042/6881
FIGURE 1878

GC GCGAGCCGCGCCGGCCCCGGTCGGGCCTCCGAAACCATGAACTTTCTGCTGTCTTGGGTGCATTGGAGCCTTG
CCTTGCTGCTCTACCTCCACCATGCCAAGTGGTCCCAGGCTGCACCCATGGCAGAAGGAGGAGGGCAGAATCATC
ACGAAGTGGTGAAGTTCATGGATGTCTATCAGCGCAGCTACTGCCATCCAATCGAGACCCTGGTGGACATCTTCC
AGGAGTACCCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCCCTGATGCGATGCGGGGGCTGCTGCA
ATGACGAGGGCCTGGAGTGTGTGCCCCTGAGGAGTCCAACATCACCATGCAGATTATGCGGATCAAACCTCACC
AAGGCCAGCACATAGGAGAGATGAGCTTCCTACAGCACAAACAAATGTGAATGCAGACCAAAGAAAGATAGAGCAA
GACAAGAAAAAAATCAGTTCGAGGAAAGGGAAAGGGGCAAAAACGAAAGCGCAAGAAATCCCGGTATAAGTCCT
GGAGCGTGACGTTGGTGCCCGCTGCTGTCTAATGCCCTGGAGCCTCCCTGGCCCCCATCCCTGTGGGCCTTGCT
CAGAGCGGAGAAAGCATTGTGTTGTACAAGATCCGCAGACGTGTAAATGTTCTGCAAAAACACAGACTCGCGTT
GCAAGGCGAGGCAGCTTGAGTTAAACGAACGTACTTGACAGATGTGACAAGCCGAGGCGGTGAGCCGGGCAGGAGG
AAGGAGCCTCCCTCAGGGTTTCGGAACCATCT

2043/6881
FIGURE 1879

TACCCCTTCATGCTCCAGTGCACCCCAGGCTTCGTGGCCAGCCTGGGAAACTGTCTCTACCCCTGGTCTCCCTTCA
GATCAGCTTCTAGAAATGTTTCGTGGCTACAGTGGCAGCACTGTTTTTCCATGATGCAAGCAGTTTGCCCTCTT
GGGCGGGGTTATCAGTGGCTGGCAGGGCTGGCACAGCGTGTCCGCCCACTGCCACCTGTGGGTTCCAGGAGGGCC
CAGCCCCCTGTGCTGATGCCCACCACCTTCTCAGCTCATGTCTGGGGAAGAGGACTGGCAGGGGGAAAGGTGCCTC
CTCCTGAAAGGTGCCTCCTCTGTTTTTGCCTAATATAGGCTTGGGAACACTTTGATGTCAGCTAATTCTGACTCC
TTTACTTACTAGCTGTGCGGCCTTGGGGCAACTTACTTAGCCTCTTTGAGCCTCCTGTTCCCCATCTGTAAAATG
GAATCTCAATAGTGTCTAATAGTACCATGTGGAGAACTTGTGTGAAATGATAGCTGTGGACTACTGTACACAGT
ACTCAGGATGTAGTAAGTGCTCAATAAACAGCTGTTGGTATGGTTGACGTTATGGTAGTGTTGTGGGGAGGACG
TAGGAAACTGGAGACTAGCTTGGCAAAGCTGGCTCTTCCTCCTTTTAGGGAAAGCTTAGAGCATCCCCATGGGGT
ATACCCATACTCAGACTGTCTCTGGCATCGAGGTTGGCCCAGGATTGAGTTCAGCTGTCACAGTGAGGTGGCGG
GATCAGATGTGGCAGGCCATGTCCCTTGGAACCTGAGTACATCGTGTGATCTCTGGAATGAAAACAGGCCTTCAC
CAGTGTTGATGGTGGAAAGCTTAGGGAAGTGCTTCAAACACAGTAGGAGGGACTTACGTTAGATTTTGGAAAGGAC
TTGCTGATTGGAAGCTCCAAAGAGTGGCATTACAGAGCTGGGTGGAGAGAGGGGGCTAGCCATCTTTTGTGTGCG
CCCACCGGGCTCATGTGTCTATCGCCTCTCATGCACTGGTGAAGTTTATGGATGTCTATCAGCGCAGCTACTGCCA
TCCAATCGAGACCCTGGTGGACATCTTCCAGGAGTACCCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGT
GCCCCTGATGCGATGCGGGGGCTGCTGCAATGACGAGGGCCTGGAGTGTGTGCCCCACTGAGGAGTCCAACATCAC
CATGCAGGTFGGGCATCTTTGGGAAGTGGGGCAAGGGGGGGATAGGGAGGGGGGTAACACTTTGGGAACAGGTGGT
CCCAGGTCGTTTTCTGGCTAGATTTGCCTTGTCTGGCTCCTGCCCTGAGTTGCACAGGGGAGGTATGGTGGGGT
CTTGCTTCTGTGGAGAAGATGCTTTCATTCCCAGCCCAGGTTCCCAGCAAGCCCCAACCATCTCCTTCTCCCTGA
TGTTTGCCCATGGGCTCAGGAGGGGACAGATGGATGCCTGTGTGAGGAGCCCCCTCTCTCCCTCTCTTGAGAGAG
TCCTGAGTGCCCCCTTCTTGGGGGCTTTGTTTGGGAAGCTGGATGAGCCTGGTCCATGGAGAGTTTAAAAAGT
CTTTTGGTGTTACCTGGTAATGGGGCACATCTCAGCCCAGATAGGGTGGGAGGGAGCTGTGAAACACAGGGAGGG
GGTTGCTTTCGGGTATCTACTAGGAGTCAGGGTGAAGCCTAGAGAGGATGAAAGAAGGGGAGGGGATGGGGAGTG
GTAAGAACCTAGGATTTGAATTCCAGCCTGGCCAACCCTTGCAGCCATGTCTTGGCCTCAAGTGAACAAGGGC
TCCTTGAGGCCAGCAGGGTTGGGGGAGTTGGGGTGGGCCTGAGCCTCTTTCCTGCTAGAGCTCTTGGTCTCCTCCT
GCCTCCACCACCCATCCCTGCTCTGCAGAACCCCTGGGTGCTGAGTGGCAGGAGCCCCAGGGTTGTCCCATCTGG
GTATGGCTGGCTGGGTCACTAACCTCTGTGATCTGCTTCCCTTCCAGATTATGCGGATCAAACCTCACCAA
GGCCAGCACATAGGAGAGATGAGCTTCCTACAGCACAACAAATGTGAATGCAGGTGAGGATGTAGTCACGGATTC
ATTATCAGCAAGTGGCTGCAGGGTGCCTGATCTGTGCCAGGGTTAAGCATGCTGTACTTTTTGGCCCCCGTCCAG
CTTCCCGCTATGTGACCTTTGGCATTCTTACTTCAATGTGCCTCAGTTTCTACATCTGTAAAATGGGCACAATAGT
AGTATACTTCATAGCATTGTTATAATGATTAAACAAGTTATATATGAAAAGATTAAACAGTGTTGCTCCAT

2044/6881
FIGURE 1880

AGGTTTTTGAAGATGGCGGCCCTCAAGGCTCTGGTGTCCGGCTGTGGGCGGCTTCTCCGTGGGCTACTAGCGGGC
CCGGCAGCGACCAGCTGGTCTCGGCTTCCAGCTCGCGGGTTCAGGGAAGTGGTGGAGACCCAAGAAGGGAAGACA
ACTATAATTGAAGGCCGTATCACAGCGACTCCCAAGGAGAGTCCAAATCCTCCTAACCCCTCTGGCCAGTGCCCC
ATCTGCCGTTGGAACCTGAAGCACAAGTATAACTATGACGATGTTCTGCTGCTTAGCCAGTTCATCCGGCCTCAT
GGAGGCATGCTGCCCCGAAAGATCACAGGCCTATGCCAGGAAGAACACCGCAAGATCGAGGAGTGTGTGAAGATG
GCCCCACCGAGCAGGTCTATTACCAAATCACAGGCCTCGGCTTCCTGAAGGAGTTGTTCCGAAGAGCAAACCCCAA
CTCAACCGGTACCTGACGCGCTGGGCTCCTGGCTCCGTCAAGCCCATCTACAAAAAAGGCCCCCGCTGGAACAGG
GTGCGCATGCCCCGTGGGGTCACCCCTTCTGAGGGACAATGCTGCTACTCAAGAACACCTTGGAAGCTGTATCAC
TGACAGAGAGCAGTGCTTCCAGAGTTCCTCCTGCACCTGTGCTGGGGAGTAGGAGGCCCCTCACAAGCCCTTGG
CCACAACCTATACTCCTGTCCCACCCACACGATGGCCTGGTCCCTCCAACATGCATGGACAGGGGACAGTGGGA
CTAACTTCAGTACCCTTGGCCTGCACAGTAGCAATGCTGGGAGCTAGAGGCAGGCAGGGCAGTTGGGTCCCTTGC
CAGCTGCTATGGGGCTTAGGCCATGCTCAGTGCTGGGGACAGGAGTTTGGCCAAACGCAGTGTCATAAACTGGGT
TCATGGGCTTACCCATTGGGTGTGCGCTCACTGCTTGGGAAGTGCAGGGGGTCTGGGCACATTGCCAGCTGGGT
GCTGAGCATTGAGTCACCTGATCTCTTGTGATGGGGCCAATGAGTCAATTGAATTCATGGGCCAAACAGGTCCCAT
CCTCTTCATG

2045/6881
FIGURE 1881

MAALKALVSGCGRLLRGLLAGPAATSWSRLEPARGFREVVETQEGKTTIIEGRITATPKESNPFPNPSGQCPICRW
NLKHKYNYDDVLLLSQFIRPHGGMLPRKITGLCQEEHRKIEECVKMAHRAGLLPNHRPRLPEGVVPKSKPQLNRY
LTRWAPGSVKPIYKKGPRWNRVRMPVGSPLLRDNVCYSRTPWKLYH

2046/6881
FIGURE 1882A

AGCTGTCTGCTCGCTCGTGGTCCCGGGACTGCAGTGGTGTGCGCTCTCGGCGCGTGGCGCTAGGCATGGCGATGGAT
CAAGTAAACGCGCTGTGCGAGCAGCTGGTGAAAGCGGTGACGGTCATGATGGACCCCAACTCCACCCAGCGCTAC
CGGCTGGAAGCCCTCAAGTTTTGTGAGGAGTTTTAAAGAAAAGTGTCTATCTGTGTCCCTGTGGCTTGAGGTTG
GCTGAGAAAACACAAGTTGCCATCGTCAGACATTTTGGCCTTCAGATCCTGGAACACGTTGTCAAGTTTCGGTGG
AACGGCATGTCTCGATTGGAGAAGGTGTATCTGAAGAACAGTGTATGGAGCTGATTGCAAATGGAACATTGAAC
ATTTTGAAGAGGAGAACCATATTAAAGATGCTCTGTCTCGAATTGTAGTGGAATGATCAAGCGAGAGTGGCCA
CAGCATTGGCCTGACATGCTAATAGAATTGGACACTCTTTCCAAACAAGGGGAAACACAGACAGAATTGGTGATG
TTTATCCTTTTGGCGACTGGCAGAGGATGTAGTGACTTTTCAGACACTTCCCCCTCAAAGAAGAAGGGACATCCAG
CAAACATTAACCCAGAACATGGAAAGGATCTTCAGTTTTCTGCTTAACACACTTCAAGAAAATGTAAACAAGTAT
CAGCAAGTGAAGACAGATACTTCTCAGGAGTCAAAGGCGCAAGCAAACCTGTGAGTAGGAGTTGCAGCACTGAAT
ACTCTAGCAGGCTATATTGACTGGGTGTCTATGAGTCACATCACTGCTGAAAACCTGTAAACTCCTGGAGATACTG
TGTTTGCTGTTGAATGAACAGGAACTTCAGTTGGGAGCCGCTGAGTGTCTTCTCATTGCAGTCAGCAGAAAAGGC
AAGTTGGAAGACCGGAAGCCCTTGATGGTCTTATTTGGAGATGTTGCCATGCATTATATACTCTCCGCCGCACAG
ACTGCTGATGGAGGAGGTTTGGTAGAAAAACACTACGTCTTTCTGAAGAGGCTCTGTGAGGTGTTGTGTGCGCTG
GGCAATCAGCTGTGTGCATTGCTGGGTGCAGATTCTGATGTAGAAAACACCATCAAACCTTGGAAAATACCTGGAA
TCTTTTCTTGCTTTTACAACCCATCCAAGTCAGTTTCTACGCTCTTCAAACCTCAGATGACTTGGGGAGCCCTCTTC
AGGCATGAAATCCTGTCCCGTGATCCTTGGCTATTAGCAATAATACCAAAAATATCTTCGTGCTTCCATGACTAAC
TTGGTCAAGATGGGCTTTCTTTCTAAACAGACAGCCCTAGCTGTGAATATTTCTCGGTTTGATTTTGATAGCGAT
GAGGACTTCAATGCTTTCTTCAAACCTCCTCCCGAGCACAACAAGGAGAGGTGATGAGGTTGGCATGTCGTTTGGAT
CCCAAACTAGCTTCCAGATGGCTGGGGAGTGGCTAAAGTATCAACTATCAACTTTTCTTGATGCTGGTTCTGTG
AATTCTTGTTCTGCAGTTGGAACCTGGAGAAGGAAGCCTCTGTTCCGTCTTCTCACCTTCATTCTGTCAGTGGGAA
GCCATGACTCTTTTTTTTGGAAAGTGTTATCACCCAGATGTTTTCGAACACTAAATAGAGAAGAAATTCCTGTTAAT
GATGGAATAGAGCTATTGCAGATGGTTCTGAACCTTTGATACCAAGGATCCCCCTCATCCTGTCTGCGTCTTACT
AATGTCTCTGCACTCTTTCCATTTGTACCTACAGACCAGAGTTTCTGCCCCAGGTCTTCTCTAAGCTATTTTCA
TCTGTCACTTTTGAAACTGTTGAAGAAAGTAAGGCCCCCAGAACCCGGGCAGTGAGGAATGTGAGGAGGCATGCT
TGTTCCCTCCATCATCAAGATGTGTGCTGACTACCCCCAGCTTGTGCTGCCCAATTTTGACATGCTTTATAACCAT
GTGAAGCAACTCCTCTCCAATGAGCTACTCCTGACACAAATGGAGAAGTGTGCCCTCATGGAAGCCCTGGTTCTC
ATTAGCAACCAATTTAAGAACTACGAGCGTCAGAAGGTGTTCTAGAGGAGCTGATGGCACCAGTGGCCAGCATC
TGGCTTTCTCAAGACATGCACAGAGTGTGTGATGCTTTTATTGCGTATGTGGGTACAGATCAGAAG
AGCTGTGACCCAGGCCTGGAGGATCCGTGTGGCTTAAACCGTGACGAATGAGCTTTTGTGTATACAGCATTCTG
GGTGTGGTGAAACGAACCTTGCTGGCCCACTGACCTAGAAGAGGCCAAAGCTGGGGGATTTGTGGTGGGTATACA
TCCAGTGGAATCCAATCTTCCGTAACCCCTGCACAGAGCAGATTCTGAAACTTCTTGACAATTTGCTTGCCTT
ATAAGAACCACACAATACATTATATGCACCAGAAATGCTAGCCAAAATGGCAGAGCCTTTACCAAGGCTCTGGAT
ATGCTTGACGCGGAAAAATCTGCTATATTAGGATTACCTCAACCTCTCTTGGAACCTCAATGACTCTCCTGTCTTC
AAAACCGTCTTGGAAGAATGCAGCGTTTCTTCTCTACCTCTATGAAAACCTGTTTTCATATCCTAGGGAAGGCA
GGCCCTTCCATGCAGCAAGACTTCTATACTGTGGAGGACCTTGCTACCCAGCTTCTCAGCTCAGCCTTTGTCAAC
TTGAACAATATTCTTGACTACCGACTCAGACCCATGCTTCATGTCTTTGTAAAGCCTCTGGTGCTCTTCTGTCCC
CCAGAGCACTATGAAGCCCTGGTATCCCCATCCTCGGACCTCTTTTACCTACCTCCATATGAGGCTTTCTCAG
AAATGGCAAGTTATCAACCAAAGGAGCCTGCTGTGTGGAGAAGATGAGGCTGCAGATGAAAACCCAGAGTCTCAA
GAGATGCTGGAGGAGCAACTGGTGAGGATGTTAACCAGAGAAGTCATGGACCTAATCACGGTTTGCTGTGTTTCA
AAGAAGGGTGCTGACCACAGTAGTGCTCCCCCAGCAGATGGAGACGATGAAGAAATGATGGCCACAGAGGTCACC
CCCTCAGCTATGGCAGAGCTTACAGACCTGGGCAAATGTCTGATGAAGCATGAGGATGTTTGTACAGCGCTATTA
ATTACAGCCTTCAATTCCCTGGCCTGGAAGATACTCTGTCTGCCAGAGGACAACCTCACAGCTCTGCTGGCCT
CTCCTCAAACAAGTGCTGTGAGGGACACTGCTCGCAGATGCAGTTACGTGGCTTTTACCAGTGTGCTGAAAGGC
TTACAGATGCACGGGCAGCACGACGGGTGCATGGCTTCCCTGGTCCATCTGGCCTTCCAGATATACGAGGCACTG
CGCCCCAGGTACCTGGAGATAAGAGCTGTAATGGAGCAAATCCCTGAAATACAGAAGGACTCACTGGACCAGTTT
GACTGCAAGCTTTTAAACCCCTCCCTGCAGAAAGTGGCTGACAAGCGCCGAAAGGACCAATTCAAACGCCTCATT
GCTGGTTGCATTGGGAAACCCCTGGGAGAGCAGTTCCGAAAAGAAAGTTCACATTAAGAATCTTCCCTCACTTTT

2047/6881
FIGURE 1882B

AAAAAAAAACAAAGCCAATGCTGGAGACGGAGGTGCTGGACAATGATGGGGGTGGCCTGGCCACCATCTTTGAACCC
TGAATCAAGCTTTTGGGCATCCTTCCTCGGCCTTTCTTGTCATCTCTTCTTTCCCTTTGTAGCCGATCTCTAGGC
CCTTCTTGCACTGCCACCTCACTTTCCACCACTGTCAGCCTGGAAAGAGATCCAGGTCTGGAGCTGGAGAGAACA
GGCCCTGTGCAGGACCAGAAGTAATTATACTAAAGTATCAAGAAAGGGAGTTAGGGCTTAAACTATTCTGTCTAG
ATGTCCCAGATAGTTCCCATTCTACTTGGAGATTTGGCTTTTCCAAGAAAAGCTAGAGCAGAGCCCTTCTCC
CACAAGCCCTCCCACCCCGTGCAGCCACATACCTGTACAGAATGGTAACCTAAGGGTGCTGTGCCCAACCCTGCG
ACTAGCAAGGCTCGCAGCAAGAGCACAGCCCTCACTACTTGTGCCAGAGTTTCTCTTGGACCACTCCAACCTCCC
ACTGAGCCCTTTTGCTGCTGGGCTGGCAGGAACTTTCCCACTCCCTAAGGGGCATGTCTGGGTTAGGTGCTAA
GTGCTGAAGAGAACTTGGTCAGTTCTCTCACTTTGCTTTGGGCAAGAATCTGGTCACCTGATGGGATCCATGGT
ACAGGCTACTGCTAAACTTGGCACAGTATCAAGTATAGTACCTCCAAGGACCAGGGCTGGGAAGTCTTTAGTGCT
AACATCCCCTTTAGAGTTCACACATCTTGCCCTTCCATGAATGACCCCTCAGTCTGGCCTCCCAGCCTCAAGGT
CCACTCAGGCACAAGAGCCACAGTACCCCTAGATAGTGTACATGACACCGTTGTCATCCAAGGATAATACAGACC
AACTAGGCTACATCTGTGATGAGCAGCTAGCAAAGCCGCTGGTCTTCTCCTAGGACTAAGTCCAGGTGCCTTCCA
CAATCTCATGGTCTTTTCAGGTCCCTGGTTACTTTTCTCAAAGGCCATTTCCAAAAGAATACATGCCTTCACATCA
CAACCTGTACTGTGAGTCCATTCTAGAGGTCACTGAAAGGCCCTGTAAAGAGAGGACATGGATACGGGACCTGGC
CCTGAGGTTATTACTGGCCGTAAGGCAGAGTTAATCCATACAGAAACCAGTGTGTCCATGTGCTCTGCACAAAAA
CAGACCTGTTGTCCATCCAGTCCACTGACAAGAGGGTTTCCCCGAGAGCCGAAGTGGACTGAAGCTACAGTTTTT
AGCTGGTGCGGGCCACAGGCAGGGTCAGATTGAGAAGAAGCAAAGCTGGGGAAGCAGAAGTTGGGAGTCTTGTGT
TGCTCCCTCTTCCTGTGTGGTGCTCTGGGTTTCTGTGGATCGTGAAGGCGATCTCAAGAGTGTTCCTCCAAAC
CTGATAGCTGCCTATTCTGTCTGGTTGGGGCTGTGGAGGATGTAGTTGTATTTATTGCATTGTAATATTTTTAA
CATCCTGTGACTTCATGCTAGAAATTTCTATTGTTTATAGAACTTTTGTAGAAACATTAACCTCTAAAGCACA
TCTGCATGTCAGTAAAAATCTCAGTTTCGTACAG

2048/6881
FIGURE 1883

CACCAAATGGCGGATGACGCCGGTGCAGTGGGGGGCCTGGAGGCCCTGGTGGCCCTGGGATGGGGAACCGCGGT
GGCTTCCGCAGAGGTTTCGCCAGTGGCATCCGGGGCCGGGGTTCGCAGCCGTGGACCGGGCCGGGGCTGAGGCCGC
GGAGCTCGCGGAGGCAAGGCCAAAGATAAGGAGTGGATGCCCCTCACCAAGCTGGGCCGCTTGGTCAAGGACATG
AAGATCAAGTCCCTGGAGGAGATCTATCTCTTCTCCCTGCCCATTAAGGAATCAGAGATCATTGACTTTTTCTG
GGGGCCTCTCTCAAGGATGAGGTTTTGAAGATTATGCCAGTGCAGAAGCAGACCCGTGCTGGCCAGCGCACCAGG
TTCAAGGTGACAGGCCGCCGTGGCTCTGTGCTGGTGCCTCATCCCTGCACCCAGGGGCACTGGCATTGTCTCC
GCACCTGTGCCCAAGAAGCTGCTCATGATGGCTGGTATCGATGACTGCTACACCTCAGCCCAGGGCTGCACTGCC
ACCCTGGGCAACTTCGCCAAGGCCACCTTTGATGCCATTTCTAAGACCTACAGCTACCTGACCCCCGACCTCTGG
AAGGAGACTGTATTTACCAAGTCTCCCTATCAGGAATTCAGTACCACCTCGTCAAGACCCACACCAGAGTCTCT
GTGCAGCAGACCCAGGCTCCAGCTGTGGCTACAACATAGGGTTTTTATACAAGAAAAATAAAGTGAATTAAGCGT
G

2049/6881
FIGURE 1884

CGCGGAGCTCGCGGAGGCAAGGCCAAAGATAAGGAGTGGATGCCCCGTCACCAAGCTGGGCCGCTTGGTCAAGGAC
ATGAAGATCAAGTCCCTGGAGGAGATCTATCTCTTCTCCCTGCCCATTAAGGAATCAGAGATCATTGACTTTTTTC
CTGGGGGCCTCTCTCAAGGATGAGGTTTTGAAGATTATGCCAGTGCAGAAGCAGACCCGTGCTGGCCAGCGCACC
AGGGCTCTCCATTGTCCCCGTGCACAGAGGCTACTAGGGGAACAAGATCGGCAAGCCCCACACCGTCCCCTGCAA
GGTGACAGGCCGCCGTGGCTCTGTGCTGGTGCGCTCATCCCTGCACCCAGGGGCACTGGCATTGTCTCCGCACC
TGTGCCCAAGAAGCTGCCATTTCTAAGACCTACAGCTACCTGACCCCCGACCTCTGGAAGGAGACTGTATTTACC
AAGTCTCCCTATCAGGAATTCAGTACCACCTCGTCAAGACCCACACCAGAGTCTCTGTGCAGCAGACCCAGGCT
CCAGCTGTGGCTACAACATAGGGTTTTTATACAAGAAAAATAAAGTGAATTAAGCGTG

2050/6881
FIGURE 1885

MPVTKLGRLVKDMKIKSLEEIYLFSLPIKES¹IIDFFLGDSLKDEVLKIMPVQKQTRAGQRTLHCPRAQRLIGE
QDRQAPHRPLQGDRPLRLCAGAPH²PCTQGHWHRLRTCAQELMPSLRPTAT

2051/6881
FIGURE 1886

GTGTTCCGGCCGATCCACCTCTTCTCGACCTGGACGTCTACCTTCCGGAGGCCACATCTTGCCCACTCCGCG
CGCGGGGCTAGCGCGGGTTTTCAGCGACGGGAGCCCTCAAGGGACATGGCAACTACAGCGGCGCCGGCGGGCGGCG
CCCGAAATGGAGCTGGCCCGGAATGGGGAGGGTTCGAAGAAAACATCCAGGGCGGAGGCTCAGCTGTGATTGACA
TGGAGAACATGGATGATACCTCAGGCTCTAGCTTCGAGGATATGGGTGAGCTGCATCAGCGCCTGCGCGAGGAAG
AAGTAGACGCTGATGCAGCTGATGCAGCTGCTGCTGAAGAGGAGGATGGAGAGTTCCTGGGCATGAAGGGCTTTA
AGGGACAGCTGAGCCGGCAGGTGGCAGATCAGATGTGGCAGGCTGGGAAAAGACAAGCCTCCAGGGCCTTCAGCT
TGTACGCCAACATCGACATCCTCAGACCCTACTTTGATGTGGAGCCTGCTCAGGTGCGAAGCAGGCTCCTGGAGT
CCATGATCCCTATCAAGGTGGTCAACTTCCCCCAGAAAATTGCAGGTGAACTCTATGGACCTCTCATGCTGGTCT
TCACTCTGGTTGCTATCCTACTCCATGGGATGAAGACGCTCTGACACTATTATCCGGGAGGGCACCTGATGGGCA
CAGCCATTGGCACCTGCTTCGGCTACTGGCTGGGAGTCTCATCCTTCATTTACTTCCTTGCCCTACCTGTGCAACG
CCCAGATCACCATGCTGCAGATGTTGGCACTGCTGGGCTATGGCCTCTTTGGGCATTGCATTGTCTGTTTCATCA
CCTATAATATCCACCTCCACGCCCTCTTCTACCTCTTCTGGCTGTTGGTGGGTGGACTGTCCACACTGCGCATGG
TAGCAGTGTGGTGTCTCGGACCGTGGGCCCCACACAGCGGCTGCTCCTCTGTGGCACCTGGCTGCCCTACACA
TGCTCTTCCTGCTCTATCTGCATTTTGCCTACCACAAAGTGGTAGAGGGGATCCTGGACACACTGGAGGGCCCCA
ACATCCCGCCCATCCAGAGGGTCCCCAGAGACATCCCTGCCATGCTCCCTGCTGCTCGGCTTCCCACCACCGTCC
TCAACGCCACAGCCAAAGCTGTTGCGGTGACCCTGCAGTCACACTGAACCCACCTGAAATTCTTGGCCAGTCCTC
TTTCCCGCAGCTGCAGAGAGGAGGAAGACTATTAAAGGACAGTCCTGATGACATGTTTCGTAGATGGGGTTTGCA
GCTGCCACTGAGCTGTAGCTGCGTGAGTACCTCCTTGATGCCTGTGCGCACTTCTGAAAGGCACAAGGCCAAGAA
CTCCTGGCCAGGACTGCAAGGCTCTGCAGCCAATGCAGAAAATGGGTGAGCTCCTTTGAGAACCCCTCCCCACCT
ACCCCTTCCTTCCTCTTTATCTCTCCACATTGTCTTGCTAAATATAGACTTGGTAATTAATAATGTTGATTGAAG
TCTGG

2052/6881
FIGURE 1887

MATTAAPAGGARNGAGPEWGGFEENIQGGGSAVIDMENMDDTSGSSFEDMGELHQRLREEEVDADAADAAAAEEE
DGEFLGMKGFGQLSRQVADQMWOAGKRQASRAFSLYANIDILRPYFDVEPAQVRSRLLESMIPIKVVNFPQKIA
GELYGPLMLVFTLVAILLHGMKTSDTIIREGILMGTAGTCFGYWLGVSSFIYFLAYLCNAQITMLQMLALLGYG
LFGHCIVLFITYNIHLHALFYLFWLLVGGLSTLRMVAVLVSRTVGPTQRLLLCGTLAALHMLFLLYLHFAYHKVV
EGILDTLEGPNIPPIQRVPRDIPAMLPAARLPTTVLNATAKAVAVTLQSH

2053/6881
FIGURE 1888

GCGGAAGCGGCGCCATTTCGTCTTCCGAGCGCTACTGCCAGCTGATGCCGGGAGCTAACTACCGCGCCGGGGCCGG
GGCCGGGGCCGGGGCCCGACGTCCCCGCGGGGCCCCGGGACCGCGAGGAGGACGGCGGGGGCCTGGAGCCCCGCGGC
CGTGGCCCCGCGACCTATTGAGGGGCACATCTAACATGTCATTTGAGGAGCTGTTGGAATTGCAGAGCCAAGTGGG
GACTAAGACGTACAAACAATTGGTAGCTGGAAATAGTCCTAAGAAACAAGCTTCTAGACCACCTATCCAAAATGC
ATGTGTTGCAGATAAGCACAGGCCTCTGGAAATGTCAGCCAAGATCCGAGTACCATTTTTACGTCAGGTTGTTCC
CATTAGTAAAAAGGTAGCCCGGGACCCTCGCTTTGATGATCTGTCAGGGGAATATAATCCTGAGGTGTTTGACAA
AACATAACCAATTCTTGAATGACATCCGAGCGAAAGAGAAAGAGTTGAAGAAGCACCTTTCAGGAGAGGAGCATGA
GAAACTGCAGCAACTGCTTCAGCGAATGGAGCAGCAAGAAATGGCACAGCAGGAACGAAAGCAACAGCAGGAGCT
GCACCTGGCCCTGAAGCAAGAACGTCGGGCTCAGGCCCAGCAGGGCCATCGGCCATACTTCCTGAAAAAATCTGA
GCAGCGCCAGTTGGCACTAGCTGAGAAGTTCAAGGAGCTGAAACGCAGCAAGAAATTGGAGAACTTCTTGAGTCG
AAAGAGGCGACGAAATGCAGGCAAGGACAGGAGACATCTCCCTTTGAGCAAAGAGTAATAAGGAACCTATCCTCTG
CTCTGCCACTGCCCCAGGGAGACATGGATCTGTGAGGACAGATTTGGCCACGGCTGGTTTCCGTTCAAGGGCAAG
GATCACAGCTGCCCTTGAATCTCATTGCCTCAGAGAAGACTAGAGGGCTCTTGGAATATCCCTAGGGCTACACAA
GAATAGTTCAGCCTTCTGCCATGCCACACAGCCTCAGCTTGAATCTGGTTTATTGCGTCCTCGTGTTCTTCTCTC
ATCCTTGCCCTTAAACCAGGGATTCTGATACCGAAGAAGAGGGGCCAATGAAAACCATGGAGTCTGTTCTGTGACTC
CCAGGGCTGGGACATTATGTAGGAGCCACTTCATAAACATTCTCTTTACTCATCTTTTTATTCTGTTTTTTGTGG
CCTTCTTTTTTGTGTTTCCCCCCCCGAAACAGAGTCTCGCTCTGTACCCAGGCTAGAGTACAGTGGTGCAATCTCG
CCTCACTGCAACCTCCACCTCCCAGGTTCAAGTGATTCTTGTGCCTCAGCCTCCCGAGTAGCTGACATCCGCCAC
CAAGCCCAGCTAATT

2054/6881
FIGURE 1889

MPGANYRAGAGAGAGARRPRGARDREEDGGGLEPAAVARDLLRGTSNMSFEELLELSQVGTKTYKQLVAGNSPK
KQASRPPIQNACVADKHRPLEMSAKIRVPFLRQVVPISKKVARDPRFDDLSGEYNPEVFDKTYQFLNDIRAKEKE
LKKHLSGEEHEKLQQLLQRMEOQEMAQQERKQQQELHLALKQERRAQAQQGHRPYFLKKSEQRQLALAEKFKEK
RSKKLENFLSRKRRRNAGKDRRHLP LSKE

2055/6881
FIGURE 1890

GCTTGGCTGTGTTTATCTCGTTGGGGACTAAGGCGTCGGTTGGCGCGCAACGGGTTCTAGGCTGCAGGCAGCTCG
AGGACCCGCGGCCCCGCCCCGGCTCGGCCTGGCAGATAGCAGAGGCAGCAGGCCGTGCCGGGGGGGCATGTTGCT
GTAACCAGTGGCCCAGGGGATGTTACGGTGGACAGTGCACCTGGAGGGCGGGCCCCGCAGGGTGAACCATGCTGC
AGTGGCTGTGCGGCATCGGGTATACTCCTTCGGGGGTTACTGCTCTGGTGAAGACTATGAGACACTGCGTCAGAT
AGATGTGCACATTTTCAATGCAGTGTCTTTCGTTGGACAAAGCTGCCCCGGTGAAGTCTGCCATCCGTGGGCA
AGCTCCTGTGGTACCCTACATGCGCTATGGACACTCAACCGTCCTCATCGACGACACAGTCCTCCTTTGGGGCGG
GCGGAATGACACCGAAGGGGCCTGCAATGTGCTCTATGCCTTTGACGTCAATACGCACAAGTGGTTCACACCCCG
AGTGTGAGGGACAGTTCCTGGGGCCCGGGATGGACATTACGCCTGTGTCCTAGGCAAGATCATGTACATTTTGG
GGGCTACGAGCAGCAGGCGGACTGTTTTTCCAATGACATTACAAAGCTAGATACCAGCACCATGACATGGACTCT
TATCTGTACAAAGGGCAGCCCTGCACGCTGGAGGGACTTCCACTCAGCCACAATGCTGGGAAGTCACATGTATGT
CTTTGGGGGCCGTGCCGACCGCTTTGGGCCATTCCATTCCAACAATGAGATTTACTGCAACCGCATTTCGAGTCTT
TGACACCAGAACTGAGGCTTGGCTGGACTGTCCCCGACTCCAGTGTGCTGAGGGGGCGCCGGAGCCACTCGGC
CTTTGGCTACAATGGGGAGCTGTACATCTTTGGTGGTTATAATGCAAGGCTGAACCGGCATTCCATGACCTCTG
GAAGTTTAATCCTGTGTCTTTACCTGGAAAAAGATTGAACCGAAGGGGAAGGGGCCATGTCCCCGCCGGCGCCA
GTGCTGCTGTATTGTTGGTGACAAGATTGTCTCTTTGGGGGTACCAGTCCATCTCCTGAGGAAGGCCTGGGAGA
TGAATTTGACCTTATAGATCATTCTGACTTACACATTTTGGACTTTAGCCCTAGTCTGAAGACTCTGTGCAAACT
GGCCGTGATTAGTATAACCTAGACCAGTCTGTTTGCCTCATGATATCAGGTGGGAGCTGAATGCCATGACCAC
CAACAGCAATATCAGTCGCCCCATCGTCTCCTCCCATGGGTAGGAGGAAGTTTCTGCCACCTCCCCTCCTGAGCC
TGCTGTCATCTTCACTGCCCCCTGCCCATCTGTCACCCACCTGCTCCTTTGACCCCTGGACTTGGTATACCTCCAT
GTGGAGTTGTTGGGCGAGAGGTGTTCTCTGTGCTGTGAATTCAGTGGGGAGCTGTAGCGGGGTGGGGGCTAGGTT
CCTCCCCCCTTGGGCCGAGGGCCCCCTTCCCCTTGGTGTCTGTGCTCCCATCCACCTCCTTTCAGCTGCTCCTGGGC
CTCAGCTCTGCCCAGGGCCAGCCAGGTTCTGCTGGGAAGGGAAGGGAATGGGGAGAAGGGAGAAGCAAGCAGTGT
CTGAGCCTCAGGAGCTTCCCCCTCCCCCTTGCCTATCCCCTCCCCTCTGCTTGAGCCTTGAGCCTTGACTGGGA
GCTGAAAGGAGTTGCAGCTGTTGGCATGAGACCTCCTTCTCCCCGTCTTGGGGAGGTGGGGACCAGCAGATAAAT
CCCACCCTTCTTGAGCTGTGCTGTACTCTGAAGTTCAGCCAGCTCAGATTTTATAAAAATTAATTAAAATCTC
CAAA

2056/6881
FIGURE 1891

MLRWTVHLEGGPRRVNHA AVAVGHRVYSFGGYCSGEDYETLRQIDVHIFNAVSLRWTKLPPVKS AIRGQAPVVPY
MRYGHSTVLIDDTVLLWGGRNDTEGACNVLYAFDVNTHKWFTPRVSGTVPGARDGHSACVLGKIMYIFGGYEQQA
DCFSNDIHKLDTSTMTWTLIC TKGSPARWRDFHSATMLGSHMYVFGGRADRF GPFHSNNEIYCNRIRVFDTRTEA
WLD CPPTFVLPEGRRSHSAFGYNGELYIFGGYNARLNRHFHDLWKFN PVSFTWKKIEPKGKGPCPRRRQCCCI VG
DKIVLFGGTSPSP EEG LGDEFDLIDHSDLHILDFSPSLKTLCKLAVIQYNLDQSCLP HDIRWELNAMTTNSNISR
PIVSSHG

2057/6881
FIGURE 1892

CCTTCAATGTGAAGCTAATATCTCCTATAGCATAGTTAATGTTTATTCAACAAATATTCATGCAGCGGAGTCAAG
AACACACCACGATGGCGGAGAAAGGAAGAGACGCCGAGCGGCCGAGTGC GGCCGAGCAAAGCCGGAGCCGGAGCG
GGGCGCGCAGGAGACGGGCCGGGTCCGGACGGGCGGAGATGCCCTATAAACTGAAAAAGGAGAAGGAGCCCCCAA
GGTTGCCAAATGCACAGCCAAGCCTAGCAGCTCGGGCAAGGATGGTGGAGGCGAGAACA CTGAGGAGGCCAGCC
GCAGCCCCAGCCCCAGCCCCAGCCCCAAGCCCAGTCTCAGCCACC GTCATCCAACAAGCGTCCCAGCAATAGCAC
GCCGCCCCCAGCGCAGCTCAGCAAAATCAAGTACTCAGGGGGGCCCCAGATTGTCAAGAAGGAGCGACGGCAAAG
CTCCTCCCGCTTCAACCTCAGCAAGAATCGGGAGCTGCAGAAGCTTCCTGCCCTGAAAGATTCCGCAACCCAGGA
GCGGGAGGAGCTGTTTATCCAGAAGCTACGCCAGTGCTGTGTCCTCTTTGACTTCGTGTCAGACCCACTCAGTGA
CCTCAAATTC AAGGAGGTGAAGCGGGCAGGACTCAACGAGATGGTGGAGTACATCACC CATAGCCGTGATGTTGT
CACTGAGGCCATTTACCCTGAGGCTGTCACCATGTTTTCAGTGAACCTCTTCGGACGCTGCCACCTTCATCGAA
TCCCACAGGGGCTGAGTTTGACCCAGAGGAAGATGAGCCCACCCTGGAAGCTGCTTGCCACATCTCCAGCTCGT
GTATGAGTTCTTCTTACGTTTTCCTTGAGTCTCCTGATTTCCAGCCAAACATAGCCAAGAAGTACATCGACCAGAA
GTTTGTACTTGCTCTCCTAGACCTATTTGACAGTGAGGATCCTCGAGAGCGGGACTTCCTCAAGACCATTTTGCA
TCGCATCTATGGCAAGTTTTTGGGGCTCCGGGCTTATATCCGTAGGCAGATCAACCACATCTTCTACAGGTT CAT
CTACGAGACGGAGCATCACAACGGGATTGCTGAGCTCCTGGAGATCCTGGGCAGCATCATCAATGGCTTTGCTCT
GCCCCTTAAAGAAGAGCACAAAGATGTTCCCTCATCCGTGTCCTACTTCCCCTTCACAAGGTCAAGTCCCTGAGTGT
CTACCACCCCTCAGCTGGCATACTGTGTGGTACAATTCCTGGAGAAGGAGAGCAGTCTGACTGAGCCGGTAATTGT
GGGACTTCTCAAGTTTTTGGCCCAAGACCCACAGCCCCAAGGAGGTGATGTTCTTGAATGAGCTGGAGGAGATTCT
GGACGTCAATTGAACCTTCTGAGTTTCAGCAAAGTGATGGAACCCCTCTTCCGCCAGCTGGCCAAGTGCTGTCTCTAG
CCCCCATTTCCAGGTGGCAGAGCGTGCTCTCTATTACTGGAACAATGAGTACATCATGAGCCTGATAAGTGACAA
TGCTGCCCCGAGTCCTCCCCATCATGTTCCCTGC ACTCTACAGGAACCTCCAAGAGCCACTGGAACAAGACAATCCA
TGGACTGATCTATAATGCCCTGAAGTTGTTTATG GAAATGAATCAGAAGCTGTTTGATGACTGCACACAACAATA
CAAGGCAGAGAAGCAGAAGGGCCGGTTCCGAATGAAGGAAAGGGAAGAGATGTGGCAAAAAATCGAGGAGCTGGC
CCGGCTTAATCCCCAGTATCCCATGTTCCGAGCCCCCTCCACC ACTGCCCCCTGTGTACTCGATGGAGACAGAGAC
CCCCACAGCTGAGGACATCCAGCTTCTGAAGAGGACTGTGGAGACTGAGGCTGTTTCAGATGCTAAAAGACATCAA
GAAGGAGAAAAGTGCTGCTGCGGAGGAAGTCGGAGCTGCCCCAGGACGTGTACACCATCAAGGC ACTGGAGGCGCA
CAAGCGGGCGGAAGAGTTCTTAAGTCCAGCCAGGAGGCTCTCTGACCCCTCACGTTCTTACCACAGGGCCACAG
CCCACACAGCCCTGGGACACTGCCCTGGCCCTCCATACTCTGCTCCCTACTGGCTGTCTTGGGGGAAGGCAGCGC
CTCTCTAGCTACTCAAGGGAGGGGGATGTGGGCACTTGAAGCAGGGACACCCACAGAATGGTCCCTCTTCTCCCC
AAAAGGTGTT CATGCCTCCCTGTGGCTAGTACAGGCTGAGCACTAAGATGCTTAGTGCTCAGACAACCTGGGGAT
GCCTGTCCCCTACCTGCTCCTCACCCACAGCTACCTGAGGCTGCTCTGAGAAGTACACACAGGAATACATACGCT
CCTCTATTCTTCCCTTCATCCTCATTTGAACGCCAGGTATCTCCCCTCCTCTCTCTCCCCTGCAGAGGCATGTAG
GGAACAGCAGGAGATTATTCTCACCAAAGTTATGTCAAGCCCCATTGGTCCCAGAGTAGCTGAAGGGAAGCCAAC
CCCCCTGCAGCACAAATAGGCCCCCCCAGTCCCAGCCGTGTGCTGGCAGATAGGGTTGTATTATTTCTTCTTACCC
CATGCCTGACCAAGGGAGGTCAAAGGAGAGAAAAGTATAGGCTGTGGACAATAACTGATGAATATAGGGCCCAGAT
GGACCAAGTGGGGCCGGGGAGGGATGAATAAACACCCTACCCCGTGCCCTGTCTTTGGTGAGCAGCAGCCCTGGG
GTCACAGACATGGAAGGGACCACCCTGGGGCTGACTGCTTTTCTGTGCTGTTGGTTCCCAAACTAGAAAGAAGG
AAGCAGGGAGCGGTGCCCCAAGCATGGCTCCTGCCAACACCTATTTATTTCTTGTGCTATGCTGGGCAGG
CCTTCTCTTGTCCCTTATAGGTACCTTGGAGGGGGCCAGGGGCTGAGGAAGGCCGACCCAGGTTCAGGGGCGCA
GGCAGTGCGGCTTTTGGCTGTGTACATAGGGTGCTTTATTCTCCACAGAGTGATACATGCTAAGGTGGGTGGGC
TTGGACCGATGTCCC CATATGTACAGAACTGAATAAAGTGGGTCTCTG

2058/6881
FIGURE 1893

MPYKLLKKEKEPPKVAKCTAKPSSSGKDGGGENTEEAQFQFQFQFQFQAQSQPPSSNKRPSNSTPFPPTQLSKIKYS
GGPQIVKKERRQSSSRFNLSKNRELQKLPALKDSPTQEREELFIQKLRQCCVLFDFVSDPLSDLKFKEVKRAGLN
EMVEYITHSRDVVTEAIYPEAVTMFSVNLFRITLPPSSNPTGAEFDPEEDEPTLEAAWPHLQLVYEFFLRFLFLESPD
FQPNIAKKYIDQKFVLALLDLFDSEDPRERDFLKTILHRIYGKFLGLRAYIRRQINHIFYRFIYETEHNGIAEL
LEILGSIINGFALPLKEEHKMFLIRVLLPLHKVKSLSVYHPQLAYCVVQFLEKESSLTEPVIVGLLKFWPKTHSP
KEVMFLNELEEILDVIEPSEFSKVMEPLFRQLAKCVSSPHFQVAERALYYWNNEYIMSLISDNAARVLPIMFPAL
YRNSKSHWNKTIHGLIYNALKLFMEMNQKLFDDCTQQYKAQKQGRFRMKEREEMWQKIEELARLNPQYPMFRAP
PPLPPVYSMETETPTAEDIQLLKRTVETEAVQMLKDIKKEKVLLRRKSELPQDVYTIKALEAHKRAEEFLTASQE
AL

2059/6881
FIGURE 1894

GAATTCCGCCCAGACGCAGGCTTCTTCTCGGGTCTTGGTCCTGCATCCTCTCTCTCCAGAGCCTCCGTTAGGGG
GTGGGAAAGGACTTTGCCATAGGTCGCTGAGGCCACCATCTGCTCTCTTACTGGCCAAGGGCGTAAAAAGATAGT
CTTCCCATTAGCTAGAGAGCAAACCCAGAAAGCCTATTGGTTGCGCCGTCCGCGGGCCTTGGTCCGCTTTGAAG
GCGGGCTGCGGCTGCGAGAGGAGGGCGGGCGGGAGGCTAGCTGTTGTCGTGGTTGCTCGGAGGCACGTGTGCAGT
CCCGGAAGCGGCGAGGGGAAACTGCTCCGCGCGCGCCCGCGGGAGGAGGAACCGCCCGGTCTTTAGGGTCCGGG
CCCGGCCGGGCCATGGATTCAATGCCTGAGCCCGGTCCCGCTGTCTTCTGCTTCTTCCCTTGCTGCTGCTGCTG
CTGCTGCTGCTGCCGGCCCCGAGCTGGGCCCCGAGCCAGGCCGAGCTGAGGAGAACGACTGGGTTCGCCTGCCC
AGCAAATGCGAAGTGTGTAAATATGTTGCTGTGGAGCTGAAGTCAGCCTTTGAGGAAACCGGCAAGACCAAGGAG
GTGATTGGCACGGGCTATGGCATCCTGGACCAGAAGGCCTCTGGAGTCAAATACACCAAGTCGGACTTGCGGTTA
ATCGAAGTCACTGAGACCATTTGCAAGAGGCTCCTGATTATAGCCTGCACAAGGAGAGGACCGGCAGCAATCGAT
TTGCCAAGGGCATGTCAGAGACCTTTGAGACATTACACAACCTGGTACACAAAGGGGTCAAGGTGGTTGATGGACA
TCCCCATATGAGCTGTGGAACGAGACTTCTGCAGAGGTGGCTGACCTCAAGAAXCAGTGTGATGTGCTGGTGGAAG
AGTTTGAGGAGGTGATCGAGGACTGGTACAGGAACCACCAGGAGGAAGACCTGACTGAATTC

2060/6881
FIGURE 1895

MDSMPEPASRCLLLLPLLLLLLLLLLPAPELGPSQAGAEENDWVRLPSKCEVCKYVAVELKSAFEETGKTKEVIGT
GYGILDQKASGVKYTKSDLRLIEVTETICKRLLIIACTRRGPAAIDLPRACQRPLRHYYTTWYTKGSRW

2061/6881
FIGURE 1896

TGATGAAACTGTAACTTACAAGAAAAGGGCTGGGTTTTGAAAATAACACAGGCTCTAAAAACCCTAAGAAGCGGT
GCAACTTTTGGCAGGAATCGGGGTTAGCGGGACCTCAAGGGCTCACTGCGGCTAAGTGAACGCTGACTGGTCCTC
CAGCGTGAGCTAGAACAGACGTCTCTATGGTCAAGTAAACAGAGCGTGTGCTGTCTTCCCCATGTGGTGGGGTTG
CGCATGATCAGTAGCTGCACCCTAGAAAGATGGCGGAGCAAGAGCAAAGAAAAATCCCTTTGGTTCCAGAAAAAT
CTCCTGAAAAAGAGGAAGGCTTATCAAGCCCTCAAAGCCACCCAGGCAAAGCAGGCACCTTTTGGCAAAGAAGGAG
CAGAAGAAAGGAAAAGGGCTCAGGTTTAAGCGACTGGAATCATTCTACATGATTCTTGGCGGCAGAAACGTGAC
AAGGTGCGTCTCAGACGACTAGAAGTGAACCTCATGCCTTGGAATTGCCAGATAAACATTCTTGGCCTTTGTT
GTACGCATCGAAAGGATTGACGGCGTGAGTTTACTGGTGCAGAGAACCATTGCAAGACTTCGCCTAAAGAAAAAT
TTTAGTGGTGTCTTTGTAAAAGTCACCCCCCAGAATCTAAAAATGCTGCGTATAGTGGAACCTTATGTGACCTGG
GGATTTCCAAATCTGAAGTCTGTCCGAGAACTCATTTTGAAACGTGGACAAGCCAAGGTCAAGAATAAGACCATC
CCTCTGACAGACAATACAGTGATTGAGGAGCACCTGGGGAAGTTTGGCGTCATTTGCTTGGAAGACCTCATTCTAT
GAAATTGCCTTCCCAGGGAAGCATTTCAGGAGATCTCATGGTTCTTGTGCCCTTTCCACCTCTCAGTGGCCCGT
CATGCTACCAAAAATAGAGTGGGCTTCCTCAAGGAGATGGGCACACCTGGCTATCGGGGTGAACGCATCAATCAG
CTCATCCGTCAGCTGAACTAGACCCAAGGTGCCAAACTGCGGTAAATTTTTTATCAGTGAAGTGGAAGCATGTGTT
TTGTTTTTGAAATTTTTATCAAGTATCTTCAGAGAAGATTATTTCTGCTTTATCTTCAGAACTGGAAAGGGTC
AAAGAAAAGACAGTAGCTGGCCGGTTCGTGGTGGCTCATGCCTGTAATCCCAACACTTAGGGAGGCTGAGGTGGGC
AGATCACCTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACATGGAGAAATGCCATCTCTACTAAAAATACAAAA
ATTAGCCGGGCATGGTGGCACGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATCGCTTGAACCT
GGGAGGTGGAAGTTGCAGTGAGCTGAGATCACGCCATTGCACTCCAGCCTGGGCAACAAGCGAAACTCTGTCTCA
AAAAAAAAGAAAAGACAGTAGCATATGTTTCATGTCAAGCACCTCTCATCACAGTCGAGTTCCAAGGAAAAATTCC
AGTGTTTTCTGCATTGGGTGCTGTGTCTATCTGAAATCGGCACATTCCATGGAGGAAGGAGTCCTGCTTTGTTGCA
TGTATCCTAGGGTTTAATGTTGGTAAATGAGTCACTCTAGCATTTGTAGAAGGCTCCCTGAGACTCCTGCAGCAG
TCGACCAAGCCCAAGGACATAAATTGAATCTGGAGAGTCCTGGGGCCTTGTTTTGAAAAAGACTTGAAATACACAT
AGGAAGAAAGGCATAAAAAATAAATGTTCACTTGTCTCTGC

2062/6881
FIGURE 1897

MISSCTTRKMAEQEQRKIPLVPENLLKKRKAYQALKATQAKQALLAKKEQKKGKGLRFKRLESFLHDSWRQKRDK
VRLRRLEVKPHALELPDKHSLAFVVRIERIDGVSLLVQRTIARLRLKKIFSGVFVKVTPQNLKMLRIVEPYVTWG
FPNLKSVRELILKRGQAKVKNKTIPLTDNTVIEEHLGKFGVICLEDLIHEIAFPKGKHFQEISWFLCPFHLSVARH
ATKNRVGFLKEMGTPGYRGERINQLIRQLN

2063/6881
FIGURE 1898

GCGCCTGTCAGGGAAGCGGCGCGCGCGCGGGCGGGCGGGCTGGGGATCCGCCGCGCAGTGCCAGCGCCAG
CGCCAGACCCGCGCCCCGCGCTCTCCGGCCCGTCGCCTGCCCTTGGGACTCGCGAGCCCGCACTCCCGCCCTGCCT
GTTGCTGCCCCAGTATGGAGCTGCTGTGTTGCGAAGGCACCCGGCACGCGCCCCGGGCCGGGCCGACCCGCGG
CTGCTGGGGGACCAGCGTGTCTGTCAGAGCCTGCTCCGCCTGGAGGAGCGCTACGTACCCCGCGCCTCCTACTTC
CAGTGCGTGTCAGCGGGAGATCAAGCCGCACATGCGGAAGATGCTGGCTTACTGGATGCTGGAGGTATGTGAGGAG
CAGCGCTGTGAGGAGGAAGTCTTCCCCCTGGCCATGAACTACCTGGATCGCTACCTGTCTTGCGTCCCCACCCGA
AAGGCGCAGTTGCAGCTCCTGGGTGCGGTCTGCATGCTGCTGGCCTCCAAGCTGCGCGAGACCACGCCCCTGACC
ATCGAAAACTGTGCATCTACACCGACCACGCTGTCTCTCCCGCCAGTTGCGGGACTGGGAGGTGCTGGTCCTA
GGGAAGCTCAAGTGGGACCTGGCTGCTGTGATTGCACATGATTTCTGGCCTTCATTCTGCACCGGCTCTCTCTG
CCCCGTGACCGACAGGCCTTGGTCAAAAAGCATGCCAGACCTTTTTGGCCCTCTGTGCTACAGATTATACCTTT
GCCATGTACCCGCCATCCATGATCGCCACGGGCAGCATTTGGGGCTGCAGTGCAAGGCCTGGGTGCCTGCTCCATG
TCCGGGGATGAGCTCACAGAGCTGCTGGCAGGGATCACTGGCACTGAAGTGGACTGCCTGCGGGCCTGTCAGGAG
CAGATCGAAGCTGCACTCAGGGAGAGCCTCAGGGAAGCCTCTCAGACCAGCTCCAGCCCAGCGCCCAAAGCCCC
CGGGGCTCCAGCAGCCAAGGGCCCAGCCAGACCAGCACTCTACAGATGTCACAGCCATACACCTGTAGCCCTGG
AGAGGCCCTCTGGAGTGGCCACTAAGCAGAGGAGGGGCCGCTGCCACCCACCTCCCTGCCTCCAGGAACACACC
ACATCTAAGCCTGAAGGGGCGTCTGTTCCTCTTCAAAAGCCCAAGGGATCTGGTCCCTACCCATCCCCGCAGTG
TGCACTAAGGGGCCCCGCCAGCCATGTCTGCATTTTCGGTGGCTAGTCAAGCTCCTCCTCCCTGCATCTGACCAGC
AGCGCCTTTCCCAACTCTAGCTGGGGGTGGGCCAGGCTGATGGGACAGAATTGGATACATACACCAGCATTCTTT
TTGAACGCCCCCCCCACCCCTGGGGGCTCTCATGTTTTCAACTGCCAAAATGCTCTAGTGCCTTCTAAAGGTGT
TGTCCCTTCTAGGGTTATTGCATTTGGATTGGGGTCCCTCTAAAATTTAATGCATGATAGACACATATGAGGGGG
AATAGTCTAGATGGCTCCTCTCAGTACTTTGGAGGCCCTATGTAGTCCGTGCTGACAGCTGCTCCTAGAGGGAG
GGGCCTAGGCCTCAGCCAGAGAAGCTATAAATTCCTCTTTGCTTTGCTTTCTGCTCAGCTTCTCCTGTGTGATTG
ACAGCTTTGCTGCTGAAGGCTCATTTTAATTTATTAATTGCTTTGAGCACAACTTTAAGAGGACATAATGGGGGC
CTGGCCATCCCAAGTGGTGGTAACCCCTGGTGGTTGCTGTTTTCTCCTCCTTCTGCTACTGGCAAAGGATCTTT
GTGGCCAAGGAGCTGCTATAGCCTGGGGTGGGGTCATGCCCTCCTCTCCCATTTGTCCCTCTGCCCCATCCTCCAG
CAGGGAAAATGCAGCAGGGATGCCCTGGAGGTGGCTGAGCCCTGTCTAGAGAGGGAGGCAAGCCCTGTTGACAC
AGGTCTTTCTAAGGCTGCAAGGTTTAGGCTGGTGGCCCAGGACCATCATCCTACTGTAATAAAGATGATTGTGA
AATAAACTGGCTTTGGCTTCTTGGAATAA

2064/6881
FIGURE 1899

MELLCCEGTRHAPRAGPDPRL LGDQRVLQSLRLLEERYVPRASYFQCVQREIKPHMRKMLAYWMLEVCEEQRCEE
EVFPLAMNYLD RYLSCVPTRKAQLQLLGAVCM LLASKLRETTPLTIEKLCIYTDHAVSPRQLRDWEVLVLGKLKW
DLAAVIAHD FLAFILHRLSLPRDRQALVKKHAQTFLALCATDYTFAMYPPSMIATGSIGAAVQGLGACSMGDEL
TELLAGITGTEVDCLRACQEQIEAALRESLREASQTSSSPAPKAPRGSSSQGPSQTSTPTDVTAIHL

2065/6881
FIGURE 1900

CACCGCGCAAGCGCATCCTGGCCTTTCTTCAGTCCCCACGTGCGATCCTTCCCGGCAACTTTTTTCGAGAAAAATG
CCCAAATTCAAGGCGGCCCGTGGGGTGGGGGTGAGGAAAAACATGCGCCCTGGCCGATCAGATCCTGGCTGGG
AATGCGGTGCGGGCGGGGTCCGGGAGAAGCGGCGGGGTGCGGGGACAGGAGAAGCGGAGGAAGAGTATGTGGG
CCCCGGCTGAGCCGACGGATTTTGCAGCAAGCACGGCAGCAACAGGAGGAACTCGAGGCCGAGCATGGGACTGGG
GACAAGCCCGCGGCGCCGCGGGAACGCACCACGCGGTGGGTCCAAGAATGCCTCAGGATGGATCAGATGACGAG
GACGAGGAGTGGCCACCCTGGAGAAGGCTGCCACAATGACAGCAGCGGGCCATCATGCAGAGGTGGTTGTGGAC
CCTGAGGATGAGCGTGCCATAGAGATGTTCAATGAACAAGAACCCTCCTGCCAGGCGCACCTGGCTGACATCATC
ATGGAGAAGCTGACTGAGAAGCAGACAGAGGTTGAGACAGTCATGTCAGAGGTGTCGGGCTTCCCTATGCCCCAG
CTGGACCCCCGGGTCTAGAAAGTGTACAGGGGGTCCGGGAGGTATTATCTAAGTACCGCAGTGAAAACTGCCC
AAGGCATTTAAGATCATCCCTGCACTCTCCAACCTGGGAGCAAATCCTCTACGTCACAGAGCCGGAGGCCTGGACT
GCAGCTGCCATGTACCAGGCCACCAGGATTTTGCCTCTAACCTGAAGGAACGCATGGCCAGCGCTTCTACAAC
CTTGTCCTGCTCCCTCGAGTACGAGATGACGTTGCTGAATACAAACGACTCAACTTCCATCTCTACATGGCTCTC
AAGAAGGCCCTTTTCAAACCTGGAGCCTGGTTCAAAGGGATCCTGATTCCACTGTGCGAGTCTGGCACTTGTACC
CTCCGGGAAGCCATCATTGTGGGTAGCATCATCACCAGTGCTCCATCCCTGTGTTGCACTCCAGTGCGGCCATG
CTGAAAATTGCTGAGATGGAATACAGCGGTGCCAACAGCATCTTCCTGCGACTGCTGCTGGATAAGAAGTATGCA
CTGCCTTACCGGGTGCTGGATGCCCTAGTCTTCCACTTCCTGGGGTTCCGGACAGAGAAGCGTGAAGTGCCTGTG
CTGTGGCACCAGTGCTCCTGACTTTGGTCCAGCGCTACAAGGCCGACTTGGCCACAGACCAGAAAGAGGCCCTC
TTAGAACTGCTCCGGCTGCAGCCCCATCCACAGCTATCGCCGAAATCAGGCGTGAGCTTCAGAGTGCAGTCCCC
CGCGATGTGGAAGATGTTCCCATCACCGTGGAGTGAGGAAAACAGTCAGCTGTCTGGCCAAAGGGTTTGAAG
GACACCAAGACCCCCGTTGGTGACTGAAGATGACACTGAGCTTTAATGGCTGAAGACCCAGATCAGGGCAGTGAC
AGATCACAGGGACATCTGTGGCTCCCAGTCCAGGACAGGAAGGACTGAGGGTCTGGCTGGTTCCCTCTTCCATTC
TAGGCCCTTATCCCTGTTTAGTTCTGAGAGCCAACTTGAGATACCATATGCTAGCATTCCCAGTCCCCAGCTGGG
GCTTGGTGTGAGTACTTTTTCTATGGCTATTGTGTGAGGTCACTGTGGATAAAGGCAAAGACAGATATTTATTGA
AAAAAAAAAAAAAAAAAAAAAAAAA

2066/6881
FIGURE 1901

MNKNPPARRTLADIIMEKLTEKQTEVETVMSEVSGFPMPQLDPRVLEVYRGVREVL SKYRSGKLPKAFKIIPALS
NWEQILYVTEPEAWTAAAMYQATRIFASNLKERMAQRFYNLVLLPRVRDDVAEYKRLNFHLYMALKKALFKPGAW
FKGILIPLCESGTCTLREAIIVGSIITKCSIPVLHSSAAMLKIAEMEYSGANSIFLRLLLDKKYALPYRVLDALV
FHFLGFRTEKRELPVLWHQCLLTLVQRYKADLATDQKEALLELLRLQPHPQLSPEIRRELQSAVPRDVEDVPITV
E

2067/6881
FIGURE 1902

CTTGGGGTGGGGGACGGGGTGAGGGGCCCTGACGGCAGAGTTCGGTCCAGAAGTGCCTGGGACGACGACGCACACGACGAG
GAGCCAAAATGGAAGAGGGGTGCAAGTCCCCTCCTGGGGCCCCAGACGCCCCCTCCTTTCTTGCTGCCTGGAGCAG
GGGCAGTGTCTGTTAGTGGCTACTCCTGGTGTGAACAGCCCATCCTGGCCACCTTCCACAGGAAACCTGACCTGAA
GGACAGAAGAGGAAGGAAGCAGGCTTTTGCCACAAATGTCACTGTCAGTGCAGAACTCTGGCTGGCCCCACCAAGAAGACAG
CCCCAAGCCCCAGGATCCAGGTCCACCAGCCAACTCAGACAGTGAAGTCTGAGGCCACCTGCCGGGGGAGGACCCTGA
GGATACCCATGTCTCAGGAATTCCTGTCTCTGCACCTGCTTAGAACATGGGGTTTTGACTTTAAACTCATTACAT
GAGTATTCAATTATCTCTCCTAGGGGGTCTGTATTGTCAAACCAGACTCTAGGGGCTTTGGCCCCAAGGCGTGAAG
GGGGTTAAGAAGGGAAAGCATAAGAAGGGAAGCTGTTTTGGGGTGTGGGGCCTCCCCAGCCTCCCTCAAGGAAGA
CCACACATGCAGGCATCAGTCAGCTATCCTTGCACCTCAGTGAGGATCTGCAAGGAGGACCCTCCCAAATGGAGGG
CATGCTTAGAAGCTGCTCTAGATTGGAGAAGAGGTGGCAATGATGAGGGGGAAAGAAGGAGAAAGGAAAGAAAAA
CCTAGTTTTACTCCTCCCCTTCTTCCATGTCTCCTCAGGGTCTGCACTTCTGAGCTTGGGTTCCCTTTGCCTGG
ACACCAACCAAGCCCCCAACTGGACTGGACTTCAGACCCTCCTGCAGCAACTCCCTCCGACAGGACATTGATGAGC
GCTACTGCCTGGCCCTTGGGGAGGAGGAGCGGGCCGAGCTGCAGCTCTTCTGTGCCAGGCGGAAGCAGGAAGCCC
TGGGACAGGGGGTAGCCCGCTGGTACTTCCCAAGCTTGAAGGACACACCTGTGAGAAGTGTAGGGAGTTGCTGA
AGCCAGGGGAGTACGGAGTGTGTTGCAGCCCGGGCAGGGGAACAGCGCTGCTGGCACCAGCCTTGCTTTGCCTGCC
AGGCTGTGGCCAGGCCCTGATAAACCTCATCTACTTCTACCATGATGGACAACCTCTACTGCGGCCGTCTCATG
CAGAGTTGCTGCGCCCGCTGCCCCGGCTTGTGACCAGCTGATCTTCTCCTGGCGCTGCACCAGGCGGAGGGAC
AGCGCTGGCATGAGAACCACCTTCTGTTGCCAGGACTGCGCCGGGCCCTCTGGGCGGGGGACGTTATGCCCTGCCCTG
GGGGAAGCCCCCTGCTGCCCCAGCTGCTTTCGAGAACCGCTACTCGGATGCAGGCTCGAGCTGGGCCGGGGCACTGG
AAGGGCAGGCATTCTTGGAGCGCCCCACCGCACCCCCCAGACCCAAGCCTCGGGGCCCGCAGCTCTCACCGCG
CATCCCTGGCCGGAGCGTTCCAAGGGCCGCCCGAACCCACCCCGCGCGCGGTTCGGGTTGCGGCGCCAGACTCC
CTCCCAGGCGCGGGAGGCGGACGCCCTCTGGTGGAGGCGGGGGACCTGGCGAGGACTCTCGGCGGCGGCGGCGG
CGCGCACGGCCCAGGGGCTGGGCGGGGCGGGAGGCTGGGCCTACCCCCACTAGCTGCGGTGTAGGTCCAGCTCC
GCGGCTCTGAGACCAGCGTTTCCGACCCGGCCCCGGAACAGGGGAGACTGGACTCGACCGAACTGAAGGAAGGGAC
CAAACCTCGGTGAACCTCTGCAACCTCTCCCCGAACACTCCTTGCTGCTGCCGGCGGTTCCAGCCTGCAAACTCAG
AGGGGGCTGCCTGGATCCAGTCCCCAGCAGGAGAACCGACCTGGGGACAAAGCGGAGGCACCCAAAGGGCAGGAG
CAATGCCGCCTGGAGACTATTCTGTATCCCAAGGACACCCCTTCTCCACCTGCTCCTCCTCTGACTCGGAA
CCTGAAGGATTTTTCTTAGGCGAGCGCTTCCCCAGTCTTGAAGACCCCCGGAAGCCTCCAAGCAGAGGACAGC
AACGCCTCTAAGACGCACTGCACCATGTGCTAGTGGCGCAGCTCAGAGAGGGGATGTGAGTGGGAGGAAAGGGGT
CTGTAAAGCGGGAGAACAAGGCTAGCCTCCCCCTAACAATCCTAGACTGAGACGCAGTCAGGCGCACGCCCCGAA
GAGGCGGCGAGGTGACAAGTTTGAGTGTGCGCCCCCTTCACTACTGCGGTTCTAAGACTTTTGGCGGAGACTTCT
TTGGCAAAACCCATTCCCCAAAGCTACGCTTCCCCTGCTGAGATAGCCCCCTACCCCCACCTCCACAGGCTGGGAC
AGCCCCGTCCCCACCATCCTCCTCCCAAGCCAATTAAATGATCACAGCACGCGTGACAGTTACCGGCTGGAGAGC
CGGAGGTGGGACCGGGAGCAGGGGACCGTAGAACCGGGCCGCGCTCCTCCCCTCCTAGAGTTCTGTGGAGGCGCAG
CAGAGGGCCGTCCCTCTTCCGGATGTGCGACTAAGCGAACAGCGCCCCCACTGCCGGCCGGTAGCAGCCGGAAGT
GCCAGACCGGAGGTGCGTCATTACCGGCGACGCCGATACGGTTCTCCAGCGAGGCCCATGCGAAGCTTTCCAC
TATGGCTTCCAGCACTGTCCCGGTGAGCGCTGCTGGCTCGGCTAATGAAACTCCCGAAATACCGGACAACGTGGG
AGATTGGCTTCGGGGCGTCTACCGCTTTGCCACTGATAGGAATGACTTCCGGAGGAACCTTGATACTAAATTTGGG
ACTCTTTGCTGCGGGAGTTTGGCTGGCCAGGAACCTTGAGTGACATTGACCTCATGGCACCTCAGCCAGGGGTGTA
GCCAAGTAGTTCTAATGCCACCTGTGCTTATCATCTGATTGCAGACAAATGGAATCCTGTGCTGAACCCGAAT
CTTCCAAAAAACAGCCTACAATCTGTGACCACCACAAGATGTGCCCTGATGGCAGCTGAAGTTTGATTGAGATGG
GCACTTTTCTTCCCCTTCCCTGCCTAGTTTCTTTTGTTCCTTGAGTCCACGCAGAATTCCATTCTCTGCTCAG
AGACAGGCTTAAGCTAAAGTATTGCCTCTATTCTGTAAAGTTCTGTACATAGTTCCCAAGCTTCTGCAGGGGGTG
ATTTTTGCTCTTGTCTGAGAAATAACAGTGCTGTTTTTAAAAAACATTTGAAATAAATACCGCACACAAAGGAAA
AAAAAAAAAAAAAAAAA

2068/6881
FIGURE 1903

MSPQGPAVLSLGSCLDTNQAPNWTGLQTLLOQLPQQDIDERYCLALGEEERAELQLFCARRKQEALGQGVARLV
LPKLEGHTCEKCRELLKPGEYGVFAARAGEQRCWHQPCFACQACGQALINLIYFYHDGQLYCGRHHAELLRPRCP
ACDQLIFSWRCTEAEQQRWHENHFCCQDCAGPLGGGRYALPGGSPCCPSCFENRYSDAGSSWAGALEGQAFLGAP
PPHPPDFSLGARSSHRASLAGAFQGPPEPTPRRGRGCGARLPRRGRRTPSGGGGGPWRGLSAAAAARTAQGLGG
AGGWASPPPLAAV

2069/6881
FIGURE 1904

CTAGTTAAGGCGGCACAGGGCCGAGGCGTAGTGTGGGTGACTCCTCCGTTCCCTTGGGTCCCGTCGTCTGTGATAC
TGCAGTTCAGCCATGGCAGAACCGCAGCCCCCGTCCGGCGGCCTCACGGACGAGGCCGCCCTCAGTTGCTGCTCC
GACGCGGACCCAGTACCAAGGATTTTCTATTGCAGCAGACCATGCTACGAGTGAAGGATCCTAAGAAGTCACTG
GATTTTTATACTAGAGTTCTTGGAATGACGCTAATCCAAAAATGTGATTTTCCATTATGAAGTTTTCACTCTAC
TTCTTGGCTTATGAGGATAAAAATGACATCCCTAAAGAAAAAGATGAAAAAATAGCCTGGGCGCTCTCCAGAAAA
GCTACACTTGAGCTGACACACAATTGGGGCACTGAAGATGATGCGACCCAGAGTTACCACAATGGCAATTCAGAC
CCTCGAGGATTCGGTCATATTGGAATTGCTGTTCCCTGATGTATACAGTGCTTGTAAGGTTTGAAGAAGTGGGA
GTCAAATTTGTGAAGAAACCTGATGATGGTAAAATGAAAGGCCTGGCATTATTCAAGATCCTGATGGCTACTGG
ATTGAAATTTGAATCCTAACAAAATGGCAACCTTAATGTAGTGCTGTGAGAATTCTCCTTTGAGATTTCAGAAG
AAAGGAAACAATGTGATTCAAGATATTTACATACCAGAAGCATCTAGGACTGATGGATCACTGTCCCGATTCAA
TTATTCTTCAGTCCATTTCCCTTCCCTATTTCAGCTGTTCCTTTTACCTAACTGTTTCAGTCATTCTGGTTTTCA
AGCAGTGCTTTATCTCATGTCTTGAATATAGTTGTGTAACCTTTATTTTTTAGGTAATAATTAGAAGAGTTCCCT
TCAGAGGCTGCATTTGCCTTCTTCTGCCACCTAAATATTACTTCCCTTCAAATCTGCCTTTGAATCATCATTTTT
AAAAAAAAAATTAACATGTTTTTGTGTAGTTATCTTCTGGGGTTTCAATTCCTCAGAAACAACTTTTTTCACAAC
GGAAAGGAAAGAACACTAGTGTTCTTTCAGTAAAGTACAAAGTGTTTATTTTACAAAAGAGTAGGTACTCTTGAG
AGCAATTCAAATCATGCTGACAAGGATACTGATAGAAAAAGTGATTTCTTCTTATTATAAAGTACATTTAAAGTT
CAAGGACTAACCTTATTTATTTGGGAAAGGGGAGGAGGAAGGAAATGATATGGTACCCAGACACTGGGCTAGGCT
GCAACTTTATCTCATTTAATACTCCCAGCTGTGATGTGAGAAAGAAAGCAGGCTAGGCATGTGAAATCACTTTCA
TGGATTATTAATGGATTTAAGAGGGCATCAATCAGCTCAACTCAAGATTTTCATAATCATTTTTTAGTATTTAGATT
GTGCCTCAAAGTTGTAGTACCTCACAATACCTCCACTGGTTTTCTGTTGTAAAAACCTTCAGTGAGTTTGACCAT
TGTGCTCTTGGCTCTTGGGCTGGAGTACCGTGGTGAGGGAGTAAACACTAGAAGTCTTTAGTACAAAACCTGCTCT
AGGGACACCTGGTGATTCCTACACAAGTGATGTTTATATTTCTCATAAAGAGTCTTCCCTATCCCAAGGTCTTCA
TGATGCCAGTAGCCATATATGATAAATTATGTTTCAGTGATAACTTAGTTATCAGAAATCAGCTCAGTGGTCTTCC
CCGCCATGATTCACATTTGATGAGTTTTTAAAAATCAAAGTGATTTTGAAAATCTCTAATGGCTCAGAAAATAAA
AACATCCAGTTTGTGGATGACTATATTTAGATTTCTCTAGACTCTAGTGGAAGACCTTTGGAAAGGCCATGCCAA
CCGTGCTTGTACTGCTAGAAGCACTTTATGTTTCCTTTTTGGGTGAAATGGATTTATGTGAGTGCTTTAAACAAA
TAGCAATACTTATAGACTGAAATAAAATGAAACTTCAAATAAG

2070/6881
FIGURE 1905

MAEPQPPSGGLTDEAALSCCSDADPSTKDFLLQQTMLRVKDEPKKSLDFYTRVLGMTLIQKCDFFIMKFSLYFLAY
EDKNDIPKEKDEKIAWALSRKATLELTHNWGTEDDATQSYHNGNSDPRGFGHIGIAVPDVYSACKRFEELGVKFV
KKPDDGKMKGLAFIQDPDGYWIEILNPNKMATLM

2071/6881
FIGURE 1906

ATGGGAGCTTCGGACCCGGAAGTGGCGCCCTGGGCTCGCGGCGGTGCCGCGGGGATGGCGGGAGCCGGAGCTGGA
GCCGGAGCTCGCGGCGGAGCGGCGGGGGTTCGAGGCTCGAGCTCGCGATCCACCGCCCGCGCACCGCGCACAT
CCTCGCCACCCTCGGCCTGCGGCTCAGCCCTCGGCGCGGCGTACGGCGCTCAGCCATCCCCTGCTC
GACAACGCCCCGACCACTGAGGCTCTTTTCGTGGCACTGGGCGCGGGCGTGACGGCGCTCAGCCATCCCCTGCTC
TACGTGAAGCTGCTCATCCAGGTGGGTTCATGAGCCGATGCCCCCACCCTTGGGACCAATGTGCTGGGGAGGAAG
GTCCTCTATCTGCCGAGCTTCTTACCTACGCCAAGTACATCGTGCAAGTGGATGGTAAGATAGGGCTGTTCCGA
GGCCTGAGTCCCCGGCTGATGTCCAACGCCCTCTCTACTGTGACTCGGGGTAGCATGAAGAAGGTTTTCCCTCCA
GATGAGATTGAGCAGGTTTTCCAACAAGGATGATATGAAGACTTCCCTGAAGAAAGTTGTGAAGGAGACCTCCTAC
GAGATGATGATGCAGTGTGTGTCCCGCATGTTGGCCCCACCCCTGCATGTCATCTCAATGCGCTGCATGGTCCAG
TTTGTGGGACGGGAGGCCAAGTACAGTGGTGTGCTGAGCTCCATTGGGAAGATTTTCAAAGAGGAAGGGCTGCTG
GGATTCTTCGTTGGATTAATCCCTCACCTCCTGGGCGATGTGGTTTTCTTGTGGGGCTGTAACCTGCTGGCCCAC
TTCATCAATGCCTACCTGGTGGATGACAGCTTCAGCCAGGCCCTGGCCATCCGGAGCTATACCAAGTTCGTGATG
GGGATTGCAGTGAGCATGCTGACCTACCCCTTCCCTGCTAGTTGGCGACCTCATGGCTGTGAACAACTGCGGGCTG
CAAGCTGGGCTCCCCCTTACTCCCCAGTGTTCAAATCCTGGATTCACTGCTGGAAGTACCTGAGTGTGCAGGGC
CAGCTCTTCCGAGGCTCCAGCCTGCTTTTCCGCCGGGTGTCATCAGGATCATGCTTTGCCCTGGAGTAACTGAA
TCATCTAAAAAACACGGTCTCAACCTGGCCACCGTGGGTGAGGCCTGACCACCTTGGGACACCTGCAAGACGACT
CCAACCCAACAACAACCAGATGTGCTCCAGCCCAGCCGGGCTTCAGTTCATATTTGCCATGTGTCTGTCCAGAT
GTGGGGTTGAGCGGGGGTGGGGCTGCACCCAGTGGATTGGGTACCCGGCAGACCTAGGGAAGGTGAGGCGAGGT
GGGGAGTTGGCAGAATCCCCATACCTCGCAGATTTGCTGAGTCTGTCTTGTGCAGAGGGCCAGAGAATGGCTTAT
GGGGGCCCAGGTTGGATGGGGAAAGGCTAATGGGGTCAGACCCACCCCGTCTACCCCTCCAGTCAGCCCAGCGC
CCATCCTGCAGCTCAGCTGGGAGCATATTCTCCTGCTTTGTACATAGGGTGTGGTCCCCTGGCACGTGGCCACC
ATCATGTCTAGGCCTATGCTAGGAGGCAAATGGCCCAGCTCTGCCTGTGTTTTTCTCAACACTACTTTTCTGATA
TGAGGGCAGCACCTGCCTCTGAATGGGAAATCATGCAACTACTCAGAATGTGTCCTCCTCATCTAATGCTCATCT
GTTTAATGGTGTATGCCTCGCGTACAGGATCTGGTTACCTGTGCAGTTGTGAATACCCAGAGGTTGGGCAGATCAG
TGTCTCTAGTCCTACCCAGTTTTAAAGTTCATGGTAAGATTTGACCTCATCTCCCGCAAATAAATGTATTGGTGA
TTTGGA

2072/6881
FIGURE 1907

MGASDPEVAPWARGGAAGMAGAGAGAGARGGAAAGVEARARDPPPAHRAHPRHPRPAAQPSARRMDGGSGLGSG
DNAPTTEALFVALGAGVTALSHPLLYVKLLIQVGHEPMPTLTGTNVLGRKVLVLPSTFTYAKYIVQVDGKIGLFR
GLSPRLMSNALSTVTRGSMKKVFPPDEIEQVSNKDDMKTSLKVVKETS YEEMMQCVSRMLAHPLHVISMRCMVQ
FVGREAKYSGVLSSIGKIFKEEGLLGFFVGLIPHLLGDVVFLWGCNLLAHFINAYLVDDSFSSQALAIRSYTKFVM
GIAVSMLTYPFLLVGDLMAVNNCGLQAGLPPYSPVFKSWIHCWKYLSVQGQLFRGSSLLFRRVSSGSCFALE

2073/6881
FIGURE 1908

TGTTCTTGAGCCCAGCTTCTTCTCGTCTCCCACCCCAGCTTCCCGGCATTGGAAGAAGGGACCGTCCTCTTCCTT
GTCTTGGCCACCCAAATCCTGGTATCGAAAGGGTTGAACGGACCGGAAGTGTGCAGCAGCGACGGGTCCCCAGCT
AATCGACGCCGGAAGTAGCAATTACTAGACAAGCATTCCGCCGCCGGCTTCGCTATGGCGGCAATTCCCCCAGAT
TCCTGGCAGCCACCCAACGTTTACTTGGAGACCAGCATGGGAATCATTGTGCTGGAGCTGTACTGGAAGCATGCT
CCAAAGACCTGTAAGAACTTTGCTGAGTTGGCTCGTCGAGGTTACTACAATGGCACAAAATTCCACAGAATTATC
AAAGACTTCATGATCCAAGGAGGTGACCCAACAGGGACAGGTCGAGGTGGTGCATCTATCTATGGCAAAACAGTTT
GAAGATGAACTTCATCCAGACTTGAAATTCACGGGGGCTGGAATTCTCGCAATGGCCAATGCGGGGCCAGATACC
AATGGCAGCCAGTTCTTTGTGACCCTCGCCCCCACCCAGTGGCTTGACGGCAAACACACCATTTTTTGGCCGAGTG
TGTCAGGGCATAGGAATGGTGAATCGCGTGGGAATGGTAGAAAACAACTCCCAGGACCGCCCTGTGGACGACGTG
AAGATCATTAAGGCATACCCTTCTGGGTAGACTTGCTACCCCTCTTGAGGCAGCTCTTCTGAGATGGCCCCAGTGAA
CCAGCTTCTAGATGACATAGAATGACATGTAATGCTAAATTTTCAATTTTGGCTTTTGCAAGTCATGAAGCTTAGGAG
GCCTGGCATCTTGGGTGAGTTAGAGATGGAAGTACATTTTAATAGGATGCTTCTTTTCTCTTCCCCCAGTGCCTA
GGTTGCCAGAGCATTTCACAAAATGCCCTGTTTATCAATAGGTGACTACTTACTACACATGAACCATAATGCTG
CTTCTTGTGCATGTCTGCTCTGATATACGTCGAACAATGTAGCAGCCACTGTCATTTCTCAGTGGTTTTGCCTAA
CCAACTTCTTCCCTAAGGAGATTTATATTCTGGCCTACACAGCAGTCCTTGATGGCTGACAGCCACAGAATTCCA
AACCAAGTAGTGCTGTCTCAGCCCTCTTAAGTCTGTGCACGCCCTATTTTCACTTTTACATTTGTTCTTCTAGGG
AATGTATGCATCTCTATATATATTTTTCCCTCTCAAAACCAGAACATCAACAGTGCTGTTTCTGACACTTCAGACA
TCCCACGCAAAGCCACATTGAATTTTTGCCAAATGAAAAACACATCCAACAATCAAGTTTCTAAGAAGGTGTCAA
GTGGGGAATAATAATAATGTATAATAATCAAGAAATTAGTTTATTAAAAGGAAGCAGAAGCATTGACCATTTTTT
CCCAGAGAAGAGGAGAAATCTGTAGTGAGCAAAGGACAGACCATGAATCCTCCTTGAGAAGTAGTACTCTCAGAA
AGGAGAAGCGCCACTCAAGTTCTTTTAACCCAAGACTTTAGAGAAATTAGGTCCAAGATTTTTATATGTTTCAAGTT
GTTTATGTATAAAAAATACTTTCTGGATTTTGTGGGGAGGAGCAGGAGAGGAAGGAAGTTAATACCTATGTAATA
CATAGAACTTCCACAATAAAATGCCATTGATGGTTGAAAAAAAAAAAAAAAAAAAAA

2074/6881
FIGURE 1909

MAAIPDPSWQPPNVYLETSMGIIVLELYWKHAPKTCKNFAELARRGYNGTKFHRIKDFMIQGGDPTGTGRGGA
SIYGKQFEDELHPDLKFTGAGILAMANAGPDINGSQFFVTLAPTQWLDGKHTIFGRVCQGIGMVNRVGMVETNSQ
DRPVDDVKI IKAYPSG

2075/6881
FIGURE 1910

CGTCAGAACCCATGCGGCAGCAAGGCCTGCCGCCGCCTCTTCGGCCCAGTGGACAGCGAGCAGCTGAGCCGCGAC
TGTGATGCGCTAATGGCGGGCTGCATCCAGGAGGCCCCGTGAGCGATGGAACCTCGACTTTGTCACCGAGACACCA
CTGGAGGGTGACTTCGCCTGGGAGCGTGTGCGGGGCCTTGGCCTGCCCAAGCTCTACCTTCCCACGGGGCCCCGG
CGAGGCCGGGATGAGTTGGGAGGAGGCAGGCGGCCTGGCACCTCACCTGCTCTGCTGCAGGGGACAGCAGAGGAA
GACCATGTGGACCAGCCTGGCCAACATGGTGAAATCTCTACTAAAAATACAAAAATTAGCTGGGCATGGTGGTGC
ACGCTTGTAATCCCAGCTACTTGGAAGGCTGAGGTGGGAGGATCACTTGAACCCAGGAGGCAGAGGTTGCAGTCA
GCTGAGATCATAACCACTGTACTCCAGCCTCTTCCAGGGTGACAGTGAGATTCATCTCAAATTAAATACATAAATAA
AAACTGTTTGGTAATATCTTCT

2076/6881
FIGURE 1911

MAGCIQEARERWNFDFVTETPLEGDFAWERVRLGLPKLYLPTGPRRGRDELGGRRPGTSPALLQGTAEEDHVD
QPGQHGEISTKNTKISWAWWCTLVIPATWKAEVGGSLEPRRQRLQSAEIIPLYSSLFQGDSEIHLK

2077/6881
FIGURE 1912

AGCTGAGGTGTGAGCAGCTGCCGAAGTCAGTTCCCTTGTGGAGCCGGAGCTGGGCGCGGATTGCGCGAGGCACCGA
GGCACTCAGAGGAGGTGAGAGAGCGGCGGCAGACAACAGGGGACCCCGGGCCGGCGGCCAGAGCCGAGCCAAGC
GTGCCCCGCTGTGTCCCTGCGTGTCCGCGAGGATGCGTGTTCGCGGGTGTGTGCTGCGTTTCACAGGTGTTTCTGC
GGCAGGCGCCATGTCAGAACCGGCTGGGGATGTCCGTCAGAACCCATGCGGCAGCAAGGCCTGCCGCGCCTCTT
CGGCCCAGTGGACAGCGAGCAGCTGAGCCGCGACTGTGATGCGCTAATGGCGGGCTGCATCCAGGAGGCCCGTGA
GCGATGGAACTTCGACTTTGTACCGAGACACCACTGGAGGGTGACTTCGCCTGGGAGCGTGTGCGGGGCCTTGG
CCTGCCCAAGCTCTACCTTCCCACGGGGCCCCGGCGAGGCCGGGATGAGTTGGGAGGAGGCAGGCGGCCTGGCAC
CTCACCTGCTCTGCTGCAGGGGACAGCAGAGGAAGACCATGTGGACCTGTCACTGTCTTGTACCCTTGTGCCTCG
CTCAGGGGAGCAGGCTGAAGGGTCCCCAGGTGGACCTGGAGACTCTCAGGGTCGAAAACGGCGGCAGACCAGCAT
GACAGATTTCTACCACTCCAAACGCCGGCTGATCTTCTCCAAGAGGAAGCCCTTAATCCGCCCACAGGAAGCCTGC
AGTCTTGGAAGCGCGAGGGCCTCAAAGGCCCGCTCTACATCTTCTGCCTTAGTCTCAGTTTGTGTGTCTTAATTA
TTATTTGTGTTTTAATTTAAACACCTCCTCATGTACATACCCTGGCCGCCCCCTGCCCCCAGCCTCTGGCATT
GAATTATTTAAACAAAACTAGGCGGTTGAATGAGAGGTTCTTAAGAGTGCTGGGCATTTTATTTTATGAAATA
CTATTTAAAGCCTCCTCATCCCGTGTTCTCCTTTTCTCTCTCCCGAGGTTGGGTGGGCGCGCTTCATGCCAGC
TACTTCCTCCTCCCCACTTGTCCGCTGGGTGGTACCCTCTGGAGGGGTGTGGCTCCTTCCCATCGCTGTACAGG
CGGTATATGAAATTCACCCCTTTTCTGGACACTCAGACCTGAATTCCTTTTTCATTTGAGAAGTAAACAGATGGCA
CTTTGAAGGGGCCTCACCGAGTGGGGGCATCATCAAAACCTTTGGAGTCCCCTCACCTCCTCTAAGGTGGGCAG
GGTGACCCTGAAGTGAGCACAGCCTAGGGCTGAGCTGGGGACCTGGTACCCTCCTGGCTCTTGATACCCCTCTCT
GTCTTGTGAAGGCAGGGGGAAGGTGGGGTCTTGAGCAGACCACCCCGCCTGCCCTCATGGCCCTCTGACCTGC
ACTGGGGAGCCCGTCTCAGTGTTGAGCCTTTTCCCTCTTTGGCTCCCCTGTACCTTTTGGAGAGCCCCAGCTACC
CTTCTTCTCCAGCTGGGCTCTGCAATTCCTCTGTGCTGTCCCTCCCCCTTGTCCCTTCCCTTCAGTACCCTC
TCAGCTCCAGGTGGCTCTGAGGTGCCTGTCCACCCCCACCCCCAGCTCAATGGACTGGAAGGGGAAGGGACACA
CAAGAAGAAGGGCACCTAGTTCTACCTCAGGCAGCTCAAGCAGCGACCGCCCCCTCCTCTAGCTGTGGGGGTGA
GGGTCCCATGTGGTGGCACAGGCCCTTGGAGTGGGGTTATCTCTGTGTTAGGGGTATATGATGGGGGAGTAGAT
CTTTCTAGGAGGGAGACACTGGCCCTCAAATCGTCCAGCGACCTTCCTCATCCACCCATCCCTCCCCAGTTCA
TTGCACTTTGATTAGCAGCGGAACAAGGAGTCAGACATTTTAAGATGGTGGCAGTAGAGGCTATGGACAGGGCAT
GCCACGTGGGCTCATATGGGGCTGGGAGTAGTTGTCTTTCTGGCACTAACGTTGAGCCCTGGAGGCACTGAAG
TGCTTAGTGTACTTGGAGTATTGGGGCTGACCCCAAACACCTTCAGCTCCTGTAACATACTGGCCTGGACTGT
TTTCTCTCGGCTCCCCATGTGTCTTGGTTCCTGTTCTCCACCTAGACTGTAAACCTCTCGAGGGCAGGGACCAC
ACCCTGTACTGTTCTGTGTCTTTCACAGCTCCTCCACAATGCTGAATATACAGCAGGTGCTCAATAAATGATTC
TTAGTGACTTTAAAAAAAAAAAAAAAAAAAAA

2078/6881
FIGURE 1913

MSEPAGDVRQNPCGSKACRRLFGPVDSEQLSRDCDALMAGCIQEARERWNFDFVTETPLEGDFAWERVRLGLPK
LYLPTGPRRGRDELGGRRPGTSPALLQGTAEEDHVDLSLSCTLVPRSGEQAEGSPGGPGDSQGRKRRQTSMTDF
YHSKRRLIFSRRKP

2079/6881
FIGURE 1914

AATAAAGGCGAGGAGAAGGCGGTGGTCCGCCATTTTCGTGGACGCCGGGTGAGTGAGAGAGTTGGTTGGTGTGGG
CCGGAGGAAAGCGGGAAGACTCATCGGAGCGTGTGGATTGAGCCGCCGATTTTTTAAACCCTAGATCTCGAAAT
GCATCGTGATTCTGTCCATTGGACTGTAAGGTTTATGTAGGCAATCTTGGAACAATGGCAACAAGACGGAATT
GGAACGGGCTTTTGGCTACTATGGACCACTCCGAAGTGTGTGGGTTGCTAGAAACCCACCCGGCTTTGCTTTTGT
TGAATTTGAAGATCCCCGAGATGCAGCTGATGCAGTCCGAGAGCTAGATGGAAGAACACTATGTGGCTGCCGTGT
AAGAGTGGAACGTGTCGAATGGTGAAAAAGAAGTAGAAATCGTGGCCACCTCCCTCTTGGGGTCGTGCGCCCTCG
AGATGATTATCGTAGGAGGAGTCCCTCCACCTCGTCGCAGAGTCACCATCATGTCTCTTCTCACCACCCTCTGAAT
CTGCATTAGCCAGTCAACTAGCCCTTTTCAGCGTCATGTGACCAGCGCGCCCCATTTCAGCTTGGCTGGTGTCTGTTT
CACATGACCCAGGCTGGCCAGTCGTTCAGGTTGCACCGCCCTTTGGTTCCCGAGCATGCTGTTTTCTCTCAGCCTT
CTCTCCAACCTTAACCAAAATCGGCAGCAGCCACCTCGACCGCCACACATTCCTGGCCAATCAGCTCAGCTGTTT
ATTTACCAATGTCTTCACAACAACCTACAGCAGCAGCCTTCGGCTAACAAAAAGCAGGAAAAATCCACAACACC
CCCTTCGCCAACCAACTAAATCCAACGCAACATCTGGCAAAACCTTTTCAGCAAATTCTTCCTGGCCGTCAGTCC
GGCAGCCTCACCTACCATTTCTAGCTTGTGTAACCCAAAACTAATCTCCAAGAAGGAGAAGCTTCTCTCGCAG
CCGGAGCAGGTCCCTTTCTAGAGATAGGAGAAGAGAGAGATCGCTGTCTCGGGAGAGAAATCACAAGCCGTCCCCG
ATCCTTCTCTAGGTCTCGTAGTCGATCTAGGTCAAATGAAAGGAAATAGAAGACAGTTTGCAAGAGAAGTGGTGT
ACAGGAAATTACTTCATTTGACAGGAGTATGTACAGAAAATTCAAGTTTTGTTTGAGACTTCATAAGCTTGGTGC
ATTTTTAAGATGTTTTAGCTGTTCAAATCTGTTTGTCTCTTGAAACAGTGACACAAAGGTGTAATTCTCTATGGT
TTGAAATGGATCATACGAGGCATGTAATACCAAGAATTGTTACTTTACAATGTTCCCTTAAGCAAAATTGAATTT
GCTTTGAACTTTTAGTTATGCACAGACTGATAATAAACCTCTAAACCTGCCAGCGGAAGTGTGTTTTTTTTTAA
ATTTAAATACAGAAACAACCTGGCAAAAAATTGAACTAAGATTTACTTTTTTTTCCATAGCTGGGATATAGGCTGCA
GCTATAGTTGAACAAGCAGTCTTTAAAACTGCTGTGAAACACAGGCCATCAGGGAAAACGAAATGCTGCACTAT
TAAATTAGAGGTTTTTTGAAAAATCCAACCTCTCATCCTGGGCAGAGGTTGCCTAGTTGGTATAGAATGTTAAGTTT
CAAGAAAGTTTACCTTTGCTTTAGGTCATAAGTTCCTTATTTGATTGCTGTATATGGATACATGGCTGTTCTGTA
CATTCTTTATGTGCAAATTTGTGATTTCAAAAATGTCCTGCCAGTTTAAGGGTACATTGTAGAGCCGAACCTTTGA
GTTACTGTGCAAGATTTTTTTTTTTCATGCTGTCATTTGTAATATGTTTTGTGAGAATCCTTGGGATTAAAGTTTTG
GTTACAAATTGTTCTTTAACTTGAAAGCCTGTTTTTCTTGCAAACTCAAATCTGTGAGCTTGGTACCAAGTCCA
GGTATAACATTTCCTATTGGAAGCCATACTTATATTTTCTTGTAAGTGCTTTTGAATTAATAAAATATTAGCATA
ATTGTGTATAGTCAGTTGAACCCACTGTTACCATTGTTCTTATCCCATGGGAAGCAGTTGGTTACACGATTCTTA
TTTTATAAGAAACAGCTGAGAGGCACTATGGATTAGTCTTCTGAAGTGAAGGAAATATAGATGTCACCTAAGTGA
TAGTTAACCCTTTTTTTTTTTTTTAGGCATAGAAGCCAGTTTCAGGGTCCATAATATTTAGTGACCAACATTTTA
AAGTATAGCAGCAACCTGGTTCTTAAACACAAAGTAAGTTGCCCATTAACAAATGGCTTTTATCTTTAGCATGAA
AACTTTCCACAGGTCTAAAATTGCTTCCATTTTATAATTTGAGGTGTTGCATGGGAATTCTAAGCTGATCCATC
ATGATGTAAAAGTTCACAATATGGTTCAAATGTAACAGTGCAGAATTGAATATGGAGGCATGCATAACCTTCCTC
TTAGAAAATGGCAGGTGTTGTAATTTCAAATTTTGTGCAATTAGATTAAATCATAATGCAACAGT

2080/6881
FIGURE 1915

MHRDSCPLDCKVYVGNLGNNGNKTELERAFFGYYGPLRSVWVARNPPGFVFEFEDPRDAADAVRELDGRTLGCGR
VRVELSNGEKRSRNRGPPPSWGRRPRDDYRRRSPPPPRRRVTIMSLTTL

2081/6881
FIGURE 1916A

GGTCTCACCATGGAGCGGAAAGTGCTTGCGCTCCAGGCCCGAAAGAAAAGGACCAAGGCCAAGAAGGACAAAGCC
CAAAGGAAATCTGAACTCAGCACCGAGGCTCTGCTCCCCACTCTGAGAGTGATCTACCAGAGCAGGAAGAGGAG
ATTCTGGGATCTGATGATGATGAGCAAGAAGATCCTAATGATTATTGTAAAGGAGGTTATCATCTTGTGAAAATT
GGAGATCTATTCAATGGGAGATACCATGTGATCCGAAAGTTAGGCTGGGGACACTTTTCAACAGTATGGTTATCA
TGGGATATTCAAGGGGAAGAAATTTGTGGCAATGAAAGTAGTTAAAAGTGCTGAACATTACACTGAAACAGCACTA
GATGAAATCCGGTTGCTGAAGTCAGTTCGCAATTCAGACCCTAATGATCCAAATAGAGAAATGGTTGTTCAACTA
CTAGATGACTTTAAATATCAGGAGTTAATGGAACACATATCTGCATGGTATTTGAAGTTTGGGGCATCATCTG
CTCAAGTGGATCATCAAATCCAATTATCAGGGGCTTCCACTGCCTTGTGTCAAAAAATTATTAGCAAGTGTTA
CAGGGTCTTGATTATTTACATACCAAGTGCCGTATCATCCACACTGACATTAAACCAGAGAACATCTTATTGTCA
GTGAATGAGCAGTACATTCCGAGGCTGGCTGCAGAAGCAACAGAATGGCAGCGATCTGGAGCTCCTCCGCCTTCC
GGATCTGCAGTCAGTACTGCTCCCCAGCCTAAACCAGCTGACAAAATGTCAAAGAATAAGAAGAAGAAATTGAAG
AAGAAGCAGAAGCGCCAGGCAGAATTACTAGAGAAGCGAATGCAGGAAATTGAGGAAATGGAGAAAGAGTCGGGC
CCTGGGCAAAAAAGACCAACAAGCAAGAAGAATCAGAGAGTCCTGTTGAAAGACCCTTGAAAGAGAACCCACCT
AATAAAATGACCCAAGAAAACTTGAAGAGTCAAGTACCATTGGCCAGGATCAAACGCTTATGGAACGTGATACA
GAGGGTGGTGCAGCAGAAATTAATTGCAATGGAGTGATTGAAGTCATTAATTATACTCAGAACAGTAATAATGAA
ACATTGAGACATAAAGAGGATCTACATAATGCTAATGACTGTGATGTCCAAAATTTGAATCAGGAATCTAGTTTC
CTAAGCTCCCCAAATGGAGACAGCAGCACATCTCAAGAAACAGACTCTTGTACACCTATAACATCTGAGGTGTCA
GACACCATGGTGTGCCAGTCTTCCTCAACTGTAGGTGAGTCATTGAGTGAACAACACATTAGCCAACCTTCAAGAA
AGCATTCGGGCAGAGATACCCTGTGAAGATGAACAAGAGCAAGAACATAACGGACCCTGGACAACAAAGGAAAA
TCCACGGCTGGAAATTTTCTTGTTAATCCCTTGAGCCAAAAAATGCAGAAAAGCTCAAGGTGAAGATTGCTGAC
CTTGAAATGCTTGTGGCACAACATTTCACTGAAGATATTCAAACAAGGCAATATCGTTTCCTTGGAAGTTCTA
ATCGGATCTGGCTATAATACCCCTGCTGACATTTGGAGCACGGCATGCATGGCCTTTGAACTGGCCACAGGTGAC
TATTTGTTTGAACCTCATTCAGGGGAAGAGTACACTCGAGATGAAGATCACATTGCATTGATCATAGAATCTCTG
GGGAAGGTGCCTCGCAAGCTCATTGTGGCAGGAAAATATTCCAAGGAATTTTTCACCAAAAAGGTGACCTGAAA
CATATCAGCAAGCTGAAACCTTGGGGCCTTTTTGAGGTTCTAGTGGAGAAGTATGAGTGGTGCAGGAAGAGGCA
GCTGGCTTCACAGATTTCTTACTGCCCATGTTGGAGCTGATCCCTGAGAAGAGAGCCACTGCCGCCGAGTGTCTC
CGGCACCCTTGGCTTAACCTCCTAAGCCCCCTGCCAGCACCACAGCAGAGATCACACACTGACCCTCCGCCCTTCC
CCTTCAAGCATTTTCTCTTCCCTTTTCAGGGTGAAGCTCTTCCCTCAAGAGTTTCTAGATCTTGTTTTTTTTTT
AATCCAACATGTTTCAATTTGGGTTTGCTTACTTGACCCTGTGGAGATCCCCACAGCCATTGGGCATCCTAGGTGAA
TTTGGCCTTGGTTGGGCTCTGCCAAAGACTAATGGACTAAAATGTGAAACAGCCTCTTGCCCTGTACCTTTCTCT
CCCATTAGGACATCCTTTAAATTATAAGCATCCTTTTTGAAAAGAGCTATGAAGGTGTATGAGCCCATCCTTTTA
TTCATTGACTCTAAGAGTCAAATTTTCTAGTGCATATCCTATTGCCAGCATAAGGATGAGGAGGGGGAAAGGGTC
TTAATTCTATGTACAGCAGAGACATTAACTTGCTGTGTCCGGGCTGCATCATCTTCTGGACTGTTTCTGTTGT
TCTCTGTGTTACATTTTTTCTGCAACTTTTAAGCTACTGTCTTTTTTAAATAGCTATATGAACACCAAATTTG
GGTACCATTTTATCACTGTTCAAAGCACGTGCAAATTCCTTTTATCTCTTTAATAGTTAAGATCTTTGAATCTTCA
GTCTGATTTTTTAATGTAAGCAAAAACAGAACCATTGAATAGTAATTTCTTGAGAACCTCAGGTGTTCTATAAACA
GTCCTTTCTGTATGTCTTCTATTACCTAAGACCAGAGTTATTTTGGTTGGTTGTTTTGTTTTATTTTTTGT
TTGTATCCATGGCTGGCACTTTACTCATTTGCACTTGAGTTTATTGCCCCATAACTAAAGGATCAGGATGATGGTA
GAACGGAGATCTGGGTTTCAGAGCTTTCCCATTTAAGAAAAATAGATCTTGAGATTCTGATTCTTTTCCAAACAG
TCCCCTGCTTTTATGTACAGCTTTTTCTTTACCTTACCCAAAATTCTGGCCTTGAAGCAGTTTCTCTATGGCT
TTGCCTTTCTGATTTTCTCAGAGGCTCGAGTCTTTAATATAACCCCAAATGAAAGAACCAAGGGGAGGGGTGGGA
TGGCACTTTTTTTTTGTTGGTCTTGTTTTTGTTTTGTTTTTGGTTGGTTGGTTGTTTTTAAAGATTAGCCAT
TCTCTGCTGCTATTTCCCTACATAATGTCAATTTTTTAACCATAATTTTGACATGATTGAGATGTACTTGAGGCTT
TTTTGTTTTAATTGAGAAAAGACTTTGCAATTTTTTTTTTAGGATGAGCCTCTCCTAGACTTGACCTAGAATATT
ACATATTCCTCCAGTAAGTAATACTGAAGAGCAAAAGAGAGGCAGGATTGGGGTCACAGCCGCTTCTTCAGCATG
GACCAAGTGGGCCTTGGGGATTGCAGCGTTCTCGAAGTGGCTGTAGGACTCGAATTTACAGAAAGCCACAGAGGT
GCAACTTGAGGCTCTGCTAGCAAGCCACCAGTGAGGCTATTGGGTAACCACTTTCTATACAGGAGATTGGAATC
TACTTTGTCAATTTATCCACCACAGTGACAAAGGAAAAGTGGTGCCGTTATGCAATCCATTTAACTCATAAACATA

2082/6881
FIGURE 1916B

TTACTCTGAGTAACTGGCCAGCCATTTCATCGGATCCTTCATTGGGTACTCCTGAAATCAGACATGTTCCCTGTAGA
AAGAATTTTAAGTTAGGCTTTCTATGCACCTATCAAGAATCAAGAGAATAGATTGTATCAAACAACGGCAGGGAA
ATCCTTCAGCAATTCTAATCCACTTTGGGTTTTTCAGCTGTTTTTACATCTAAAGCAATAGACTAGAACTGAATTA
TCTTCTACATAGTAAAATCACAATTGTGGAATTACAGGAATTCTGGTGATATTAAGGTGAAATAACAAAACACAA
AAGGCCCTATTTTAACAGTTGATGTGACAGTAAGTTTTAATAGAACCTGTAACCTTCATTTTGGAAATGCTTCTCC
ACCAAATAAGGGCTTTTTCCCCTATTTAAGGAGCCAGATGGATTGAAAGATGTGGAAATAGGCAGCTGTAGATCT
TGATCTTCCAGGTACCCCATGTACCTTTATTGAGCTTAATTATAATACTGTCAAATTGCCACGATCTCACTAAAG
GATTTCTATTTGCTGTCAGTTAAAAATAAAGCCCTAAATACATTTTTATTCTTTCTACTGAGGGCATTGCTCTGTT
TTCTTTGTAAATGCCGTACAATAAACAAATTATTTAATAACCTA

2083/6881
FIGURE 1917

MERKVLALQARKKRTKAKKDKAQRKSETQHRGSAPHSESDLPEQEEIILGSDDDEQEDPNDYCKGGYHLVKIGDL
FNGRYHVIRKLGWGHFSTVWLSWDIQGKKFVAMKVVKSAEHYTETALDEIRLLKSVRNSDPNDPNREMVVQLDD
FKISGVNGTHICMVFEVLGHLLKWI IKSNYQGLPLPCVKKI IQQVLQGLDYLHTKCRI IHTDIKPENILLSVNE
QYIRRLAAEATEWQRSGAPPPSGSAVSTAPQPKPADKMSKNKKKKLKKKQKRQAELLEKRMQEIEEMEKESGPGQ
KRPNKQEESESPVERPLKENPPNKMTQEKLEESSTIGDQTLMERDTEGGAAEINCNGVIEVINYTQNSNNETLR
HKEDLHNANDCDVQNLNQESSFLSSQNGDSSTSQETDCTPITSEVSDTMVCQSSSTVGQSFSEQHISQLQESIR
AEIPCEDEQE QEHNGLDNKGKSTAGNFLVNPLEPKNAEKLKVKIADLGNACWHKHFTEDIQTRQYRSLEVLIGS
GYNTPADIWSTACMAFELATGDYLFEPHSGEETYTRDEDHIALI IELLGKVPRKLIVAGKYSKEFFTCKGDLKHIT
KLKPWGLFEVLVEKEYEWSQEEAAGFTDFLLPMLLELIPEKRATAAECLRHPWLNS

2084/6881
FIGURE 1918A

GGGCCGGCTCGCGGGCGCTGCCAGTCTCGGGCGGCGGTGTCCGGCGCGCGGGCGGCCTGCTGGGCGGGCTGAAGG
GTTAGCGGAGCACGGGCAAGGCGGAGAGTGACGGAGTCGGCGAGCCCCGCGGCGACAGGTTCTCTACTTAAAAG
ACAATGACTACTGATGAAGGTGCCAAGAACAATGAAGAAAAGCCCCACAGCCACTGTTGCTGAGCAGGGAGAGGAT
ATTACCTCCAAAAAAGACAGGGGAGTATTAAAGATTGTCAAAAGAGTGGGGAATGGTGAGGAAACGCCGATGATT
GGAGACAAAAGTTTATGTCCATTACAAAGGAAAAATTGTCAAATGGAAAGAAGTTTGATTCCAGTCATGATAGAAAT
GAACCATTTGTCTTTAGTCTTTGGCAAAGGCCAAGTCATCAAGGCATGGGACATTGGGGTGGCTACCATGAAGAAA
GGAGAGATATGCCATTTACTGTGCAAACCAGAATATGCATATGGCTCGGCTGGCAGTCTCCCTAAAATTCCCTCG
AATGCAACTCTCTTTTTTTGAGATTGAGCTCCTTGATTTCAAAGGAGAGGATTTATTTGAAGATGGAGGCATTATC
CGGAGAACCACGGAAGGAGAGGGATATTCAAATCCAAACGAAGGAGCAACAGTAGAAAATCCACCTGGAAGGC
CGCTGTGGTGGAAAGGATGTTTACTGTCAGAGATGTGGCATTCACTGTGGGCGAAGGAGAAGACCACGACATTCCA
ATTGGAATTGACAAAGCTCTGGAGAAAATGCAGCGGAAGAACAATGTATTTTATATCTTGGACCAAGATATGGT
TTTGGAGAGGCAGGGAAGCCTAAATTTGGCATTGAACCTAATGCTGAGCTTATATATGAAGTTACACTTAAGAGC
TTCGAAAAGGCCAAAGAATCCTGGGAGATGGATACCAAAGAAAAATTGGAGCAGGCTGCCATTGTCAAAGAGAAG
GGAACCGTATACTTCAAGGGAGGCAAATACATGCAGGCGGTGATTCACTATGGGAAGATAGTGTCTTGGTTAGAG
ATGGAATATGTTTTATCAGAAAAGGAATCGAAAGCTTCTGAATCATTTCTCCTTGCTGCCTTTCTGAACCTGGCC
ATGTGCTACCTGAAGCTTAGAGAATACACCAAAGCTGTTGAATGCTGTGACAAGGCCCTTGGACTGGACAGTGCC
AATGAGAAAGGCTTGTATAGGAGGGGTGAAGCCCAGCTGCTCATGAACGAGTTTGAGTCAGCCAAGGGTGACTTT
GAGAAAGTGCTGGAAGTAAACCCCCAGAATAAGGCTGCAAGACTGCAGATCTCCATGTGCCAGAAAAGGCCAAG
GAGCACAACGAGCGGGACCGCAGGATATACGCCAACATGTTCAAGAAGTTTGCAGAGCAGGATGCCAAGGAAGAG
GCCAATAAAGCAATGGGCAAGAAGACTTCAGAAGGGGTCACTAATGAAAAAGGAACAGACAGTCAAGCAATGGAA
GAAGAGAAACCTGAGGGCCACGTATTGACCGCCACGCCAAGGAGGGAAGAGTCCCAGTGAACTCGGCCCCCTCCTCAA
TGGGCTTTCCCCCAACTCAGGACAGAACAGTGTTTAATGTAAAGTTTGTATAGTCTATGTGATTCTGGAAGCAA
ATGGCAAACCAGTAGCTTCCCCAAAAACAGCCCCCTGCTGCTGCCCCGAGGGTTCACTGAGGGGTGGCACGGGA
CCACTCCAGGTGGAACAAACAGAAATGACTGTGGTGTGGAGGGAGTGAGCCAGCAGCTTAAGTCCAGCTCATTTT
AGTTTCTATCAACCTTCAAGTATCCAATTACAGGGTCCCTGGAGATCATCCTAACAATGTGGGGCTGTTAGGTTTT
ACCTTTGAACCTTTCATAGCACTGCAGAAACCTTTTAAAAAAAATGCTTCATGAATTTCTCCTTTTCTACAGTTG
GGTAGGGTAGGGGAAGGAGGATAAGCTTTTGTTTTTTAAATGACTGAAGTGCTATAAATGTAGTCTGTTGCATTT
TTAACCAACAGAACCCACAGTAGAGGGTCTCATGTCTCCCCAGTTCCACAGCAGTGTCACAGACGTGAAAGCCA
GAACCTCAGAGGCCACTTGCTTGCTGACTTAGCCTCCTCCCAAAGTCCCCCTCCTCAGCCAGCCTCCTTGAGAG
GTGGCTTTCTACCACACACAGCCTGTCCCTGGGGGAGTAATTCGTGTCATTCTTAAACACCCTTCAGCAATGATA
ATGAGCAGATGAGAGTTTCTGGATTAGCTTTTCTTATTTTCGATGAAGTTCTGAGATACTGAAATGTGAAAAGAG
CAATCAGAATTGTGCTTTTCTCCCTCCTCTATTCTTTTAGGGAATAATATTCAATACACAGTACTTCTCTCC
AGCATTGCTACTGCTCAGCTTCTTCTTCTATTCTAATCCTTGCTATTAAGAATTTAAGACTTGTGCTTACAATAT
TTTTGACCTGGAGTGGATCTATTTACATAGTCATTTAGGATCCATGCAGCTTTTTTGTCTTTTTTAAGATTATTG
GCTCATAAGCATATGTATACTGGTTTATGGAACTTTATTTACACTCCTCTATCATGCAAAAAAATTTTGACTTTT
TAGTACTAAGCTTAATTTTTTAAAAACAAAATCTGTAGTGTGACAAATAAATAGTTGCTCTTCTACACTAGGGGT
TTCACCTGCAGGTTTGACACGCAGTTGCTCGCTTTTCTGCCCCTGTCAAGCTTCTCTGTTCTGGCGTGAGTTGTG
AAAGAGTTGAAGACAGCTTCCCATGCCGGTACACAGCCAGTAGCCTAAATCTCCAGTACTTGAGCTGACCATTGA
ACTAGGGCAAGTCTTAAATGTGTACATGTAGTTGAATTTCACTCCTTACGGGTAAACAGATTGAGCATGGCTCTC
TATTCCTCAGCCTAAGAAACACTCATGGGAATGCATTTGGCAACCCAAGGAACCATTGTGCTTAAACCTGGAACA
TCTCACCTTTTTTAAATCCTAAAAACACTGGCAGTTATATTTTAAATTAGTTTTTATTTTTATGATGGTTTTATC
AAAAGACTTTTTATTATTAGATTGGGACCCCTTCAAACCTAAAAATCAAGTTATTTCTTTTATAATACTTTTCT
TCCCCATGGAACAAATGGGATCAATTTGTGAGTTTTTTTCTTTAATGATAACTAAAATCCCTCTAATTTCTCAT
TATGCTTTTGTCTTTTTTATGAAATATTTCTTTTAAAAGCCCCAGTCTCACCTACGAAATATGAAGAGCAAAAGC
TGATTTTGTCTTACTTGCTAAACTGTTGGGAAAGCTCTGTAGAGCATGGTTCCAGTGAGGCCAAGATTGAAATTTG
ATACTAAAAGGCCACCTAGCTTTTTTGAGATAACAAACAAGAAAGCTATTCCAAGACTCAGATGATGCCAGCTG
TCTCCACGTGTGTATTATGGTTACCAGGGGGAAGTGGCAAAAGTGTTGTGTGGGGAGGGGAAGGGTGTGTGAGT
GGTTCTGAGCAAATAACTACAGGGTGCCATTACCACTCAAGAAGACACTTCACGTATTCTTGTATCAAATTCAA

2085/6881
FIGURE 1918B

TAATCTTAAACAATTTGTGTAGAAGTCCACAGACATCTTTCAACCACCTTTTAGGCTGCATATGGATTGCCAAGT
CAGCATATGAGGAATTAAAGACATTGTTTTTAAAAAAAAAAAAATCATTTAGATGCACTTTTTTGTGTGTTCTTTA
AATAAATCCAAAAAAAAATGTGAAAAAAAAA

2086/6881
FIGURE 1919

MTTDEGAKNNEESPTATVAEQGEDITSKKDRGVLKIVKRVNGEETPMIGDKVYVHYKGKLSNGKKFDSSHDRNE
PFVFSLGKGQVIKAWDIGVATMKKGEICHLLCKPEYAYGSAGSLPKIPSNATLFFEIEILLDFKGEDLFEDGGIIR
RTKRKGEGYSNPNEGATVEIHLEGRCGGRMFDCRDVAFTVGEGEDHDIPIGIDKALEKMQRREEQCILYLGPYGF
GEAGKPKFGIEPNAELIYEVTLSFEKAKESWEMDTKEKLEQAAIVKEKGTVYFKGGKYMQAVIQYGKIVSWLEM
EYGLSEKESKASESFLLAFLNLMCYLKLREYTKAVECCDKALGLDSANEKGLYRRGEAQLLMNEFESAKGDFE
KVLEVNPQNKAARLQISMCQKKAKEHNERDRRIYANMFKKFAEQDAKEEANKAMGKKTSEGV TNEKGTDSQAMEE
EKPEGHV

2087/6881
FIGURE 1920

CGCCACCATGGTGTGCGTGAACGTCCTGGCCGATGCTCTCAAGAGCATCAACAATGCCGAAAAGAGAGGCAAACG
CCCAGTGCTTATTAGGCCGTGCTCCAACTCATCGTCCGGTTTCTCACTGTGATGATGAAGCATGGTTACATTGG
CGAATTTGAAATCATTGATGATCGCAGAGCTGGGAAAAATTGTTGCGAACCTCACAGGCAGGCTAAACAAGTGTGG
AGTGATCAGCCCCAGATTCGGTGTGCAACTCAAAGATCTAGAAAATGGCAGAATAATCTGCTTCCATCCCACCAG
TTTGGTTTCATTGTACTGACAACCTCAGCTGGCATCATGGACCATGAAGAAGCAAGACGAAAACACACAGGAGGG
AAAATCCTGGGATTCTTTTCTAGGGATGTAATACATATTTACAAATAAAATGTCTCATGGAAAAAAAAGAAA
AAAGACAGGAAAAAAAAAAAAAAAAAAAAAAT

2088/6881
FIGURE 1921

GCCTCCCGCTCCAGCCCGGCTCATTCCGCACATTCCGGCCAGCCCCCTCCCCACGACCCCCCTTCCCCGGCCCCC
CTTGCGGCTCCCTCGGGCCCGGCGGAGCGGCCCCGGCCGGAGCGCCCCCGCGAGCTCGGACCAGGCTCAGCCGCCC
AGTGGGCTCAGGCCCAGAGCCCAGAGCAACCAGCACAAATAGCGTCCAACAGCTGGAACGCCAGCAGCAGCCCCGG
GGAGGCCCCGGGAGGATGGGCCCCGAGGGCCTGGACAAGGGGCTGGACAACGATGCGGAGGGCGTGTGGAGCCCCGA
CATCGAGCAGAGCTTCCAGGAGGCCCTGGCCATCTACCCGCCCTGCGGCCGGCGGAAGATCATCTGTCTCAGACGA
GGGCAAGATGTACGGCCGAAATGAGTTGATTGCACGCTATATTAACTGAGGACGGGGAAGACTCGGACGAGAAA
ACAGGTGTCCAGCCACATACAGGTTCTAGCTCGGAAGAAGGTGCGGGAGTACCAGGTTGGCATCAAGGCCATGAA
CCTGGACCAGGTCTCCAAGGACAAAGCCCTTCAGAGCATGGCGTCCATGTCTCTGCCCAGATCGTCTCTGCCAG
TGTCTGCGAACAAGTTCAGCCCACCTTCCCCTCTGCCCCAGGCCGTCTTCTCCACTTCTCGCGGTTCTGGAG
CAGCCCCCTCTCCTGGGACAGCAGCCTGGACCCTCTCAGGACATCAAGCCCTTTGCACAGCCAGCCTACCCCAT
CCAGCCGCCCCCTGCCGCCGACGCTCAGCAGTTATGAGCCCCCTGGCCCCGCTCCCCTCAGCTGCTGCCTCTGTGCC
TGTGTGGCAGGACCCTACCATTTGCCTCCTCCCGGCTGCGGCTCCTGGAGTATTAGCCTTCATGGAGGTGCAGCG
AGACCCTGACACGTACAGCAAACACCTGTTTGTGCACATCGGCCAGACGAACCCCGCCTTCTCAGACCCACCCCT
GGAGGCAGTAGATGTGCGCCAGATCTATGACAAATTCCCCGAGAAAAAGGGAGGATTGAAGGAGCTCTATGAGAA
GGGGCCCCCTAATGCCTTCTTCTTGTCAAGTTCTGGGGCCGACCTCAACAGCACCATCCAGGAGGGCCCCGGGAGC
CTTCTATGGGGTCAGCTCTCAGTACAGCTCTGCTGATAGCATGACCATCAGCGTCTCCACCAAGGTGTGCTCCTT
TGGCAAACAGGTGGTAGAGAAGGTGGAGACTGAGTATGCCAGGCTGGAGAACGGGCGCTTTGTGTACCGTATCCA
CCGCTCGCCCATGTGCGAGTACATGATCAACTTCATCCACAAGCTGAAGCACCTGCCCGAGAAGTACATGATGAA
CAGCGTGCTGGAGAACTTCACCATCCTGCAGGTGGTCACGAGCCGGGACTCCCAGGAGACCCTGCTTGTCTATTGC
TTTTGTCTTCGAAGTCTCCACCAGTGAGCACGGGGCCCAGCACCATGTCTACAAGCTCGTCAAAGACTAGGGTGC
CCTCTGCGCCTCCTTAAGGATGCAGGGTGAGCATCTCCTCTCCACACCTGCCTGGCACCCCTGGGGGGGTCCAGG
ATTGAGGATTCATCTACCTGCCAGGCCTCAGGCCCAGGACCAGGAGGCCTCCCCACCTACCCAGCACACACAC
TCCCTGCCACTGTTCTGCGCTTTAATTGTGGGAGAAGAGAGGAGAGGAGGGCTCAGCGGTGGGGCAGCCTGTCCG
GGGCGCTGACCCACCATACCCCTGCTCTGCCCAGCCTCGCGTGACCTCAGAGAGGTGGGGATAGGGGACACCTTC
AGCCTCCAGCATGTGTGGCCACTGTACCCCCACCCACCCTTGGGGGAGCATGATGGGCAGGTGAGGGCAGGATGG
AGACCAAGGGAGTCAGTGAGCAGAGGCCCTGGGAGTGTCCGGTTGGGGTTGGACTGAGGACAGAGGGGCCACAC
TTCCTTGCCCCCTTGTGTCTCCAGGCCTGGTGCCAGACTCCTTGTCATGGCTTGTGTGGTCTCAGACTCCGCACA
GCGAGCGTAGGTCTCTGGGTTTTAGATGAAGTGCCAGGCTCCAGGAAGTTGAGGGACCCACAGGAGAGGTGGGC
AGAGCTGGAGTTCTCATCCAGGGCTGCTTGTCCCCAGAGCCAGGTTTATACTACCTCCCTGGGGCGGGGGCTGG
CCGAGGGGTAGGGGAGAGGCTCTGCAGTGTGGAGTGGAGCCTCATCGAGGGGCGCTGGGTTAGGGGAGCACCTGT
TTCAGACTGGGCATGAAGAAGGGAGCACAGCAGCTACTAGACCCCATTAGCACCTCATTAGCCCAAGCCAGCC
AGGGGCCCCAGGAAGATGGGGCACCCCCAGCACCCCTCCAGATTGAGAGCAAGGTAGAGGAAGGAGTCCCAGCCT
CTGGGCAGACCAGAGGCCAGAGGGAGAGAGTAGCAGAAGGCTTTTGATTTTTCTCTTGCTGAGGCTTGAATCT
GACAAACCCCTTGGTGGGCACTGCTCCCTTAGGTTCTTCCCCACCTCAATCTACCTGCCTAGAGTAGCAGCTCCCA
GACCCAGTTCTGGGACTGAAGGTTAACCCTTCACCTGCTGTCCCTTCTTAACACCCAGGCCCCCAGAGCCAGCTG
GGCCTGTCCAGCAGCCACCTGTGGGTATTTATGAGTTTCATATGAAGTACTGTGCCCCCTTCCCTTCTCATCCCG
ACCCTGCCCCGAGCTTCTGAAGGTCTCACTGTTTGATATCGCTCAGGCCACCTCCAAACCCACCTAGGTTTT
ATAATGTATATTATATATTTTTTTTTGTGTATTTTTTAAATCCAGCTGTGATGGGTTATATCATAAATGCAGCTTGG
GGTTGGAGCAGGGGCCCTCAAAGGCCAGCTCCTGCTC

2089/6881
FIGURE 1922

GCGGCGTGAGAAGCCATGAGCAGCAAAGTCTCTCGCGACACCCTGTACGAGGCGGTGCGGGAAGTCCTGCACGGG
AACCAGCGCAAGCGCCGCAAGTTCCTGGAGACGGTGGAGTTGCAGATCAGCTTGAAGAACTATGATCCCCAGAAG
GACAAGCGCTTCTCGGGCACCGTCAGGCTTAAGTCCACTCCCCGCCCTAAGTTCTCTGTGTGTGTCTTGGGGGAC
CAGCAGCACTGTGACGAGGCTAAGGCCGTGGATATCCCCACATGGACATCGAGGCGCTGAAAAAACTCAACAAG
AATAAAAACTGGTCAAGAAGCTGGCCAAGAAGTATGATGCGTTTTTGGCCTCAGAGTCTCTGATCAAGCAGATT
CCACGAATCCTCGGCCCAGGTTTAAATAAGGCAGGAAAGTTCCTTCCCTGCTCACACACAACGAAAACATGGTG
GCCAAAGTGGATGAGGTGAAGTCCACAATCAAGTTCCAAATGAAGAAGGTGTTATGTCTGGCTGTAGCTGTTGGT
CACGTGAAGATGACAGACGATGAGCTTGTGTATAACATTACCTGGCTGTCAACTTCTTGGTGTGATTGCTCAAG
AAAACTGGCAGAATGTCCGGGCCTTATATATCAAGAGCACCATGGGCAAGCCCCAGCGCCTATATTAAGGCACA
TTTGAATAAATTCTATTACCAGTTC

2090/6881
FIGURE 1923

MSSKVSRTLYEAVREVLHGNQRKRRKFLETVELQISLKNYDPQDKRFSGTVRLKSTPRPKFSVCVLGDQQHCD
EAKAVDIPHMDIEALKKLNKNKKLVKKLAKKYDAFLASESLIKQIPRILGPGLNKAGKFPSLLTHNENMVAKVDE
VKSTIKFQMKKVLCLAVAVGHVKMTDDELVYNIH LAVNFLVSLKKNWQNVRALYIKSTMGKPQRLY

2091/6881
FIGURE 1924

GTGAGTTTACCCCTATGAGACTGTGAGAGGCCCGGGGCCTACCTCAAAGGAGCGGGGTCGCGAAGCTAGCTAGCA
GCGGCCCCCTCCAGGTCCCCGGGCCCCGGCGCGCGCGGCTTGGTTGTGAAGAGGCGGGGAAGCGGGTGTG
CGGTCCCCGCCATGGAGGGCATGGACGTAGACCTGGACCCGGAGCTGATGCAGAAGTTCAGCTGCCTGGGCACCA
CCGACAAGGACGTGCTCATCTCCGAGTTCCAGAGGCTGCTCGGCTTCCAGCTCAATCCTGCCGGTTGCGCCTTCT
TCCTGGACATGACCAACTGGAACCTACAAGCAGCAATTGGCGCCTATTATGACTTTGAGAGCCCAAACATCAGTG
TGCCCTCTATGTCCTTTGTTGAAGATGTCACCATAGGAGAAGGGGAGTCAATACCTCCGGATACTCAGTTTGTA
AAACATGGCGGATCCAGAATTCTGGGGCAGAGGCCTGGCCTCCAGGGGTTTGTCTTAAATATGTCGGGGGAGACC
AATTTGGACATGTGAACATGGTGATGGTGAGATCGCTAGAGCCCCAAGAGATTGCAGATGTCAGCGTCCAGATGT
GCAGCCCCAGCAGAGCAGGAATGTATCAGGGACAGTGGCGGATGTGCACTGCTACAGGACTCTACTATGGAGATG
TCATCTGGGTGATTCTCAGTGTGGAGGTGGGTGGACTTTTAGGAGTAACGCAGCAGCTGTCATCTTTTGAAACGG
AGTTCAACACACAGCCGCATCGTAAGGTAGAAGGAACTTCAACCCTTTTGCTCTCCCCAAAAGAACCGACAAT
CAGATGAAAACAACCTTAAAGACCCTGGGGGCTCCGAGTTCGACTCGATCAGCAAAAACACATGGGCTCCTGCTC
CTGACACATGGGCTCCTGCTCCTGACCAAACTGAGCAAGACCAGAATAGACTGTCACAGAACTCTGTAAATCTGT
CTCCAGCAGTCACGCAAACAACCTTATCAGTAGTGACTTACAGTAAGGGGCTCCATGGGCCTTACCCCTTCGGCC
AGTCTTAAACGGGTGTCAGCAAAAAAAAAAAAAAAAAAA

2092/6881
FIGURE 1925

MEGMDVDLDPELMQKFSCLGTTDKDVLISEFORLLGFQLNPAGCAFFLDMTNWNLQAAIGAYYDFESPNISVP
SM
SFVEDVTIGEGESIPPDQTQFVKTWRIQNSGAEAWPPGVCLKYVGGDQFGHVNMMVMRSLEPQEIADVSVQMCSP
S
RAGMYQGQWRMCTATGLYYGDVIWVILSVEVGGLLGVTQQLSSFETEFNTQPHRKVEGNFNPFASPQKNRQSD
EN
NLKDPGGSEFDSISKNTWAPAPDTWAPAPDQTEQDQNRLSQNSVNLSPSSHANNLSVVTYISKGLHGYPYFGQS

2093/6881
FIGURE 1926

GGCACGAGGGGGTGTAGGGTCTGCCTGCCTGTTTCTGTCTGGGTGTCTGAGTTCCAAAAATGTGTGTTGTTTGT
CCTCCTCATCCTCTTCTGAGACTGTTGTTTTTTTAGAGCTTGATTGTGGGAGAAAAGCTTGTTGTGAAATTCCTC
TTCACCTCCCCACCCCCAAAAATAAAAGGGGGCATAACTTTATTCCACTGGAGAAGCCCTGGGGGTGGCTGG
AGCCAGCCTGCTGAGAAGCGTGGTGCAGCTGGGTCTGGGACTTCACTAGAGCTTACTCTGGAGCACCTATTTTCT
GTGCACATGGGAGTGTCTCACTCCCTAGCAGAGCAGAGGGAAGTCTCTGCCAGGTACCCACGCCACAGGCCTCAG
GATGGCTTTTTGTCTGAGGGCCTCATTAGGCCCAGACTGCTGCTGCTGGTACCAGTCTCCTGAGACACTGCCTCC
CTGGAGCCCATGCATGCCCAGCTGTTCTTACTGCTTAGTAGCCTTGAAGCAGCACATCTCCACTGTCCCTGGCAG
GATTGTGGGAGGCTTCACAACCCCTGCTTTTCTGACTTCCTCTTCTGCCAACACTGGGTGCCCTTCCCAGTTT
CCCAGCAGGGGCTTCATGGGCCACCGTCAGTGGGTCTGGGCCTGCCAGAGTCGTCTTGCTCTTCCCTCTTGCTTCT
AGGCAACCACACTTGGAAGTTAAATGTCCCAAGCACCTTGTCTCCCTTCCCAAGAACAAACCATTTCTGTGCAC
ATCCTTGGAGGCGAGATGAGCTCCTTGCAAGGGCCAGAGTAAGTGCAAGTCATGGAGTGCAGGCAGAGGGGTCC
ATGGCTTCCCCAGCCCAGGGAGGGTATCAGTATCATTTCATTCTCTCTCCCTCACTGGTATGGGTTCAGAGCAAT
GCCTAGGGCCCCCTCTCTGCTCCCCTGCCTAGTGGGGTGGTAGTGGCTACCTCTCAGCCCCAATAGTCCCTGCTCC
TCTTAGAATCTTACCAAGTGGCAGGCCACCTCTGGGCAGGACCACCTGCGTCTGGCACCCAGGAGGTGAGGCAG
ACACCATGGTTAGGTGATAGGGTCTGAACCCAGTTGGGGAGACAGAGGGGTTCAGACTTGGGAAGAATCTGTCAG
TGTGCATGGAGTGAAGTGTGTGTGTGTGGATGGATGTGCACGTGTGCATGCTTTTTTTCTTTTTGCCGTGAGGAC
AGTTGAATTTGGGGCATTTTTCTACAAGAAGCAGTCAGCCTTCTCTCCCCATAAGGACTGGCTGTAACCTTAAG
CCCATCAAAGTTACTTCCAGCCTGGAGAGAACCTCACAAACAGCTGGTGTGGCCTGAGGGTGGCCATGGTGGGA
AATGGGCATGAGAATAAATACCTCCCCAAATTCAATCTGAGCCCAGCAGGAGAGGATGGTAGGGTTGCCAGGGCT
CAGAAGTGCAAGCTGATTACTACCCCCACCTGCCTCGCCGCACCTTTCCTTTGTTTCCTTGGGTGAATGCAGGA
GCAGCAGTGGCTGCCCTTCCCACCTGGACAGTGGTGTGTGTAGAAAGCCAGCTGGATGTTTGTGGTGGGGCCTCA
TGGTGCCTAGGAGGAGATAAAGATGAGGAGGTTTTTCCTTATTGTATAAATGAATATTTGTATGATTAAATTAAC
ACACACACCAAAAAAAAAAAAAAAAAAAAAA

2094/6881
FIGURE 1927

MAFCLRASLGPDCCWYQSPETLPPWSPCMFSCSYCLVALKQHISTVPGRIVGGFTTPAFLTSSSAQHWVPLPSF
PAGASWATVSGSGPARVLLFLLLLGNHTWQVKCPKHLVSLPKNKPFLCTSLEAR

2095/6881
FIGURE 1928

AGAGTCGTCTTGCTCTTCCTCTTGCTTCTAGGCAACCACACTTGGCAAGTTAAATGTCCCAAGCACCTTGTCTCC
CTTCCCAAGAACAACCATTTTTTCTTTTGGCGTGAGGACAGTTGAATTTGGGGCATTTTTCTACAAGAAGCA
GTCAGCCTTCTCTCCCCATAAGGACTGGCTGTAACCTTAAGCCCATCAAAGTTACTTCCAGCCTGGAGAGAACC
TCACCAAACAGCTGGTGTGGCCTGAGGGTGGCCATGGTGGGAAATGGGCATGAGAATAAATACCTCCCCAAATTC
AATCTGAGCCCAGCAGGAGAGGATGGTAGGGTTGCCAGGGCTCAGAAGTGCAAGCTGATTACTCACCCACCCTG
CCTCGCCGCACCTTTCCTTTGTTTCCTTGGGTGAATGCAGGAGCAGCAGTGGCTGCCCTTCCACCTGGACAGTG
GTGTGTGTAGAAAGCCAGCTGGATGTTTGTGGTGGGGCCTCATGGTGCCTAGGAGGAGATAAAGATGAGGAGGTT
TTCCTTATTGTATAAATGAATATTTGTATGATTAAATTAACACACACACCAAAAAAA

2096/6881
FIGURE 1929

GTCTGACTTCCTCCCAGCACATTCTGCACTCTGCCGTGTCCACACTGCCCCACAGACCCAGTCCTCCAAGCCTG
CTGCCAGCTCCCTGCAAGCCCCTCAGGTTGGGCCTTGCCACGGTGCCAGCAGGCAGCCCTGGGCTGGGGGTAGGG
GACTCCCTACAGGCACGCAGCCCTGAGACCTCAGAGGGCCACCCCTTGAGGGTGGCCAGGCCCCCAGTGGCCAAC
CTGAGTGCTGCCTCTGCCACCAGCCCTGCTGGCCCCCTGGTTCCGCTGGCCCCCAGATGCCTGGCTGAGACACGC
CAGTGGCCTCAGCTGCCCACACCTCTTCCCGGCCCTGAAGTTGGCACTGCAGCAGACAGCTCCCTGGGCACCAG
GCAGCTAACAGACACAGCCGCCAGCCCAAACAGCAGCGGCATGGGCAGCGCCAGCCCGGGTCTGAGCAGCGTATC
CCCCAGCCACCTCCTGCTGCCCCCGACACGGTGTGCGGGACAGGCTTGGAGAAGGCGGCAGCGGGGGCAGTGGG
TCTCGAGAGACGGGACTGGAGTCCCAGTCCACCCGCCACGCCGAGCAGGGCCTGTCCGCTTCTACCTCTCCTA
CTTTGACATGCTGTACCCTGAGGACAGCAGCTGGGCAGCCAAGGCCCTGGGGCCAGCAGTCGGGAGGAGCCACC
TGAGGAGCCTGAGCAGTGCCCGGTCAATTGACAGCCAAGCCCCAGCGGGCAGCCTGGACTTGGTGCCCGCGGGCT
GACCTTGGAGGAGCACTCGCTGGAGCAGGTGCAGTCCATGGTGGTGGGCGAAGTGCTCAAGGACATCGAGACGGC
CTGCAAGCTGCTCAACATCACCGCAGATCCCATGGACTGGAGCCCCAGCAATGTGCAGAAGTGCTCCTGTGGAC
AGAGCACCAATACCGGCTGCCCCCATGGGCAAGGCCTTCCAGGAGCTGGCGGGCAAGGAGCTGTGCGCCATGTC
GGAGGAGCAGTTCGCGCAGCGCTCGCCCCCTGGGTGGGGATGTGCTGCACGCCACCTGGACATCTGGAAGTCAGC
GGCCTGGATGAAAGAGCGGACTTCACCTGGGGCGATTCACTACTGTGCCTCGACCAGTGAGGAGAGCTGGACCGA
CAGCGAGGTGGACTCATCATGCTCCGGGCAGCCCATCCACCTGTGGCAGTTCCTCAAGGAGTTGCTACTCAAGCC
CCACAGCTATGGCCGCTTCATTAGGTGGCTCAACAAGGAGAAGGGCATCTTCAAATGAGGACTCAGCCAGGT
GGCCCGGCTGTGGGGCATCCGCAAGAACCGTCCCGCCATGAACTACGACAAGCTGAGCCGCTCCATCCGCCAGTA
TTACAAGAAGGGCATCATCCGGAAGCCAGACATCTCCAGCGCCTCGTCTACCAGTTCGTGCACCCCATCTGAGT
GCCTGGCCCAGGGCCTGAAACCCGCCCTCAGGGGCCTCTCTCCTGCCTGCCTCAGCCAGGCCCTGAGATG
GGGGAAAACGGGCAGTCTGCTCTGCTGCTCTGACCTTCCAGAGCCCAAGGTCAGGGAGGGGCAACCAACTGCCCC
AGGGGGATATGGGTCTCTGGGGCCTTCGGGACCATGGGGCAGGGGTGCTTCCTCCTCAGGCCAGCTGCTCCCC
TGAGGACAGAGGGAGACAGGGCTGCTCCCCAACACCTGCCTCTGACCCAGCATTTCCAGAGCAGAGCCTACAG
AAGGGCAGTGACTCGACAAAGGCCACAGGCAGTCCAGGCCTCTCTGCTCCATCCCCCTGCCTCCCATTTCTGCA
CCACACCTGGCATGGTGCAGGGAGACATCTGCACCCCTGAGTTGGGCAGCCAGGAGTGCCCCCGGAATGGATAA
TAAAGATACTAGAGAACTG

2097/6881
FIGURE 1930

MGSASPGGLSSVSPSHLLLPPDTVSRTGLEKAAAGAVGLERRDWSPSPPATPEQGLSAFYLSYFDMLYPEDSSWAA
KAPGASSREEPPEEPEQCPVIDSQAPAGSLDLVPGGLTLEEHSLQVQSMVVGEVLKDIETACKLLNITADPMDW
SPSNVQKWLWTEHQYRLPPMGKAFQELAGKELCAMSEEQFRQRSPLGGDVLHAHLDIWKSAAWMKERTSPGAIH
YCASTSEESWTDSEVDSSCSGQPIHLWQFLKELLLKPHSYGRFIRWLNKEKGIFKIEDSAQVARLWGIRKNRPAM
NYDKLSRSIRQYYKKGIIRKPDISQRLVYQFVHP I

2098/6881
FIGURE 1931

CGGCGGCCGAGCTCGCGCATCCCAGCCATCACTCTTCCACCTGCTCCTTAGAGAAGGGAAGATGAGTGAGTCGAG
CTCGAAGTCCAGCCAGCCCTTGGCCTCCAAGCAGGAAAAGGACGGCACTGAGAAGCGGGGCCGGGGCAGGCCGCG
CAAGCAGCCTCCGGTGAGTCCCGGGACAGCGCTGGTAGGGAGTCAGAAGGAGCCCAGCGAAGTGCCAACACCTAA
GAGACCTCGGGGCGGACCAAAGGGAAGCAAAAACAAGGGAGAAGGAGGAAGAGGAGGGCATCTCGCAGGAGTCCT
CGGAGGAGGAGCAGTGACCCATGCGTGCCGCTGCTCCTCACTGGAGGAGCAGCTTCCTTCTGGGACTGGACAGC
TTTGCTCCGCTCCCACCGCCCCCACCCCTTCCCCAGGCCACCATCACCACCGCTCTGGCCGCCACCCCATCT
TCCACCTGTGCCCTCACCACCACACTACACAGCACACCAGCCGCTGCAGGGCTCCCATGGGCTGAGTGGGGAGCA
GTTTTCCCCTGGCCTCAGTTCCCAGCTCCCCCGGCCACCCACGCATACACACATGCCCTCCTGGACAAGGCTAA
CATCCCACCTTAGCCGCACCCTGCACCTGCTGCGTCCCCACTCCCTTGGTGGTGGGGACATTGCTCTCTGGGCTTT
TGGTTTGGGGGCGCCCTCTCTGCTCCTTCACTGTTCCCTCTGGCTTCCCATAGTGGGGCCTGGGAGGGTTCCCT
GGCCTTAAAAGGGGCCCCAAGCCCCATCTCATCCTGGCAGCCCTACTCCACTGCCCTGGCAGCAGCAGGTGTGGC
CAATGGAGGGGGGTGCTGGCCCCCAGGATTCCCCCAGCCAAACTGTCTTTGTCACCACGTGGGGCTCACTTTTCA
TCCTTCCCCAACTTCCCTAGTCCCCGTACTAGGTTGGACAGCCCCCTTCGGTTACAGGAAGGCAGGAGGGGTGAG
TCCCCTACTCCCTCTTCACTGTGGCCACAGCCCCCTTGCCCTCCGCCTGGGATCTGAGTACATATTGTGGTGATG
GAGATGCAGTCACTTATTGTCCAGGTGAGGCCCAAGAGCCCTGTGGCCGCCACCTGAGGTGGGCTGGGGCTGCTC
CCCTAACCCCTACTTTGCTTCCGCCACTCAGCCATTTCCCCCTCCTCAGATGGGGCACCAATAACAAGGAGCTCAC
CCTGCCCCGCTCCCAACCCCCCTCCTGCTCCTCCCTGCCCCCAAGGTTCTGGTTCCATTTTTCTCTGTTCACAA
ACTACCTCTGGACAGTTGTGTTGTTTTTGTTCATGTTCCATTCTTCGACATCCGTCATTGCTGCTGCTACCAG
CGCCAAATGTTATCCTCATTGCCTCCTGTTCTGCCCACGATCCCCTCCCCAAGATACTCTTTGTGGGGAAGAG
GGGCTGGGGCATGGCAGGCTGGGTGACCGACTACCCAGTCCCAGGGAAGGTGGGGCCCTGCCCCTAGGATGCTG
CAGCAGAGTGAGCAAGGGGGCCCAAATCGACCATAAAGGGTGTAGGGGCCACCTCCTCCCCCTGTTCTGTGGGG
AGGGGTAGCCATGATTGTCCCAGCCTGGGGCTCCCTCTCTGGTTTCTATTGTCAGTTACTTGAATAAAAAAAA
TATCCTTTTCTGG

2099/6881
FIGURE 1932

GGTGGCCACAGAGCAACTTCCTCTAGAGGGAGCTGATTGGAGCCGGGTGCCGCTGGCACCTCTATGATCACTGGA
GTCTCGCGGGTCCCTCGGGCTGCACAGGGACAAGTAAAGGCTACATCCAGATGCCGGGAATGCACTGACGCCC
TCCTGGAAACTGGGCTCCCACTCAGCCCCCTGGGAGCAGCAGCCGCCAGCCCCCTCGGGACCTCCATCTCCACCCTG
CTGAGCCACCCGGGTGGGCCAGGATCCCGGCAGGCTGATCCCGTCTCCACTGAGACCTGAAAAATGGCTTCGG
GGCAAGGCCCAGGTCTCTCCAGGCAGGAGTGGGAGAGCCTGCCCTGCCCTCTGCTTCTGCAGGAACAGGAGGCT
GAAGGGGTGGCTGCCCTGCCGACCCAGAGATGGTCACCTTACCTCTGCAACCTACAGCACCATGGGGCAGGTGG
GACGGCAGCTCGCCATCATCGGGGACGACATCAACCGACGCTATGACTCAGAGTTCCAGACCATGTTGCAGCACC
TGCAGCCCACGGCAGAGAATGCCTATGAGTACTTCACCAAGATTGCCACCAGCCTGTTTGAGAGTGGCATCAATT
GGGGCCGTGTGGTGGCTCTTCTGGGCTTCGGCTACCGTCTGGCCCTACACGTCTACCAGCATGGCCTGACTGGCT
TCCTAGGCCAGGTGACCCGCTTCGTGGTTCGACTTCATGCTGCATCACTGCATTGCCCGGTGGATTGCACAGAGGG
GTGGCTGGGTGGCAGCCCTGAACCTGGGGCAATGGTCCCATCCTGAACGTGCTGGTGGTTCTGGGTGTGGTTCTGT
TGGGCCAGTTTGTGGTACGAAGATTCTTCAAAATCATGACTCCCAAGGGTGCCCTTTGGGGTCCCGGTTCCAGACCC
CTGCCCTGGACTTAAGCGAAGTCTTTGCCCTCTCTGTTCCCTTGAGGGGTCCCCCTCAAGAGTACAGAAGCTTT
AGCAAGTGTGCACTCCAGCTTCGGAGGGCCCCTGCGTGGGGGCCAGTCAGGCTGCAGAGGCACCTCAACATTGCA
TGGTGCTAGTGGGCCCTCTCTCTGGGGCCAGGGGCTGTGGCCGTCTCCTCCCTCAGCTCTCTGGGACCTCCTTAG
CCCTGTCTGCTAGGCGCTGGGGAGACTGATAACTTGGGGAGGCAAGAGACTGGGAGCCACTTCTCCCCAGAAAGT
GTTTAACGGTTTTAGCTTTTTATAATACCTTGTGAGAGCCATTCCACCATTCTACCTGAGGCCAGGACGTCT
GGGGTGTGGGGATTGGTGGGTCTATGTTCCCCAGGATTGAGCTATTCTGGAAGATCAGCACCTAAGAGATGGGA
CTAGGACCTGAGCCTGGTCTCGCCGTCCCTAAGCATGTGTCCAGGAGCAGGACCTACTAGGAGAGGGGGGCCA
AGGTCCTGCTCAACTCTACCCCTGCTCCCATTCCTCCCTCCGGCCATACTGCCTTTGCAGTTGGACTCTCAGGGA
TTCTGGGCTTGGGGTGTGGGGTGGGGTGGAGTCGCAGACCAGAGCTGTCTGAACTCACGTGTCAGAAGCCTCCAA
GCCTGCCTCCCAAGGTCTCTCAGTTCTCTCCCTTCCTCTCTCCTTATAGACACTTGCTCCCAACCCATTCACTA
CAGGTGAAGGCTCTCACCCCATCCCTGGGGGCCTTGGGTGAGTGGCCTGCTAAGGCTCCTCCTTGCCAGACTA
CAGGGCTTAGGACTTGGTTTGTATATCAGGGAAAAGGAGTAGGGAGTTCATCTGGAGGGTTCTAAGTGGGAGAA
GGACTATCAACACCACTAGGAATCCCAGAGGTGGGATCCTCCCTCATGGCTCTGGCACAGTGTAAATCCAGGGGTG
TAGATGGGGGAACTGTGAATACTTGAACCTGTGTTCCCCCACCCTCCATGCTCCTCACCTGTCTAGGTCTCCTCAG
GGTGGGGGGTGACAGTGCCTTCTCTATTGGGCACAGCCTAGGGTCTTGGGGGTGAGGGGGGAGAAGTTCTTGATT
CAGCCAAATGCAGGGAGGGGAGGCAGATGGAGCCCATAGGCCACCCCTATCCTCTGAGTGTTTGGAAATAAACT
GTGCAATCCCCTC

2100/6881
FIGURE 1933

MGQVGRQLAIIGDDINRRYDSEFQTMLOHLOPTAENAYEYFTKIATSLFESGINWGRVVALLGFGYRLALHVVYQH
GLTGFLGQVTRFVVDFMLHHCIARWIAQRGGWVAALNLGNGPILNVLVVLGVVLLGQFVVRFFKS

2101/6881
FIGURE 1934

GGCCGGAGCCGTGCGAGTTCTCTACCCTGCTTCGCGAGCGGGCGAGAGAACGCGAGTCCCAGGATCCCCGGCACC
CAGTTCTCTTCCACTGCATGATTTTTCTTTGACCGGGTATTCCCACCAGGAAGTGGACAGGATGAAGTGTTTGA
AGAGATTGCCATGCTTGTCCAGTCAGCCCTGGATGGCTATCCAGTATGCATCTTTGCCTATGGCCAGACAGGCAG
TGGCAAGACCTTCACAATGGAGGGTGGGCCTGGGGGAGACCCCCAGTTGGAGGGGCTGATCCCTCGGGCCCTGCG
GCACCTCTTCTCTGTGGCTCAGGAGCTGAGTGGTCAGGGCTGGACCTACAGCTTTGTAGCAAGCTACGTAGAGAT
CTACAATGAGACTGTCCGGGACCTGCTGGCCACTGGAACCCGGAAGGGTCAAGGGGGCGAGTGTGAGATTGCGCG
TGCAGGGCCAGGGAGTGAGGAGCTCACTGTCACCAATGCTCGATATGTCCCTGTCTCCTGTGAGAAAAGAAGTGGA
CGCCCTGCTTCATCTGGCCCGCCAGAATCGGGCTGTGGCCCGCACAGCCAGAAATGAACGGTCATCACGCAGCCA
CAGTGTATTCCAGCTACAGATTTCTGGGGAGCACTCCAGCCGAGGCCTGCAGTGTGGGGCCCCCTCAGTCTTGT
GGACCTGGCCGGGAGTGAGCGACTTGACCCCGGCTTAGCCCTCGGCC

2102/6881

FIGURE 1935

MDPQ RSP LLEV KGNIELKRPLIKAPS QLP LSG SRLKRRPD QMEDGLEPEKKRTRGLGATTKITTSHPRVPSLT TV
PQTQGQTTAQKVS KKTGPRCSTAIATGLKNQKPVPAVPVQKSGTSGVPPMAGGKKPSKRPAWDLKGQLCDLNAEL
KRCRERTQTLDQENQQLQDQLRDAQQOVKALGTERTTLEGH LAKVQAQAEQGQQLK NLRACVLELEERLSTQEG
LVQELQKKQVELQEERRGLMSQLEEKERRLQTSEAALSSSQAEVASLRQETVAQAALLTEREERLHGLEMERRRL
HNQLQELKGNIRVFCRVRPVLPG EPTPPPGLLLFP SGPGGPSDPPTRLSLSRSDERRGTL SGAPAPPTRHDFSFD
RVFPPGSGQDEVFEEIAMLVQSALDGY PVCIFAYGQTGSGKTFTMEGGPGGDPQLEGLIPRALRHLFSVAQELSG
QGWTYSFVASYVEIYNETVRDLLATGTRKGQGGECEIRRAGPGSEELTVTNARYVPVSCEKEVDALLHLARQNRA
VARTAQNERSSRSHSVFQLQISGEHSSRGLQCGAPLSLVDLAGSERLDPGLALGPGERERLRETQAINSSLSTLG
LVIMALSNKESHVPYRNSKLT YLLQNSLGGSAKMLMFVNI SPLEENVSESLNSLRFASKVNQC VIGTAQANRK

2103/6881
FIGURE 1936

CTCTCGGCTTTCGGCTCGGAGGAGGCCAAGGTGCAACTTTCTTCGGTCATCCTGAATCTGGGTTCATCCGACACC
AGCTGCCTCCACCATGCCACCGAAGTTCGACCCCAACGAGATCAAGGTCGTATACCTGAGGTGCACCAGAGGTGA
AGTCGGGTGCCACTTCTGCCCTGGCCCCCAAGATCGGCCCCCTGGGTCTGTCTCCAAAAAGGTTGGTGATGACAT
TGCCAAGGCAACGGGTGACTGGAAGGGCCTGAGGATTACAGTGAAACTGACCATTGAGAACAGACAGGCCCAGAT
TGAGGTGGTGCCCTTCTGCCTCTGCCCCGATCATCAAAGCCCTCAAGAAACCACCAAGAGACAGAAAGAAACAGAA
AAACATTAAACACAATGGGAATATCACTTTTGATGAGATCGTCAACATTGCTCGACAGATGCGGCACCGATCCTT
AGCCAGAGAACTCTCTGGAACCATTAAAGAGATTCCGGGGACTGCCAGTCTATGGGCTGTAATGTTGATGGCCA
CCACCCTCATGACATCATAGATGACATCAACAGTGGTGCTGTGGAATGCCAGCTAGTTAAGCACAAAGGAAAAT
ATTTCATAAAAGGATCATTGACAACCTGGT

2104/6881
FIGURE 1937

GTTCCGGCGGGGGCGGCCGAGGGGGAAGAGTGTGTGTCTGCGGGAGAAAGAGGAGAATCACCCAAGCGGCCTCAG
AAGTCCCAGGGAGTGGAGGCCCTGCCATGGAGCCGTGTGGTGTATGTGTGGTAACACCATGTCTGTGCCCTGC
TCAACGATGCTGCCACCGTGTCTGGAGCTGAGCGGGAACGGCCGTGGTTATTTTTTTTACATGGACTTGGAGACA
CAGGGCACAGCTGGGCTGACGCCCTCTCCACCATTCGGCTCCCTCACGTCAAGTACATCTGTTCCCATGAGCCTA
GGATCCCTGTGACCCTCAACATGAAGATGGTGTATGCCCTCCTGGTTTGACCTGATGGGGCTGAGTCCAGATGCCC
CAGAGGACGAGGCTGGCATCAAGAAGGCAGCAGAGAACATCAAGGCCTTGATTGAGCATGAAATGAAGAACGGGA
TCCCTGCCAATCAAATCATCCTGGGAGGCTTTTACAGGGCCGGGCCCTGTCCCTCTACATGGCCCTCACCTGCC
CCCACCTCTGGCTGGCATCCTGGCTTTGAGCTGCTGGCCGCTCTGCACCGGGCCTTCCCCCAGGCAGCTAATG
GCAGTGCCAAGGACCTGGCCATCCTCCAGTGCCATGGGGAGCTGGACCCCATGGTGCCCGTACGGTTTGGGGCCC
TGATGGCTGAGAAGCTCCGGTCTGTTGTACACCTGCCAGGGTCCAGTTCAGACATACTGGGTGTCATGCACA
GCTCCTGTCTCAGGAGATGGCAGCTGTGAAGGAATTTCTTGAGAAGCTGCTGCCTCCTGTCTAACTAGTCGCTG
GCCCCAGTGCACTACCCAGCTCATGGGGGACTCAGCAAGTAAGCATGGCACCATCTTGGGTCTGAGCTGGTCGA
GCCCCGTGTCCCCACCTTCTGACCTGTCTTTTCCACAGGCCTCTAGGGGCAGGTGGCAAGGCCTGGCTGGGC
CTTCTTCTTGGCCTCAGCCACCTGGCTCTGTCTGCAGTAGGGGCAGGCTGCTTTCTTATCCCATTTCCCTGGAG
GCGGGCCCCCTGGCAGCAGTATTGGAGGGGCTACAGGCAGCTGGAGAAAGAGGCCAGCCACTGACCCACTCAC
TCAGGACCTCACTCACTAGCCCCACTTTGGGCCCCCTCCTGTAACTTAGGGTTTGGCCCATGGGGCCCTCCCAG
GCCCCTGCCCCAACTGATTCTGCCCAGATAATCTTGTGTCTCCTGCCTCCACTCAGCTGCTTCTCAGTCATGAAC
GTGGCCATGGCCCCGGGGGTCCCTTGTCTGTGGGCTCCCTGTCCCTGGGCAGGAGTGCTGGTGAGGAGGTGG
AGCCTTTTGAGGGGGGCTTCCCTCAGCTGTTTCCCCACACTGGGGGGCTGGGGCCCTGCCTCCCCGTTACCCTCC
TTCCCTGCAGGCCTGGAGCCTGTAGGGCTGGACTGAGGTTTCAGGTCTCCCCCAGCTGTCTCACCCCCACTTTGT
CCCCACTCTAGAGCAGGGAGGCAGTGGGGGAGGAGTTGTGTCTTGTCTTCTGTCTCCATGTGGTTTTTGGGTGT
TTTCTTCTTGTGTCTCCTGGATTCTGATAAAATTAAAGAAATTGCTTCCTC

2105/6881
FIGURE 1938

GTGTGTCTGCGGGAGAAAGAGGAGAATCACCCAAGCGGCCTCAGAAGTCCCAGGGAGTGGAGGCCCCCTGCCATGG
AGCCGTGTGGTGTATGTGTGGTAACACCATGTCTGTGCCCCTGCTCAACGATGCTGCCACCGTGTCTGGAGCTGA
GCGGGAAACGGCCGTGGTTATTTTTTTTACATGGACTTGGAGACACAGGGCACAGCTGGGCTGACGCCCTCTCCAC
CATTCGGCTCCCTCACGTCAAGTACATCTGTTCCCATGAGCCTAGGATCCCTGTGACCCTCAACATGAAGATGGT
GATGCCCTCCTGTCAAGGCCTTGATTGAGCATGAAATGAAGAACGGGATCCCTGCCAATCAAATCATCCTGGGAG
GCTTTTCACAGGGCCGGGCCCTGTCCCTCTACATGGCCCTCACCTGCCCCCACCCTCTGGCTGGCATCCTGGCTT
TGAGCTGCTGGCCGCCTCTGCACCGGGCCTTCCCCCAGGCAGCTAATGGCAGTGCCAAGGACCTGGCCATCCTCC
AGTGCCATGGGGAGCTGGACCCCATGGTGCCCGTACGGTTTGGGGCCCTGATGGCTGAGAAGCTCCGGTCTGTTG
TCACACCTGCCAGGGTCCAGTTCCAGACATACTGGGTGTCATGCACAGCTCCTGTCCTCAGGAGATGGCAGCTG
TGAAGGAATTTCTTGAGAAGCTGCTGCCTCCTGTCTAACTAGTCGCTGGCCCCAGTGCAGTACCCACGCTCATGG
GGGACTCAGCAAGTAAGCATGGCACCATCTTGGGTCTGAGCTGGTCGAGCCCCTGTCCCCACCCTTCCTGACCTG
TCCTTTTCCCACAGGCCTCTAGGGGCAGGTG

2106/6881
FIGURE 1939

GAAAGAGGAGAATCACCCAAGCGGCCTCAGAAAGTCCCAGGGAGTGGAGGCCCCCTGCCATGGAGCCGTGTGGTGTA
TGTGTGGTAACACCATGTCTGTGCCCCCTGCTCAACGATGCTGCCACCGTGTCTGGAGCTGAGCGGGAAACGGCCG
TGGTTATTTTTTTACATGGACTTGGAGACACAGGGCACAGCTGGGCTGACGCCCTCTCCACCATTCGGCTCCCTC
ACGTCAAGTACATCTGTTCCCATGAGCCTAGGATCCCTGTGACCCTCAACATGAAGATGGTGATGCCCTCCTGGT
TTGACCTGATGGGGCTGAGTCCAGATGCCCCAGAGGACGAGGCTGGCATCAAGAAGGCAGCAGAGAACATCAAGG
CCTTGATTGAGCATGAAATGAAGAACGGGATCCCTGCCAATCAAATCATCCTGGGAGGCTTTTCACAGGGCCGGG
CCCTGTCCCTCTACATGGCCCTCACCTGCCCCCACCCTCTGGCTGGCATCCTGGCTTTGAGCTGCTGGCCGCCTC
TGCACCGGGCCTTCCCCCAGGGTCCAGTTCCAGACATACCTGGGTGTCATGCACAGCTCCTGTCCCTCAGGAGATG
GCAGCTGTGAAGGAATTTCTTGAGAAGCTGCTGCCTCCTGTCTAACTAGTCGCTGGCCCCAGTGCAGTACCCAG
CTCATGGGGGACTCAGCAAGTAAGCATGGCACCATCTTGGGTCTGAGCTGGTCGAGCCCCCTGTCCCCACCCTTCC
TGACCTGTCCTTTTCCACAGGCCTCTAGGGGCAGGTGGCAAGGCCTGGCTGGGCCTTCCTTCCTGGCCTCAGCC
ACCTGGCTCTGTCTGCAGTAGGGGCAGGCTG

2107/6881
FIGURE 1940

GTTATTTTTTTTACATGGACTTGGAGACACAGGGCACAGCTGGGCTGACGCCCTCTCCACCATTCGGCTCCCTCAC
GTCAAGTACATCTGTTCCCATGAGCCTAGGATCCCTGTGACCCCTCAACATGAAGATGGTGATGCCCTCCTGGTTT
GACCTGATGGGGCTGAGTCCAGATGCCCCAGAGGACGAGGCTGGCATCAAGAAGGCAGCAGAGAACATCAAGGCC
TTGATTGAGCATGAAATGAAGAACGGGATCCCTGCCAATCAAATCATCCTGGGAGGCTTTTCACAGGGCCGGGCC
CTGTCCCTCTACATGGCCCTCACCTGCCCCCAGCTGTCTCACCCCCACTTTGTCCCCACTCTAGAGCAGGGAGGC
AGTGGGGGAGGAGTTGTGTCTTGTCTTCTGTCTCCATGTGGTTTTTGGGTGTTTTTCTTCTTGTGTCTCGGATT
TGATAAAATTAAAGAAATTGCTTCCTC

2108/6881
FIGURE 1941

ACATGAAGATGGTGATGCCCTCCTGGTTTGACCTGATGGGGCTGAGTCCAGATGCCCCAGAGGACGAGGCTGGCA
TCAAGAAGGCAGCAGAGAACATCAAGGCCTTGATTGAGCATGAAATGAAGAACGGGATCCCTGCCAATCAAATCA
TCCTGGGAGGCTTTTCACAGGGCCGGGCCCTGTCCCTCTACATGGCCCTCACCTGCCCCACCCCTCTGGCTGGCA
TCCTGGCTTTGAGCTGCTGGCCGCCTCTGCACCGGGCCTTCCCCCAGGCAGCTAATGGCAGTGCCAAGGACCTGG
CCATCCTCCAGTGCCATGGGGAGCTGGACCCCATGGTGCCCGTACGGTTTGGGGCCCTGATGGCTGAGAAGCTCC
GGTCTGTTGTCACACCTGCCAGGGTCCAGTTCCAGACATACTGGGTGTCATGCACAGCTCCTGTCCTCAGGAGA
TGGCAGCTGTGAAGGAATTTCTTGAGAAGCTGCTGCCTCCTGTCTAACTAGTCGCTGGCCCCAGTGCAGTACCCC
AGCTCATGGGGGACTCAGCAAGTAAGCATGGCACCATCTTGGGTCTGAGCTGGTCGAGCCCCCTGTCCCCACCCCTT
CCTGACCTGTCCTTTTCCCACAGGCCTCTAGGGGCAGGTGGCAAGGCCTGGCTGGGCCTTCCCTTCCTGGCCTCAG
CCACCTGCCTCCACTCAGCTGCTTCTCAGTCATGAACGTGGCCATGGCCCCGGGGGTCCCCCTTGCTGCTGTGGGC
TCCCTGTCCCTGGGCAGGAGTGCTGGTGAGGAGGTGGAGCCTTTTGAGGGGGGCCTTCCCTCAGCTGTTTCCCCA
CACTGGGGGGCTGGGCCCTGCCTCCCGTTACCCCTCCTTCCCTGCAGGCCTGGAGCCTGTAGGGCTGGACTGAGG
TTCAGGTCTCCCCCAGCTGTCTACCCCCACTTTGTCCCCACTCTAGAGCAGGGAGGCAGTGGGGGAGGAGTTG
TGTCTTGTCTTCTGTCTCCATGTGGTTTTTTGGGTGTTTTTCTTCTTGTGTCCTGGATTCTGATAAAATTAAAGAA
ATTGCTTCCTC

2109/6881
FIGURE 1942

CGGCACGAGGCGGTGGGAGTGGGAAGGAAGGCGGAGGGAACCATGCGAGGTTCTGAGAATTGCGGCGAGGGTCGC
CTCGAGAGACGGTTTCTGAGCAGGAATTCTGAAATCCCCACCACTTCCTCCCTCCGGGGGATTTGATCCCCT**ATG**

GCCACCGCTAACAGCATCATCGTGCTGGATGATGATGACGAAGATGAAGCAGCTGCTCAGCCAGGGCCCTCCAC
CCTCTCCCAATGCGGCCTCACCTGGGGCAGAAAGCCCCTAGCTCCTCTGAGCCTCATGGGGCCAGAGGAAGCAGT
AGTTCGGGCGGCAAGAAATGCTACAAGCTGGAGAATGAGAAGCTGTTTGAAGAGTTTCTTGAACCTTTGTAAGATG
CAGACAGCAGACCACCTGAGGTGGTCCCATTCCTCTATAACCGGCAGCAACGTGCCCCACTCTCTGTTTTTGGCC
TCGGCGGAGTTCTGCAACATCCTCTCTAGGGTCTGTCTCGGGCCCGGAGCCGGCCAGCCAAGCTCTATGTCTAC
ATCAATGAGCTCTGCACTGTTCTCAAGGCCCCACTCAGCCAAAAAGAAGCTGAACTTGGCCCCCTGCCGCCACCACC
TCCAATGAGCCCTCTGGGAATAACCTTCCCACACACCTCTCCTTGGACCCCAAAATGCTGAAAACACTGCCTCT
CAGTCTCCAAGGACCCGTGGTTCCCGGCGGCAGATCCAGCGTTTGGAGCAGCTGCTGGCGCTCTATGTGGCAGAG
ATCCGGCGGCTGCAGGAAAAGGAGTTGGATCTCTCAGAATTGGATGACCCAGACTCCGCATACCTGCAGGAGGCA
CGGTTGAAGCGTAAGCTGATCCGCCTCTTTGGGCGACTATGTGAGCTGAAAGACTGCTCTTCACTGACCGGCCGT
GTCATAGAGCAGCGCATCCCCTACCGTGGCACCCTGCTACCCAGAGGTTAACAGGCGCATTGAGCGGCTCATCAAC
AAGCCAGGGCCTGATACCTTCCCTGACTATGGGGATGTGCTTCGGGCTGTAGAGAAGGCAGCTGCCCGACACAGC
CTTGGCCTCCCCGACAGCAGCTCCAGCTCATGGCTCAGGATGCCTTCCGAGATGTGGGCATCAGGTTACAGGAG
CGACGTCACCTCGATCTCATCTACAACCTTTGGCTGCCACCTCACAGATGACTATAGGCCAGGCGTTGACCCTGCA
CTATCAGATCCTGTGTTGGCCCCGGCGCTTCGGGAAAACCGGAGTTTGGCCATGAGTCGGCTGGATGAGGTCATC
TCCAAATACGCAATGTTGCAAGACAAAAGTGAGGAGGGCGAGAGAAAAAAGAGAAGAGCTCGGCTCCAAGGCACC
TCTTCCCACTCTGCAGACACCCCCGAAGCCTCCTTGGATTCTGGTGAGGGCCCTAGTGGAATGGCATCCCAGGGG
TGCCCTTCTGCCTCCAGAGCTGAGACAGATGACGAAGACGATGAGGAGAGTGATGAGGAAGAGGAGGAGGAGGAG
GAAGAAGAAGAGGAGGAGGCCACAGATTCTGAAGAGGAGGAGGATCTGGAACAGATGCAGGAGGGTCAGGAGGAT
GATGAAGAGGAGGACGAAGAGGAAGAAGCAGCAGCAGGTAAAGATGGAGACAAGAGCCCCATGTCCTCACTACAG
ATCTCCAATGAAAAGAACCTGGAACCTGGCAAACAGATCAGCAGATCTTCAGGGGAGCAGCAAAACAAAGGACGC
ATAGTGTCACCATCGTTACTGTCAGAAGAACCCCTGGCCCCCTCCAGCATAGATGCTGAAAGCAATGGAGAACAG
CCTGAGGAGCTGACCCTGGAGGAAGAAAGCCCTGTGTCTCAGCTCTTTGAGCTAGAGATTGAAGCTTTGCCCTG
GATACCCCTTCTCTGTGGAGACGGACATTTCTCTTCCAGGAAGCAATCAGAGGAGCCCTTCACTGTCTTA
GAGAATGGAGCAGGCATGGTCTCTTCTACTTCTTCAATGGAGGCGTCTCTCCTCACAACCTGGGGAGATTCTGGT
CCCCCTGCAAAAAATCTCGGAAGGAGAAGAAGCAAACAGGATCAGGGCCATTAGGAAACAGCTATGTGGAAAGG
CAAAGGTCAGTGCATGAGAAGAATGGGAAAAAGATATGTACCCTGCCAGCCACCTTCCCCCTTGGCTTCTCTG
GCCCCAGTTGCTGATTCTCTCCACGAGGGTGGACTCTCCAGCCATGGCCTGGTGACCAGCTCCCTCTGCATCCCT
TCTCCAGCCCGGCTGTCCCAAACCCCCATTACAGCCTCCTCGGCCTGGTACTTGCAAGACAAGTGTGGCCACA
CAATGCGATCCAGAAGAGATCATCGTGCTCTCAGACTCTGAT**TAACT**GCCTCCCCCTTCTCCCTGCCTCCAGAATG
TTCTGGGATAACATTTGGAGGAAGGTGGGAAGCAGATGACTGAGGAAGGGATGGACTAAGCTAATCCCCTTTTGG
TGGTGTTTCTTT

2110/6881
FIGURE 1943

MATANSIIVLDDDDDEDEAAAQPGPSHPLPNAASPGAEAPSSSEPHGARGSSSSSGGKKCYKLENEKLFEFFLELCK
MQTADHPEVVPFLYNRQQRHSLFLASAEFCNILSRVLSRARSRAKLYVYINELCTVLKAHSAKKKLNLA PAAT
TSNEPSGNNPPTHLSLDPTNAENTASQSPRTGRSRRQIQRLQQLALYVAEIRRLQEKELDLSELDDPD SAYLQE
ARLKRKLIRLFGRLCELKDCSSLTGRVIEQRIPIYRGTRYPEVNRRIERLINKPGPDTFPDYGDVLR AVEKAAARH
SLGLPRQQLQLMAQDAFRDVGIRLQERRHLDLIYNFGCHLTDDYRPGVDPALSDPVLARRLRENRLAMSR LDEV
ISKYAMLQDKSEEGERKKRRARLQGTSSHSADTPEASLDSGEGPSGMASQGCPSASRAETDDEDDEESDEEEEEE
EEEEEEEATDSEEEEDLEQM QEGQEDDEEEDEEEEAAGKDGDKSPMSSLQISNEKNLEPGKQISRSSGEQQNKG
RIVSPSLLSEEPLAPSSIDAESNGEQPEELTLEESPVSQLFELEIEALPLDTPSSVETDISSSRKQSEEPFTTV
LENGAGMVSSTSFNGGVSPHNWGDSPGPPCKKSRKEKKQTGSGPLGNSYVERQSVHEKNGKKICTLPSPPSPLAS
LAPVADSSTRVDSPSHGLVTSSLCIPSPARLSQTPHSQPPRPGTCKTSVATQCDPEEIIVLSDSD

2111/6881
FIGURE 1944

GGCACGAGGGCTGAGAAGAGTTTTGCACGTGGATCGCCGTTTCGGGTGGGCGAGATGGAGACAGCCCCAAGCCGG
GCAAGGATGTCCCGCCCAAGAAAGACAACTTCAGACCAAGAGAAAGAAACCGCGGCGATACTGGGAGGAAGAGA
CCGTTCCGACCACAGCCGGAGCCTCTCCAGGGCCTCCTCGTAACAAGAAGAATCGGGAGCTCCGTCCTCAGAGAC
CAAAAAATGCTTACATCTTAAAGAAGTCTCGGATCTCTAAGAAGCCTCAGGTCCCGAAGAAACCCGAGAATGGA
AGAACCCGGAGTCCAGCGCGGCTTGTCCGGGGCCCAAGATCCATTCCCAGGCCCCGCCCCGTCCTGTGGAAG
TGGTCCAGAAGTTCTGTGCGATTGACAAATCCCGAAAGCTACCAATTCTAAAGCCAAAACCTCGAAGCCGACTTG
AGGTGGCTGAAGCTGAGGAAGAGGAAACAAGTATCAAAGCTGCTCGTTCTGAGCTGCTGCTTGCTGAAGAACCTG
GGTTTCTGGAAGGGGAGGATGGGGAAGACACAGCAAAGATATGCCAGGCTGACATTGTGGAGGCTGTGGACATTG
CAAGTGCAGCCAAGCACTTTGACTTGAATCTGCGGCAGTTTGGACCCTACAGACTAAACTACTCTCGAACTGGAA
GACACCTGGCTTTTGGAGGGCGCCGAGGTTCATGTGGCTGCCCTTGATTGGGTAAACAAAGAAGCTTATGTGCGAGA
TCAACGTCATGGAGGCGGTGCGGGACATCCGTTTCTCCATTCTGAGGCACTGCTTGCTGTTGCTCAGAACCCTG
GGCTCCACATCTATGACAATCAGGGCATTTGAGCTCCACTGTATCCGCCGCTGTGACCGAGTAACACGGCTTGAGT
TCCTGCCCTTCCACTTCCTCCTGGCTACAGCTTCAGAAACAGGGTTTCTAACCTACCTGGATGTGTGCTAGTGGGGA
AGATTGTGGCAGCTCTGAATGCTCGAGCTGGGCGGCTCGATGTTATGAGTCAGAACCCCTTACAATGCCGTATCC
ATCTCGGACACAGCAATGGTACTGTGTCTTTATGGAGTCCAGCTATGAAGGAGCCACTGGCAAAGATTCTCTGTCT
ATCGTGGTGGGGTCCGGGCTGTGGCAGTAGATTCTACAGGCACGTACATGGCCACCTCTGGCCTAGACCACCAGC
TGAAGATCTTTGACTTGCGAGGGACGTACCAGCCTCTGAGCACTCGGACCCTGCCCCATGGAGCAGGGCACCTGG
CCTTCTCCAGAGGGGACTGCTGGTGGCGGGAATGGGTGACGTTGTCAACATCTGGGCAGGGCAGGGCAAGGCCA
GCCCCACCTCCCTTGAACAGCCCTACCTCACCCACCGGCTCTCAGGCCCTGTGCATGGCCTTCAGTTCTGCCCCCT
TTGAAGATGTGCTGGGGGTGGGGCACACTGGGGGCATCACCAGCATGCTGGTCCCTGGGGCCGGTGAGCCCAACT
TCGATGGCCTGGAGAGTAATCCATACAGAAGCCGGAAGCAGCGCCAGGAGTGGGAGGTGAAGGCCCTGCTAGAGA
AGGTACCTGCAGAGCTTATTTGTCTGGACCCACGAGCCCTGGCCGAGGTGGATGTCATCTCCCTGGAGCAGGGAA
AGAAGGAGCAGATAGAGAGGCTGGGCTATGACCCGAGGCTAAGGCTCCCTTCCAGCCAAAGCCAAAGCAGAAGG
GCCGAGCTCCACGGCAAGCCTGGTGAAGAGGAAGAGGAAGGTGATGGATGAGGAACACAGGGACAAGGTCCGGC
AGAGCCTTCAGCAGCAGCATCATAAGGAGGCGAAGGCCAAGCCACGGGGGCCCGGCCATCTGCCCTGGACAGAT
TTGTGCGCTTGAGCCAGACTCCAGGGTTGCCTGGGAACAGTCTCTCCCAAGATCACCTGTAGGGAAATGAGTGT
CCCTGGAACAAGGAGGTGGGGGCAGTGTGGCCCCTTCCCCAACTGGGGGTGGACAGCTGTCTCCTGGGGTGGGTT
GGTATTAAAGAGGAAAAGCGATTTTTTGGAAAAAAAAAAAAAAAAAAAAA

2112/6881
FIGURE 1945

METAPKPGKDVPPKKDKLQTKRKKPRRYWEEETVPTTAGASPGPPRNKKNRELRPQRPKNAYILKKSRI SKKPQV
PKKPREWKNPESQRGLSGAQDPFPGPAPVPVEVVQKFCRIDKSRKLP HSKAKTRSRLEVAEAE EEEETS IKAARSE
LLLAEEP GFLEGEDGEDTAKICQADIVEAVD IASAAKHFDLNL RQFGPYRLNYSRTGRHLAFGGRRGHVAALDWV
TKKLMCEINVMEAVRDIRFLHSEALLAVAQNRWLHIYDNQGIELHCIRRCDRVTRLEFLPFHFL LATASETGFLT
YLDVSVGKIVAALNARAGRLDVMSQNPYN AVIHLGHSNGTVSLWSPAMKEPLAKILCHRGGVRAVAVDSTGT YMA
TSGLDHQLKIFDLRGTYQPLSTRTLPHGAGHLAFSQRGLLVAGMGDVVNIWAGQGKASPPSLEQPYLTHRLSGPV
HGLQFCPFEDVLGVGHTGGITSM LVPGAGEPNFDGLESNPYRSRKQRQEW EVKALLEKVPAELICLDPRALAEVD
VISLEQ GKKEQIERLG YDPQAKAPFQPKPKQKGRSSTASLVKRKRKVMDEEHRDKVRQSLQQQH HKEAKAKPTGA
RPSALDRFVR

2113/6881

FIGURE 1946

CTCTCTTCCACAGGAGGCCTACACGCCGCCGCTTGTGCTGCAGCCATGTCTCTAGTGATCCCTGAAAAGTTCCAG
CATATTTTGCAGTACTCAACACCAACATCGATGGGCGGCGGAAAATAGCCTTTGCCATCACTGCCATTAAAGGGT
GTGGGCCGAAGATATGCTCATGTGGTGTGAGGAAAGCAGACATTGACCTCACCAAGAGGGCGGGAGAACTCACT
GAGGATGAGGTGGAACGTGTGATCACCATTATGCAGAATCCACGCCAGTACAAGATCCCAGACTGGTTCTTGAAC
AGACAGAAGGATGTAAAGGATGGAATAACAGCCAGGTCCTAGCCAATGGTCTGGACAACAAGCTCCGTGAAGAC
CTGGAGCGACTGAAGAAGATTCGGGCCCATAGAGGGCTGCGTCACCTTCTGGGGCCTTCGTGTCCGAGGCCAGCAC
ACCAAGACCACTGGCCGCCGTGGCCGCACCGTGGGTGTGTCCAAGAAGAATAAGTCTGTAGGCCTTGTCTGTTA
ATAAATAGTTTATATACAAAAAA

2114/6881
FIGURE 1947

MSLVIPEKFQHILRVLNTNIDGRRKIAFAITAIGVGRRYAHVVLRKADIDLTKRAGELTEDEVERVITIMQNPR
QYKIPDWFLNRQKDVKGKYSQVLANGLDNKLREDLERLKKIRAHRLRHFHWGLRVRGQHTKTTGRRGRTVGVSK
KK

2115/6881
FIGURE 1948

GGAGAGGATCCCGGAGCCGGTGAGAATTCTCTGTTTTTCTCTACCATCCTTTCCAGGCCTTTTCCTCACCTAAT
GAGTCGTAGAGACGAGGGCCCAGAGAGTCTGTAAAGTGGCTGGTGAAAGATTAGTGTCCCAGGGCCCTACATCCG
GGAGGTGGTTTCGGGATAAAGAGAACTAGTCTTGGGAACAATGTAGGTGGAACTTAAGGGAATGGGAGAGCGGCC
CATAGAGGTGGACGGAGGGCGCGATTGGAGTAAAGCGGACCCGTGTGTAGGTATAGAGTTGAGTCAAGTGGAGTCA
CTGCCTCTGTCCCTCTGGTCAGCGTGATGGCCAGAGGCCTGGGGGGCCCCCACTGGGTGGCCGTGGGACTGCTGA
CCTGGGCGACCTTGGGGCTTCTGGTGGCTGGACTCGGGGGTTCATGACGACCTGCACGACGATCTGCAAGAGGACT
TCCATGGCCACAGCCACAGGCACTCACATGAAGATTCCACCATGGCCACAGCCATGCCCATGGCCATGGCCACA
CTCACGAGAGCATCTGGCATGGACATAACCCACGATCACGACCATGGACATTACATGAGGATTTACACCATGGCC
ATAGCCATGGCTACTCCCATGAGAGCCTCTACCACAGAGGACATGGACATGACCATGAGCATAGCCATGGAGGCT
ATGGGGAGTCTGGGGCTCCAGGCATCAAGCAGGACCTGGATGCTGTCACTCTCTGGGCTTATGCACTGGGGGCCA
CAGTGCTGATCTCAGCAGCTCCATTTTTTGTCTCTTCCCTTATCCCCGTGGAGTCAACTCTCCCCGGCATCGCT
CTCTACTTCAGATCTTGCTCAGTTTTTGTCTCCGGTGGGCTCCTGGGAGATGCTTTCTGCACTCATTCCTCATG
CTCTTGAACCTCATTCTCACCACACTCTGGAGCAACCCGGACATGGACACTCCACAGTGGCCAGGGCCCCATT
TGTCTGTGGGACTGTGGGTCTCAGTGAATTGTTGCCTTTCTTGTCTGTGGAGAAATTTGTGAGACATGTGAAAG
GAGGACATGGTCACAGTCATGGACATGGACACGCTCACAGTCATACACGTGGAAGTCATGGACATGGAAGACAAG
AGCGTTCTACCAAGGAGAAGCAGAGCTCAGAGGAAGAAGAAAAGGAAACAAGAGGGGTTTCAAGAGGCGAGGAG
GGAGCACAGTACCCAAAGATGGGCCAGTGAGACCTCAGAACGCTGAAGAAGAAAAAGAGGCTTAGACCTGCGTG
TGTCGGGGTACCTGAATCTGGCTGCTGACTTGGCACACAACCTTCACTGATGGTCTGGCCATTGGGGCTTCCTTC
GAGGGGGCCGGGGACTAGGGATCCTGACCACAATGACTGTCCTGCTACATGAAGTGCCCCACGAGGTCGGAGACT
TTGCCATCTTGGTCCAGTCTGGCTGCAGCAAAAAGCAGGCGATGCGTCTGCAACTACTGACAGCAGTAGGGGCAC
TGGCAGGCACAGCCTGTGCCCTTCTCACTGAAGGAGGAGCAGTGGGCAGTGAAATTGCAGGTGGTGCAGGTCCTG
GCTGGGTCTGCCATTTACTGCAGGTGGCTTTATCTACGTAGCAACAGTGTCTGTGTTGCCGAGCTGCTGAGGG
AGGCATCACCATTGCAATCACTTCTGGAGGTGCTGGGGCTGCTGGGGGGAGTTATCATGATGGTGCTGATTGCCC
ACCTTGAGTGAGGGGTGGATAAACTACCCCTGCCCCAAACCTCTACCCCTAACTCCAGGTCAGGGGTGCGTAGAG
GTTGGGGGCCCTGGCCAGGGACATCTGCCAAAGGAAGGAACTGTAGCCTGGGAGAATGGTTACTTTGGCATTAGG
GCCTTCAAGGGCTGGCAGTCTTACAGAGGCTGGAGCGGTGAGAATGAGAGGCCAGAGGGACCATAGTGTGGGCA
CTGTCTGACCATGTTGCATTTGGAAGGCTAAATGGGGCCATGAAGAAGGCTGGAAGGGACAGGGGGTGATGGCAG
CCTACCTGGTGTCCCTACCCACCTGTTCTCGGAGAACCAAGTTGCTACACAGGAAGTTCTCCAAGGTCCAGTT
TCCTTTCTCCCACAGTTGGTGGAGGCTTCAGGGAAGACCAGAGTCCTGGACAGAGAGGGTAACAGGAGGAGTCG
GGGATAAACATCAAACATCAATCGTGTGTCTGATTGGGAGTGATTGGGGGGATGGGGTGGGAGAGGGTTAGTT
GGTATTCTCATGGCCTGATTTTTTTTTGTTTCTATTCCCTTTTATATCACTGTGTTTGAATCGAGGGGGAGGGGTGG
TAACCGGAAATAAAGACCTCCGATCTTCCGCCCC

2116/6881
FIGURE 1949

GCTCACAGTCATCAATTATAGACCCCAACAAC**ATG**CGCCCTGAAGACAGAATGTTCCATATCAGAGCTGTGATCTT
GAGAGCCCTCTCCTTGGCTTTTCCTGCTGAGTCTCCGAGGAGCTGGGGCCATCAAGGCGGACCATGTGTCAACTTA
TGCCGCGTTTGTACAGACGCATAGACCAACAGGGGAGTTTATGTTTGAATTTGATGAAGATGAGATGTTCTATGT
GGATCTGGACAAGAAGGAGACCGTCTGGCATCTGGAGGAGTTTGGCCAAGCCTTTTCCTTTGAGGCTCAGGGCGG
GCTGGCTAACATTGCTATATTGAACAACAACCTGAATACCTTGATCCAGCGTTCCAACCACACTCAGGCCACCAA
CGATCCCCCTGAGGTGACCGTGTTTCCCAAGGAGCCTGTGGAGCTGGGGCCAGCCCAACACCCTCATCTGCCACAT
TGACAAGTTCTTCCCACCAGTGCTCAACGTACGTGGCTGTGCAACGGGGAGCTGGTCACTGAGGGTGTCGCTGA
GAGCCTCTTCTGCCCAGAACAGATTACAGCTTCCACAAGTTCCATTACCTGACCTTTGTGCCCTCAGCAGAGGA
CTTCTATGACTGCAGGGTGGAGCACTGGGGCTTGGACCAGCCGCTCCTCAAGCACTGGGAGGCCCAAGAGCCAAT
CCAGATGCCTGAGACAACGGAGACTGTGCTCTGTGCCCTGGGCCTGGTGCTGGGCCTAGTCGGCATCATCGTGGG
CACCGTCCTCATCATAAAGTCTCTGCGTTCTGGCCATGACCCCCGGGGCCAGGGGACCCT**GTGA**AATACTGTAAA
GGTGACAAAATATCTGAACAGAAGAGGACTTAGGAGAGATCTGAACTCCAGCTGCCCTACAACTCCATCTCAGC
TTTTCTTCTCACTTCATGTGAAAATACTCCAGTGGCTGACTGAATTGCTGACCCTTCAAGCTCTGTCTTATCC
ATTACCTCAAAGCAGTCATTCCCTTAGTAAAGTTTCCAACAAATAGAAATTAATGACACTTTGGTAGCACTAATAT
GGAGATTATCCTTTCATTGAGCCTTTTATCCTCTGTTCTCCTTTGAAGAACCCTCACTGTACCTTCCCGAGAA
TACCCTAAGACCAATAAATACTTCAGTATTTT

2117/6881
FIGURE 1950

MRPEDRMFHIRAVILRALSLAFLLSLRGAGAIKADHVSTYAAFVQTHRPTGEFMFEFDEDEMFYVDLDKKETVWH
LEEFQQAFSFEAQGGLANIAILNNNLNTLIQRSNHTQATNDPPEVTVPKEPVELGQPNTLICHIDKFFPPVLNV
TWLCNGELVTEGVAESLFLPRTDYSFHKFHLYTFVPSAEDFYDCRVEHWGLDQPLLKHWEAQEP IQMPETTETVL
CALGLVLGLVGIIVGTVLIKSLRSGHDPRAQGT

2118/6881
FIGURE 1951A

GGACTGCGGGATAGGAAGCTGGGGATATGGACAAGCAGCAGCGTTATAGCGCTCTGGGTTTCGGGACATAGGCCT
GGGCCATGCGGCCCCCTTGCCCCCTTGCGCGGACCCCCAGGAACGTTTCGAAAGCTGGTCCTCGTGGCTGGGGGA
AAGGCGGGGGGTGGGGGGGAAGCGGGCACGTGACCCCGGTACGCCAATCTGGGTGCTGCTGACGTACGCGCGCGG
CCCCGATGCTCTCCCCACCCCCCAGCCCGTTCGGGAAGGGAGGGGCTGGGGGCTACGCCCCATCCCCAGCAG
GCTTCGTTTTCTGGGGGGGGGTTGACACCCCGATTACATAACCCGTACCAAGCCGAGGGCAACTTTGGAGGCC
CCTGGAAGGCTTTAGGATCCAGATTCTTCGCTGCTGCTGCCTTACCGCCGAGAACACCACCCGCCAGGCGTCTT
GCGGCCACACCCCTGGCGGGTTCAGGCAGGCTACGCCCACGCGACCCCTCCCGTTTCCCTGCTTTGGCCAATGGA
GGAGCTACGAATGGCACGACCTGCTCGAGCTTGGCAGTCTCCAGTTGGGCTGTGCATGGAAGCTTGGGAAGACTT
TGTTGGAAGGGGAGGCGGGGAGAGAGTGTGGAGGCTCTGGGGCGATGGCTTCCGCACCTCTTCCAACCACCCCTC
TTTCCCTGGAGTCGGCGGACCACAGCTCAGCCAATTGGCTTGGAGATGTGGCGGGTTGCCACTTCCCTGTGGGTC
TCTGCGGCACTCTTCTGCCCTGGTGACTGACACCTTGGAAATGAAGTTTATGACGTCATCGTTGCGGCTGGCCAAT
AGAAAAAGCTCCCCGCGGAGAGGTGTTCTTCCCTTTCGACTCAGCTTCTTACCCGCGTGAGCGAGCGCGCGCGC
GCGGAGGGGGTGGGGAAAATCTCAAGCAGGGTGGCGCGCATGAGCGGCGAAGCTCCTCCTCCCCGCTATATATA
AAGGGCTGGCGCGGGGCTCGGCGGCGCCATTTCTGTGCTGGAGTGGAGCAGCCTCTAGAACGAGCTGGAGGATTCT
GCCTACCGATACAGAGCCTTCGAGTCGTCCGGGGCCGCCATTACAATCCACCTCCATCCGCTTGGAAATGGCCTT
CGTCCCGGCCTATGACTGGTCCCAGCGGGCAGTACAGACCCCTTAGAAGCCCTTGAGCTCCCTTTTTTCGGGCC
CCGCCAATCCTCGAGTCTGTCCACCCCTCTACTCCGCCCTCAAGAGGATTTCAAAGATGGAGGCGGCGGCTC
CCTAAACCACTTTTCGTGTTTCATCCGCTCCATCCGAGATCGAAACGGGACCTCGTCGGCCCCGTAGGGGCCGA
CAAGAAGAGGGAATCCCTGCAGACCAACAGCGGGCTATATTGACGACGGTGTCTGAGATCGGGGACCGTCTTTTG
AAGAGTCAGTCCCTCCTTAGTTGCCCGCCTCAGCTGAGGCCGCGCCATTTTCTTGCTGTCCGCGCTCTGCAGAG
CGCGCCAAGCTGCCCGGAGCTCTCCGAGAGGGCCCCAAGAGACTGCTTTCGTGCCGGCCAGGCAGGGGGTTTGT
GCCTGGAGGCCCCAAGAGGAACGGCCTCCCCCAACTTAGCGGGTTATGCTGGACGGGGCGGTGAGGGGAACCGAG
GCCACCCGGACTTTCCGCGGCTGAGGGCAGCGCCGGTTCCTTGCGGTCAAGATGCTGCAAAACGTGACTCCCCAC
AATAAGCTCCCTGGGGAAGGGAATGCAGGGTGTGCTGGGGCTGGGCCCAGAAGCAGCAGCACCAGGGAAAAGGATT
CGAAAACCTCTCTCTTGATGAGGGCTTTGAGAGCCCCACAATGGCTTCGGTGCCTGCTTTGCAACTTACCCCT
GCCAACCCACCACCCCGGAGGTGTCCAATCCAAAAAGCCAGGACGAGTTACCAACCAGCTGCAATACCTACAC
AAGGTAGTGATGAAGGCTCTGTGGAACATCAGTTTCGATGGCCATTCCGGCAGCCTGTGGATGCTGTCAAACCTG
GGTCTACCGGATTATCACAAAATTATAAAACAGCCTATGGACATGGGTACTATTAAGAGGAGACTTGAAAAAAT
TATTATTGGGCTGCTTCAGAGTGTATGCAAGATTTTAATACCATGTTACCAACTGTTACATTTACAACAAGCCC
ACTGATGATATTGTCTAATGGCACAAACGCTGGAAGAGATATTCCTACAGAAGGTTGCATCAATGCCACAAGAA
GAACAAGAGCTGGTAGTGACCATCCCTAAGAACAGCCACAAGAAGGGGGCCAAGTTGGCAGCGCTCCAGGGCAGT
GTTACCAGTGCCCATCAGGTGCCGTGCCGTCTCTTCTGTGTACACACAGCCCTGTATACTCCTCCACCTGAGATA
CCTACCAGTGTCTTCAACATTCCCCACCCATCAGTCATTTCTCTCCACTTCTCAAGTCCTTGCACTCTGCTGGA
CCCCGCTCCTTGCTGTTACTGCAGCTCCTCCAGCCAGCCCCCTTGCCAAGAAAAAAGGCGTAAAGCGGAAAAGCA
GATACTACCACCCCTACACCTACAGCCATCTTGGCTCCTGGTTCTCCAGCTAGCCCTCCTGGGAGTCTTGAGCCT
AAGGCAGCACGGCTTCCCCCTATGCGTAGAGAGAGTGGTGCGCCCATCAAGCCCCACGCAAAGACTTGCCCTGAC
TCTCAGCAACAACACCAGAGCTCTAAGAAAGGAAAGCTTTCAGAACAGTTAAAACATTGCAATGGCATTTTGAAG
GAGTTACTCTCTAAGAAGCATGCTGCCTATGCTTGGCCTTTCTATAAACCAGTGGATGCTTCTGCACTTGCCCTG
CATGACTACCATGACATCATTAAGCACCCCATGGACCTCAGCACTGTCAAGCGGAAGATGGAGAACCCTGATTAC
CGGGATGCACAGGAGTTTGCTGCTGATGTACGGCTTATGTTCTCCAAGTGTATAAGTACAATCCCCAGATCAC
GATGTTGTGGCAATGGCACGAAAGCTACAGGATGTATTTGAGTTCGGTTATGCCAAGATGCCAGATGAACACTA
GAACCAGGGCCTTTACCAGTCTCTACTGCCATGCCCCCTGGCTTGGCCAAATCGTCTTCAGAGTCTTCCAGTGAG
GAAAGTAGCAGTGAGAGCTCCTCTGAGGAAGAGGAGGAGGAAGATGAGGAGGACGAGGAGGAAGAAGAGAGTGAA
AGCTCAGACTCAGAGGAAGAAAGGGCTCATCGCTTAGCAGAACTACAGGAACAGCTTCGGGCAGTACATGAACAA
CTGGCTGCTCTGTCCAGGGTCCAATATCCAAGCCCAAGAGGAAAAGAGAGAAAAAAGAGAAAAAGAAGAACGG
AAGGCAGAGAAGCATCGAGGCCGAGCTGGGGCCGATGAAGATGACAAGGGGCCTAGGGCACCCCGCCACCTCAA
CCTAAGAAGTCCAAGAAAGCAAGTGGCAGTGGGGGTGGCAGTGTGCTTTAGGCCCTTCCGGCTTTGGACCTTCT
GGAGGAAGTGGCACCAAGCTCCCCAAAAGGCCACAAAGACAGCCCCACCTGCCCTGCCTACAGGTTATGATTCA

2119/6881

FIGURE 1951B

GAGGAGGAGGAAGAGAGCAGGCCCATGAGTTACGATGAGAAGCGGCAGCTGAGCCTGGACATCAACAAATTACCT
GGGGAGAAGCTGGGCCGAGTTGTGCATATAATCCAAGCCAGGGAGCCCTCTTTACGTGATTCAAACCCAGAAGAG
ATTGAGATTGATTTTGAAACACTCAAGCCATCCACACTTAGAGAGCTTGAGCGCTATGTCCTTTCCTGCCTACGT
AAGAAACCCCGGAAGCCCTACACCATTAAAGAAGCCTGTGGGAAAGACAAAGGAGGAAGTGGCTTTGGAGAAAAAG
CGGGAATTAGAAAAGCGGTTACAAGATGTCAGCGGACAGCTCAATTCTACTAAAAAGCCCCCAAGAAAGCGAAT
GAGAAAACAGAGTCATCCTCTGCACAGCAAGTAGCAGTGTACGCCTTAGCGCTTCCAGCTCCAGCTCAGATTCC
AGCTCCTCCTCTTCCCTCGTCGTCTTCAGACACCAGTGATTGAGCTCAGGCTAAGGGGTGAGGCCAGATGGG
GCAGGAAGGCTCCGCAGGACCGGACCCCTAGACCACCCTGCCCCACCTGCCCCTTCCCCCTTTGCTGTGACACTT
CTTCATCTCACCCCCCCTGCCCCCTCTAGGAGAGCTGGCTCTGCAGTGGGGGAGGGATGCAGGGACATTTACT
GAAGGAGGGACATGGACAAAACAACATTGAATTCCCAGCCCCATTGGGGAGTGATCTCTTGGACACAGAGCCCCC
ATTCAAATGGGGCAGGGCAAGGGTGGGAGTGTGCAAAGCCCTGATCTGGAGTTACCTGAGGCCATAGCTGCCCT
ATTCACTTCTAAGGGCCCTGTTTTGAGATTGTTTGTCTAATTTATTTTAAGCTAGGTAAGGCTGGGGGGAGGGT
GGGGCCGTGGTCCCCCTCAGCCTCCATGGGGAGGGAAGAAGGGGGAGCTCTTTTTTTACGTTGATTTTTTTTTTC
TACTCTGTTTTCCCTTTTTCCCTCCGCTCCATTTGGGGCCCTGGGGGTTTCAGTCATCTCCCCATTTGGTCCCCT
GGACTGTCTTTGTTGATTCTAAGTGTAAATAAGAAAATATT

2120/6881
FIGURE 1952

GGGCAGAAAGGGCACGCTCTTGTGGGTGACTACAGGTTAGGAGACCGTTGAACCTGGAGGGGCCCTAGGATGGAC
CCCGTGGAAGATTTCAGAGACTGCGCCCTCTCCCTGGCGCCGCCTTCCCCTACACGCGGGCGGTATATTCTGTTG
CAGTTGGCCCAGGACCTGTTTCCAAGACTCTGCCCCCTCGCACTTCCGTCCCTCCTGGTTTTGTAAAGTGATGCT
CATAGGAACCCCCACCCCGCGTGACACTACTCCCAGCTCCTGGCTGACTTCTAGTCTTCTGGTTGAAGCTGCGCC
TTTAGATGACACGACCCTACCCACCCCTGTTTCCAGCGGATGCCCGGGCCTGGAGCCCACAGAATTCTTCCAGTC
CCTGGGTGGGGACGGAGAAAGGAACGTTTCAGATTGAGATGGCCCATGGCACCACCACGCTCGCCTTCAAGTTCCA
GCATGGAGTGATTGCAGCAGTGGATTCTCGGGCCTCAGCTGGGTCTTACATTAGTGCCTTACGGGTGAACAAGGT
GATTGAGATTAAACCCTTACCTGCTTGGCACCATGTCTGGCTGTGCAGCAGACTGTCAGTACTGGGAGCGCCTGCT
GGCCAAGGAATGCAGGCTGTACTATCTGCGAAATGGAGAACGTATTTTCAGTGTGGCAGCCTCCAAGCTGCTGTC
CAACATGATGTGCCAGTACCGGGGCATGGGCCTCTCTATGGGCAGTATGATCTGTGGCTGGGATAAGAAGGGTCC
TGGACTCTACTACGTGGATGAACATGGGACTCGGCCTCTCAGGAAATATGTTCTCCACGGGTAGTGGGAACACTTA
TGCCTACGGTGTCTATGGACAGTGGCTATCGGCCTAATCTTAGCCCTGAAGAGGCCTATGACCTTGGCCGCAGGGC
TATTGCTTATGCCACTCACAGAGACAGCTATTCTGGAGGCGTTGTCAATATGTACCACATGAAGGAAGATGGTTG
GGTGAAAGTAGAAAGTACAGATGTCAGTGACCTGCTGCACCAGTACCGGGAAGCCAATCAATTAATGGTGGTGGTG
GCAGCTGGGCAGGTCTCCTCTGGGAGGTCTTGGCCGACTCAGGGACCTAAGCCACGTTAAGTCCAAGGAGAAGAA
GAGGCCTAGCCTGAGCCAAAGAGAGAGTACGGGCTCAGCAGCCAGAGGAGGCCGGTGAAGTGCATCTTCTGCGTG
TTCTC

2121/6881
FIGURE 1953

MLIGTPTPRDTPSSWLTSSLLVEAAPLDDTTLPTPVSSGCPGLEPTEFFQSLGGDGERNVQIEMAHGTTTLAFK
FQHGVIAAVDSRASAGSYISALRVNKVIEINPYLLGTMSGCAADCQYWERLLAKECRLYYLNRNGERISVSAASKL
LSNMMCQYRGMGLSMGSMICGWDKKGPGLYYVDEHGTRLSGNMFSTGSGNTYAYGVMDSGYRPNLSPEEAYDLGR
RAIAYATHRDSYSGGVNMYHMKEDGWVKVESTDVSDLLHQYREANQ

2122/6881
FIGURE 1954

ATTCTTGTCTGTTCTGCCTCACTCCCGAGCTCTACTGACTCCCAACAGAGCGCCCAAGAAGAAAATGGCCATAAG
TGGAGTCCCTGTGCTAGGATTTTTTCATCATAGCTGTGCTGATGAGCGCTCAGGAATCATGGGCTATCAAAGAAGA
ACATGTGATCATCCAGGCCGAGTTCTATCTGAATCCTGACCAATCAGGCGAGTTTATGTTTGACTTTGATGGTGA
TGAGATTTTCCATGTGGATATGGCAAAGAAGGAGACGGTCTGGCGGCTTGAAGAATTTGGACGATTTGCCAGCTT
TGAGGCTCAAGGTGCATTGGCCAACATAGCTGTGGACAAAGCCAACCTGGAAATCATGACAAAGCGCTCCAACCTA
TACTCCGATCACCAATGTACCTCCAGAGGTAACCTGTGCTCACGAACAGCCCTGTGGAACCTGAGAGAGCCCAACGT
CCTCATCTGTTTCATAGACAAGTTCACCCCAACAGTGGTCAATGTCACGTGGCTTCGAAATGGAAAACCTGTCAC
CACAGGAGTGTGAGAGACAGTCTTCTGCCCAGGGAAGACCACCTTTTCCGCAAGTTCCACTATCTCCCCTTCCT
GCCCTCAACTGAGGACGTTTACGACTGCAGGGTGGAGCACTGGGGCTTGGATGAGCCTCTTCTCAAGCACTGGGA
GTTTGATGCTCCAAGCCCTCTCCCAGAGACTACAGAGAACGTGGTGTGTGCCCTGGGCCTGACTGTGGGTCTGGT
GGGCATCATTATTGGGACCATCTTCATCATCAAGGGATTGCGCAAAAGCAATGCAGCAGAACGCAGGGGGCCTCT
GTAAGGCACATGGAGGTGATGGTGTCTTCTTAGAGAGAAGATCACTGAAGAACTTCTGCTTTAATGGCTTTACAA
AGCTGGCAATATTACAATCCTTGACCTCAGTGAAAGCAGTCATCTTCAGCATTTTCCAGCCCTATAGCCACCCCA
AGAGTGGTTATGCCTCCTCGATTGCTCCATACTCTAACATCTAGCTGGCTTCCCTGTCTATTGCCTTTTCCTGTA
TCTATTTTCTCTATTTCCCTATCATTTTATTATCACCATGCAATGCCTCTGGAATAAAACATACAGGAGTCTGTC
TCTGCTATGGAATGCCCCATGGGGCATCTCTTGTGTACTTATTGTTTAAGGTTTCCTCAAACCTGTGATTTTTCTG
AACACAATAAACTATTTTGAAGATCTTGGGTGGAA

2123/6881
FIGURE 1955

GCCGTCTTATCTAAGTCAGAGTCTCCTAAAGAGCCAGAACAACCTGAGGAAGCTCTTCATTGGAGGGTTGAGCTTT
GAAACAACCTGATGAGAGCCTGAGGAGCCATTTTGAGCAGTGAGGGACACTCCCGGACAGTGTGGTCATGAGAGAT
CCAAACCCAAGCGCTCCAGGGGCTTTGGATTTTTACATATGCCACTGTGGAGGAGGTGGATGCAGCCGTGAATG
CAAGGCCACACAAGGTGGATGGAAGAGCTGTGGAACCAAAGAGAGCTGTCTCAAGAGAAGATTCTCAAATACCAG
GTGCCCCTTAACCTGTGAAAAAGATATATGCTGGTGGCATTAAAGAAGACACTGAAGAAATCACCTAAGAAATTA
TTTTGAGTAGTATGGAAAAATTGAAGTGATTGAAAACATGACTGACCGAGGCAGTTGCAAGAAAAGGGGCTTTGC
CTTTGTAACCTTTGATGACCATGACTCCGTGGATAAGACTGTTCATTGAGAAATACCACAGTGTGAATGGCCACAA
CTGTGAAGTTAGGAAAAGCCTGTCAAAGCAAGAGATGGCTAGTGCTCCATCCAGCCGAAGAGGTGGAAGTGGTTCT
GGAAACTTTGGTGGTGGTCATGGAGGTGGTTTTCGGTGGGAATGACAACTTTGATCATGGAGGAACTTCAGTGGT
TGTGGTAGCTTTGGTGGCAGCTGTGGTGGTGGTGGATATGGTGGCAGTGAGGATGGCTATAATGGATTTGGTAAT
GATGGGAGCAATTTTGGAGGTGGTGAAGCTACAATGATTTTGGCAATTACAACAATCAGTCTTCAAATTTTGA
CCCATGAAGGGAGGAAACTTTTGGAGGCAGAAGCTGTGGCCTCTATGGTGGTGGAGGCCAATACTTTGCCAAACCA
TGAAACCAAAGTGGCTATTGTGGTTCCAGTAGCAGCAGTAGCTATGGCAGTGGCAGAAGATTTTAATTAGGAAAC
AAAGCTTAGCAGGAGAGGAGAGCCAGAGAAGTGACAGGGAAGCTACAGGTTACAACAGATTTGTGAACTCAGCCA
AGCACAGTGGTGGCAGGGCCTAGCTGGTACAAAGAAGACATGTTTTAGACAAATACTCATGTGTATGGGCAAAAA
ACTCGAGGACTGTATTTGTGACTAATTGTATAACAGGTTATTTTAGTTTCTGTTCTGTGGAAAGTGTAAGCATT
CCAACAAAGGGTTTTAATGTAGATTTTTTTTTTGCACCCATGCTGTTTATTGCTAAATGTAATAGTCTGATCGTGA
CACTGAAAAAA

2124/6881
FIGURE 1956

ATGGACGAACGGCTACTGGGGCCGCCCCCTCCAGGCGGGGGCCGGGGGGCCTGGGATTGGTGAGTGGGGAGCCT
GGGGGCCCTGGCGAGCCTCCCGGTGGCGGAGACCCCGGTGGGGGTAGCGGGGGGGTCCCGGGAGGCCGAGGGAAG
CAAGACATCGGGGACATTCTGCAGCAGATAATGACCATCACCGACCAGAGCCTGGACGAGGCCCAGGCCAAGAAA
CACGCCCTAAACTGCCACCGAATGAAGCCTGCTCTCTTTAGCGTCCTGTGTGAAATCAAGGAGAAAACTGGCCTC
AGCATTTCGGAGCTCCCAGGAGGAGGAGCCGGTGGACCCACAGCTGATGCGCTTGGACAACATGCTTCTGGCAGAG
GGTGTGGCTGGGCCCCGAGAAAGGGGGCGGCTCAGCAGCAGCAGCTGCAGCCGCTGCAGCCTCTGGTGGTGGTGTG
TCCCCTGACAACTCCATCGAACACTCGGACTATCGCAGCAAACCTTGCCAGATCCGTCACATATACCACTCGGAG
CTGGAGAAGTATGAGCAGGCATGTAATGAGTTACGACCCATGTCATGAACCTGCTGAGGGAGCAGAGCCGCACC
AGGCCCCGTGGCCCCCAAAGAGATGGAACGCATGGTGAGCATCATCCATCGAAAGTTTCAGCGCCATCCAGATGCAG
CTGAAGCAGAGCACCTGCGAGGCTGTGATGATCCTGCGCTCCCGTTTCTGGATGCCAGACGAAAGCGCCGTAAC
TTCAGCAAACAGGCCACTGAGGTCTTAAATGAGTATTTCTACTCCACCTGAGTAACCCATATCCTAGTGAGGAG
GCCAAGGAGGAGCTTGCCAAGAAGTGTGGCATCACCGTGTCTCAGGTCTCCAACCTGGTTTGGCAACAAGAGGATT
CGCTATAAGAAAAACATCGGAAAGTTCCAAGAGGAGGCAAACATCTATGCTGTCAAGACCGCCGTGTCAGTCACC
CAGGGGGGCCACAGCCGCACCAGCTCCCCGACACCCCCTTCTCTGCAGGCTCTGGCGGCTCTTTCAATCTCTCA
GGATCTGGAGACATGTTTCTGGGGATGCCTGGGCTCAACGGAGATTCTTATTCTGCTTCCCAGGTGGAATCACTC
CGACACTCGATGGGGCCAGGGGGCTATGGGGATAACCTCGGGGGAGGCCAGATGTACAGCCCACGGGAAATGAGG
GCAAAATGGCAGCTGGCAAGAGGCTGTGACCCCTCTTCAGTGACATCCCCAACGGAGGGACCAGGGAGTGTTCAC
TCTGATACCTCCAACCTGATCTTGCCCCCTCAGGGTCACAGGGGTGGGGCTCTCACAAGGCGACTTGAAGAGGACG
CAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGACAGAGAAGGGCCAATGGGGTTCATCCCTCCCT
AACGAGACTCTCTGTGCTGGGGGTGCTAATTACATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGGTCTG
TCTCTCCCTTTTTTCCATCTTTTTCTCTCTCGTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTA
TTTCTCAGACCCCTTTTTCTCTCTGTCTTTCTCTCTCCCTCTCCACACCTCACACACACATACTCCCACTTGC
AACTATTCTGTTTCTCTCTGGGCTCCCCACTTTCCCTTCCCCACCCCACTTGTATGCTCTGGAATCTGTGGAG
ACGCCAGCCCTGCCCAATCAGAGATGCCAAAAATGGGGACATGACTTCTGGACAGAGGACATGGGCCACGCCCCC
ATGCATCCCCACCCCGCCCCCTCCGGACGGCTTACTTACCTCATACGCAGCTCATCTTAAACCAATAGAATCGCT
CGGTGGACGAGAGTGTCTGACTCAGATATCTACCTCGGAGGGAGTTTCTGCTACTTTAGGGAATTATTGACTGGG
CTTTGGGGTTGAACTTTTTTTTTTTTTAAAGAAAGAAAAAGAAACCCTGGGATCCATCTGTTTTTTTTTGTGTGT
TGTTGTTTTTGTGTGTGTGGTGGTGGTGGTGGTGGTCTTAATTTTTTAATTTAGTTTGGGGAAGTAGCTTG
TTTTTTTTTTTTATAAATATGTTGATTCTTGTCTTTTTTTTTTTATTTCTTACTTTCCCATATTAGGGGTGATAGC
CAAAGGGGTTCTGGTAAGAGAAAGGGGGACAAACAGAACTGGTAAAGAGGCCCCCTGGCTCCAGGCCTGTCCAT
CAGGAAGTAAATTTTACAGGGCACCAAGCTTTGCCCCCTAAAATCCCTTAGGTGTTCTTTGTTTCATGCAGGCAGG
TTTCTGCCGCAATTTGATGTGGAGGCAGTGAAGGGCTTGCCCTGCTGGCCTCTCATCCCCCTTCTTCCCACAACCC
TTGGGCAGGGCTGGACTCAGTAATTTTGAGGAAATTGAAGATGCCATCTTCCCCTGTGAGTGACATGTCTTTAAT
TTTTTAAAAAACTACTATTTGAAAATTGGAGGGGAAGAATGGGAAGGGAGTTATTGCCAAATATGTTAAATATG
GGTGGGGTGCTTGATATATGATCTTCTCAATTTCCCATAAATGAGGTATCTTTTTGTACACCAAAAATCAAG
GGGTAGGGAGAGGGAGGAGGTTGCAAAAAGCCAGATGTGGGGGAAAAGTAACATCAACACTGTCCCATCCTCAGC
CCTGAAGTAGCTACCATCTGATCCCCCTCAGACATTCTCAGGATTTTACAAGACTGTCAGAGTGGGGAACCCCTCC
CATTAAAGATCCGGGCAGGACTGGGGACAGGTTGGAAGTGTGATGGGTGGGGGGTGGGAGGCATGGGCCGGGGG
CAGTTCTCTCTCACTTGTAACCTTGTGTAGTTTACAGAAAAAAAACAAAATGCAGTTTTAAATAAAGAAATTT
CTTTTT

2125/6881
FIGURE 1957A

AGAAGGTAGCAGACAGACAGACGGATCTAACCTCTCTTGGATCCTCCAGCCATGAGGCTGCTCTGGGGGCTGATC
TGGGCATCCAGCTTCTTCACCTTATCTCTGCAGAAGCCCAGGTTGCTCTTGTTCTCTCCTTCTGTGGTTCATCTG
GGGGTCCCCCTATCGGTGGGGGTGCAGCTCCAGGATGTGCCCCGAGGACAGGTAGTGAAAGGATCAGTGTTTCCTG
AGAAACCCATCTCGTAATAATGTCCCCTGCTCCCCAAAGGTGGACTTCACCCTTAGCTCAGAAAGAGACTTCGCA
CTCCTCAGTCTCCAGGTGCCCTTGAAAGATGCGAAGAGCTGTGGCCTCCATCAACTCCTCAGAGGCCCTGAGGTC
CAGCTGGTGGCCCATTCGCCATGGCTAAAGGACTCTCTGTCCAGAACGACAAACATCCAGGGTATCAACCTGCTC
TTCTCCTCTCGCCGGGGGCACCTCTTTTTGTCAGACGGACAGCCCATTTACAACCCTGGCCAGCGGGTTCGGTAC
CGGGTCTTTGCTCTGGATCAGAAGATGCGCCCCGAGCACTGACACCATCACAGTCATGGTGGAGAACTCTCACGGC
CTCCGCGTGCGGAAGAAGGAGGTGTACATGCCCTCGTCCATCTTCCAGGATGACTTTGTGATCCCAGACATCTCA
GAGCCAGGGACCTGGAAGATCTCAGCCCATTCTCAGATGGCCTGGAATCCAACAGCAGCACCCAGTTTGAGGTG
AAGAAATATGTCTTCCCAACTTTGAGGTGAAGATCACCCCTGGAAAGCCCTACATCCTGACGGTGCCAGGCCAT
CTTGATGAAATGCAGTTAGACATCCAGGCCAGGTACATCTATGGGAAGCCAGTGCAGGGGGTGGCATATGTGCGC
TTTGGGCTCCTAGATGAGGATGGTAAGAAGACTTTCTTTCGGGGGCTGGAGAGTCAGACCAAGCTGGTGAATGGA
CAGAGCCACATTTCCCTCTCAAAGGCAGAGTTCCAGGACGCCCTGGAGAAGCTGAATATGGGCATTACTGACCTC
CAGGGGCTGCGCCTCTACGTTGCTGCAGCCATCATTGAGTATCCAGGTGGGGAGATGGAGGAGGCAGAGCTCACA
TCCTGGTATTTTGTGTCTATCTCCCTTCTCCTTGGATCTTAGCAAGACCAAGCGACACCTTGTGCTGGGGCCCC
TTCTGCTGCAGGCCTTGGTCCGTGAGATGTCAGGCTCCCAGCTTCTGGCATTCTGTCAAAGTTTCTGCCACG
GTGTCTTCTCCTGGGTCTGTTTCTGAAGTCCAGGACATTCAGCAAAACACAGACGGGAGCGGCCAAGTCAGCATT
CCAATAATTATCCCTCAGACCATCTCAGAGCTGCAGCTCTCAGTATCTGCAGGCTCCCCACATCCAGCGATAGCC
AGGCTCACTGTGGCAGCCCCACCTTCAGGAGGCCCCGGGTTTCTGTCTATTGAGCGGCCGGATTCTCGACCTCCT
CGTGTGGGGACACTCTGAACCTGAACCTGCGAGCCGTGGGCAGTGGGGCCACCTTTTCTCATTACTACTACATG
ATCCTATCCCGAGGGCAGATCGTGTTCATGAATCGAGAGCCCAAGAGGACCCTGACCTCGGTCTCGGTGTTTGTG
GACCATCACCTGGCACCCCTCCTTCTACTTTGTGGCCTTCTACTACCATGGAGACCACCCAGTGCCAACTCCCTG
CGAGTGGATGTCCAGGCTGGGGCCTGCGAGGGCAAGCTGGAGCTCAGCGTGGACGGTGCCAAGCAGTACCGGAAC
GGGAGTCCGTGAAGCTCCACTTAGAAACCGACTCCCTAGCCCTGGTGGCGCTGGGAGCCTTGACACAGCTCTG
TATGCTGCAGGCAGCAAGTCCCACAAGCCCCCTCAACATGGGCAAGGTCTTTGAAGCTATGAACAGCTATGACCTC
GGCTGTGGTCCCTGGGGGTGGGGACAGTGCCCTTCAGGTGTTCCAGGCAGCGGGCCTGGCCTTTTCTGATGGAGAC
CAGTGGACCTTATCCAGAAAGAGACTAAGCTGTCCCAAGGAGAAGACAACCCGAAAAAGAGAAACGTGAACCTC
CAAAAGGCGATTAAATGAGAAATTGGGTGAGTATGCTTCCCCGACAGCCAAGCGCTGCTGCCAGGATGGGGTGACA
CGTCTGCCCATGATGCGTTTCTGCGAGCAGCGGGCAGCCGCGTGCAGCAGCCGGACTGCCGGGAGCCCTTCCTG
TCCTGCTGCCAATTGTGCTGAGAGTCTGCGCAAGAAGAGCAGGGACAAGGGCCAGGCGGGCCTCCAACGAGCCCTG
GAGATCCTGCAGGAGGAGGACCTGATTGATGAGGATGACATTCCCGTGCAGCTTCTTCCCAGAGAAGTGGCTC
TGGAGAGTGGAACAGTGGACCGCTTTCAAATATTGACACTGTGGCTCCCCGACTCTCTGACCACGTGGGAGATC
CATGGCCTGAGCCTGTCCAAAACCAAAGGCCTATGTGTGGCCACCCAGTCCAGCTCCGGGTGTTCCGCGAGTTC
CACCTGCACCTCCGCTGCCATGTCTGTCCGCCGCTTTGAGCAGCTGGAGCTGCGGCCTGTCTCTATAACTAC
CTGGATAAAAACCTGACTGTGAGCGTCCACGTGTCCCCAGTGGAGGGGCTGTGCTGGCTGGGGGCGGAGGGCTG
GCCCAGCAGGTGCTGGTGCCTGCGGGCTCTGCCCCGCCGTGTTGCCCTTCTCTGTGGTGCCACGGCAGCCGCCGCT
GTGTCTCTGAAGGTGGTGGCTCGAGGGTCCCTTCGAATTCCCTGTGGGAGATGCGGTGTCCAAGGTTCTGCAGATT
GAGAAGGAAGGGGCCATCCATAGAGAGGAGCTGGTCTATGAACCTCAACCCCTTGAGACCACCGAGCCGGACCTTG
GAAATACCTGGCAACTCTGATCCCAATATGATCCCTGATGGGGACTTTAACAGCTACGTCAGGGTTACAGCCTCA
GATCCATTGGACACTTTAGGCTCTGAGGGGGCCTTGTACACAGGAGCGTGGCCTCCCTCTTGAGGCTTCCTCGA
GGCTGTGGGGAGCAAACCATGATCTACTTGGCTCCGACACTGGCTGCTTCCCGCTACCTGGACAAGACAGAGCAG
TGGAGCACACTGCCTCCGAGACCAAGGACCACGCCGTGGATCTGATCCAGAAAGGCTACATGCGGATCCAGCAG
TTTCGGAAGGCGGATGGTTTCTATGCGGCTTGGTTGTACGGGGCAGCAGCACCTGGCTCACAGCCTTTGTGTTG
AAGGTCTGAGTTTGGCCAGGAGCAGGTAGGAGGATCGCCTGAGAACTGCAGGAGACATCTAACTGGCTTCTG
TCCAGCAGCAGGCTGACGGCTCGTTCCAGGACCTCTCTCCAGTGATACATAGGAGCATGCAGGGGGGTTTGGTG
GGCAATGATGAGACTGTGGCACTCACAGCCTTTGTGACCATCGCCCTTCATCATGGGCTGGCCGTCTTCCAGGAT
GAGGGTGCAGAGCCATTGAAGCAGAGAGTGGAAGCCTCCATCTCAAAGGCAAGCTCATTTTTGGGGGAGAAAGCA

2126/6881
FIGURE 1957B

AGTGCTGGGCTCCTGGGTGCCCACGCAGCTGCCATCACGGCCTATGCCCTGACACTGACCAAGGCCCTGCGGAC
CTGCGGGGTGTTGCCCACAACAACCTCATGGCAATGGCCCAGGAGACTGGAGATAACCTGTACTGGGGCTCAGTC
ACTGGTTCTCAGAGCAATGCCGTGTCGCCCCACCCGGCTCCTCGCAACCCATCCGACCCCATGCCCCAGGCCCA
GCCCTGTGGATTGAAACCACAGCCTACGCCCTGCTGCACCTCCTGCTTCACGAGGGCAAAGCAGAGATGGCAGAC
CAGGCTGCGGCCTGGCTCACCCGTCAGGGCAGCTTCCAAGGGGGATTCCGCAGTACCCAAGACACGGTGATTGCC
CTGGATGCCCTGTCTGCCTACTGGATTGCCTCCCACACCACTGAGGAGAGGGGTCTCAATGTGACTCTCAGCTCC
ACAGGCCGGAATGGGTTCAAGTCCCACGCGCTGCAGCTGAACAACCGCCAGATTTCGCGGCCTGGAGGAGGAGCTG
CAGTTTTCTTGGGCAGCAAGATCAATGTGAAGGTGGGAGGAAACAGCAAAGGAACCTGAAGGTCCTTCGTACC
TACAAATGTCCTGGACATGAAGAACACGACCTGCCAGGACCTACAGATAGAAGTGACAGTCAAAGGCCACGTCGAG
TACACGATGGAAGCAAACGAGGACTATGAGGACTATGAGTACGATGAGCTTCCAGCCAAGGATGACCCAGATGCC
CCTCTGCAGCCCGTGACACCCCTGCAGCTGTTTGAGGGTCGGAGGAACCGCCGAGGAGGGAGGCGCCCAAGGTG
GTGGAGGAGCAGGAGTCCAGGGTGCACTACACCGTGTGCATCTGGCGGAACGGCAAGGTGGGGCTGTCTGGCATG
GCCATCGCGGACGTCACCCCTCCTGAGTGGATTCCACGCCCTGCGTGCTGACCTGGAGAAGCTGACCTCCCTCTCT
GACCGTTACGTGAGTCACTTTGAGACCGAGGGGCCCCACGTCCTGCTGTATTTTGACTCGGTCCCCACCTCCCGG
GAGTGCGTGGGCTTTGAGGCTGTGCAGGAAGTGCCGGTGGGGCTGGTGCAGCCGGCCAGCGCAACCTGTACGAC
TACTACAACCCCGAGCGCAGATGTTCTGTGTTTTACGGGGCACCAAGTAAGAGCAGACTCTTGGCCACCTTGTTG
TCTGCTGAAGTCTGCCAGTGTGCTGAGGGGAAGTGCCCTCGCCAGCGTCGCGCCCTGGAGCGGGTCTGCAGGAC
GAGGATGGCTACAGGATGAAGTTTGCTGCTACTACCCCGTGTGGAGTACGGCTTCCAGGTAAAGTTCTCCGA
GAAGACAGCAGAGCTGCTTTCCGCCTCTTTGAGACCAAGATCACCAAGTCCTGCACTTCACCAAGGATGTCAAG
GCCGCTGCTAATCAGATGCGCAACTTCTGGTTTCGAGCCTCCTGCCGCTTCGCTTGGAACCTGGGAAAGAATAT
TTGATCATGGGTCTGGATGGGGCCACCTATGACCTCGAGGGACACCCCAAGTACCTGCTGGACTCGAATAGCTGG
ATCGAGGAGATGCCCTCTGAACGCCTGTGCCGGAGCACCCGCCAGCGGGCAGCCTGTGCCCAGCTCAACGACTTC
CTCCAGGAGTATGGCACTCAGGGGTGCCAGGTGTGAGGGCTGCCCTCCCACCTCCGCTGGGAGGAACCTGAACCT
GGGAACCATGAAGCTGGAAGCACTGCTGTGTCCGCTTTCATGAACACAGCCTGGGACCAGGGCATATTAAAGGCT
TTTGGCAGCAAAGTGTCAGTGTTGGC

2127/6881
FIGURE 1958

MRLWGLIWASSFFTLSQLKPRLLLFSPSVVHLGVPLSVGVQLQDVPRGQVVKGSVFLRNP SRNNVPCSPKVDFT
LSSERDFALLSLQVPLKDAKSCGLHQLLRGPEVQLVAHSPWLKDSLSRTTNIQGINLLFSSRRGHLFLQTDQPIY
NPGQVRVYRVFALDQKMRPSTDTITVMVENSHGLRVRKKEVYMPSSIFQDDFVIPDISEPGTWKISARFSDGLES
NSSTQFEVKKYVLPNFVKITPGKPYILTVPGHLDQMQLDIQARYIYGKPVQGVAYVRFGLLDEDGKKTTFRGLE
SQTCLVNGQSHISLSKAEFQDALEKLNMGITDLQGLRLYVAAAIIEYPPGEMEEAELTSWYFVSSPFSLDLSKTK
RHLVPGAPFLLQALVREMSGSPASGIPVKVSATVSSPGSVPEVQDIQQNTDGSQVSIPIIIPQTISELQLSVSA
GSPHPAIARLTVAAPSGGPGFLSIERPDSRPPRVGDTLNLNLRAVGSGATFSHYYYMILSRGQIVFMNREP KRT
LTSVSFVDHHLAPSFYFVAFYYHGDHPVANSLRVDVQAGACEGKLELSVDGAKQYRNGESVKLHLETDSLALVA
LGALDTALYAAGSKSHKPLNMGKVFEAMNSYDLGCGPGGGDSALQVFAQAGLAFSDGDQWTL SRKRLSCPKEKTT
RKKRNVN FQKAIN EKLQGYASPTAKRCCQDGVTRLPM MRSCEQRAARVQQPDCREPF LSCCQFAESLRKKS RDKG
QAGLQRALEILQEEDLIDEDDIPVRSFFPENWLWRVETVDRFQILTLWL PDSLTTWEIHGLSLSKTKGLCVATPV
QLRVFREFHHLRLPMSVRRFEQLELRPVLYNYLDKNLTVSVHVSPVEGLCLAGGGGLAQQVLVPAGSARPVAFS
VVPTAAA AVSLKVVARGSFEFPVGDAVSKVLQIEKEGAIHREELVYELNPLDHRGRTLEIPGNSDPNMIPDGD FN
SYVRVTASDPLDTLGSEGALSPGGVASLLRLPRGCGEQTM IYLAPTLAASRYLDKTEQWSTLPPETKDHAVDLIQ
KGYMRIQQFRKADGSYAAWLSRGSSTWLTAFVLKVLSLAQEQVGG SPEKLQETSNWLLSQQQADGSFQDLSPVIH
RSMQGGVLVGNDETVALTAFVTIALHHGLAVFQDEGAEP LKQ RVEASISKASSFLGEKASAGLLGAHAAAI TAYAL
TLTKAPADLRGVAHNNLMAMAQETGDNLYWGSVTGSQSNAVSP TPAPRNP SDPMPQAPALWIETTAYALLHLLLH
EGKAEMADQAAAWLTRQGSFQGGFRSTQD TVIALDAL SAYWIASHTTEERGLNVTLSSTGRNGFKSHALQLNNRQ
IRGLEEELQFSLGSKINVKVG GNSKGT LKVLRTYNVLD MKNTTCQDLQIEVTVKGHVEYTMEANEDYEDY EYDEL
PAKDDPDAPLQPVTP LQLFEGRNRNRREAPKVVEEQESRVHYTVCIWRNGKVGLSGMAIADVTL LSGFHALRAD
LEKLTSLSDRYVSHFETEGPHVLLYFDSVPTSRECVGFEAVQEV PVGLVQPASATLYDYNPERRCSVFY GAPS K
SRLLATLCSAEVCQCAEGKCPRQRALERGLQDEDDGYRMKFACYYPRVEYGFQVKVLREDSRAAFRLFETKITQV
LHFTKDVKAAANQMRNFLVRASCRLRLEPGKEYLIMGLDGATYDLEGHPQYLLDSNSWIEEMP SERLCRSTRQRA
ACAQLNDFLQ EYGTQGCQV

2128/6881
FIGURE 1959

AGGGGAAGGGAATGTGACCAGGTCTAGGTCTGGAGTTTCAGCTTGGACACTGAGCCAAGCAGACAAGCAAAGCAA
GCCAGGACACACCATCCTGCCCCAGGCCCAGCTTCTCTCCTGCCTTCCAACGCCATGGGGAGCAATCTCAGCCCC
CAACTCTGCCTGATGCCCTTTATCTTGGGCCTCTTGCTGGAGGTGTGACCACCACTCCATGGTCTTTGGCCCAG
CCCCAGGGATCCTGCTCTCTGGAGGGGGTAGAGATCAAAGGCGGCTCCTTCCGACTTCTCCAAGAGGGGCCAGGCA
CTGGAGTACGTGTGTCCTTCTGGCTTCTACCCGTACCCGTGTGCAGACACGTACCTGCAGATCTACGGGGTCCTGG
AGCACCCCTGAAGACTCAAGACCAAAAGACTGTGAGGAAGGCAGAGTGCAGAGCAATCCACTGTCCAAGACCACAC
GACTTCGAGAACGGGGAATACTGGCCCCGGTCTCCCTACTACAATGTGAGTGATGAGATCTCTTTCCACTGCTAT
GACGGTTACACTCTCCGGGGCTCTGCCAATCGCACCTGCCAAGTGAATGGCCGGTGGAGTGGGCAGACAGCGATC
TGTGACAACGGAGCGGGGTACTGCTCCAACCCGGGCATC¹CCCATTTGGCACAAGGAAGGTGGGCAGCCAGTACCGC
CTTGAAAGACAGCGTCACCTACCACTGCAGCCGGGGGGCTTACCCTGCGTGGCTCCCAGCGGCCGAACGTGTCAGGAA
GGTGGCTCTTGAGCGGGACGGAGCCTTCTGCCAAGACTCCTTCATGTACGACACCCCTCAAGAGGTGGCCGAA
GCTTTCTGTCTTCCCTGACAGAGACCATAGAAGGAGTGCATGCTGAGGATGGGCACGGCCCAGGGGAACAACAG
AAGCGGAAGATCGTCTGACACCCTCAGGCTCCATGAACATCTACCTGGTGCTAGATGGATCAGACAGCATTGGG
GCCAGCAACTTCACAGGAGCCAAAAAGTGTCTAGTCAACTTAATTGAGAAGGTGGCAAGTTATGGTGTGAAGCCA
AGATATGGTCTAGTGACATATGCCACATACCCCAAATTTGGGTCAAAGTGTCTGAAGCAGACAGCAGTAATGCA
GACTGGGTACGAAGCAGCTCAATGAAATCAATTATGAAGACCACAAGTTGAAGTCAGGGACTAACACCAAGAAG
GCCCTCCAGGCAGTGTACAGCATGATGAGCTGGCCAGATGACGTCCCTCCTGAAGGCTGGAACCGCACCCGCCAT
GTCATCATCCTCATGACTGATGGATTGCACAACATGGGCGGGGACCCAATTACTGTCATTGATGAGATCCGGGAC
TTGCTATACATTGGCAAGGATCGCAAAAACCCAAGGGAGGATTATCTGGATGTCTATGTGTTTGGGGTCGGGCCT
TTGGTGAACCAAGTGAACATCAATGCTTTGGCTTCCAAGAAAGACAATGAGCAACATGTGTTCAAAGTCAAGGAT
ATGGAAAACCTGGAAGATGTTTTCTACCAAATGATCGATGAAAGCCAGTCTCTGAGTCTCTGTGGCATGGTTTGG
GAACACAGGAAGGTACCGATTACCACAAGCAACCATGGCAGGCCAAGATCTCAGTCATTGCGCCCTTCAAAGGGA
CACGAGAGCTGTATGGGGCTGTGGTGTCTGAGTACTTTGTGCTGACAGCAGCACATTGTTTCACTGTGGATGAC
AAGGAACACTCAATCAAGGTCAGCGTAGGAGGGGAGAAGCGGGACCTGGAGATAGAAGTAGTCCTATTTACCCC
AACTACAACATTAATGGGAAAAAAGAAGCAGGAATTCCTGAATTTTATGACTATGACGTGGCCCTGATCAAGCTC
AAGAATAAGCTGAAATATGGCCAGACTATCAGGCCCATTTGTCTCCCCTGCACCGAGGGAACAACCTCGAGCTTTG
AGGCTTCCTCCAACCTACCACTTGCCAGCAACAAAAGGAAGAGCTGCTCCCTGCACAGGATATCAAAGCTCTGTTT
GTGTCTGAGGAGGAGAAAAAGCTGACTCGGAAGGAGGTCTACATCAAGAATGGGGATAAGAAAGGCAGCTGTGAG
AGAGATGCTCAATATGCCCCAGGCTATGACAAAGTCAAGGACATCTCAGAGGTGGTCACCCCTCGGTTCTTTGT
ACTGGAGGAGTGAGTCCCTATGCTGACCCCAATACTTGACAGAGGTGATTCTGGCGGCCCTTGATAGTTTACAAG
AGAAGTCGTTTCATTCAAGTTGGTGTAAATCAGCTGGGGAGTAGTGGATGTCTGCAAAAACCAGAAGCGGCAAAAG
CAGGTACCTGCTCACGCCCAGACTTTTACATCAACCTCTTTCAAGTGCTGCCCTGGCTGAAGGAGAACTCCAA
GATGAGGATTTGGGTTTTCTATTAAGGGGTTTCTGCTGGACAGGGCGTGGGATTGAATTAACAGCTGCGACA
AC

2129/6881
FIGURE 1960

MGSNLSPQLCLMPFILGLLSGGVTTTPWSLAQPQGSCLLEGVEIKGGSFRLQEGQALEYVCPSGFYYPVQTRT
CRSTGWSWTLKTQDQKTVRKAECRAIHCPRPDHFENGEYWPRSPYYNVSD EISFHCYDGYTLRGSANRTCQVNGR
WSGQTAICDNGAGYCSNPGIPIGTRKVG SQYRLED SVTYHCSRGLTLRGSQRRTCQEGGSWSGTEPSCQDSFMYD
TPQEVAEAFLLSSLTETIEGVDAEDGHGPGEQQKRKIVLDPGSMNIYLVLDGSDSIGASNFTGAKKCLVN LIEKV
ASYGVKPRYGLVTYATYPKIWVKVSEADSSNADWVTQQLNEINYEDHKLKSGTNTKKALQAVYSMMSWPDDVPPE
GWNRTRHVIILMTDGLHNMGGDPITVIDEIRDLLYIGKDRKNPREDYLDVYVFGVGPLVNQVNINALASKKDNEQ
HVFKVKDMENLEDV FYQMIDESQSLSLCGMVWEHRKGT DYHKQPWQAKISVIRPSKGHESCMGAVVSEYFVLTA A
HCFTVDDKEHSIKVSVGGEKRDLEIEVVLFHPNYNINGKKEAGIPEFYDYDVALIKLKNKLKYGQTIRPICLPCT
EGTTRALRLPPTTTCQQQKEELLPAQDIKALFVSEEEKLTRKEVYIKNGDKKGGSCERDAQYAPGYDKVKDISEV
VTPRFLCTGGVSPYADPNTCRGDSGGPLIVHKRSRFIQVGVISWGVVDVCKNQKRQKQVPAHARDFHINLFQVLP
WLKEKLQDEDLGFL

2130/6881
FIGURE 1961

GGTCCCAAGGCTTTCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGTGTGAGTTTCCGGCGTTCCGAAGGAC
TGAGCTCTTGTCGCGGATCCCGTCCGCCGTTTCCAGCCCCAGTCTCAGAGCGGAGCCCACAGAGCAGGGCACCG
GC**ATG**GCCAAAGCCGCGGCGATCGGCATCGACCTGGGCACCACCTACTCCTGCGTGGGGGTGTTCCAACACGGCA
AGGTGGAGATCATCGCCAACGACCAGGGCAACCGCACCACCCCACTACGTGGCCTTACGGACACCGAGCGGC
TCATCGGGGATGCGGCCAAGAACCAGGTGGCGCTGAACCCGCAGAACACCGTGTTTGACGCGAAGCGGCTGATCG
GCCGCAAGTTCGGCGACCCGGTGGTGCAGTCGGACATGAAGCACTGGCCTTTCCAGGTGATCAACGACGGAGACA
AGCCCAAGGTGCAGGTGAGCTACAAGGGGGAGACCAAGGCATTCTACCCCGAGGAGATCTCGTCCATGGTGCTGA
CCAAGATGAAGGAGATCGCCGAGGCGTACCTGGGCTACCCGGTGACCAACGCGGTGATCACCGTGCCGGCCTACT
TCAACGACTCGCAGCGCCAGGCCACCAAGGATGCGGGTGTGATCGCGGGGCTCAACGTGCTGCGGATCATCAACG
AGCCACGCGCCGCCCATCGCCTACGGCTGGACAGAACGGGCAAGGGGGAGCGCAACGTGCTCATCTTTGACC
TGGGCGGGGGCACCTTCGACGTGTCCATCCTGACGATCGACGACGGCATCTTCGAGGTGAAGGCCACGGCCGGGG
ACACCCACCTGGGTGGGGAGGACTTTGACAACAGGCTGGTGAACCACTTCGTGGAGGAGTTCAAGAGAAAACACA
AGAAGGACATCAGCCAGAACAAGCGAGCCGTGAGGCGGCTGCGCACCGCCTGCGAGAGGGGCCAAGAGGACCCTGT
CGTCCAGCACCCAGGCCAGCCTGGAGATCGACTCCCTGTTTGAGGGCATCGACTTCTACACGTCCATCACCAGGG
CGAGGTTTCGAGGAGCTGTGCTCCGACCTGTTCCGAAGCACCTGGAGCCCGTGGAGAAGGCTCTGCGCGACGCCA
AGCTGGACAAGGCCCAGATTACAGACCTGGTCCCTGGTCGGGGGCTCCACCCGCATCCCCAAGGTGCAGAAGCTGC
TGCAGGACTTCTTCAACGGGCGCGACCTGAACAAGAGCATCAACCCCGACGAGGCTGTGGCCTACGGGGCGGCGG
TGCAGGCGGCCATCCTGATGGGGGACAAGTCCGAGAAGCTGCAGGACCTGCTGCTGCTGGACGTGGCTCCCCTGT
CGCTGGGGCTGGAGACGGCCGGAGGCGTGATGACTGCCCTGATCAAGCGCAACTCCACCATCCCCACCAAGCAGA
CGCAGATCTTACCACCTACTCCGACAACCAACCCGGGGTGCTGATCCAGGTGTACGAGGGCGAGAGGGCCATGA
CGAAAGACAACAATCTGTTGGGGCGCTTCGAGCTGAGCGGCATCCCTCCGGCCCCAGGGGCGTGCCCCAGATCG
AGGTGACCTTCGACATCGATGCCAACGGCATCCTGAACGTCACGGCCACGGACAAGAGCACCGGCAAGGCCAGCA
AGATCACCATCACCAACGACAAGGGCCGCCCTGAGCAAGGAGGAGATCGAGCGCATGGTGCAGGAGGCGGAGAAGT
ACAAAGCGGAGGACGAGGTGCAGCGCGAGAGGGTGTGAGCCAAGAACGCCCTGGAGTCCTACGCCCTCAACATGA
AGAGCGCCGTGGAGGATGAGGGGCTCAAGGGCAAGATCAGCGAGGCGGACAAGAAGAAGGTTCTGGACAAGTGTC
AAGAGGTGATCTCGTGGCTGGACGCCAACACCTTGCCGAGAAGGACGAGTTTGAGCACAAGAGGAAGGAGCTGG
AGCAGGTGTGTAACCCCATCATCAGCGGACTGTACCAGGGTGCCGGTGGTCCCGGGCCTGGGGGCTTCGGGGCTC
AGGGTCCCAAGGGAGGGTCTGGGTGAGGCCCTACCATTTGAGGAGGTGGAT**TAG**GGGCCTTTGTTCTTTAGTATGT
TTGTCTTTGAGGTGGACTGTTGGGACTCAAGGACTTTGCTGCTGTTTTCTATGTCAATTTCTGCTTCAGCTCTTT
GCTGCTTCACTTCTTTGTAAAGTTAAGTTGTAACCTGATGGTAATTAGCTGGCTTCATTATTTTGTAGTACAAC
CGATATGTTTATTAGAATTCTTTGCATTTAATGTTGATACTGTAAGGGTGTTCGTTCCCTTTAAATGAATCAAC
ACTGCCACCTTCTGTACGAGTTTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGCTTGGCGAAAACACTACAAAGGC
TGGAATGTATGTTTTTATAATTTGTTTATTTAAATATGAAAAATAAATGTTAACTTT

2131/6881
FIGURE 1962

MAKAAAIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALNPQNTVFDAKRLIG
RKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEISSMVLTKMKEIAEAYLGYPVTNAVITVPAYF
NDSQRQATKDAGVIAGLNLVRIINEPTAAAIAYGLDRTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGD
THLGGEDFDNRLVNHFVEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA
RFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDNLKSINPDEAVAYGAAV
QAAILMGDKSENVQDLLLLLDVAPLSLGLETAGGVM TALIKRNSTIPTKQTQIFTTYSNQPGLIQVYEGERAMT
KDNLLGRFELSGIPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKASKITITNDKGRLSKEEIERMVQEAEKY
KAEDEVQRERVSAKNALESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELE
QVCNPIISGLYQGAGGPGPGGFGAQGPKGSGSGPTIEEVD

2132/6881
FIGURE 1963

GCTGCTGCGACAGTCCACTACCTTTTTTCGAGAGTGA TCTCCCGTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCG
GCTGCAGGCACCGGCGCGTTCGAGTTTCCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTT
CCAGCCCCCAATCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGGCATGGCCAAAGCCGCGGCGATCGGCATCG
ACCTGGGCAACCACCTACTCCTGCGTGGGGGTGTTCCAACACGGCAAGGTGGAGATCATCGCCAACGACCAGGGCA
ACCGCACCAACCCCAAGCTACGTGGCCTTCACGGACACCGAGCGGCTCATCGGGGATGCGGCCAAGAACCAGGTGG
CGCTGAACCCGCGAGAACACCGTGTTTTGACGCGAAGCGGCTGATCGGCCGCAAGTTCGGCGACCCGGTGGTGCAGT
CGGACATGAAGCACTGGCCTTTCCAGGTGATCAACGACGGAGACAAGCCCAAGGTGCAGGTGAGCTACAAGGGGG
ACACCAAGGCATTCTACCCCGAGGAGATCTCGTCCATGGTGCTGACCAAGATGAAGGAGATCGCCGAGGCGTACC
TGGGCTACCCGGTGACCAACGCGGTGATCACCGTGCCGGCCTACTTCAACGACTCGCAGCGCCAGGCCACCAAGG
ATGCGGGTGTGATCGCGGGGCTCAACGTGCTGCGGATCATCAACGAGCCACCGGCCCGCCATCGCCTACGGCC
TGGACAGAACGGGCAAGGGGGAGCGCAACGTGCTCATCTTTGACCTGGGCGGGGGACCTTCGACGTGTCCATCC
TGACGATCGACGACGGCATCTTCGAGGTGAAGGCCACGGCCGGGGACACCCACCTGGGTGGGGAGGACTTTGACA
ACAGGCTGGTGAACCACTTCGTGGAGGAGTTCAAGAGAAAACACAAGAAGGACATCAGCCAGAACAAGCGAGCCG
TGAGGCGGCTGCGCACCGCCTGCGAGAGGGCCAAGAGGACCCTGTCTCCAGCACCCAGGCCAGCCTGGAGATCG
ACTCCCTGTTTGAGGGCATCGACTTCTACACGTCCATCACCAGGGCGAGGTTTCGAGGAGCTGTGCTCCGACCTGT
TCCGAAGCACCTTGAGCCCGTGGAGAAGGCTCTGCGCGACGCCAAGCTGGACAAGGCCAGATTACGACCTGG
TCCTGGTTCGGGGCTCCACCCGCATCCCCAAGGTGCAGAAGCTGCTGCAGGACTTCTTCAACGGGCGCGACCTGA
ACAAGAGCATCAACCCGACGAGGCTGTGGCCTACGGGGCGGCGGTGCAGGCGGCCATCCTGATGGGGGACAAGT
CCGAGAACGTGCAGGACCTGCTGCTGCTGGACGTGGCTCCCCTGTCTGCTGGGGCTGGAGACGGCCGGAGGCGTGA
TGACTGCCCTGATCAAGCGCAACTCCACCATCCCCACCAAGCAGACGCAGATCTTACCACCTACTCCGACAACC
AACCCGGGGTGTGATCCAGGTGTACGAGGGCGAGAGGGCCATGACGAAAGACAACAATCTGTTGGGGCGCTTCG
AGCTGAGCGGCATCCCTCCGGCCCCCAGGGGCGTGCCCCAGATCGAGGTGACCTTCGACATCGATGCCAACGGCA
TCCTGAACGTACGGCCACGGACAAGAGCACCGGCAAGGCCAACAAGATCACCATCACCAACGACAAGGGCCGCC
TGAGCAAGGAGGAGATCGAGCGCATGGTGCAGGAGGCGGAGAAGTACAAAGCGGAGGACGAGGTGCAGCGCGAGA
GGGTGTAGCCAAGAACGCCCTGGAGTCCTACGCCTTCAACATGAAGAGCGCCGTGGAGGATGAGGGGCTCAAGG
GCAAGATCAGCGAGGCCGACAAGAAGAAGGTGCTGGACAAGTGTCAAGAGGTGATCTCGTGGCTGGACGCCAACA
CCTTGGCCGAGAAGGACGAGTTTGAGCACAAAGGAAGGAGCTGGAGCAGGTGTGTAACCCCATCATCAGCGGAC
TGTACCAGGGTGCCGGTGGTCCCGGGCCTGGGGGCTTCGGGGCTCAGGGTCCCAAGGGAGGGTCTGGGTGAGGCC
CCACCATTGAGGAGGTAGATTAGGGGCCTTTCCAAGATTGCTGTTTTTTGTTTTGGAGCTTCAAGACTTTGCATTT
CCTAGTATTTCTGTTTGTGCTGCTCTCAATTTCTGTGTTTGCAATGTTGAAATTTTTTGGTGAAGTACTGAACTT
GCTTTTTTTCCGGTTTCTACATGCAGAGATGAATTTATACTGCCATCTTACGACTATTTCTTTTAAATACAC
TAACTCAGGCCATTTTTTAAGTTGGTTACTTCAAAGTAAATAAACTTTAAAATTCAAGTGA

2133/6881
FIGURE 1964

MAKAAAIGIDLGTITYSCVGVFQHGKVEIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALNPNQNTVFDKRLIG
RKFGDPVVQSDMKHWPQVINDGDKPKVQVSYKGDTKAFYPEEISSMVLTKMKEIAEAYLGYPVTNAVITVPAYF
NDSQRQATKDAGVIAGLNLRIINEPTAAAIAYGLDRTGKGERNVLIFDLGGGTDFDVSILTIIDGIFEVKATAGD
THLGGEDFDNRLVNHFFVEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA
RFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLNKSINPDEAVAYGAAV
QAAILMGDKSENVQDLLLLLDVAPLSLGLTAGGVM TALIKRNSTIPTKQTQIFTTYSNQPGLIQVYEGERAMT
KDNLLGRFELSGIPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQEAKEY
KADEVQRERVSAKNALESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELE
QVCNPIISGLYQGAGGPGPGGFGAQGPKGGSGSGPTIEEVD

2134/6881
FIGURE 1965

GGCTTCCTCCTCCCCTCTACTCTACCCAGCTTGCGCTCCCCAGCCGCAAGTCGGCCGCGCTTTGCCCCTCAGCGC
TTGGAGCTTTCTGCGTCGCTTCCCGCTGCGCCTGCGCGGTCCCGCCTCGCCCCACGCGCGGGCTCGCGCTTCGGT
TTCCCCAGACCTGCTCGCAGCACCTGCTGTCTTCCCGGTCCGGCCCGCTGCCCCGCGGCGCCAGCACCAATGCTCT
TCTATTCTTTTTTCAAGTCCCTTGTGGGCAAGGATGTGGTCGTGGAATAAAGAATGACCTGAGCATCTGTGGAA
CCCTCCATTCTGTGGATCAGTATCTCAACATCAAATACTGACATCAGTGTACAGACCCTGAGAAATACCCTC
ACATGTTATCAGTGAAGAACTGCTTCATTCGGGGCTCAGTGGTCCGATACGTGCAGCTGCCAGCAGATGAGGTCG
ACACACAGTTGCTACAGGATGCGGCAAGGAAGGAAGCCCTGCAGCAGAAACAGTATGATGGCTCCTCCTCCTCTTCC
CCTCCCTCTTTCATTGGTGACCCATAACCCCAAGTCCCAGCCCAGAACCCCTAACCCCAATACTTGAAGGGGTT
TTGTTTTTTTTACTAATGATGGTTTTGTGGTTTTTTTTTAAGGGATGAGTGGATGAGAGGAGTAATAGGGAACAGC
TATCCTCTCTTGAGAAGGGGAGGATAAGTAGGCTGGGAACTTCAAAGCCTTCCCAGTCCCCAGCACCTGCCTTT
CTCACTACTTCTCTGGAGATGGTAGGAGAGTTTCCTAGGTCTTCCAGGGCAGCATGTGATTTCATTTGGGGATGG
AAGGAATCTGTCCCGCATCGGGAATAAAATTTATGATGC

2135/6881
FIGURE 1966

MLFYSEFKSLVGKDVVELKNDLSICGTLHSVDQYLNILKLTDISVTDPEKYPHMLSVKNCFIRGSVVRVYVQLPAD
EVDLTQLLQDAARKEALQQKQ

2136/6881
FIGURE 1967A

GTCACAAAGGGGGGAACACGTGGGCGCCGGCTGCCGGGGCGGCGATCTTAGGGAACTAGGGTACCTGGAGAGCC
GCCCACCGTCTCTGCCCGCTCGACTCCTCCGCCCCGGCGCTCGGCCGGTCCAGCCGCGGGCCGGCGCTGGCTGT
GAGGTGGATTCCCGGGCCAGTCTGACCATCTCCCTCCAGTTTTTTCCACTTCGTTTCGGACCTTCTCATAACTATGT
CCACCTCTACGTCTCCCTCACCCAGATGCCTTCCCCAGCCTCCGAGCCCTCATAGCCGCTCGCTATGGGGAGG
CTGGGGAGGGTCCCGGATGGGGAGGAGCCACCCCCGCATCTGTCTCCAGCCACCCCCGACTAGCAGGACTCCCT
TTCCCCACCCCGCTGCCGGCCCTGGAGCAGGGGCCCCGGTGGGCTCTGGGTGTGGGGGGCCACGGCTGTGGCCC
AGCTGCTGTGGCCAGCAGGCCTGGGGGGCCAGGGGGCAGCCGGGCGGCTGTCTTGTCCAACAGTGGGTCACTT
ACGCCGACACGGAGTTAATACCAGCTGCCTGTGGAGCAACGCTGCCGGCCCTGGGACTCCGAAGCTCGGCCCAGG
ACCCCCAGGCTGTGCTGGGGGGCCCTGGGCAGGGCCCTGAGCCCCCTTGGAGGAGTGGCTTCGGCTGCACACCTACT
TGGCCGGGGAGGCCCCACTCTGGCTGACCTGGCGGCTGTACAGCCTTGCTGCTGCCTTTCCGATACGTCCTAG
ACCCACCTGCCCCCGGATCTGGAATAATGTGACTCGCTGGTTTGTACAGTGTGTCCGGCAGCCAGAATTCCGAG
CCGTGCTAGGAGAAGTGGTTCTATACTCAGGAGCCAGGCCTCTCTCTCATCAGCCAGGCCCCGAGGCTCCTGCCC
TCCCAAAGACAGCTGCTCAGCTCAAGAAAGAGGCAAGAAACGGGAGAAGCTAGAGAAATTCCAACAGAAGCAGA
AGATCCAACAGCAGCAGCCACCTCCAGGGGAGAAGAAACCAAAACCAGAGAAGAGGGAGAAACGGGATCCTGGGG
TCATTACCTATGACCTCCCAACCCACCCGGGAAAAGAAAGATGTCACTGGCCCCATGCCGACTCCTACAGCC
CTCGGTATGTGGAGGCTGCCTGGTACCCTTGGTGGGAGCAGCAGGGCTTCTTCAAGCCAGAGTATGGGCGTCCTA
ATGTGTCAAGCAGCAAAATCCCCGAGGTGTCTTCATGATGTGCATCCACCCCCCAATGTGACAGGCTCCCTGCACC
TGGGCCATGCACTACCAACGCCATCCAGGACTCCCTGACTCGATGGCACCAGCATGCGTGGGGAGACCACCTGT
GGAACCTTGGCTGTGACCATGCAGGTATTGCCACCCAGGTGGTGGTGGAGAAGAAGCTATGGCGTGAGCAGGGAC
TGAGCCGGCACCAGCTGGGCCGCGAGGCCTTTCTACAGGAAGTCTGGAAGTGGAGGAGGAGAAAGGTGACCGGA
TTTACCACCAGTTGAAGAAGCTTGGCAGCTCCTTGGACTGGGATCGAGCCTGTTTACCATGGACCCTAAACTCT
CAGCAGCTGTGACAGAGGCCTTTGTCCGGCTTACAGAGGAAGGCATCATCTATCGCAGTACCCGCCTTGTAACT
GGTCTGCAACCTCAACTCCGCCATCTCTGACATTGAGGTGGATAAGAAGGAGCTGACAGGTGACACCCTGCTCT
CCGTGCCTGGCTACAAGGAGAAGGTGGAGTTCGGGGTCTCGTGTCTTTGCCTATAAGGTCCAAGGCTCAGATA
GCGACGAGGAGGTGGTGGTGGCAACAACCTCGGATCGAGACAATGCTGGGAGATGTGGCTGTAGCTGTGCACCCCCA
AAGATACCAGATAACCAGCACCTGAAGGGGAAGAACGTGATCCACCCATTCTGTCTCGGAGCCTTCCCATTGTCT
TCGATGAATTTGTGGACATGGACTTTGGCACAGGTGCTGTGAAGATCACCCCCGCACATGACCAAAATGACTATG
AAGTTGGGCAGCGGCACGGGCTGGAGGCCATCAGCATCATGGACTCCCGGGGGGCCCTCATCAATGTGCCTCCGC
CTTCTCTGGGCTGCCAGGTTTGAGGCCAGGAAAGCGGTGCTGGTGGCGCTGAAGGAGCGGGGACTGTTCCGTG
GCATTGAGGACAACCCCATGGTGGTGCCACTTTGCAACCGGTGCAAGGACGTGGTAGAGCCTCTGCTGCGGCCGC
AGTGGTACGTTTCGTGCGGGGAGATGGCCCAGGCTGCCAGCGCCGCTGTGACTCGGGGTGACCTCCGCATCCTGC
CTGAGGCCCATCAGCGCACATGGCATGCCTGGATGGACAACATCCGGGAGTGGTGCATTTCCAGGCAGCTGTGGT
GGGGCCATCGCATCCCAGCCTACTTTGTCACTGTCACTGACCCAGCGGTGCCCCCTGGGGAGGACCCTGATGGGC
GGTACTGGGTGAGTGGACGCAATGAGGCGGAGGCCCGGGAGAAGGCAGCCAAGGAGTTCGGAGTGTCCCCTGACA
AGATCAGTCTCCAGCAAGATGAGGATGTATTGGATACCTGGTTCTCCTCTGGCCTCTTCCCCTTATCCATTTTG
GCTGGCCCAACCAGTCAGAAGACCTGAGTGTGTTCTACCCGGGACACTGCTGGAGACCGGTCATGACATCCTCT
TCTTCTGGGTGGCCCGGATGGTCACTGCTGGGCCTGAAGCTCACGGGAGGCTGCCCTTTAGAGAGGTCTACCTCC
ATGCCATCGTGCAGATGCTCACGGCCGGAAGATGAGCAAGTCTCTAGGCAATGTCATCGATCCCCTGGATGTCA
TCTATGGAATCTCCCTGCAGGGCCTCCACAACCAGCTGCTGAACAGCAACCTGGATCCCAGCGAGGTGGAGAAGG
CCAAAGAAGGGCAGAAAGCTGACTTCCCAGCGGGGATTCTGAATGTGGCACCGATGCTCTCCGGTTTGGATTAT
GTGCCTACATGTCCCAGGGTCGTGACATCAACCTGGATGTGAACCGGATACTGGGTTACCGCCACTTCTGCAACA
AGCTCTGGAATGCCACCAAGTTTGGCCTTCGTGGCCTTGGGAAGGGTTTTGTGCCCTCACCCACCTCCCAGCCCG
GAGGCCATGAGAGCCTGGTGGACCGCTGGATCCGCAGCCGCCTGACAGAGGCTGTGAGGCTCAGCAATCAAGGCT
TCCAGGCCTACGACTTCCCGGCCGTACCACTGCCCAGTACAGCTTCTGGCTCTATGAGCTCTGTGATGTCTACT
TGGAGTGCTGAAACCTGTACTGAATGGGGTGGACCAGGTGGCAGCTGAGTGTGCCCCGCCAGACCCTGTACACTT
GCCTGGACGTTGGCCTGCGGCTGCTCTCACCTTTCATGCCCTTCGTGACGGAGGAGCTGTTCCAGAGGCTGCCCC
GGAGGATGCCGCAAGCTCCCCCTAGCCTCTGTGTTACCCCCCTACCCGGAGCCCTCAGAGTGTCTTGAAGGACC
CCGAGGCAGAAGCCGCCCTTGAAGTGGCGCTAAGCATCACGCGAGCCGTGCGCTCCCTGCGGGCCGACTACAACC

2137/6881
FIGURE 1967B

TCACCCGGATCCGGCCTGACTGTTTCCTGGAAGTGGCGGATGAGGCCACGGGCGCCCTGGCATCGGCGGTGTCGG
GCTACGTGCAGGCCCTGGCCAGCGCAGGTGTGGTGGCTGTTCTGGCCCTGGGGGCTCCCGCCCCCAGGGTTGCG
CTGTGGCTCTGGCTTCTGATCGCTGCTCCATCCACCTGCAGCTTCAGGGGCTGGTGGACCCTGCACGGGAGCTGG
GCAAGCTGCAAGCCAAGCGAGTTGAGGCCAGCGGCAGGCCAGCGTCTGCGGGAACGCCGTGCTGCCTCGGGCT
ATCCTGTCAAGGTGCCGCTCGAAGTCCAGGAGGCAGATGAAGCCAAGCTCCAACAGACAGAAGCAGAGCTCAGGA
AGGTGGATGAGGCCATCGCCCTATTCCAGAAGATGCTGTGATCCACCACCCAGCTTCACCCCTCACCCCAGCGG
CTCACCATGGGGATGGCAGCAATAAAATATTTTCCCACAAAA

2138/6881
FIGURE 1968

MSTLYVSPHPDAFFPSLRALIAARYGEAGEGPGWGGAHPRICLQPPPTSRTPFPPPRLPALQGGGLWVWGATAV
AQLLWPAGLGGPGGSRAAVLVQQWVSADTELIPAACGATLPALGLRSSAQDPQAVLGALGRALSPLEEWLRLHT
YLAGEAPTLADLAAVTALLLPFRYVLDPPARRIWNVTRWFTCVRQPEFRAVLGEVVLVYSGARPLSHQPGPEAP
ALPKTAAQLKKEAKKREKLEKFQQKQKIQQQQPPPGGEKKPKPEKREKRDPGVITYDLPTPPGEKKDVSGMPDSY
SPRYVEAAWYPWWEQQGFFKPEYGRPNVSAANPRGVFMMCIPEPNTGSLHLGHALTNAIQDSLTRWHRMRGETT
LWNPFGCDHAGIATQVVVEKKLWREQGLSRHQLGREAFLOEVWKWKEEKGDRIYHQLKKLGSSLDWDRACFTMDPK
LSAAVTEAFVRLHEEGIYRSTRLVNWSCTLNSAISDIEVDKKELTGRTLLSVPGYKEKVEFGVLVSFAYKVQGS
DSDEEVVVATTRIETMLGDVAVAVHPKDTRYQHLKGKNIHPFLSRSLPIVFDEFVDMDFGTGAVKITPAHDQND
YEVGQRHGLEAISIMDSRGALINVPPFPLGLPRFEARKAVLVALKERGLFRGIEDNPMVVPCLNRSKDVVEPLLR
PQWYVRCGEMAQAASAAVTRGDLRILPEAHQRTWHAWMDNIREWCISRQLWWGHRIPAYFVTVSDPAVPPGEDPD
GRYWVSGRNEAEAREKAAKEFGVSPDKISLQQDEVDLDTWFSGLFPLSLIGWPNQSEDLSVFYPGTLLLETGHI
LFFWVARMVMLGLKLTGRLPFREVYLHAIVRDAHGRKMSKSLGNVIDPLDVIYGISLQGLHNQLLNSNLDPSEVE
KAKEGQKADFPAGIPECGTDALRFGLCAYMSQGRDINLDVNRILGYRHFCNKLWNATKFALRGLGKGFVPSPTSQ
PGGHESLVDRWIRSLTEAVRLSNQGFQAYDFPAVTTAQYSFWLYELCDVYLECLKPVLNGVDQVAAECAQTLY
TCLDVGLRLLSPFMPFVTEELFQRLPRRMPQAPPSLCVTPYPEPSECSWKDPEAEAALELALSITRAVRSRADY
NLTRIRPDCFLEVADEATGALASAVSGYVQALASAGVVAVLALGAPAPQGCALASDRCSIHLQLQGLVDPARE
LGKLQAKRVEAQRQAQRLRERRAASGYPVKVPLEVQEADEAKLQQTEAELRKVDEAIALFQKML

2139/6881
FIGURE 1969

GCGGCTCTCTGATCCAGCCCGGGAGAGGACCGAGCTGGAGGAGCTGGGTGTGGGGTGCGTTGGGCTGGTGGGGAG
GCCTAGTTTGGGTGCAAGTAGGTCTGATTGAGCTTGTGTTGTGCTGAAGGGACAGCCCTGGGTCTAGGGGAGAGA
GTCCCTGAGTGTGAGACCCGCCTTCCCCGGTCCCAGCCCCCTCCAGTTCCCCCAGGGACGGCCACTTCCTGGTCC
CCGACGCAACC**ATGG**CTGAAGAACAACCGCAGGTCGAATTGTTTCGTGAAGGCTGGCAGTGATGGGGCCAAGATTG
GGAAGTGGCCATTCTCCCAGAGACTGTTTCATGGTACTGTGGCTCAAGGGAGTCACCTTCAATGTTACCACCGTTG
ACACCAAAAGGCGGACCGAGACAGTGCAGAAGCTGTGCCCAGGGGGGCAGCTCCCATTCCTGCTGTATGGCACTG
AAGTGACACACAGACACCAACAAGATTGAGGAATTTCTGGAGGCAGTGCTGTGCCCTCCCAGGTACCCCAAGCTGG
CAGCTCTGAACCCCTGAGTCCAACACAGCTGGGCTGGACATATTTGCCAAATTTTCTGCCTACATCAAGAATTCAA
ACCCAGCACTCAATGACAATCTGGAGAAGGGACTCCTGAAAGCCCTGAAGGTTTTAGACAATTACTTAACATCCC
CCCTCCCAGAAGAAGTGGATGAAACCAGTGCTGAAGATGAAGGTGTCTCTCAGAGGAAGTTTTTGGATGGCAACG
AGCTCACCCCTGGCTGACTGCAACCTGTTGCCAAAGTTACACATAGTACAGGTGGTGTGTAAGAAGTACCGGGGAT
TCACCATCCCCGAGGCCTTCCGGGGAGTGCATCGGTACTTGAGCAATGCCTACGCCCCGGGAAGAATTCGCTTCCA
CCTGTCCAGATGATGAGGAGATCGAGCTCGCCTATGAGCAAGTGGCAAAGGCCCTCAAA**TAA**GCCCCCTCCTGGGA
CTCCCTCAACCCCTCCATTTTCTCCACAAAGGCCCTGGTGGTTTCCACATTGCTACCCAATGGACACACTCCAA
AATGGCCAGTGGGCAGGGAATCCTGGAGCACTTGTTCCGGGATGGTGTGGTGAAGAGGGGATGAGGGAAAGAAA
TGGGGGGCCTGGGTCAGATTTTTATTGTGGGGTGGGGTGAGTAGGACAACATATTTAGTAATAAAATACAGAAT
AAAAATCAAGTGTTTTTAAAAAAA

2140/6881
FIGURE 1970

MAEEQPQVELFVKAGSDGAKIGNCPFSQRLEFMVLWLKGVTFNVTTVDTKRRTETVQKLCPPGGQLPFLLYGTEVHT
DTNKIEEFLEAVLCPPRYPKLAALNPESNTAGLDIFAKFSAYIKNSNPALNDNLEKGLLKALKVLDNYLTSPLPE
EVDETSAEDEGVSQRKFLDGNELTLADCNLLPKLHIVQVCKKYRGFTIPEAFRGVHRYLSNAYAREEFASCPD
DEEIELAYEQVAKALK

2141/6881
FIGURE 1971

ATGAGCAGCTCAGAGGAGGTGTCCTGGATTTCTGGTTCTGTGGGCTCCGTGGCAATGAATTCTTCTGTGAAGTG
GATGAAGACTACATCCAGGACAAATTTAATCTTACTGGACTCAATGAGCAGGTCCCTCACTACCGACAAGCTCTA
GACATGATCTTGGACCTGGAGCCTGATGAAGAACTGGAAGACAACCCCAACCAGAGTGACCTGATTGAGCAGGCA
GCCGAGATGCTTTATGGATTGATCCACGCCCGCTACATCCTTACCAACCGTGGCATCGCCCAGATGTTGGAAAAG
TACCAGCAAGGAGACTTTGGTTACTGTCCTCGTGTGTACTGTGAGAACCAGCCAATGCTTCCCATTGGCCTTTCA
GACATCCCAGGTGAAGCCATGGTGAAGCTCTACTGCCCCAAGTGCATGGATGTGTACACACCCAAGTCATCAAGA
CACCATCACACGGATGGCGCCTACTTCGGCACTGGTTTCCCTCACATGCTCTTCATGGTGCATCCCGAGTACCGG
CCCAAGAGACCTGCCAACCAGTTTGTGCCCAGGCTCTACGGTTTCAAGATCCATGCGATGGCCTACCAGCTGCAG
CTCCAAGCCGCCAGCAACTTCAAGAGCCCAGTCAAGACGATTCTGCTTGA

2142/6881
FIGURE 1972

MSSSEEVSWISWFCGLRGNEFFCEVDEDYIQDKFNLTGLNEQVPHYRQALDMILDLEPDEELEDNPNQSDLIEQA
AEMLYGLIHARYILTNRGIAQMLEKYQQGDFGYCPRVYCENQPMPLIGLSDIPGEAMVKLYCPKCMDVYTPKSSR
HHHTDGAYFGTGFPHMLFMVHPEYRPFKR PANQFVPRLYGFKIHAMAYQLQLQAASNFKSPVKTI R

2143/6881
FIGURE 1973A

TAGTGCACGCACGCAGGCGTAGTACGGTCCCCCGGGCGACAGCGGTGGCGGCTCCTCGGGGTGCTCGGCTCCCT
 CCCACCTAGGCCGGCCCCGGCCCCGACTCGCCCTCAGAACTCACTGTTTGGGGCTGCGGACTTTCTCGTCGTGCC
 CCACAAAAGTAAAGCTTGGGGACCTGGGGGGAGCCGGAAGTATCGCTTCGAGATCCCCAAATACTATCGGGGAAA
 CGGAAGTGGCCGTCGGTGGCAGGTTTGGGGGAGACCGGAAGTGACGAGACCTGTCGGGCC**ATG**GAGCCTAATGATA
 GTACCAGTACCGCTGTGGAGGAGCCTGACAGCTTGGAGGTGTTGGTGAAGACCTTGGACTCTCAAACCTCGTACCT
 TTATTGTGGGGGCCAGATGAATGTAAAAGAGTTTAAGGAGCACATTGCTGCCTCTGTCAGCATCCCATCTGAAA
 AACAAACGGCTCATTTACCAGGGACGAGTTCTGCAAGATGATAAGAAGCTTCAGGAATACAATGTTGGGGGAAAGG
 TTATCCACCTGGTGAACGGGCTCCTCCTCAGACTCACCTCCCTTCTGGGGCATCTTCTGGGACGGGGTCTGCCT
 CAGCCACTCATGGTGGGGGATCCCCCCTGGTACTCGGGGGCTGGGGCCTCTGTTTCATGACCGGAATGCCAACA
 GCTATGTCATGGTTGGAACCTTCAATCTTCCTAGTGACGGCTCTGCTGTGGATGTTTCACATCAACATGGAACAGG
 CCCCATTTCAGAGTGAGCCCCGGGTACGGCTGGTGATGGCTCAGCACATGATCAGGGATATACAGACCTTACTAT
 CCGGATGGAGACTCTCCCTACCTTCAGTGTCGAGGAGGGCCCCAACCCGACGACAGTCAGCCGCCCCCGCAGC
 CACCGGCTGTGACCCCGGAGCCAGTAGCCTTGAGCTCTCAAACATCAGAACCAGTTGAAAGTGAAGCACCTCCCC
 GGGAGCCCATGGAGGCAGAAGAAGTGGAGGAGCGTGCCCCAGCCAGAACC CGGAGCTCACTCCTGGCCCAGCCC
 CAGCGGGCCCAACACCTGCCCCGAAACAAATGCACCCAACCATCCTTCCCCTGCGGAGTATGTCGAGGTGCTCC
 AGGAGCTACAGCGGCTGGAGAGTCGCCTCCAGCCCTTCTTGACGCGCTACTACGAGGTCTGCGGTGCTGCTGCCA
 CCACGGACTACAATAACAATCACGAGGGCCGGGAGGAGGATCAGCGGTTGATCAACTGGTAGGGGAGAGCCTGC
 GACTGCTGGGCAACACCTTTGTTGCACTGTCTGACCTGCGCTGCAATCTGGCCTGCACGCCCCCACGACACCTGC
 ATGTGGTCCGGCCTATGTCTCACTACACCACCCCATGGTGCTCCAGCAGGCAGCCATTCCCATAACAGATCAATG
 TGGAACCACTGTGACCATGACAGGAAATGGGACTCGGCCCCCCCCAACTCCCAATGCAGAGGCACCTCCCCCTG
 GTCTGGGCAGGCCTCATCCGTGGCTCCGCTTCTACCAATGTGAGTCCTCAGCTGAGGGGGCTCCCCGCCAG
 GTCCAGCTCCCCGCCAGCCACCAGCCACCCGAGGGTCATCCGGATTTCCCACCAGAGTGTTGAACCCGTGGTCA
 TGATGCACATGAACATTCAAGATTCTGGCACACAGCCTGGTGGTGTTCAGAGTGCTCCCACTGGCCCCCTGGGAC
 CCCCTGGTCATGGCCAAACCTGGGACAGCAGGTGCCAGGCTTCCCAACAGCTCCAACCCGGGTGGTGATTGCC
 GGCCCACTCCTCCACAGGCTCGGCCTTCCCATCCTGGAGGGCCCCCAGTCTCTGGGACACTGCAGGGCGCCGGTC
 TGGGTACCAATGCCTCGTTGGCCCAGATGGTGAGCGGCCTTGTGGGGCAGCTTCTTATGCAGCCAGTCCTTGTGG
 CTCAGGGGACCCAGGTATGGCTCCACCGCCAGCCCTGCCACTGCTTCTGCCAGTGCTGGCACCACCAACACAG
 CTACCACAGCTGGCCCCGCTCCTGGGGGGCTGCCAGCCTCCACCCACCCCTCAACCCCTCATGGCTGATCTTC
 AGTTCTCTCAGCTTCTGGGGAACCTGCTAGGGCCTGCAGGGCCAGGGGCTGGAGGGCTGGTGTGGCTTCTCCCA
 CCATCACTGTGGCGATGCCTGGTGTCCCTGCCTTTCTCCAAGGCATGACTGACTTCTTGACAGGCAACACAGACAG
 CCCCTCCACCACCCCACTCCTCCACCCCACTGCCCCAGAGCAGCAGACCATGCCCCACCCAGGCTCCC
 CTTCTGGTGGCGCAGGGAGTCCCTGGAGGCCTGGGTCTTGAGAGCCTGTCACCGGAGTTTTTTACCTCAGTGGTGC
 AGGGTGTGCTCAGCTCCCTGCTGGGCTCCCTGGGGGCTCGGGCTGGCAGCAGTGAAGTATTGCTGCCTTCATAC
 AACGCCTCAGTGGATCCAGCAACATCTTTGAGCCTGGAGCTGATGGGGCCCTTGGATTCTTTGGGGCCTTGCTTT
 CTCTTCTGTGCCAGAACTTCTCTATGGTGGACGTAGTGATGCTTCTCCATGGGCATTTCCAGCCACTACAACGGC
 TCCAGCCCCAGCTGCGATCCTTCTCCACCAGCACTACCTGGGTGGTCAGGAGCCACACCCAGTAACATCCGGA
 TGGCAACCCACACATTGATCACGGGGCTAGAAGAGTATGTGCGGGAGAGTTTTCTTGGTGCAGGTTTCAGCCAG
 GTGTGGACATCATCCGGACAAACCTGGAATTTCTCCAAGAGCAGTTAATAGCATTGCTGCGCATGTGCTGCATT
 GCACAGATAGTGGATTGTTGGGGCCCGTTGCTGGAGTTGTGTAACCAAGGCCTGTTTGAATGCCTGGCCCTAAACC
 TGCATGCTTGGGGGGACAGCAGATGGAGCTTGTGCTGTTATCAATGGCCGAATTCGTGCTATGTCTCGTGGGG
 TGAATCCCTCCTTGGTGAGCTGGCTGACCACTATGATGGGACTGAGGCTTCAGGTGGTACTGGAGCACATGCCTG
 TAGGCCCTGATGCCATTCTCAGATACGTTTCGAGGGTTGGTGATCCCCCCCAGCCACTTCTGAGGAGCCAATGG
 AAGTTCAGGGAGCAGAAAGAGCTTCCCCTGAGCCTCAGCGGGAGAATGCTTCCCCAGCCCCCTGGAACAACAGCAG
 AAGAGGCCATGTCCCGAGGTCCACCTCCTGCTCCTGAGGGGGGCTCCCGGGATGAACAGGATGGAGCTTCAGCTG
 AGACAGAACCTTGGGCAGCTGCAGTCCCCCAGAATGGGTCCCTATTATCCAGCAGGACATTAGAGCCAGCGGA
 AGGTGAAACCGCAGCCCCCTCTGAGTGATGCCTACCTCAGTGGTATGCCTGCCAAGAGACGCAAGACGATGCAGG
 GTGAGGGCCCCCAGCTGCTTCTCTCAGAGGCTGTGAGCCGGGCAGCTAAGGCAGCCGGAGCTCGGCCCTGACGA
 GCCCCGAGAGCCTGAGCCGGGACCTGGAGGCACCAGAGGTTTCAGGAGAGCTACAGGCAGCAGCTCCGGTCTGATA

2144/6881
FIGURE 1973B

TACAAAAACGACTGCAGGAAGACCCCAACTACAGTCCCCAGCGCTTCCCCAATGCCAGCGGGCCTTTGCTGATG
ATCCT**TAG**CTCTTTGCTCTATGGCCCTTCCTCATCAGGGGACCGTTCCCCCTCTTCCTTCACAGTATTAAAGA
AATAAAAGTCGGATTTTCTGGC

2145/6881
FIGURE 1974

MEPNDSTSTAVEEPDSLEVLVKTLDSQTRTFIVGAQMNVKEFKEHIAASVSIPSEKQRLIYQGRVLQDDKKLQEY
NVGGKVIHLVERAPPQTHLPSGASSGTGSASATHGGGSPPGTRGPGASVHDRNANSYVMVGTFNLPSDGSAVDVH
INMEQAPIQSEPRVRLVMAQHMIQTLTLLSRMETLPYLQCRGGPQPQHSQPPPQPPAVTPEPVALSSQTSEPVE
SEAPPREPMEAEVEERAPAQNPETPGPAPAGPTPAPETNAPNHPSPA EYVEVLQELQRLSRLQPFLLQRYEY
LGAAATTDYNNNHEGREEDQRLINLVGESLRLLGNTFVALSDLRCNLACTPPRHLHVVRPMSHYTTPMVLQQAII
PIQINVGTTVTMTGNGTRPPPTPNAEAPPPGPGQASSVAPSSSTNVESAEAGAPPPGPA PPPATSHPRVIRISHQS
VEPVVMMHMNIQDSGTQPGGVPSAPTGPLGPPGHGQTLGQQVPGFPTAPTRVVIARPTPPQARPSHPGGPPVSGT
LQGAGLGTNASLAQMVSGLVGQLLMQPVLV AQGTPGMAPPPAPATASASAGTTNTATTAGPAPGGPAQPPPTPQP
SMADLQFSQLLGNLLGPAGPGAGGPGVASPTITVAMPGVPAFLQGMTDFLQATQTAPPPPPPPPPPPPAPEQQTM
PPPGSPSGGAGSPGGLGLESLSPEFFTSVVQGVLSLLGSLGARAGSSESIAAFIQRLSGSSNIFEPGADGALGF
FGALLSLLCQNF SMVDVVMLLHGHFQPLQRLQPQLRSFFHQHYLGQEQPTPSNIRMATHTLITGLEEYVRESFSL
VQVQPGVDIIRTNLEFLQEQFNSIAAHVLHCTDSGFGARLLELCNQGLFECLALNLHCLGGQQMELAAVINGRIR
RMSRGVNPSLVSWLTMMGLRLQVVLEHMPVGEDAILRYVRRVGDPPQPLPEEPMEVQGAERASPEPQRENASPA
PGTTAEEMS RGPPEPAGGSRDEQDGASAETEPWAAVPEWVPIIQQDIQSQRKVQPPLSDAYLSGMPAKR
RKTMQEGEPQLLLSEAVSRAAKAAGARPLTSPELSRDL EAPVQESYRQQLRSDIQKRLQEDPNYSPQRF PNAQ
RAFADDP

2146/6881
FIGURE 1975A

TAGTGCACGCACGCAGGCGTAGTACGGTCCCCCGGGCGACAGCGGTGGCGGCTCCTCGGGGTGCTCGGCTCCCT
CCCACCTAGGCCGGCCCCGGCCCCGACTCGCCCTCAGAACTCACTGTTTGGGGCTGCGGACTTTCTCGTCGTGCC
CCACAAAAGTAAAGCTTGGGGACCTGGGGGGAGCCGGAAGTATCGCTTCGAGATCCCCAAATACTATCGGGGAAA
CGGAAGTGGCCGTGGTGGCAGGTTTGGGGGAGACCGGAAGTGACGAGACCTGTGGGCCATCGAGCCTAATGATA
GTACCAGTACCGCTGTGGAGGAGCCTGACAGCTTGGAGGTGTTGGTGAAGACCTTGGACTCTCAAACCTCGTACCT
TTATTGTGGGGGCCAGATGAATGTAAAAGAGTTAAGGAGCACATTGCTGCCTCTGTGAGCATCCCATCTGAAA
AACACGGGCTCATTTACCAGGGACGAGTTCTGCAAGATGATAAGAAGCTTCAGGAATACAATGTTGGGGGAAAGG
TTATCCACCTGGTGGAACGGGCTCCTCCTCAGACTCACCTCCCTTCTGGGGCATCTTCTGGGACGGGGTCTGCCT
CAGCCACTCATGGTGGGGGATCCCCCCTGGTACTCGGGGGCCTGGGGCCTCTGTTTCATGACCGGAATGCCAACA
GCTATGTTCATGGTTGGAACCTTCAATCTTCTAGTGACGGCTCTGCTGTGGATGTTTCACATCAACATGGAACAGG
CCCCGATTAGAGTGTGAGGAGGGCCCCAACCAGCAGCAGTACAGCCGCCCCCGCAGCCACCGGCTGTGACCCCGG
AGCCAGTAGCCTTGAGCTCTCAAACATCAGAACAGTTGAAAGTGAAGCACCTCCCCGGGAGCCCATGGAGGCAG
AAGAAGTGGAGGAGCGTGCCCCAGCCAGAACCCGAGCTCACTCCTGGCCCAGCCCCAGCGGGCCCAACACCTG
CCCCGAAACAAATGCACCAACCATCCTTCCCTTGCAGGAGTATGTGAGGTGCTCCAGGAGCTACAGCGGCTGG
AGAGTCGCCTCCAGCCCTTCTTGCAGCGCTACTACGAGGTTCTGGGTGCTGCTGCCACCACGGACTACAATAACA
ATCAGAGGGCCGGGAGGAGGATCAGCGGTTGATCAACTTGGTAGGGGAGAGCCTGCGACTGCTGGGCAACACCT
TTGTTGCACTGTCTGACCTGCGCTGCAATCTGGCCTGCACGCCCCACGACACCTGCATGTGGTCCGGCCTATGT
CTCACTACACCACCCCATGGTGTCTCAGCAGGCAGCCATTCCCATACAGATCAATGTGGGAACCACTGTGACCA
TGACAGGAAATGGGACTCGGGCCCCCCCCAACTCCCAATGCAGAGGCACCTCCCCCTGGTCTGGGCAGGCCTCAT
CCGTGGCTCCGTCTTCTACCAATGTGAGTCTCAGCTGAGGGGGCTCCCCCGCCAGGTCCAGCTCCCCCGCCAG
CCACCAGCCACCCGAGGGTTCATCCGGATTTCACCACAGAGTGTGGAACCCGTGGTTCATGATGCACATGAACATTC
AAGATTCTGGCACACAGCCTGGTGGTGTTCGAGTGTCTCCACTGGCCCCCTGGGACCCCTGGTTCATGGCCAAA
CCCTGGGACAGCAGGTGCCAGGCTTCCCAACAGCTCCAACCCGGGTGGTGATTGCCCGGCCCACTCCTCCACAGG
CTCGGCCTTCCCATCCTGGAGGGCCCCCAGTCTCTGGGACACTGCAGGGCGCCGGTCTGGGTACCAATGCCTCGT
TGGCCCAGATGGTGAGCGGCCTTGTGGGGCAGCTTCTTATGCAGCCAGTCTTGTGGCTCAGGGGACCCAGGTA
TGGTCCACCGCCAGCCCCCTGCCACTGCTTCTGCCAGTGTGGCACCACCAACACAGCTACCACAGCTGGCCCCG
CTCCTGGGGGGCCTGCCAGCCTCCACCCACCCCTCAACCCTCCATGGCTGATCTTCAGTTCTCTCAGCTTCTGG
GGAACCTGCTAGGGCCTGCAGGGCCAGGGGCTGGAGGGTCTGGTGTGGCTTCTCCCACCATCACTGTGGCGATGC
CTGGTGTCCCTGCCTTTCTCCAAGGCATGACTGACTTCTTGAGGCAACACAGACAGCCCCCTCCACCACCCAC
CTCCTCCACCCCAACACCTGCCCCAGAGCAGCAGACCATGCCCCACAGGCTCCCTTCTGGTGGCGCAGGGA
GTCCTGGAGGCCTGGGTCTTGAGAGCCTGTACCGGAGTTTTTTACCTCAGTGGTGCAGGGTGTGCTCAGCTCCC
TGCTGGGCTCCCTGGGGGCTCGGGCTGGCAGCAGTGAAGTATTGCTGCCTTCATACACGCCTCAGTGGATCCA
GCAACATCTTTGAGCCTGGAGCTGATGGGGCCCTTGGATTCTTTGGGGCCTTGCTTTCTCTTGTGCCAGAACT
TCTCTATGGTGGACGTAGTGATGCTTCTCCATGGGCATTTCAGCCACTACAACGGCTCCAGCCCCAGCTGCGAT
CCTTCTTCCACCAGCACTACCTGGGTGGTCAGGAGCCACACCCAGTAACATCCGGATGGCAACCCACACATTGA
TCACGGGGCTAGAAGAGTATGTGCGGGAGAGTTTTTCTTGGTGCAGGTTTCAGCCAGGTGTGGACATCATCCGGA
CAAACCTGGAATTTCTCCAAGAGCAGTTTAATAGCATTGCTGCGCATGTGCTGCATTGCACAGATAGTGGATTTG
GGGCCCGGTTGCTGGAGTTGTGTAACCAAGGCCTGTTTGAATGCCTGGCCCTAAACCTGCACTGCTTGGGGGGAC
AGCAGATGGAGCTTGTGCTGTTATCAATGGCCGAATTGCTGCTATGTCTCGTGGGGTGAATCCCTCCTTGGTGA
GCTGGCTGACCACTATGATGGGACTGAGGCTTTCAGGTGGTACTGGAGCACATGCCTGTAGGCCCTGATGCCATT
TCAGATACGTTTCGACGGGTTGGTGATCCCCCCCAGCCACTTCTGAGGAGCCAATGGAAGTTTCAGGGAGCAGAAA
GAGCTTCCCTGAGCCTCAGCGGGAGAATGCTTCCCCAGCCCTGGAACAACAGCAGAAGAGGCCATGTCCCGAG
GTCCACCTCCTGCTCCTGAGGGGGGCTCCCGGGATGAACAGGATGGAGCTTCAGCTGAGACAGAACCTTGGGCAG
CTGCAGTCCCCCAGAATGGGTCCCTATTATCCAGCAGGACATTTCAGAGCCAGCGGAAGGTGAAACCGCAGCCCC
CTCTGAGTGATGCCTACCTCAGTGGTATGCCTGCCAAGAGACGCAAGACGATGCAGGGTGGAGGGCCCCAGCTGC
TTCTCTCAGAGGCTGTGAGCCGGGCAGCTAAGGCAGCCGGAGCTCGGCCCCTGACGAGCCCCGAGAGCCTGAGCC
GGGACCTGGAGGCACCAAGGTTTCAGGAGAGCTACAGGCAGCAGCTCCGGTCTGATATACAAAACGACTGCAGG

2147/6881
FIGURE 1975B

AAGACCCCAACTACAGTCCCCAGCGCTTCCCCAATGCCCAGCGGGCCTTTGCTGATGATCCTTTAGCTCTTTGCTC
TATGGCCCTTCCTCATCAGGGGACCGTTTCCCCCTCTTCCTTCACAGTATTTAAGAAATAAAAAGTCGGATTTTT
CTGGC

2148/6881
FIGURE 1976

MEPNDSTSTAVEEPDSLEVLVKTLD SQTRTFIVGAQMNVKEFKEHIAASVSIPSEKQRLIYQGRVLQDDKKLQEY
NVGGKVIHLVERAPPQTHLPSGASSGTGSASATHGGGSPPGTRGPGASVHNRNANSYVMVGTFNLPSDGSADVH
INMEQAPIQSEPRVRLVMAQHMRDIQTLLSRMECRGGPQPQHSQPPPPQPPAVTPEPVALSSQTSEPEVESEAPPR
EPMEAEVEEERAPAQNPELTPGPAPAGPTPAPETNAPNHPSPA EYVEVLQELQRLSRLQPFLLQRYEVLGAAAT
TDYNNNHEGREEDQRLINLVGESLRLLGNTFVALSDLRCNLACTPPRHLHVVRPMSHYTTMPVLQQA AIP IQINV
GTTVTMTGNGTRPPPTPNAEAPPPGPGQASSVAPSSTNVESSAEGAPPPGPAPPPATSHPRVIRISHQSVEPVVM
MHMNIQDSGTQPGGVPSAPTGPLGPPGHGQTLGQQVPGFPTAPTRVVIARPTPPQARPSHPGGPPVSGTLQGAGL
GTNASLAQMVSGLVGQLMQPVLVAQGTPGMAPPPAPATASASAGTTNTATTAGPAPGGPAQPPPTPQPSMADLQ
FSQLLGNNLLGPAGPGAGGSGVASPTITVAMPGVPAFLQGMTDFLQATQTAPPPPPPPPPPPPPAPEQQTMPPPGSP
SGGAGSPGGLGLESLSPEFFTSVVQGVLSLLGSLGARAGSSIESIAAFIQRLSGSSNIFEPGADGALGFFGALLS
LLCQNFMSMVDVVMLLHGHFQPLQRLQPLRSFFHQHYLGQEQPTPSNIRMATHTLITGLEEYVRESFSLVQVQPG
VDIIRTNLEFLQE QFNSIAAHVLHCTDSGFGARLLELCNQGLFECLALNLHCLGGQQMELAAVINGRIRMSRGV
NPSLVSWLTTMMGLRLQVVLEHMPVGPDAILRYVRRVGDPPQPLPEEPMEVQGAERASPEPQRENASPA PGTTAE
EAMSRGPPPAPEGGSRDEQDGASAETEPWAAAVPPEWVPIIQQDIQSQRKVKPQPPLSDAYLSGMPAKRRKTMQG
EGPQLLLSEAVSRAAKAAGARPLTSPESLSRDLEAPEVQESYRQQLRSDIQKRLQEDPNYSPQRFPNAQRAFADD
P

2149/6881
FIGURE 1977A

TAGTGCACGCACGCAGGCGTAGTACGGTCCCCCGGGCGACAGCGGTGGCGGCTCCTCGGGGTGCTCGGCTCCCT
CCCACCTAGGCCGGCCCCGGCCGACTCGCCCTCAGAACTCACTGTTTGGGGCTGCGGACTTTCTCGTCGTGCC
CCACAAAAGTAAAGCTTGGGGACCTGGGGGGAGCCGGAAGTATCGCTTCGAGATCCCCAAATACTATCGGGGAAA
CGGAAGTGGCCGTCGGTGGCAGAGACCTGTCCGGCCATCGAGCCTAATGATAGTACCAGTACCGCTGTGGAGGAGC
CTGACAGCTTGGAGGTGTTGGTGAAGACCTTGGACTCTCAAACCTCGTACCTTTATTGTGGGGGGCCAGATGAATG
TAAAAGAGTTTAAAGGAGCACATTGCTGCCTCTGTGACATCCCATCTGAAAAACAACGGCTCATTTACCAGGGAC
GAGTTCTGCAAGATGATAAGAAGCTTCAGGAATACAATGTTGGGGGAAAGGTTATCCACCTGGTGGAAACGGGCTC
CTCCTCAGACTCACCTCCCTTCTGGGGCATCTTCTGGGACGGGGTCTGCCTCAGCCACTCATGGTGGGGGATCCC
CCCCTGGTACTCGGGGGCCTGGGGCCTCTGTTTCATGACCGGAATGCCAACAGCTATGTATGGTTGGAACCTTCA
ATCTTCCTAGTGACGGCTCTGCTGTGGATGTTACATCAACATGGAACAGGCCCCGATTAGAGTGAGCCCCGGG
TACGGCTGGTGATGGCTCAGCACATGATCAGGGATATACAGACCTTACTATCCCGGATGGAGTGTCGAGGAGGGC
CCCAACCGCAGCACAGTCAGCCGCCCCCGCAGCCACCGGCTGTGACCCCGGAGCCAGTAGCCTTGAGCTCTCAA
CATCAGAACCAGTTGAAAGTGAAGCACCTCCCCGGGAGCCCATGGAGGCAGAAGAAGTGGAGGAGCGTGCCCCAG
CCCAGAACC CGGAGCTCACTCCTGGCCCCAGCCCCAGCGGGCCCAACACCTGCCCCGAAACAAATGCACCCAACC
ATCCTTCCCCTGCGGAGTATGTGAGGTGCTCCAGGAGCTACAGCGGCTGGAGAGTGCCTCCAGCCCTTCTTGC
AGCGCTACTACGAGGTTCTGGGTGCTGCTGCCACCACGGACTACAATAACAATCACGAGGGCCGGGAGGAGGATC
AGCGGTTGATCAACTTGGTAGGGGAGAGCCTGCGACTGCTGGGCAACACCTTTGTTGCACTGTCTGACCTGCGCT
GCAATCTGGCCTGCACGCCCCACGACACCTGCATGTGGTCCGGCCTATGTCTCACTACACCACCCCATGGTGC
TCCAGCAGGCAGCCATTCCCATAACAGATCAATGTGGGAACCACTGTGACCATGACAGGAAATGGGACTCGGCCCC
CCCCAATCCCAATGCAGAGGCACCTCCCCCTGGTCTGGGCAGGCCTCATCCGTGGCTCCGTCTTCTACCAATG
TCGAGTCTCAGCTGAGGGGGCTCCCCGCCAGGTCCAGCTCCCCGCCAGCCACCAGCCACCCGAGGGTTCATCC
GGATTTCCACCAGAGTGTGGAACCCGTGGTCATGATGCACATGAACATTCAAGATTCTGGCACACAGCCTGGTG
GTGTTCCGAGTGCTCCCACTGGCCCCCTGGGACCCCTGGTTCATGGCCAAACCCCTGGGACAGCAGGTGCCAGGCT
TCCCAACAGCTCCAACCCGGGTGGTGATTGCCCGGGCCACTCCTCCACAGGCTCGGCCTTCCATCCTGGAGGGC
CCCCAGTCTCTGGGACACTGCAGGGCGCCGGTCTGGGTACCAATGCCTCGTTGGCCCAGATGGTGAGCGGCCTTG
TGGGGCAGCTTCTTATGCAGCCAGTCCTTGTGGCTCAGGGGACCCAGGTATGGCTCCACCGCCAGCCCCTGCCA
CTGCTTCTGCCAGTGCTGGCACCAACACAGCTACCACAGCTGGCCCCGCTCCTGGGGGGCCTGCCAGCCTC
CACCCACCCCTCAACCCTCCATGGCTGATCTTCAGTTCTCTCAGCTTCTGGGGAACCTGCTAGGGCCTGCAGGGC
CAGGGGCTGGAGGGTCTGGTGTGGCTTCTCCACCATCACTGTGGCGATGCCTGGTGTCCTTCTTCTCCAAG
GCATGACTGACTTCTTGACAGGCAACACAGACAGCCCTCCACCACCCCACTCCTCCACCCCACTACCTGCC
CAGAGCAGCAGACCATGCCCCCACCAGGCTCCCCTTCTGGTGGCGCAGGGAGTCTGGAGGCCTGGGTCTTGAGA
GCCTGTACCGGAGTTTTTTTACCTCAGTGGTGCAGGGTGTGCTCAGCTCCCTGCTGGGCTCCCTGGGGGCTCGGG
CTGGCAGCAGTGAAAGTATTGCTGCCTTCATACAACGCCTCAGTGGATCCAGCAACATCTTTGAGCCTGGAGCTG
ATGGGGCCCTTGATTCTTTGGGGCCTTGCTTTCTCTCTGTGCCAGAACTTCTCTATGGTGGACGTAGTGATGC
TTCTCCATGGGCATTTCCAGCCACTACAACGGCTCCAGCCCCAGCTGCGATCCTTCTTCCACCAGCACTACCTGG
GTGGTCAGGAGCCACACCCAGTAACATCCGGATGGCAACCCACACATTGATCACGGGGCTAGAAGAGTATGTGC
GGGAGAGTTTTTCTTGGTGCAGGTTTCAGCCAGGTGTGGACATCATCCGGACAAACCTGGAATTTCTCCAAGAGC
AGTTTAATAGCATTGCTGCGCATGTGCTGCATTGCACAGATAGTGGATTGGGGCCCGTTGCTGGAGTTGTGTA
ACCAAGGCCTGTTTGAATGCCTGGCCCTAAACCTGCACTGCTTGGGGGGACAGCAGATGGAGCTTGCTGCTGTTA
TCAATGGCCGAATTCGTGCTATGTCTCGTGGGTGAATCCCTCCTTGGTGAGCTGGCTGACCACTATGATGGGAC
TGAGGCTTCAGGTGGTACTGGAGCACATGCCTGTAGGCCCTGATGCCATTCTCAGATACGTTTCGAGGGTTGGTG
ATCCCCCCCAGCCACTTCTGAGGAGCCAATGGAAGTTCAGGGAGCAGAAAGAGCTTCCCCTGAGCCTCAGCGGG
AGAATGCTTCCCCAGCCCCCTGGAACAACAGCAGAAGAGGCCATGTCCCGAGGTCCACCTCCTGCTCCTGAGGGGG
GCTCCCGGGATGAACAGGATGGAGCTTCAGCTGAGACAGAACCTTGGGCAGCTGCAGTCCCCCAGAATGGGTCC
CTATTATCCAGCAGGACATTTCAGAGCCAGCGGAAGGTGAAACCGCAGCCCCCTCTGAGTGATGCCTACCTCAGTG
GTATGCCTGCCAAGAGACGCAAGACGATGCAGGGTGGGGCCCCCAGCTGCTTCTCTCAGAGGCTGTGAGCCGGG
CAGCTAAGGCAGCCGGAGCTCGGCCCCTGACGAGCCCCGAGAGCCTGAGCCGGGACCTGGAGGCACCAGAGGTT
AGGAGAGCTACAGGCAGCAGCTCCGGTCTGATATACAAAACGACTGCAGGAAGACCCCACTACAGTCCCCAGC

2150/6881
FIGURE 1977B

GCTTCCCAATGCCAGCGGGCCTTTGCTGATGATCCTTAGCTCTTTGCTCTATGGCCCTTCCTCATCAGGGGAC
CGTTTCCCCCTCTTCCTTCACAGTATTTAAGAAATAAAAGTCGGATTTTCTGGCAAAAAAAAAAAAAAAAAAAAA
AAAA

2151/6881
FIGURE 1978

MEPNDSTSTAVEEPDSLEVLVKTLDSTRTFIVGAQMNVKEFKEDIAASVSIPSEKQRLIYQGRVLQDDKKLQEY
NVGGKVIHLVERAPPQTHLPSGASSGTGSASATHGGGSPPGTRGPGASVHNRNANSYVMVGTFNLPSDGSADVH
INMEQAPIQSEPRVRLVMAQHMIRDIQTLLSRMECRGGPQPQHSQPPPPPPAVTPEPVALSSQTSEPVSESEAPPR
EPMEAEVEERAPAQNPETPGPAPAGPTPAPETNAPNHPSPAIEYVEVLQELQRLSRLOPFLQRYEVLGAAAT
TDYNNNHEGREEDQRLINLVGESLRLLGNTFVALSDLRCNLACTPPRHLHVVRPMSHYTTPMVLQQAAPPIQINV
GTTVTMTGNGTRPPPTPNAEAPP PGPGQASSVAPSSTNVESAEAGAPPPGPAPPPATSHPRVIRISHQSVEPVVM
MHMNIQDSGTQPGGVPSAPTGPLGPPGHGQTLGQQVPGFPTAPTRVVIARPTPPQARPSHPGGPPVSGTLQAGL
GTNASLAQMVSGLVGQLLMQPVLAQGTGPMAPPPAPATASASAGTTNTATTAGPAPGGPAQPPPTPQPSMADLQ
FSQLLGNLLGPAGPGAGGSGVASPTITVAMPGVPAFLQGMTDFLQATQTAPPPPPPPPPPPPPAPEQQTMPPPGSP
SGGAGSPGGLGLESLSPEFFTSVVQGVLSLLGSLGARAGSSEIAAFIQRLSGSSNIFEPGADGALGFFGALLS
LLCQNF SMVDVVMLLHGHFQPLQRLQPLRSFFHQHYLGGEPTPSNIRMATHTLITGLEEYVRESFSLVQVQPG
VDIIRTNLEFLQEQFNSIAAHVLHCTDSGFGARLLELCNQGLFECLALNLHCLGGQQMELAAVINGRIRMSRGV
NPSLVSWLTTMMGLRLQVLEHMPVGPDAILRYVRRVGDPPQPLPEEPMEVQGAERASPEPQRENASAPGTTAE
EAMSRGPPPAPEGGSRDEQDGASAETEPWAAVPEWVPIIQDIIQSQRKVKPQPPLSDAYLSGMPAKRRKTMQG
EGPQLLLSEAVSRAAKAAGARPLTSPELSRDLEAPEVQESYRQQLRSDIQKRLQEDPNYSPQRFPAQRAFADD
P

2152/6881
FIGURE 1979A

CCCTAGGCCCGGGTCCCGGATCCCCCGCGCACCCCGGCCAGGCTCTGGCACGTTTTTGGGGGAGGTCCTTGCAAGGACC
CAACATACTCAATGAGCTTCCAGCGCAATGTCCTCGATCGCTCGGGGCCGACTGCCAAGGGAAAGGATGGAAAGAAG
TATTCCTCGCTCAACCTGTTTGATACGTATAAGGGCAAGTCCTTAGAGATCCAGAAAACCCGCTGTTGCCCTCGC
CATGGCCTGCAGAGTCTCGGGAAAGTTGCCATTGCCCGGCGTATGCCACCTCCAGCCAACCTTCCAAGCCTGAAA
GCCGAGAACAAAGGCAATGACCCCAATGTCTCTACTAGTGCCAAAAGACGGAACAGGATGGGCAAGCAAAACAGGAG
CAGTCCGACCCCAAGAGTTCCGATGCCTCAACCGCTCAGCCGCCGGAATCGCAGCCACTGCCGGCTTCACAGACG
CCTGCCTCCAACCAGCCGAAACGACCCCCAGCAGCCCCGAGAACACTCCTTTGGTTCCAAGCGGGGTAAAGTCC
TGGGCACAAGCCAGCGTCACCCATGGAGCACATGGAGATGGTGGAAGGGCATCAAGCCTACTGTACGATTCTCT
CGAGAGGAATTTCCGACCCTGCAGGCGGCTGGCGACCAGGACAAGGCTGCCAAGGAAAGGGAGTCTGCCGAACAG
TCGTCTGGGCCCGGACCAAGCCTCCGCCCCCAAATTTCTACAACCTTGAGGGACGGAGGTGGGCGTGGCCCTGAT
GAGCTGGAGGGCCCGGACTCCAAACTTCATCATGGTCATGATCCCCGGGGTGGGCTACAGCCTTCAGGCCCCACCC
CAGTTCCTTCCCTACCGCGGAATGATGCCGCCTTTTCATGTATCCCCCATATCTCCCGTTCCCTCCGCCCTATGGA
CCCCAGGGGCCTTACCATAACCCACTCCTGATGGGCCCAGCCGTTTTTCCCGTGTGGCGGGCCCCCGAGGCTCA
GGGCCACCAATGCGCTTAGTAGAGCCTGTGGGTCTGCCCTCTATTCTCAAAGAGGATAATCTCAAAGAGTTTGAT
CAGTTGGATCAGGAGAATGATGATGGTTGGGCAGGGGCCCATGAAGAGGTTGACTTAACTGAAAAGCTCAAGTTC
AGCGATGAGGAAGATGGGCGAGACTCTGATGAGGAGGGAGCTGAGGGCCACAGGGATTCCCAATCAGCTTCTGGT
GAGGAACGGCCCCCTGAAGCAGATGGCAAAAAGGGCAACTCCCCAACAGCGAACCGCCCACTCCTAAGACGGCC
TGGGCAGAAACCTCTCGGCCCTCCAGAGACAGAGCCGGGACCTCCTGCCCCAAAGCCTCCCTTACCCCTGGGGAC
TACCCAGATCGTGGGGTCTTCCCTGCAAGCCCCCAGCACCTGAAGATGAGGATGAGGCATGGCGGCAGCGACGA
AAGCAGTCGTCACTGAGATTTCCCTGGCAGTGGAGCGGGCCCGGCGACGGCGAGAGAAGAAGAGGAGCGGCGCATG
CAAGAAGAGCGCCGGGCAGCCTGTGCTGAGAAGCTCAAGCGACTCGATGAAAAGTTTGGGGCACCTGACAAGCGG
CTCAAAGCAGAGCCTGTGCCCCACCTGTGCCCCCTTCTACCCAGCTCCACCACCTGCAGTCCCTAAAGAACTC
CCTGCACCTCCAGCTCCACCTCCAGCATCAGCCCCAACACCAGAGAAAGAACCTGAAGAGCCAGCACAGGCCCCCT
CCTGCCCAATCTACTCCTACTCCAGGTGTGGCTGCGGCTCCCACTCTGGTGAGTGGTGGTGGCAGTACCAGTAGC
ACCAGCAGTGGCAGCTTCGAAGCCAGCCCAGTGGAACCACAACCTGCCCTCAAAGAGGGTCTCTGAACCACCAGAA
GAGGTTTCTCTCTTACCACACCCCCAGTTCCAAAGGTGGAACCCAAGGGTGATGGGATTGGTCCCACCCGCCAG
CCCCCTAGTCAGGGCTTGGGCTACCCCAAATATCAGAAGTCGTTGCCTCCTCGTTTTCCAGCGGCAGCAGCAGGAG
CAGCTCCTGAAGCAGCAGCAGCAGCACCAGTGGCAGCAGCATCAACAGGGCTCTGCCCTCCTTACCCCACTGCC
CCATCACCACCACAGCCTGTGACCTGGGGGTGTGCCAGCTCCACAGGCTCCACCCCCGCCCCCAAGGCCCTG
TACCCAGGTGCTCTGGGGCCGGCCCCCACCATGCCCCCAATGAACTTTGATCCCCGATGGATGATGATTCTCTCT
TATGTGGACCCCCGGCTCCTCCAGGGTCTGCCCCCTCTAGACTTCTACCTTCCTGGTGTGCATCCCTCTGGCCTA
GTTCCCCGAGAGCGTTTACAGACAGTGGGGGCTCAAGCTCAGAGCCATTTGACCGTCATGCACCTGCTATGTTACGG
GAACGGGGCACTCCACCGGTGGATCCAAAGTTGGCTGGGTAGGAGATGTCTTCACCGCCACACCCGCTGAACCC
CGCCCCACTTACCTCACCCTCTGCGCCAGGCTGCGGATGAGGATGACAAGGGGATGAGGAGCGAGACTCCTCCAGTA
CCTCCCCCACCACCTATCTGCCAGTTATCCAGGCTTTCTGAGAATGGAGCCCTGGGGCCCCCAATCTCTCGC
TTTTCTCTGGAGGAACCAGGGCCCCGTCCACTCCCCTGGCCCCCAGGCAGTGATGAAGTGGCCAAGATACAACT
CCACCACCCAAGAAGGAGCCCCCTAAGGAGGAGACTGCACAGCTGACGGGGCCAGAAGCAGGCCGAAAGCCTGCC
CGCGGAGTGGGAGTGGAGGCCAGGGCCCCCACCACCACGCAGAGAGTGCACAGAGACCCGCTGGGGCCCT
CGTCCAGGGAGCAGTCGTGCTGGAATCCCTCCAGAGGAGCCAGGGGCCCCACCCGCCGGGCTGGGCCTATAAG
AAACCTCCACCACCTACAAAAGTAGAAGAGCTGCCTCCCAAGCCCCCTCGAACAGGGGGATGAAACCCCCAAACCC
CCAAAGCCAGACCCACTCAAGATAACCAAGGGGAAGCTAGGGGGGCCCAAGGAGACCCACCCAATGGAATCTT
TCCCTGCCCAAGGCTTCGGAGGGACTATTGATGAAAGAGTGGGTCTTACCTCTTGCCGGGGTTCGGGGCCGA
GGCGAGTATTTTGCCAGAGGGAGGGGTTTTCGGGGGACCTATGGGGGACGAGGGCGGGGAGCCCGAAGCCGGGAA
TTCCGCAGTTACCGAGAGTTTCGAGGAGATGATGGGCGTGGAGGTGGGACAGGGGGACCAAACACCCTCTGCT
CCCCGAGGCCGCACTGCCAGCGAGACACGGAGCGAGGGTTTACAGATATGAGGAAATCCCCAAGCGGCGCCGGCAG
CGGGGCTCAGAAACAGGCAGCGAGACCCATGAGAGTGATCTGGCTCCTTCAGACAAGGAGGCTCCACACCCAAG
GAGGGAACACTCACCCAGGTCCCTCTCGCTCCCCCACCACCAGGAGCCCCACCTTCACCAGCCCCAGCCCGCTTC
ACTGCCCGGGGTGGGCGAGTCTTACTCCAGAGGGGTGCCATCTCGCCGGGGCCGAGGAGGAGGGAGGGCCCCCT

2153/6881
FIGURE 1979B

CCTCAAGTTTGGCCAGGCTGGAGCCCTCCAGCCAAGTCTCTGGCTCCCAAGAAACCTCCCACAGGCCCTTTGCCA
CCAAGTAAGGAGCCTTTGAAAGAGAAGTTGATCCCAGGGCCTCTGTCCCCTGTGGCGCGCGGAGGCAGCAATGGA
GGTAGCAATGTGGGCATGGAAGATGGGGAGCGACCCCGAAGGAGGCGACATGGGAGGGCTCAGCAGCAGGATAAA
CCGCCTCGTTTCCGGAGGCTGAAGCAGGAACGGGAGAATGCCGCAAGGGGGTCTGAGGGCAAGCCCTCCCTAACC
CTTCCAGCCTCCGCTCCTGCACCTGAGGAGGCCCTCACAACAGTCACAGTGGCCCCAGCACCTCGCCGGGCGAGCT
GCCAAGTCTCCTGATCTGTCAAACCAGAACTCAGACCAAGCCAATGAGGAATGGGAGACTGCATCAGAGAGCAGT
GACTTCACCAGTGAGCGCCGAGGGGACAAAGAGGCACCCCCACCAGTACTGCTGACACCCAAGGCTGTGGGAACCT
CCTGGGGGAGGTGGAGGTGGAGCCGTACCAGGTATTTTCAGCCATGTCCCGCGGAGATCTGAGCCAGAGAGCCAAG
GATTTGAGTAAACGGGAGCTTCTCAAGTCAGCGGCCAGGCATGGAACGGCAGAATCGGCGCCCTGGCCCCAGGGGGC
AAGGCTGGCAGCAGTGGCAGCAGCAGTGGAGGAGGCGGTGGGGGTCTTGAGGAAGGACCGGGCCAGGACGAGGC
GACAAGAGGAGCTGGCCCTCTCCCAAGAACC GAAGTCGTCTCCAGAGGAGCGTCCCCCGGGGCTTCCCTGCCT
CCCCACCTCCCAGCAGTTCTGTGTCTTCCGCCTGGACCAAGTTATCCACAGCAACCCTGTGGCATCCAACAG
GCTCTGGCCCAGCTTAGTAGCCGTCAAGGGAGTGTAAGTGCACCAAGGGGTTCATCAAGGCACAAGCCTGGGCCT
CCCCAAGCCCCCTCAGGGCCCCCTCTCCTAGGCCCCCAACCCGATACGAGCCCCAGAGGGTCAACAGCGGCCCTCAGT
TCTGACCCCCACTTTGAGGAGCCGGGGCCAATGGTGAGAGGGGTGGGTGGGACTCCTCGGGACTCTGCCGGGGTT
AGTCCCTTTCCCCCTAAACGTCGGGAGCGGCCTCCAGAAAACCAGAGCTGCTACAGGAGGAATCTTTGCCACCT
CCTCATAGCTCTGGATTCTTGGGCTCTAAGCCTGAGGGCCCAGGCCCTCAGGCAGAGTCCAGAGATACAGGCACA
GAGGCCCTGACCCCTCACATCTGGAACCGTTTACATACTGCCACTAGCCGAAAGAGTTACCGGCCAGCTCCATG
GAGCCTTGATGGAGCCCCCTGAGTCTTTTGAGGATGTGGCTGGCACAGAAATGAGTCAGTCTGACAGTGGGGTG
GACCTGAGTGGGGATTCTCAGGTGTCATCAGGTCCCTGCAGCCAGCGAAGTTCCCTTGATGGAGGACTCAAGGGG
GCAGCAGAGGGACCCCCCAAGAGGCCTGGAGGCTCCTCACCCCTGAATGCTGTTCCTTGTGAGGGTCCACCTGGC
TCTGAACCTCCTAGGAGACCACCCTGCCCCCCACGATGGGGACAGAAAGGAGCTGCCCCGGGAGCAGCCTCTG
CCCCCTGGCCCCATTGGCACAGAACGATCACAGCATAACAGACCGAGGCACAGAGCCTGGCCCCATTGCGCCATCC
CATCGACCTGGTCCCCCAGTCCAGTTTGGCACTAGTGACAAGGACTCAGACTTACGCCTAGTGGTAGGAGACAGC
TTGAAAGCAGAGAAGGAGCTAACAGCATCAGTCACTGAGGCCATTCTGTATCACGAGACTGGGAGCTGCTTCCC
AGTGCTGCTGCCTCTGCTGAGCCACAATCCAAGAACCTGGATTCTGGGCACTGTGTCCCGGAGCCCAGCTCCTCA
GGCCAGCGCCTGTATCCTGAGGTTTTCTATGGCAGTGCTGGGCCTTCCAGTTCTCAGATCTCTGGGGGAGCCATG
GACTCTCAATTACATCCAAACAGTGGAGGCTTCCGCCCTGGGACACCCTCACTGCACCCTTACAGATCACAGCCC
CTATACCTACCCCCCGGCCAGCCCCCTCCCTCAGCACTGCTCTCTGGGGTAGCTCTCAAGGGCCAGTTTCTGGAT
TTCTCCACAATGCAAGCTACAGAGCTGGGGAAAGTTGCCGGCTGGAGGAGTTCTCTACCCTCCACCTTCCTTCCTC
TACTCTCCGGCTTTCTGCCCCAGTCCCTTGCCTGACACATCGTTGCTTCAGGTACGCCAGGATCTGCCATCCCT
TCGGATTTTTATTCTACTCCTCTGCAGCCTGGTGGCCAAAGTGGCTTTCTCCCTTCAGGGGCTCCTGCCAGCAG
ATGCTTCTACCCATGGTAGACTCACAGCTGCCTGTGGTGAACCTTTGGCTCCCTGCCGCCAGCACCACCTCCTGCC
CCACCTCCCCCTTCTCTGTTACCTGTGGGCCCTGCTCTGCAGCCCCCAGCCTGGCTGTGCGGCCCCACCTGCT
CCTGCTACTCGGGTGCTGCCTTCACCTGCCAGGCCCTTCCCCGCTAGCTTGGGGCGAGCAGAGCTGCATCCAGTG
GAACTAAAGCCGTTCCAGGATTATCAAAAACCTGAGCAGCAACCTTGGGGGACCTGGATCATCACGGACTCCCCCA
ACTGGAAGGTCCTTCTCTGGCCTCAATTCCCGTCTCAAGGCCACGCCTTCCACCTACAGTGGAGTCTTCCGCACC
CAGCGCGTCGACCTTTACCAGCAGGCCTCCCCACCAGATGCCCTGCGCTGGATACCTAAGCCTTGGGAGCGGACA
GGGCTGCCACCTCGAGAAGGGCCCTCCCGACGGGCAGAGGAGCCTGGGTCCCGAGGGGACAAGGAGCCTGGGTG
CCCCACCCCGCTGAGGGAGTTCTCTTGGCCCCCTACCCCGGGGCTTGTATATAGATTATAAATATATAAGGGG
GAAAGGGGTGGGCGGGGAGGGGTGTGGGGCTGGGGCTCACTTCCCCTCCTCCCCCTTCCCCTGGTCCCCTGTC
CCTGGGGCTGTTTGTAAAAAAGAGTAATAAAAGGATT

2154/6881
FIGURE 1980

MSDRSGPTAKGKDGGKYSSSLNLFDTYKGKSLEIQKPAVAPRHGLQSLGKVAIARRMPPPPANLPSLKAENKGNDPN
VSLVPKDG TGWASKQEQSDPKSSDASTAQPPESQFLPASQTPASNQPKRPPAAPENTPLVPSGVKSWAQASVTHG
AHGDGGRASSLLSRFSREEFPTLQAAGDQDKAAKERESAEQSSGGPGLRPQNSTTWDRDGGGRGPDELEGPD SKL
HHGHDFRGGGLQPSGPPQFPPYRGMPPFFMYPPYLFPFPFYGPQGPYRYPTPDGPSRFPRVAGPRGSGPPMRLVEP
VGRPSILKEDNLKEFDQLDQENDDGWAGAHEEVDYTEKLKFSDEEDGRDSDEEGAEGHRDSQSASGEERPPEADG
KKGNSPENSEPPTPKTAWAETSRPPETEPGPPAPKPPLPPGDYPDRGGPPCKPPAPEDEDEAWRQRRKQSSSEISL
AVERARRRRREEEERMQEERRAACAEKLRLEKFGAPDKRLKAEPAAPPAAPSTPAPPPAVPKELPAPPAPPPA
SAPTPEKEPEEPAQAPPAQSTPTPGVAAAPTLLVSGGGSTSSSTSSGSFEASPVEPQLPSKEGPEPPEEVPPPTTPP
VPKVEPKGDGIGPTRQPPSQGLGYPKYQKSLPFRFQRQQEQQLLKQQQHQWQQHQQSAPPTPVPPSPPPQPVTL
GAVPAPQAPPPPPKALYPGALGRPPPMPPMNFDPWRMMIPPYVDPRLQGRPPLDFYPPGVHPSGLVPRERSDSG
GSSSEPFDRHAPAMLRERGTTPVDPKLAUVGDVFTATPAEPRELTSPLRQAADDDKGMRSCTPPVPPPPPYLAS
YPGFPENGAPGPPISRFPLEEGPRPLPWPPGSDEVAKIQTTPPKKEPPKEETAQLTGPEAGRKPARGVSGGGQG
PPPPRRSRRTETRWGPRGSSRRGIPPEEPGAPRRRAGPIKKPPPTKVEELPPKPLEQGDETPKPPKPDPLKIT
KKGKGGPKETPPNGNLSPAPRLRRDYSYERVGPTSCRGRGRGEYFARGRGFRGTYGGRGRGARSREFRSYREFRG
DDGRGGGTGGPNHPPAPRGRTASETRSEGSEYEEIPKRRRQRGSETGSETHESDLAPSDKEAPTKEGTLTQVPL
APPPPGAPPSPAPARFTARGGRVFTPRGVPSRRGRGGGRPPPQVCPGWSPPAKSLAPKKPPTGPLPPSKEPLKEK
LIPGPLSPVARGGSNGGSNVGMEDGERPRRRRHGRAQQQDKPPRFRLKQERENAARGSEGKPSLTLPASAPAPE
EALTTVTVAPAPRRRAAKSPDLNQNNSDQANEWEETASESSDFTSERRGDKEAPPPVLLTPKAVGTPGGGGGGAV
PGISAMSRGDLQRAKDLKRSFSSQRPGRMERQNRPGPGGKAGSSSSSGGGGGGGPGGRTGPRGRDKRSWPSPK
NRSRPPEERPPGLPLPPPPSSSAVFRLDQVIHNSNPAGIQQALQLSSRQGSVTAPGGHPRHKPGPPQAPQGPSP
RPPTRYEPQVRNSSLSSDPHFEEPGPMVRGVGGTTPRDSAGVSPFPKRRERPPRKPPELLQEESLPPPHSSGFLGS
KPEGPGPQAESRDTGTEALTPHIWNRLHTATSRKSYRPSMEPWMEPLSPFEDVAGTEMSQSDSGVDLSGDSQVS
SGPCSQRSSPDGGLKGAAEGPPKRPGGSSPLNAVPCGPPGSEPPRRPPAPHDGDRKELPREQPLPPGP I GTER
SQHTDRGTEPGPIRPSHRPGPPVQFGTSDKDSDLRLVVGDSLKAEKELTASVTEAIPVSRDWELLPSAAAASAEQ
SKNLDSGHCVPEPSSSGQRLYPEVFYGSAGPSSSQISGGAMDSQLHPNSGGFRPGTSLHPYRSQPLYLPPGPAP
PSALLSGVALKGQFLDFSTMQATELGKLPAGGVLYPPPSFLYSPAFCPSPLPDTSLQVRQDLPSPSDFYSTPLQ
PGGQSGFLPSGAPAQQMLLPMVDSQLPVVNFGLPPAPPPAPPPLSLLEVGPALQPPSLAVRPPAPATRVLPSP
ARPPASLGRAELHPVELKPFQDYQKLSSNLGGPGSSRTPTGRSFSGLNSRLKATPSTYSGVFRTQRVDLYQQA
SPPDALRWIPKPWERTGLPPREGPSRRAEPPGSRGDKEPGLPPPR

2155/6881
FIGURE 1981A

CCCTAGGCCCCGGGTCCCGGATCCCCGCGCACCCGGCCAGGCTCTGGCACGTTTTGGGGGAGGTGCCTGCAGGACC
CAACATACTCAATGAGCTTCCAGCGCAATGTCGGATCGCTCGGGGCCGACTGCCAAGGGAAAGGATGGAAAGAAG
TATTCTCTCGCTCAACCTGTTTGATACGTATAAGGGCAAGTCCTTAGAGATCCAGAAACCCGCTGTTGCCCCCTCGC
CATGGCCTGCAGAGTCTCGGGAAAGTTGCCATTGCCCCGGCGTATGCCACCTCCAGCCAACCTTCCAAGCCTGAAA
GCCGAGAACAAAGGCAATGACCCCAATGTCTCACTAGTGCCAAAAGACGGAACAGGATGGGCAAGCAAAACAGGAG
CAGTCCGACCCCAAGAGTTCGGATGCCTCAACCGCTCAGCCGCCGGAATCGCAGCCACTGCCGGCTTCACAGACG
CCTGCCTCCAACCAGCCGAAACGACCCCCAGCAGCCCCCGAGAACACTCCTTTGGTTCCAAGCGGGGTAAAGTCC
TGGGCACAAGCCAGCGTCACCCATGGAGCACATGGAGATGGTGGAAGGGCATCAAGCCTACTGTACAGATTCTCT
CGAGAGGAATTTCCGACCCTGCAGGCGGCTGGGCGACCAGGACAAGGCTGCCAAGGAAAGGGAGTCTGCCGAACAG
TCGTCTGGGCCCCGGACCAAGCCTCCGCCCCCAAAATTCTACAACCTTGGAGGGACGGAGGTGGGCGTGGCCCTGAT
GAGCTGGAGGGCCCCGGACTCCAAACTTCATCATGGTCATGATCCCCGGGGTGGGCTACAGCCTTCAGGCCCCACC
CAGTTCCCTCCCTACCGCGGAATGATGCCGCCTTTTCATGTATCCCCCATATCTCCCGTTCCCTCCGCCCTATGGA
CCCCAGGGGCCTTACCGATACCCCACTCCTGATGGGCCCAGCCGTTTTCCCGTGTGGCGGGCCCCCGAGGCTCA
GGGCCACCAATGCGCTTAGTAGAGCCTGTGGGTCTGTCCTCTATTCTCAAAGAGGATAATCTCAAAGAGTTTGAT
CAGTTGGATCAGGAGAATGATGATGGTTGGGCAGGGGCCCCATGAAGAGGTTGACTACACTGAAAAGCTCAAGTTC
AGCGATGAGGAAGATGGGCGAGACTCTGATGAGGAGGGAGCTGAGGGCCACAGGGATTCCAATCAGCTTCTGGT
GAGGAACGGCCCCCTGAAGCAGATGGCAAAAAGGGCAACTCCCCAACAGCGAACCGCCCACTCCTAAGACGGCC
TGGGCAGAAACCTCTCGGCCTCCAGAGACAGAGCCGGGACCTCCTGCCCCAAAGCCTCCCCTACCCCCACCTCAC
CGGGGCCCCCGCGGGAAGTGGGGCCCCCTGGGGACTACCCAGATCGTGGGGGTCTCCCTGCAAGCCCCCAGCA
CCTGAAGATGAGGATGAGGCATGGCGGCAGCGACGAAAGCAGTCGTCTGAGATTTCCCTGGCAGTGGAGCGG
GCCCGGCGACGGCGAGAAGAAGAGGAGCGGCGCATGCAAGAAGAGCGCCGGGCAGCCTGTGCTGAGAAGCTCAAG
CGACTCGATGAAAAGTTTGGGGCACCTGACAAGCGGCTCAAAGCAGAGCCTGCTGCCCCACCTGCTGCCCCCTTCT
ACCCAGCTCCACCACCTGCAGTCCCTAAAGAACTCCCTGCACCTCCAGCTCCACCTCCAGCATCAGCCCCAACA
CCAGAGAAAGAACCTGAAGAGCCAGCACAGGCCCCCTCCTGCCCAATCTACTCCTACTCCAGGTGTGGCTGCGGCT
CCCCTCTGGTGAGTGGTGGTGGCAGTACCAGTAGCACCAGCAGTGGCAGCTTCGAAGCCAGCCAGTGGAAACCA
CAACTGCCCTCAAAGAGGGTCTGAACCACCAGAAGAGTTTCTCCTCCTACCACACCCCCAGTTCCAAAGGTG
GAACCCAAAGGGTGATGGGATTGGTCCCACCCGCCAGCCCCCTAGTCAGGGCTTGGGGTACCCCAAATATCAGAAG
TCGTTGCCTCCTCGTTTCCAGCGGCAGCAGCAGGAGCAGCTCCTGAAGCAGCAGCAGCAGCAGCAGCAGCAGCAG
CATCAACAGGGCTCTGCCCCCTCCTACCCAGTGCCCCCATCACCACCACAGCCTGTGACCCTGGGGGCTGTGCCA
GCTCCACAGGCTCCACCCCCGCCCCCAAGGCCCTGTACCCAGGTGCTCTGGGCGCGCCCCCACCCTGCCCCCA
ATGAACCTTTGATCCCCGATGGATGATGATTCTCCTTATGTGGACCCCCGGCTCCTCCAGGGTCTGTCCTCCTA
GACTTCTACCCTCCTGGTGTGCATCCCTCTGGCCTAGTTCCCCGAGAGCGTTCAGACAGTGGGGGCTCAAGCTCA
GAGCCATTTGACCGTCATGCACCTGCTATGTTACGGGAACGGGGCACTCCACCGGTGGATCCAAAGTTGGCCTGG
GTAGGAGATGTCTTACCGCCACACCCGCTGAACCCCGCCCACTTACCTCACCTCTGCGCCAGGCTGCGGATGAG
GATGACAAGGGGATGAGGAGCGAGACTCCTCCAGTACCTCCCCACCACCTATCTGGCCAGTTATCCAGGCTTT
CCTGAGAATGGAGCCCCTGGGCCCCCAATCTCTCGTTTTCTCTGAGGAACCAGGGCCCCGTCCTCCTCCTGG
CCCCAGGCAGTGATGAAGTGGCCAAGATACAACTCCACCACCCAAGAAGGAGCCCCCTAAGGAGGAGACTGCA
CAGCTGACGGGGCCAGAAGCAGGCCGAAAGCCTGCCCGCGGAGTCGGGAGTGGAGGCCAGGGCCCCCACCACCA
CGCAGAGAGAGTCGCACAGAGACCCGCTGGGGCCCTCGTCCAGGGAGCAGTCGTCTGGAATCCCTCCAGAGGAG
CCAGGGGCCCCACCCCGCCGGGCTGGGCCTATAAAGAAACCTCCACCACCTACAAAAGTAGAAGAGCTGCCTCCC
AAGCCCCCTGAACAGGGGGATGAAACCCCCAAACCCCCAAAGCCAGACCCACTCAAGATAACCAAGGGGAAGCTA
GGGGGCCCCAAGGAGACCCACCCAATGGAAATCTTTCCCTGCCCAAGGCTTCGGAGGGACTATTTCGTATGAA
AGAGTGGGTCTTACCTCTTGCCGGGGTGGGGGCCGAGGCGAGTATTTTGCCAGAGGGAGGGGTTTTCGGGGGACC
TATGGGGGACGAGGGCGGGGAGCCCGAAGCCGGGAATTCCGCAGTTACCGAGAGTTTCGAGGAGATGATGGGCGT
GGAGGTGGGACAGGGGGACCAAACCAACCTCCTGCTCCCCGAGGCCGCACTGCCAGCGAGACACGGAGCGAGGGT
TCAGAGTATGAGGAAATCCCCAAGCGCGCCGGCAGCGGGGCTCAGAAACAGGCAGCGAGACCCATGAGAGTGAT
CTGGCTCCTTCAGACAAGGAGGCTCCACACCCAAGGAGGGAACACTCACCCAGGTCCCTCTCGCTCCCCACCA
CCAGGAGCCCCACCTTCACCAGCCCCAGCCGCTTCACTGCCCGGGGTGGGCGAGTCTTCACTCCCAGAGGGGTG

2156/6881
FIGURE 1981B

CCATCTCGCCGGGGCCGAGGAGGAGGGAGGCCCCCTCCTCAAGTTTGCCAGGCTGGAGCCCTCCAGCCAAGTCT
CTGGCTCCCAAGAAACCTCCACAGGCCCTTTGCCACCAAGTAAGGAGCCTTTGAAAGAGAAGTTGATCCCAGGG
CCTCTGTCCCCTGTGGCGCGCGGAGGCAGCAATGGAGGTAGCAATGTGGGCATGGAAGATGGGGAGCGACCCCGA
AGGAGGCGACATGGGAGGGCTCAGCAGCAGGATAAACCGCCTCGTTTCCGGAGGCTGAAGCAGGAACGGGAGAAT
GCCGCAAGGGGGTCTGAGGGCAAGCCCTCCCTAACCTTCCAGCCTCCGCTCCTGCACCTGAGGAGGCCCTCACA
ACAGTCACAGTGGCCCCAGCACCTCGCCGGGCAGCTGCCAAGTCTCCTGATCTGTCAAACCAGAACTCAGACCAA
GCCAATGAGGAATGGGAGACTGCATCAGAGAGCAGTGACTTCACCAGTGAGCGCCGAGGGGACAAAAGAGGCACCC
CCACCAGTACTGCTGACACCCAAGGCTGTGGGAACTCCTGGGGGAGGTGGAGGTGGAGCCGTACCAGGTATTTC
GCCATGTCCCGCGGAGATCTGAGCCAGAGAGCCAAGGATTTGAGTAAACGGAGCTTCTCAAGTCAGCGGCCAGGC
ATGGAACGGCAGAAATCGGCGCCCTGGCCCAGGGGGCAAGGCTGGCAGCAGTGGCAGCAGCAGTGGAGGAGGCGGT
GGGGGTCTCGGAGGAAGGACCGGGCCAGGACGAGGCGACAAGAGGAGCTGGCCCTCTCCCAAGAACCGAAGTCTG
CCTCCAGAGGAGCGTCCCCCGGGGCTTCCCTGCCTCCCCACCTCCCAGCAGTTCTGCTGTCTTCGCTCTGGAC
CAAGTTATCCACAGCAACCCTGCTGGCATCCAACAGGCTCTGGCCAGCTTAGTAGCCGTCAAGGGAGTGTA
GCACCAGGGGGTTCATCCAAGGCACAAGCCTGGGCCTCCCCAAGCCCTCAGGGCCCCCTCTCCTAGGCCCCCAACC
CGATACGAGCCCCAGAGGTCAACAGCGGCCTCAGTTCTGACCCCCACTTTGAGGAGCCGGGGCCAATGGTGAGA
GGGGTGGGTGGGACTCCTCGGGACTCTGCCGGGGTTAGTCCCTTTCCCCCTAAACGTCGGGAGCGGCCTCCCAGA
AAACCAGAGCTGCTACAGGAGGAATCTTTGCCACCTCCTCATAGCTCTGGATTCTTGGGCTCTAAGCCTGAGGGC
CCAGGCCCTCAGGCAGAGTCCAGAGATACAGGCACAGAGGCCCTGACCCCTCACATCTGGAACCGTTTACATACT
GCCACTAGCCGAAAGAGTTACCGGCCAGCTCCATGGAGCCTTGATGGAGCCCCTGAGTCCTTTTGGAGATGTG
GCTGGCACAGAAATGAGTCAGTCTGACAGTGGGGTGGACCTGAGTGGGGATTCTCAGGTGTATCAGGTCCCTGC
AGCCAGCGAAGTTCCCCTGATGGAGGACTCAAGGGGGCAGCAGAGGGACCCCCCAAGAGGCCTGGAGGCTCCTCA
CCCCTGAATGCTGTTTCTTGTGAGGGTCCACCTGGCTCTGAACCTCCTAGGAGACCACCACCTGCCCCCAGCAT
GGGGACAGAAAGGAGCTGCCCCGGGAGCAGCCTCTGCCCCCTGGCCCCATTGGCACAGAACGATCACAGCATACA
GACCGAGGCACAGAGCCTGGCCCCATTGCGCCATCCCATCGACCTGGTCCCCCAGTCCAGTTTGGCACTAGTGAC
AAGGACTCAGACTTACGCCTAGTGGTAGGAGACAGCTTGAAAGCAGAGAAGGAGCTAACAGCATCAGTCACTGAG
GCCATTCTGTATCACGAGACTGGGAGCTGCTTCCAGTGCTGCTGCCTCTGCTGAGCCACAATCCAAGAACCTG
GATTCTGGGCACTGTGTCCCGGAGCCCAGCTCCTCAGGCCAGCGCCTGTATCCTGAGGTTTTCTATGGCAGTGCT
GGGCCTTCCAGTTCTCAGATCTCTGGGGGAGCCATGGACTCTCAATTACATCCAAACAGTGGAGGCTTCCGCCCT
GGGACACCCTCACTGCACCCCTTACAGATCACAGCCCCTATACCTACCCCCCGGCCAGCCCCCTCCCTCAGCACTG
CTCTCTGGGGTAGCTCTCAAGGGCCAGTTTCTGGATTTCTCCACAATGCAAGCTACAGAGCTGGGGAAGTTGCCG
GCTGGAGGAGTTCTCTACCTCCACCTTCCTTCTCTACTCTCCGGCTTTCTGCCCCAGTCTTTGCTGACACA
TCGTTGCTTACAGGTACGCCAGGATCTGCCATCCCCTTCGGATTTTATTCTACTCCTCTGCAGCCTGGTGGCCAA
AGTGGCTTTCTCCCTTCAGGGGCTCCTGCCAGCAGATGCTTCTACCCATGGTAGACTCACAGCTGCCTGTGGTG
AACTTTGGCTCCCTGCCGCCAGCACCTCCTGCCCCACCTCCCCTTTCTCTGTACCTGTGGGCCCTGCTCTG
CAGCCCCCAGCCTGGCTGTGCGGCCCCACCTGCTCCTGCTACTCGGGTGCTGCCTTACCTGCCAGGCCCTTC
CCGCTAGCTTGGGGCGAGCAGAGCTGCATCCAGTGGAATAAAGCCGTCCAGGATTATCAAAAACCTGAGCAGC
AACCTTGGGGGACCTGGATCATCACGGAATCCCCAACTGGAAGGTCTTCTCTGGCCTCAATTCCCGTCTCAAG
GCCAGCCTTCCACCTACAGTGGAGTCTTCCGCACCCAGCGCGTGCACCTTACCAGCAGGCCTCCCCACCAGAT
GCCCTGCGCTGGATACCTAAGCCTTGGGAGCGGACAGGGCTGCCACCTCGAGAAGGGCCCTCCCGACGGGCAGAG
GAGCCTGGGTCCCGAGGGGACAAGGAGCCTGGGTGCCCCACCCCGCTGAGGGAGTTCTCTTGGCCCCCTACCC
CCGGGGCTTGTATATAGATTATAAATATATAAGGGGAAAGGGGTGGGCGGGGAGGGGTGTGGGGCTGGGGCCT
CACTTCCCCTCCTCCCCCTTCCCCTGGTCCCCTGTCCCTGGGGCTGTTTGTAAAAAAGAGTAATAAAAGGATTT

2157/6881
FIGURE 1982

MSDRSGPTAKGKDGGKYSSNLNLFDTYKGKSLEIQKPAVAPRHGLQSLGKVAIARRMPPPPANLPSLKAENKGNNDPN
VSLVPKDG TGWASKQE QSDPKSSDASTAQPPESQFLPASQTPASNQPKRPPAAPENTPLVPSGVKSWAQASVTHG
AHGDGGRASSLLSRFSREEFPTLQAAGDQDKAAKERESAEQSSGPGPSLRPQNSTTWDRDGGGRGPDELEGPDSKL
HHGHDFRGGGLQPSGPPQFPPYRGMPPFFMYPPYLFPFPPYGPQGPYRYPTPDGFSRFFRVAGPRGSGPPMRLVEP
VGRPSILKEDNLKEFDQLDQENDDGWAGAHEEVDYTEKLKFSDEEDGRDSDEEGAEGHRDSQSASGEERPPEADG
KKGNPNSEPPTPKTAWAETSRPPETEPGPPAPKPPFLPPPHRGPAWNWGP GDYPDRGGPFCKPPAPEDEDEAWR
QRRKQSSSEISLAVERARRRREERREERMQEERRAACAEKLRLEKFGAPDKRLKAEPAAAPPAAPSTPAPPPAVP
KELPAPPAPPPASAPTPEKEPEEPAQAAPPAQSTPTPGVAAATLVSGGGSTSSTSSGSFEASPVEPQLPSKEGPE
PPEEVPPPTTPPVKVEPKGDGIGPTRQPPSQGLGYPKYQKSLPFRFQRQQEQQLLKQQQQHQWQQHQQGSAPPT
PVPPSPFPQVTLGAVPAPQAPPPPPKALYPGALGRPPPMPPMNFDP RWMMIIPPYVDPRLQLQGRPPPLDFYPPGVHP
SGLVPRERSDSGGSSSEPFDRHAPAMLRERGTTPVDPKLAWVG DVFTATPAEPRPLTSPLRQAADDDKGM RSET
PPVPPPPPYLASYPGFENGAGPPISRFPLEEPGPRPLPWPPGSDEVAKIQTTPPKKEPPKEETAQLTGPEAGR
KPARGVGSGGQGP PPRRESRTETRWGPRPGSSRRGIPPEEPGAPRRRAGPIKKPPPPPTKVEELPPKPLEQGD ET
PKPPKPDPLKITKGKLGPKETPPNGNLSPAPRLRRDYSYERVGPTSCRGRGRGEYFARGRGFRGT YGGRGRGAR
SREFRSYREFRGDDGRGGGTGGPNHPPAPRGRTASETRSEGSEYEEIPKRRRQRGSETGSETHESDLAPSDKEAP
TPKEGTLTQVPLAPPPPGAPPSPAPARFTARGGRVFTPRGVP SRRGRGGGRPPPQVCPGWSPPAKSLAPKKPPTG
PLPPSKEPLKEKLIPGPLSPVARGGSNGGSNVGMEDGERPRRRRHGRAQQQDKPPRFRRRLKQERENAARGSEGKP
SLTLPASAPAPEEALT TVTVAPAPRRAAKSPDLNQNDSQANEWE TASESSDFTSERRGDKEAPPVLLTPKA
VGTPGGGGGGGAVPGISAMSRGDL SQRADLSKRFSFSSQRPGMERQNRPGPGGKAGSSSGSSSGGGGGGPGGRTGP
GRGDKRSWPSPKNRSRPPEERPPGLPLPPPPSSSAVFRLDQVIHSNPAGIQQALQLSSRQGSVTAPGGHPRHK
PGPPQAPQGPSPRPPTRYEPQRVNSGLSSDPHFEEPGPMVRGVGGT PRDSAGVSPFPKRRERPPRKPELLQEES
LPPPHSSGFLGSKPEGPGPQAESRDTGTEALTPHIWNRLHTATSRKSYRPSMEPWMEPLSPFEDVAGTEMSQSD
SGVDLSGDSQVSSGPCSQRSSPDGGLKGAAEGPPKRPGGSSPLNAVPCEGPPGSEPPRRPPAPHDGDRKELPRE
QFLPPGPIGTERSQHTDRGTEPGPIRPSHRPGPPVQFGTSDKDSDLRLVVGDSLKA EKELTASVTEAIPVSRDWE
LLPSAAAASAEPQSKNLD SGHCVPFEPSSSQRLYPEVFYGSAGPSSSQISGGAMDSQLHPNSGGFRPGT PSLHPYR
SQPLYLPPGPAPPSALLSGVALKGQFLDFSTMQATELGKLPAGGVLYPPPSFLYSPAFCPSPLPDT SLLQVRQDL
PSPSDFYSTPLQPGGQSGFLPSGAPAQQMLLPMVDSQLPVVNF GSLPPAPPPAPPPLSLLPVGPALQPPSLAVRP
PPAPATRVLPSPARPPASLGRAELHPVELKPFQDYQKLSSNLGGPGSSRTPTTGRSFSGLN SRLKATPSTYSGV
FRTQRVDLYQQASPPDALRWIPKPPWERTGLPPREGPSRRAEPPGSRGDKEPGLPPPR

2158/6881
FIGURE 1983

CCGAGCTTCTTAAACACAGGCCTTGGGCCTACGGCTCTGGGGGTACTTGGGGGGGCGGGGGCAGGTCTGATGAGT
AACCCCTCCCCCAGGTTCCAGAGGAAGAAGCCTCCACATCTGTCTGCCGGCCCAAGAGTTCCATGGCCTCCACT
TCCCGCCGCCAACGCCGAGAACGTCGCTTTTCGTCGTTACTTGTCTGCAGGACGGCTGGTCCGGGGCCCAGGCCCTC
CTCCAGCGACACCCAGGCCTCGATGTAGATGCTGGGCAGCCCCCACCCTGCACCGGGCCTGTGCCCGCCACGAT
GCCCCTGCCCTGTGCTGCTGCTTCGGCTCGGGGCTGACCCTGCCACCAGGACCGCCATGGGGACACGGCACTG
CATGCTGCTGCCCGCCAGGGCCCAGATGCCTACACCGATTTCCTTCCTCCCGCTGCTAAGCCGCTGTCCCTCCGCC
ATGGGAATAAAGAATAAGGATGGGGAGACCCCTGGCCAAATTTGGGCTGGGGACCCCCCTGGGATTCTGCTGAA
GAGGAGGAAGAAGATGATGCCTCCAAGGAGCGGGGAATGGAGACAGAAGCTCCAGGGTGAGCTGGAGGACGAGTGG
CAGGAAGTCATGGGGAGGTTTGAAGGTGATGCCTCCCATGAAACCCAGGAACCTGAGTCCTTCTCAGCCTGGTCA
GATCGCCTGGCCCGGGAACATGCCCAGAAGTGCCAGCAGCAGCAGCGAGAAGCAGAGGGATCCTGTGACCCCCA
CGTGCTGAGGGCTCCAGCCAGAGCTGGCGACAGCAGGAGGAGGAGCAGCGGCTCTTCAGGGAGCGAGCCCGGGCC
AAGGAGGAAGAGCTGCGTGAGAGCCGAGCCAGGAGGGCGCAGGAGGCTCTAGGGGACCGAGAACCCAAGCCAACC
AGGGCCGGGGCCAGGGAAGAGCACCCCAGAGGAGCGGGGAGGGGCAGCCTCTGGCGATTGGTGATGTGCCCTGG
CCCTGCCCTGGGGGAGGGGACCCAGAGGCCATGGCTGCAGCCCTGGTGGCCAGGGGCCCCCCTTTGGAGGAACAG
GGGGCTCTGAGGAGGTACTTGAGGGTCCAGCAGGTCCGCTGGCACCCCTGACCGCTTCCTGCAGCGATTCCGAAGC
CAGATTGAGACCTGGGAGCTGGGCCGTGTGATGGGAGCAGTGACAGCCCTTCTCAGGCCCTGAATCGCCATGCA
GAGGCCCTCAAGTGACCCTAGGGAAGAAGCAAGAACTTCGGGGCTGCAGCCTCAGGATGAGGCAGAAGGAAGGG
TAAGGGAAAGGATGGGGACCACAAGGAAGAGCCAGGTGCTGCTCAGCAGAGGATATGGGTGGGAGCGAAAGTTGT
AACAAAGTGGGGGTGGGGGGTGCGGGCCGCCACCCTGCTCCTTGACTCTGCCGTTTCCTAATAAGACCTGGTTCC
ACATCTC

2159/6881
FIGURE 1984

ACAGGCATTTTCCAAAGGCAAGCCTGGAGCGCACGGATCTGTATAACCGCGGAAGGCCCTGTTTCCGGTCCCTTG
CGCCTGCGCTCTTGCAAGCAAGAAGGCGGGAGGCTGGAGTAGAGGGAAGCCTGCAACCGGAAGTGAAGGCAGATT
TCCCTCCTTCGCTCGCTGTTGCTGCCGCCATACGCGCTCTCCCTGTTTAGTTATGGCAGAGAACGATGTGGACAAT
GAGCTCTTGGACTATGAAGATGATGAGGTGGAGACAGCAGCTGGGGGAGATGGGGCTGAGGCCCTGCCAAGAAG
GATGTCAAGGGCTCCTATGTCTCCATCCACAGCTCTGGCTTTCGTGACTTCCTGCTCAAGCCAGAGTTGCTCCGG
GCCATTGTGCGACTGTGGCTTTGAGCATCCGTGAGAAAGTCCAGCATGAGTGCATCCCTCAGGCCATTCTGGGAATG
GATGTCCCTGTGCCAGGCCAAGTCGGGCATGGGAAAGACAGCAGTGTGTTGTCTTGGCCACACTGCAACAGCTGGAG
CCAGTTACTGGGCAGGTGTCTGTGCTGGTGATGTGTACACTCGGGAGTTGGCTTTTCAGATCAGCAAGGAATAT
GAGCGCTTCTCTAAATACATGCCCAATGTCAAGGTTGCTGTTTTTTTTTGGTGGTCTGTCTATCAAGAAGGATGAA
GAGGTGCTGAAGAAGAACTGCCCCGATATCGTCGTGGGGACTCCAGGCCGTATCCTAGCCCTGGCTCGAAATAAG
AGCCTCAACCTCAAACACATTAAACACTTTATTTTGGATGAATGTGATAAGATGCTTGAACAGCTCGACATGCGT
CGGGATGTCCAGGAAATTTTTCGCATGACCCCCACGAGAAGCAGGTCATGATGTTTCAAGTGTGCTACCTTGAGCAAA
GAGATCCGTCCAGTCTGCCGCAAGTTCATGCAAGATCCAATGGAGATCTTCGTGGATGATGAGACGAAGTTGACG
CTGCATGGGTGTCAGCAGTACTACGTGAACTGAAGGACAACGAGAAGAACCGGAAGCTCTTTGACCTTCTGGAT
GTCCTTGAGTTCAACCAGGTGGTGATCTTTGTGAAGTCTGTGCAGCGGTGCATTGCCCTTGGCCCAGCTACTAGTG
GAGCAGAACTTCCCAGCCATTGCCATCCACCGTGGGATGCCCCAGGAGGAGAGGCTTCTCGGTATCAGCAGTTT
AAAGATTTTCAACGACGAATTCTTGTGGCTACCAACCTATTTGGCCGAGGCATGGACATCGAGCGGGTGAACATT
GCTTTTAATTATGACATGCCTGAGGATTCTGACACCTACCTGCATCGGGTGGCCAGAGCAGGCCGGTTTGGCACC
AAGGGCTTGGCTATCACATTTGTGTCCGATGAGAATGATGCCAAGATCCTCAATGATGTGCAGGATCGCTTTGAG
GTCAATATTAGTGAGCTGCCTGATGAGATAGACATCTCCTCCTACATTGAACAGACACGGTAGAAGACTCGCCCA
TTTTGGAATGTGACCGTCTGTCCTTCAGGAGAGGACACCAGGGTGGGGGTGAAGGAGACACTACTGCCCCACCC
CTGACAGCCCCCACCCTATGGCTTCCATCTTTTGCATCACCACCACTCCTGAACCCCATTTCTGATTTGTCAGA
ATTTTTTTTTTAACAAAATAAAAATGAAACACATGTGTCTGTGGTATCTAAAAAAAAAAAAAAAAAAAAAAAAA

2160/6881
FIGURE 1985

MAENDVDNELLDYEDDEVETAAGGDGAEAPAKKDVKGSYVSIHSSGFRDFLLKPELLRAIVDCGFEHPSEVQHEC
IPQAILGMDVLCQAKSGMGKTAVFVLATLQOLEPVTGQVSVLVMCHTRELAFQISKEYERFSKYMPNVKVAVFFG
GLSIKKDEEVLKKNCPHIVVGTGPRILALARNKSLNLKHIKHFILDEC DKMLEQLDMRRDVQEIFRMTPEKQVM
MFSATLSKEIRPVCRKFMQDPMEIFVDDETKLT LHGLQQYYVKLDNEKNRKLFDLLDVLEFNQVVIFVKS VQRC
IALAQLLVEQNFP AIAIHRGMPQEERLSRYQQFKDFQRRILVATNLFGRGMDIERVNIAFN YDMPEDSDTYLHRV
ARAGRFGTKGLAITFVSDENDAKILNDVQDRFEVNISELPDEIDISSYIEQTR

2161/6881
FIGURE 1986

ACAGGCATTTTCCAAAGGCAAGCCTGGAGCGCACGGATCTGTATAACCGCGGAAGGCCCTGTTTCCGGTCCCTTG
CGCCTGCGCTCTTGAGCCCAAGAAGGCGGGAGGCTGGAGTAGAGGGAAGCCTGCAACCGGAAGTGAAGGCAGATT
TCCCTCCTTCGTCGCTGTTGCTGCCGCCATACGCGCTCTCCCTGTTTAGCTCTTCTGTTAGAAATAGTATCTTTG
TTTTCTTTGCTGTTCCCTCAATCCCCTACTCTTCACCCCTTGTTTTCACCTATTTTGCGAGAACCCATCCAGATC
CCCCTTCCCTTCTTCCCCTGCCGGCCAGTTATGCGCAGAGAACGATGTGGACAATGAGCTCTTGGAATATGAAGA
TGATGAGGTGGAGACAGCAGCTGGGGGAGATGGGGCTGAGGCCCTGCCAAGAAGGATGTCAAGGGCTCCTATGT
CTCCATCCACAGCTCTGGCTTTTCGTGACTTCCTGCTCAAGCCAGAGTTGCTCCGGGCCATTGTGCACTGTGGCTT
TGAGCATCCGTCAGAAAGTCCAGCATGAGTGCATCCCTCAGGCCATTCTGGGAATGGATGTCTGTGCCAGGCCAA
GTCGGGCATGGGAAAGACAGCAGTGTGTTGCTTGGCCACACTGCAACAGCTGGAGCCAGTTACTGGGCAGGTGTC
TGTGCTGGTGATGTGTCACACTCGGGAGTTGGCTTTTCAGATCAGCAAGGAATATGAGCGCTTCTCTAAATACAT
GCCCAATGTCAAGGTTGCTGTTTTTTTTTGGTGGTCTGTCTATCAAGAAGGATGAAGAGGTGCTGAAGAAGAACTG
CCCGCATATCGTCGTGGGGACTCCAGGCCGTATCCTAGCCCTGGCTCGAAATAAGAGCCTCAACCTCAAACACAT
TAAACACTTTTATTTTGGATGAATGTGATAAGATGCTTGAACAGCTCGACATGCGTCGGGATGTCCAGGAAATTTT
TCGCATGACCCCCCACGAGAAGCAGGTGATGATGTTTCACTGCTACCTTGAGCAAAGAGATCCGTCCAGTCTGCCG
CAAGTTTCATGCAAGATCCAATGGAGATCTTCGTGGATGATGAGACGAAGTTGACGCTGCATGGGTTGCAGCAGTA
CTACGTGAAACTGAAGGACAACGAGAAGAACCAGGAGCTCTTTGACCTTCTGGATGTCCTTGAGTTCAACCAGGT
GGTGATCTTTGTGAAGTCTGTGCAGCGGTGCATTGCCTTGGCCAGCTACTAGTGGAGCAGAACTTCCCAGCCAT
TGCCATCCACCGTGGGATGCCCCAGGAGGAGAGGCTTTCTCGGTATCAGCAGTTTAAAGATTTTCAACGACGAAT
TCTTGTGGCTACCAACCTATTTGGCCGAGGCATGGACATCGAGCGGGTGAACATTGCTTTTAAATTATGACATGCC
TGAGGATTCTGACACCTACCTGCATCGGGTGGCCAGAGCAGGCCGGTTTGGCACCAAGGGCTTGGCTATCACATT
TGTGTCCGATGAGAATGATGCCAAGATCCTCAATGATGTGCAGGATCGCTTTGAGGTCAATATTAGTGAGCTGCC
TGATGAGATAGACATCTCCTCCTACATTGAACAGACACGGTAGAAGACTCGCCCATTTTGGAATGTGACCGTCTG
TCCTTCAGGAGAGGACACCAGGGTGGGGTGAAGGAGACACTACTGCCCCACCCCTGACAGCCCCACCCCATG
GCTTCCATCTTTTGCATCACCACCACTCCTGAACCCCCATTTCTGATTTGTCAGAATTTTTTTTTTAACAAAATA
AAAATGAAACACATGTGTCTGTGGTATCTAAAAAAAAAAAAAAAAAAAAAAAAA

2162/6881
FIGURE 1987

MAENDVDNELLDYEDDEVETAAGGDGAEAPAKKDVKGSYVSIHSSGFRDFLKPELLRAIVDCGFEHPSEVQHEC
IPQAILGMDVLCQAKSGMGKTAVFVLATLQQLPVTGQVSVLVMCHTRELAFQISKEYERFSKYPNVKVAVFFG
GLSIKKDEEVLKKNCPHIVVGTPGRILALARNKSLNLKHIKHFI LDECDKMLEQLDMRRDVQEIFRMTPEKQVM
MFSATLSKEIRPVCRKFMQDPMEIFVDDTKLTLHGLQYYVKLKDNEKNRKLFDLLDVLEFNQVVIFVKSQVRC
IALAQLLVEQNFPAAIAIHRGMPQEERLSRYQQFKDFQRRILVATNLFGRGMDIERVNIAFNYPEDSDTYLHRV
ARAGRFGTKGLAITFVSDENDAKILNDVQDRFEVNISELPDEIDISSYIEQTR

2163/6881
FIGURE 1988

AGACGCCGAGATGCTGGTCATGGCGCCCCGAACCGTCCTCCTGCTGCTCTCGGCGGCCCTGGCCCTGACCGAGAC
CTGGGCCGGCTCCCACTCCATGAGGTATTTGACACCGCCATGTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCAT
CTCAGTGGGCTACGTGGACGACACGCAGTTCGTGAGGTTGACAGCGACGCCGCGAGTCCGAGAGAGGAGCCGCG
GGCGCCGTGGATAGAGCAGGAGGGGGCCGGAGTATTGGGACCGGAACACACAGATCTTCAAGACCAACACACAGAC
TGACCGAGAGAGCCTGCGGAACCTGCGCGGCTACTACAACCAGAGCGAGGCCGGGTCTCACACCCTCCAGAGCAT
GTACGGCTGCGACGTGGGGCCGGACGGGCGCCTCCTCCGCGGGCATAACCAGTACGCCTACGACGGCAAGGATTA
CATCGCCCTGAACGAGGACCTGCGCTCCTGGACCGCGGGACACCGCGGCTCAGATCACCCAGCGCAAGTGGGA
GGCGGCCCGTGTGGCGGAGCAGGACAGAGCCTACCTGGAGGGCACGTGCGTGGAGTGGCTCCGCAGATACCTGGA
GAACGGGAAGGACACGCTGGAGCGCGCGGACCCCCCAAAGACACACGTGACCCACCACCCCATCTCTGACCATGA
GGCCACCCTGAGGTGCTGGGCCCTGGGCTTCTACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGCGAGGA
CCAAACTCAGGACACTGAGCTTGTGGAGACCAGACCAGCAGGAGATAGAACCTTCCAGAAGTGGGCAGCTGTGGT
GGTGCCTTCTGGAGAAGAGCAGAGATACACATGCCATGTACAGCATGAGGGGCTGCCGAAGCCCCTCACCCCTGAG
ATGGGAGCCGTCTTCCAGTCCACCGTCCCCATCGTGGGCATTGTTGCTGGCCTGGCTGTCTTAGCAGTTGTGGT
CATCGGAGCTGTGGTCGCTGCTGTGATGTGTAGGAGGAAGAGCTCAGGTGGAAAAGGAGGGAGCTACTCTCAGGC
TGCGTGCAGCGACAGTGCCCAGGGCTCTGATGTGTCTCTCACAGCTTGAAAAGCCTGAGACAGCTGTCTTGTGAG
GGA CTGAGATGCAGGATTTCTTCACGCCTCCCCTTTGTGACTTCAAGAGCCTCTGGCATCTCTTTCTGCAAAGGC
ACCTGAATGTGTCTGCGTCCCTGTTAGCATAATGTGAGGAGGTGGAGAGACAGCCCACCCTTGTGTCCACTGTGA
CCCCGTGTTCCCATGCTGACCTGTGTTTCCTCCCCAG

2164/6881
FIGURE 1989

MLVMAPRTVLLLLSAALALTETWAGSHSMRYFDTAMSRPGRGEPRFISVGIVDDTQFVRFDSDAASPREEPRAPW
IEQEGPEYWDNRNTQIFKTNTQTDRESLRNLRGYYNQSEAGSHTLQSMYGCDVGPDGRLLRGHNQYAYDGKDYIAL
NEDLRSWTAADTAAQITQRKWEAARVAEQDRAYLEGTCVEWLRRYLENGKDTLERADPPKTHVTHHPISDHEATL
RCWALGFYPAEITLTWQRDGEDQTQDTELVEITRPAGDRITQKWAAVVVP SGEEQRYTCHVQHEGLPKPLTLRWEF
SSQSTVPIVGIVAGLAVLAVVIGAVVAAVMCRRKSSGGKGGSYSQAACSDSAQGSVDVSLTA

2165/6881
FIGURE 1990

GCGTGATGTCTCACAGAAAGTTCTCCACTCCCAGACATGGGTCCCTCGGCTTCCTGCCTTGGAAGCGCAGCAGCA
GGCATTGTGGGAAGGTGAAGAGCTTCCCTAAGGATGACCCGTCCAAGCCGGTCCACCTCACAGCCTTCCTGGGAT
ACAAGGCTGGCATGACCCACATCGTGCGGGCTCTGGAGAAGATTGACCTTAAGTTCATTGACACCCCTCCAAGT
TTGGCCATGGCCACTTCCAGACCATGGAGGAGAAGAAAGCATTTCATGGGACCACTCAAGAAAGACCGAATTGCAA
AGGAAGAAGGAGCTTAATGCTGGGAACAGATATTGCAACTGGTGGGATCTCAATAAAAGTTATTTTCCA

2166/6881
FIGURE 1991

MSHRKFSTPRHGS LGFLPWKRSSRHCGKVKSF PKDDPSKPVHLTAFLGYKAGMTHIVRALEKID LKFIDTPSKFG
HGHFQTMEEKKAFMGPLKKDRIAKEEGA

2167/6881
FIGURE 1992

ATTCTCCCCAGAGGCCGAGATGCGGGTCATGGCGCCCCGAGCCCTCCTCCTGCTGCTCTCGGGAGGCCTGGCCCT
GACCGAGACCTGGGCCTGCTCCCACTCCATGAGGTATTTGACACCGCCGTGTCCCGCCCCGGCCGCGAGAGCC
CCGCTTCATCTCAGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTGACAGCGACGCCGCGAGTCCGAGAGG
GGAGCCGCGGGCGCCGTGGGTGGAGCAGGAGGGGCGGAGTATTGGGACCGGGAGACACAGAACTACAAGCGCCA
GGCACAGGCTGACCGAGTGAGCCTGCGGAACCTGCGCGGCTACTACAACCAGAGCGAGGACGGGTCTCACACCCT
CCAGAGGATGTATGGCTGCGACCTGGGGCCCCGACGGGCGCCTCCTCCGCGGGTATGACCAGTCCGCCTACGACGG
CAAGGATTACATCGCCCTGAACGAGGACCTGCGCTCCTGGACCGCCGCGGACACCGCGGCTCAGATCACCCAGCG
CAAGTTGGAGGCGGCCCGTGC GGCGGAGCAGCTGAGAGCCTACCTGGAGGGCACGTGCGTGGAGTGGCTCCGCAG
ATACCTGGAGAACGGAAGGAGACGCTGCAGCGCGCAGAACCCCCAAAGACACACGTGACCCACCACCCCTCTC
TGACCATGAGGCCACCCTGAGGTGCTGGGCCCTGGGCTTCTACCCTGCGGAGATCACACTGACCTGGCAGCGGGA
TGGGGAGGACCAGACCCAGGACACCGAGCTTGTGGAGACCAGGCCAGCAGGAGATGGAACCTTCCAGAAGTGGGC
AGCTGTGGTGGTGCCTTCTGGACAAGAGCAGAGATACACGTGCCATATGCAGCACGAGGGGCTGCAAGAGCCCT
CACCCCTGAGCTGGGAGCCATCTTCCCAGCCCACCATCCCCATCATGGGCATCGTTGCTGGCCTGGCTGTCCTGGT
TGTCCTAGCTGTCTTGGAGCTGTGGTCACCGCTATGATGTGTAGGAGGAAGAGCTCAGGGCATTTCCTTCCCAC
AGGTGGAAAAGGAGGGAGCTGCTCTCAGGCTGCGTGCAGCAACAGTGCCAGGGCTCTGATGAGTCTCTCATCAC
TTGTAAAGCCTGAGACAGCTGCCTGTGTGGGACTGAGATGCAGGATTTCTTCACACCTCTCCTTTGTGACTTCAA
GAGCCTCTGGCATCTCTTTCTGCAAAGGCGTCTGAATGTGTCTGCGTTTCTGTTAGCATAATGTGAGGAGGTGGA
GAGACAGCCCACCCCGTGTCCACCGTGACCCCTGTCCCCACACTGACCTGTGTTCCCTCCCCGATCATCTTTCC
TGTTCCAGAGAGGTGGGGCTGGATGTCTCCATCTCTGTCTCAAATTCATGGTGCACTGAGCTGCAACTTCTTACT
TCCCTAATGAAGTTAAGAACCTGAATATAAATTTGTGTTCTCAAATATTTGCTATGAAGCGTTGATGGATTAAAT
AAATAAGTCAATTCCTAGAAGTGAGAGAGCAAATAAAGACCTGAGAACCTTCCAG

2168/6881
FIGURE 1993

MRVMAPRALLLLLLSGGLALTETWACSHSMRYFDTAVSRPGRGEPRFISVG YVDDTQFVRFDSDAASPRGEPRAPW
VEQEGPEYWDRETQNYKRQAQADRVSLRNLRGYYNQSE DGSHTLQRMYGCDLGP DGRLLRGYDQSA YDGKDYIAL
NEDLRSWTAADTAAQITQRKLEAARAAEQ LRAYLEGTCVEWLRRYLENGKETLQRAEPPKTHVTHHPLSDHEATL
RCWALGFYPAEITLTWQRDGEDQTQDTEL VETRPAGDGT FQKWA AVVVP SGQE QRYTCHMQHEGLQEPLT LSWEP
SSQPTIP IMGIVAGLAVLVVLAVLGAVVTAMMCRRKSSGHFLPTGGKGGSCSQAACSN SAQGSDES LITCKA

2169/6881
FIGURE 1994

GGAAAGGTGTACGCAGGCGCAGTGGCGTCTAAATTTGGGCCCCACTAAATGCGTCGGAGCATCTCCGCGCCCAGGC
GGCTCCTCCTCACTGCGGCAACCCGGGAAAACCTTGTGAACATAATCAGAAAAAGTGGAAGGCGGGAGATCTTGGGG
CGCTGTCCAATGGCGCGGAAGAGAACAATGAGCTGGCCAATCGGGAACGGCACGGGGGCGGGCTCGCTCGGCGC
GAAGTTCGGGCCCCGGAATTCGAAGGAGGGGTAGGCGCTGCCCCGCGCGCAGAGGCCGCGCCCCCTCTGGCCCCG
GCTTCTTGGCTGTCAAACAGATGCAGCAACGTCGGCTCCTGCCGAGGAGCCCAAGGGGTCCCGGGATCCGCCGCA
CAGGCTGGCACTGCTTGAAGAGGAGGCTACTCGGAGACTGCGCCGCGCGGGTAGATCCGAAACGGGGCTGGGGCG
GAGTGGGAAAAGGCCGGGTATGCCTTGCATGATCGCGGGGAGCTCCTTCTGTTTTTATCCACCTAGAGAAGCC
GGGAAGTAGGGGTTTAGGTCCAATTTGTTGGAGTACTTAAGGACTCGTTTGCACTTTCTTTTGGGGGATGACAGT
GGATTCAATTGCCCTCGGAGGTTCAACCAGTTATGAGTGAGGGATTGGCCAGAAGATCGGGGCGCAGGCAAGCAGG
AGTGCTCTATTAGGATAAGCAAGTTTGACAGGAAGAAGCTGCTCTTCTCCGAATTACACAGAGGTGATGTGTTCCG
TATTGCACGTAGACGTGTGTATAACAGGACCTCCTTCCCCGCGCCCCGCCACCCCGACACACAGGAGCTGCCT
AAAGTATCCTTGCCTTGCAAGTTGGAGGCTCCCCAAATATTTTGTGATCTGAGGATCCAGCTCAAGTGAGGTGCC
ATAGGACGTGTTTCTGAGTTTGCAATGACGGAGACCTTCTTGGAAATTTTTCATTGTCAAGTCGGCTTAACCAAT
TTTGCATTGAGTCCTAGGCTGCTTGCACTCTGAATTTGGGCTATTAGGTTAGTGCTCAAAGTTGAAACCGCAT
ACAGCACAACTCAAGTTTGCATCAGACTGGGAAGCGAACTTAAGCCAGCGGTGCGTGGCCCAGGAGTGGGAAAAG
AAATGGATGCCTGAAGTGGAAGAGGTTGGTGAGAGGGGGCACCGCCCATGCTGCCCTGCTTCCAAGTGTGCGCA
TAGGGGGCGGCAGGGGCGGTGATCTCTACACCTTCCACCCCCCGCCGGGGCTGGCTGCACCTATCGCTTGGGCC
ACAGGGCCGACCTGTGTGATGTGGCCCTGCGGGCCCCAGCAGGAGCCTGGCCTCATCTCTGGGATCCACGCCGAAC
TGATGCCGAGCCCCGGGGTGATGACTGGAGGGTCAGCCTGGAAGACCACAGCAGCCAAGGTGAGCATTAAAGCAG
GGCAGCTTTGCCCTTGGGTGGTTGAAGCGCCAGGCTGGAATGAGTAAGGTCTCCACAAGACCCTGCTGCCTGCCT
CCCATACTCCCATCAGATTGGATGGATAGTCGTGGTCCAGACCTTCATCTTCCACCAGAAGTGTGCACAGTCAG
AAGCTCTCTGCCAGACTGACCCCTTTTGGTCCCGTTTAGCTCATAACAGGACCTGGGATATCATCAGAAAGATATC
ACAGTGGGGATGTTCTGAGGCCACTAGAGGCCAAGTTTAGACTTGATTGAGTTTCCAGCTTTGCTGAGGCACTCT
GTTCTTGGGTTAGGGCAGTTCTATGTTGAATAATGTTTTTAATAATCTGGGCATGTCTTTCTCCGTGACTTGAGG
CAGTTAGCCTCAGAAAGCCTAGATTCACATTTGAGTTTTGCCACTGCCTCTTGGTAAAGTCAGCTGTAGGAGTGT
TATGGTTATTAGACTATAGTAGCCAACATTCATCTAGTGCTTACTGTTATGAGCCAGGCCCTATTTTAAAGTGTAT
TGAATGTAGGTGGTACTAATATTATCCTCATTTACAGTAAAGGAAAATGAGGCACAAAGAGGTTAAGGAACTTGT
CCAGGGCTGGGCATGGTGGTTTACACCTATAATCCAGCACTTTGGGAGGCTAAGGCAGGGTGGATCACTTGAGCT
CAGGAGTTTCAGACCAGCCTGGGCAACATGGTGAAAACCTGTCTCTACCAAAAAATTAATTAATTTTTTAAAAA
AGCCTGGGCGCGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCGGAGATGGGCAGATCACGAGGTCAGGA
GTTTCGAGACCATCCTGACCAACATGTTGAAACCCATCTGTGCTGAAAAAAAATACAAAAATTAGCCAGGTGTG
GTGGCGTGCACCTGTAACCCAGCTACTCAGGAGGCTGAAGCAGCAGAATCACTTGAACCCGGGAGGCGGAGGTT
GCAGTGAGCTGAGATCGCAACACTGCCTCCAGCTTGGGCGACAGAGCGAGACTCCATCTCAAACAAACAAACAA
ACCAAAAGCTTGCCAGGGTCACATAACTGGTAAGTGGTAGAGCTAGGATCTGAACGAGCTGGAGCTGGGGGAGA
GTGAGCATGTTTGAAGAACTGGACCTTAGGGCGGGGCACGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGC
TGAGGCGGGCAGATCAGGAGGTGAGGAGTATGAGACCAGCCTGGCCAACATGGTAAAAACCTGTCTCTGCTAAAA
ATAAAAAAATTAGCCAGACGTGGTGGCACATGCCTGTAATCCAGCTACTCAGGAGGCTGAGGCAGGAGAATTGC
TTGAACCTGGGAGGCGGTTCAGCTTGGGCAATAGAGCAAACTCCATC

2170/6881
FIGURE 1995

TTGGTGGATTCTCAGTCCCTGCCGCCGCGGGGCGCCCTGGGATAGCGGCGGGGCTCCTGAACAGATCTCGGCC
CCTTTCCAAACACTCCTGATGCCTCATTGCGCTCTCGCTTCTTTTCGACCACCATTGTTGGGGGCTGAGGCACTCA
CGGGGCTCCCCAGGTTTCACTCCGTTTCTACACAGTCCGAGCCCCATGGATCTCCCATCTCCCGGAGGAACCGT
GAAGCCAAACAGAAGCGCCTGCGAGAGAAGCAGGCTACTCTGGAGGCTGAGATAGCAGGGGAGAGCAAGTCACCT
GCAGAATCCATTAAGGCCTGGAGGCCTAAGGAGTTAGTATTGTATGAAATCCCTACGAAACCCGGTGAAAAGAAA
GATGTCTCTGGGCCCCCTGCCTCCTGCATACAGCCCCGATATGTTGAGGCTGCCTGGTACCCGTGGTGGGTACGA
GAGGGCTTCTTCAAACCAGAATATCAGGCCCCGGCTGCCCAAGCTACAGGGGAGACCTTTTCCATGTGTATCCCA
CCTCCCAATGTCACTGGCTCCCTGCACATTGGCCACGCACTCACGGTGGCCATACAGGATGCCCTCGTGCGCTGG
CACCGGATGCGTGGGGATCAAGTGCTGTGGGTCCCTGGTTCAGATCATGCAGGAATTGCTACACAAGCTGTGGTG
GAGAAACAACCTGTGGAAGGAACGGGGAGTGAGGAGACATGAGCTGAGCCGGGAGGCCTTCCTTAGGGAGGTGTGG
CAGTGGAAGGAGGCGAAAGGTGGAGAGATCTGTGAGCAGCTGCGAGCTCTGGGTGCCTCCCTGGACTGGGATCGA
GAGTGTTTTACCATGGATGTTGGCTCCTCAGTGGCTGTGACTGAAGCTTTTGTGCGGCTCTACAAGGCGGGGTG
CTGTACCGGAACCATCAGCTTGTCAACTGGTCATGTGCTTTAAGATCAGCCATCTCGGACATTGAGGTGGAGAAC
CGGCCCCCTGCCCTGGCCACACACAGCTTCGACTGCCTGGCTGCCCCACCCCGTGTCTTTTGGCCTCCTATTTTCT
GTTGCCTTCCCCGTGGATGGAGAGCCTGATGCAGAGGTTGTGGTAGGAACCACAAGGCCAGAGACGCTGCCTGGA
GATGTGGCTGTGGCCGTTTCATCCAGACGACTCGCGATACACACATCTACACGGGCGACAGCTTCGTACCCCTTG
ATGGGGCAGCCTCTTCCCCTCATCACAGACTATGCTGTTTCAGCCACATGTGGGCACGGGGGCGAGTGAAGGTGACT
CCAGCTCACAGTCCCTGCCGATGCTGAGATGGGGGCCCCGACATGGCTTGAGCCCCCTTGAATGTCATTGCGGAGGAT
GGGACCATGACCTCCCTCTGCGGGGACTGGCTGCAGGGTCTTACCGGTTTGTGGCCCCGGGAAAAGATAATGTCT
GTGCTGAGTGAATGGGGCCTGTTCCGGGGCCTCCAGAACCACCCCATGGTACTGCCCATCTGCAGCCGTTCTGGG
GATGTGATAGAATACCTGCTGAAGAACCAGTGGTTTGTCCGCTGCCAGGAAATGGGGGCCCCGAGCTGCCAAGGCT
GTGGAGTCGGGGGCCCTGGAGCTCAGTCCCTCCTTCCACCAGAAGAACTGGCAGCACTGGTTTTCCCATATTGGG
GACTGGTGTGTCTCCCGGCAGCTGTGGTGGGGCCATCAGATTCCAGCCTACCTGGTTGTAGAGGACCATGCGCAG
GGAGAAGAGGACTGTTGGGTGGTTGGGCGGTGAGAGGCTGAGGCCAGAGAGGTAGCAGCGGAACCTGACAGGGAGG
CCAGGGGCAGAGCTGACCCTGGAGAGGGATCCTGATGTCTTAGACACATGGTTTTCTTCTGCCCTGTTCCCTTT
TCTGCCCTGGGCTGGCCCCAAGAGACCCAGACCTTGCTCGTTTCTACCCCTGTCACTTTTGAAACGGGCAGC
GACCTTCTGCTGTTCTGGGTGGGCCGATGGTCATGTTGGGGACCCAGCTCACAGGGCAGCTGCCCTTCAGCAAG
GTGCTTCTTCATCCCATGGTTCCGGACAGGCAGGGCCGGAAGATGAGCAAGTCCCTGGGGAATGTGCTGGACCCA
AGAGACATCATCAGTGGGGTGGAGATGCAGGTGCTGCAGGAAAAGCTGAGAAGCGGAAATTTGGACCCTGCAGAG
CTGGCCATTGTGGCTGCAGCACAGAAAAAGGACTTTCCTCACGGGATCCCTGAGTGTGGGACAGATGCCCTGAGA
TTCACACTCTGCTCCCATGGAGTTCAGGCGGGCGACTTGCACCTGTCACTCTCTGAGGTCCAGAGCTGCCGACAT
TTCTGCAACAAGATCTGGAATGCTCTTCGCTTTATCCTCAATGCTTTAGGGGAGAAATTTGTGCCACAGCCTGCT
GAGGAGCTGTCTCCCTCCTCCCCGATGGATGCCTGGATCCTGAGCCGCTTGCCCTGGCTGCCAGGAGTGTGAG
CGGGGCTTCTCACCCGAGAGCTCTCGCTCGTCACTCATGCCCTGCACCACTTCTGGCTTACAAACCTCTGTGAC
GTCTACCTGGAGGCTGTGAAGCCCGTGTGTGGCACTCGCCCCGCCCTTGGGGCCCCCTCAGGTCTGTCTCC
TGCGCTGACCTCGGCCTCCGCTCCTGGCCCCACTGATGCCCTTCTGGCTGAAGAGCTCTGGCAGAGGCTGCC
CCCAGGCCTGGTTGCCCCCTGCCCCAGCATCTCGGTTGCCCTTACCCAGCGCTGCAGCTTGGAGCACTGG
CGCCAGCCAGAGCTGGAGCGGCGCTTCTCCCGGTCCAAGAGGTGCTGCAGGTGCTAAGGGCTCTCCGAGCCAG
TACCAGCTCACCAAAGCCCGGCCCGAGTGCTGCTGCAGAGCTCAGAGCCTGGGGACAGGGCCTCTTCGAGGCC
TTCTTGGAGCCCCCTGGGCACCCTGGGCTACTGTGGGGCTGTGGGCCTGTTACCCCGAGGCGCAGCAGCTCCCTCC
GGCTGGGGCCAGGCTCCACTCAGTGACACGGCTCAAGTCTACATGGAGCTGCAGGGCCTGGTGGACCCGCAGATC
CAGCTACCTCTGTTAGCCGCCCAGAGGTACAAGTTGCAGAAGCAGCTTGACAGCCTCACAGCCAGGACCCCATCA
GAAGGGGAGGCAGGACTCAGAGGCAACAAAAGCTTCTTCCCTCCAGCTGGAATTGTCAAACCTGGACAAGGCA
GCCTCTCACCTCCGGCAGCTGATGGATGAGCCTCCAGCCCCAGGAGCCGAGCTCTAACTCATCATCCCCATC
AGTTTTCTCCCTCTCAGACCTGTCTTTGAGGACAAACAGATTTGTGAGCTGTGAGGGTGCAGTGGGACGTGAGA
GACTATGTGGTCCATCGCCTTCAATTGTGTAAATGAGGACACAGACTGGCTTGGTTCGAGTACTGTGGTGTCTT
GAGATGCTCACATTACTGCCCGGCTGCCTCCACCTGGAAGTCTGGGAATGAGGAGATTGAGATAAACTTTTGA
AATCCC

2171/6881
FIGURE 1996

MGQPLPLITDYAVQPHVGTGAVKVTPAHSPADAEMGARHGLSPLNVIAEDGTMTSLCGDWLQGLHRFVAREKIMS
VLSEWGLFRGLQNHMPVLPICSRSGDVIEYLLKNQWFVRCQEMGARA AKAVESGALELSPSFHQKNWQHWF SHIG
DWCVSRQLWWGHQIPAYLVVEDHAQGEEDCWVVG RSEAEAREVAAELTGRPGAELTLERDPDVLDTWFS SALFPF
SALGWPQETPD LARFYPLSLLETGSDLLLFVWGRMVMLGTQLTGQLPF SKVLLHPMVRDRQGRKMSKSLGNVLDP
RDIISGVEMQVLQEKLRSGNLDPAELAIVAAAQKKDFPHGIPEC GTDALRFTLCSHG VQAGDLHLSVSEVQSCRH
FCNKIWNALRFILNALGEKFVPQPAEELSPSSPMDAWILSR LALAAQECERGFLTRELSLVTHALHHFWLHNLCD
VYLEAVKPV LWHSRPLGPPQVLFSCADLGLRLLAPLMPFLAEELWQRLPPRPGCPPAPSISVAPYPSACSLEHW
RQPELERRFSRVQEVVQVLRALRATYQLT KARPRVLLQSSEPGDQGLFEAFLEPLGTLGYCGAVGLLPPGAAAPS
GWAQAPLSDTAQVYMELOGLVDPQIQLP LLAARRYKLQKQLDSL TARTPSEGEAGTQRQOKLSSLQLELSKLDKA
ASHLRQLMDEPPAPGSPEL

2172/6881
FIGURE 1997

TCCCATCTTTTCCTCGCATTTTTTTCACCATCTTTCCCTCAATCTCCAGGAGCCAATGCGAGACTTTTGGCTCCGA
TTAAGCGACGGCCCCGAGACTTGGGGTGCGCGAGGAGGATCGACAGAGTGGTGATGGGAGAGCACCCCTTCAAGGGG
ACTGAACCGAGTACACCTACAATGCAGGAATCTGCAGGAATTCTTAGGGGGCCTGAGCCCTGGGGTATTGGACCG
ATTGTATGGGCACCCTGCCACATGTCTGGCTGTCTTCAGGGAGCTCCCATCCTTGGCTAAGAACTGGGTGATGCG
GATGCTCTTTCTGGAGCAGCCTTTGCCACAGGCTGCTGTAGCTCTGTGGGTAAAGAAGGAATTCAGCAAGGCTCA
GGAGGAAAGTACAGGGCTGCTGAGCGGCCTCCGATCTGGCACACCCAGCTGCTCCCAGGCGGGCTCCAGGGCCT
CATCTCAACCCCATTTTCCGCCAGAACCTCCGCATTGCCCTTCTGGGTGGGGGAAGGCCTGGTCTGATGACAC
AAGTCAGCTGGGACCAGACAAGCATGCCCGGGACGTTCCCTCCCTTGACAAGTACGCCGAGGAGCGATGGGAGGT
GGTCTTGCACTTCATGGTGGGCTCCCCAGTGCAGCTGTCAGCCAGGACTTGGCTCAGCTCCTCAGCCAGGCTGG
GCTCATGAAGAGTACTGAACCTGGAGAGCCGCCCTGCATTACTTCCGCTGGCTTCCAGTTCCTGTTGCTGGACAC
CCCGGCTCAGCTCTGGTACTTTATGTTGCAGTATTTGCAGACAGCCCAGAGCCGGGGCATGGACCTGGTAGAGAT
TCTCTCCTTCCTCTTCCAGCTCAGCTTCTCTACTCTGGGCAAGGATTACTCTGTGGAAGGTATGAGTGATTCTCT
GTTGAACTTCCTGCAACATCTGCGTGAGTTGGGCTTGTTTTCCAGAGGAAGAGGAAATCTCGGCGTTACTACCC
CACACGCCCTGGCCATCAATCTCTCATCAGGTGTCTCTGGAGCTGGGGGCACTGTGCATCAGCCAGGTTTCATTGT
CGTGGAACCAATTACCGACTGTATGCCTACACGGAGTCGGAGCTGCAGATTGCCCTCATTGCCCTCTTCTCTGA
GATGCTCTATCGGTTCCCCAACATGGTGGTGGCGCAGGTGACCCGGGAGAGTGTGCAGCAGGCAATCGCCAGTGG
CATCACAGCCCAGCAGATAATCCATTTCCCTAAGGACAAGAGCCCACCCAGTGATGCTCAAACAGACACCTGTGCT
GCCCCCACCATCACCGACCAGATCCGGCTCTGGGAGCTGGAAAGGGACAGACTCCGGTTCAGTGGGGTGTCTCT
GTATAACCAGTTCCTGTGCGCAAGTGACTTTGAGCTGCTGCTGGCCCACGCGCGGGAGCTGGGCGTGCTCGTGTT
CGAGAACTCGGCCAAGCGGCTCATGGTGGTGACCCGGCCGGGCACAGCGACGTCAAGCGCTTTTGGAAGCGGCA
GAAACATAGCTCCTGAGAGCGCGGGACTTGGACACGGACCTCGGCGGGCGGGACTGGGCGGGCGGGGCATCAGA
ACTCAGGTGTTTTTTATTTACGCGTCAGGGCTTTTCTTGTTTAATAAGTTATGATAGCT

2173/6881
FIGURE 1998

MESTPSRGLNRVHLQCRNLQEFLLGGLSPGVLDRLYGHPATCLAVFRELP
SLAKNWVMRMLFLEQPLPQAAVALWV
KKEFSKAQEESTGLLSGLRIWHTQLLPGGGLQGLILNPIFRQNLRIALLGGGKAWSD
DTSQLGPDKHARDVP
SLDK
YAEERWEVVLHFMVGSPSAAVSQDLAQLLSQAGLMKSTEPGEPPCITSAGFQ
FLLLDTPAQLWYFMLQYLQTAQS
RGMDLVEILSFLFQLSFSTLGKDYSEGMDSLLNFLQHLREFGLVFQ
RKRKSRRYYPTRLAINLSSGVSGAGGT
VHQPGEFIVVETNYRLYAYTESELQIALIALFSEMLYRFPNMVVAQVTRESVQQA
IASGITAQQIIHFLRTRAHPV
MLKQTPVLPPTITDQIRLWELERDRLRFTEGVLYNQFLSQVDFELL
LAHARELGVLVFENSAKRLMVVTPAGHSD
VKRFRWKRQKHSS

2174/6881
FIGURE 1999A

TTAGGAAGTTATTTAACTGATCTCTGCCCTAGTTTCTTCATGTGTTAAATATGGATAGTAATAGTATCTACCTTA
TGAAGTGACTGTGAAGATAAAATTATGGATTCTGTTTAAGGGTTTAGGCCAGTGTCTGGCACAGGGGAAGCATTCT
TAAAAATATAGCTGATGCTGTTAAACAATGACTGTTGTTGTTGTTTACTGTTATTATCCCCAAAGCGGCCATT
CTGTCTGTTGCTGTCTAGCTATGACTCAGTCCCCTGATTAACTTACGCACCACCCATTTTATCCCCTGAGAGATG
CTGCCCCCACCCTTAGGCCCCGAGGGATCAGGAGCTATGGGACCAGAGGCCCTGTCATCTTTACTGCTGCTGCT
CTTGGTGCAAGTGGAGATGCTGACATGAAGGGACATTTTGATCCTGCCAAGTGCCGCTATGCCCTGGGCATGCA
GGACCGGACCATCCAGACAGTGACATCTCTGCTTCCAGCTCCTGGTCAGATTCCACTGCCGCCGCCACAGCAG
GTTGGAGAGCAGTGACGGGGATGGGGCCTGGTGCCCCGAGGGTCGGTGTTTCCCAAGGAGGAGGAGTACTTGCA
GGTGGATCTACAACGACTGCACCTGGTGGCTCTGGTGGGCACCCAGGGACGGCATGCCGGGGGCTGGGCAAGGA
GTTCTCCCGGAGCTACCGGCTGCGTTACTCCCGGGATGGTTCGCCGCTGGATGGGCTGGAAGGACCGCTGGGGTCA
GGAGGTGATCTCAGGCAATGAGGACCCTGAGGGAGTGGTGCTGAAGGACCTTGGGCCCCCATGGTTGCCCGACT
GGTTGCTTCTACCCCCGGGCTGACCGGGTCTATGAGCGTCTGTCTGCGGGTAGAGCTCTATGGCTGCCTCTGGAG
GGATGGACTCCTGTCTTACACCGCCCCCTGTGGGGCAGACAATGTATTTATCTGAGGCCGTGTACCTCAACGACTC
CACCTATGACGGACATACCGTGGGCGGACTGCAGTATGGGGTCTGGGCCAGCTGGCAGATGGTGTGGTGGGGCT
GGATGACTTTAGGAAGAGTCAGGAGCTGCGGGTCTGGCCAGGCTATGACTATGTGGGATGGAGCAACCACAGCTT
CTCCAGTGGCTATGTGGAGATGGAGTTTGAGTTTGACCGGCTGAGGGCCTTCCAGGCTATGCAGGTCCACTGTAA
CAACATGCACACGCTGGGAGCCCGTCTGCCTGGCGGGGTGGAATGTCGCTTCCGGCGTGGCCCTGCCATGGCCTG
GGAGGGGGAGCCCATGCGCCACAACCTAGGGGGCAACCTGGGGGACCCAGAGCCCGGGCTGTCTCAGTGCCCTT
TGGCGGCCGTGTGGCTCGCTTTCTGCAGTGCCGCTTCTCTTTGCGGGGCCCTGGTTACTCTTCAGCGAAATCTC
CTTCATCTCTGATGTGGTGAACAATTCTCTCCGGCACTGGGAGGCACCTTCCCGCCAGCCCCCTGGTGGCCGCC
TGGCCCACTCCCACTTACAGCAGCTTGGAGCTGGAGCCCAGAGGCCAGCAGCCCGTGGCCAAGGCCGAGGG
GAGCCCGACCGCCATCCTCATCGGCTGCCTGGTGGCCATCATCCTGCTCCTGCTGCTCATCATTGCCCTCATGCT
CTGGCGGCTGCCTGGCGCAGGCTCCTCAGCAAGGCTGAACGGAGGGTGTGGAAGAGGAGCTGACGGTTACCT
CTCTGTCCCTGGGGACACTATCCTCATCAACAACCGCCCAGGTCTTAGAGAGCCACCCCCGTACCAGGAGCCCCG
GCCTCGTGGGAATCCGCCCCACTCCGCTCCCTGTGTCCCAATGGCTCTGCGTTGCTGCTCTCCAATCCAGCCTA
CCGCTCCTTCTGGCCACTTACGCCCGTCCCCCTCGAGGCCCGGGCCCCCACACCCGCTGGGCCAAACCCAC
CAACACCCAGGCCTACAGTGGGGACTATATGGAGCCTGAGAAGCCAGGCGCCCCGCTTCTGCCCCACCTCCCCA
GAACAGCGTCCCCATTATGCCGAGGCTGACATTGTTACCCTGCAGGGCGTCAACGGGGGCAACACCTATGCTGT
GCCTGCACTGCCCCAGGGGCGAGTGGGGATGGGCCCCCAGAGTGGATTTCCTCGATCTCGACTCCGCTTCAA
GGAGAAGCTTGGCGAGGGCCAGTTTGGGGAGGTGCACCTGTGTGAGGTGCACAGCCCTCAAGATCTGGTTAGTCT
TGATTTCCCCCTTAATGTGCGTAAGGGACACCCTTTGCTGGTAGCTGTCAAGATCTTACGGCCAGATGCCACCA
GAATGCCAGGAATGATTTCTGAAAGAGGTGAAGATCATGTGAGGCTCAAGGACCCAAACATCATTCGGCTGCT
GGGCGTGTGTGTGAGGACGACCCCTCTGCATGATTACTGACTACATGGAGAACGGCGACCTCAACCACTTCT
CAGTGCCCAACAGCTGGAGGACAAGGCAGCCGAGGGGGCCCCCTGGGGACGGCAGGCTGCGCAGGGGGCCACCAT
CAGCTACCCAATGCTGCTGCATGTGGCAGCCAGATCGCCTCCGGCATGCGCTATCTGGCCACACTCAACTTTGT
ACATCGGGACCTGGCCACGCGGAACTGCCTAGTTGGGGAAAATTTACCATCAAAATCGCAGACTTTGGCATGAG
CCGGAACCTCTATGCTGGGGACTATTACCGTGTGCAGGGCCGGGCAGTGCTGCCCATCCGCTGGATGGCCTGGGA
GTGCATCCTCATGGGGAAGTTCACGACTGCGAGTGACGTGTGGGCCTTTGGTGTGACCCTGTGGGAGGTGCTGAT
GCTCTGTAGGGCCCAGCCCTTTGGGCAGCTCACCGACGAGCAGGTCAICGAGAACGCGGGGGAGTTCTTCCGGGA
CCAGGGCCGGCAGGTGTACCTGTCCCGCCGCTGCTGCCCCGAGGGCCTATATGAGCTGATGCTTCGGTGCTG
GAGCCGGGAGTCTGAGCAGCGACACCCTTTTCCAGCTGCATCGGTTCTTGGCAGAGGATGCACTCAACACGGT
GTGAATCACACATCCAGCTGCCCTCCCTCAGGGAGCGATCCAGGGGAAGCCAGTGACACTAAAACAAGAGGACA
CAATGGCACCTCTGCCCTTCCCTCCCGACAGCCCATCACCTCTAATAGAGGCAGTGAGACTGCAGGTGGGCTGG
GCCACCCAGGGAGCTGATGCCCTTCTCCCTTCTGGACACACTCTCATGTCCCTTCTGTCTTCTTCTTCT
AGAAGCCCCGTGTCGCCACCCAGCTGGTCTGTGGATGGGATCCTCTCCACCCTCTCTAGCCATCCCTTGGGGA
AGGGTGGGGAGAAATATAGGATAGACACTGGACATGGCCCATGGAGCACCTGGGCCCCACTGGACAACACTGAT
TCTTGGAGAGGTGGCTGCGCCCCCAGCTTCTCTCTCCCTGTACACACTGGACCCCACTGGCTGAGAATCTGGGG
GTGAGGAGGACAAGAAGGAGAGGAAAATGTTTCTTGTGCTGCTCCTGTACTTGTCTCTCAGCTTGGGCTTCTTC

2175/6881

FIGURE 1999B

CTCCTCCATCACCTGAAACACTGGACCTGGGGGTAGCCCCGCCCCAGCCCTCAGTCACCCCCACTTCCCCTTGC
AGTCTTGTAGCTAGAACTTCTCTAAGCCTATACGTTTCTGTGGAGTAAATATTGGGATTGGGGGGAAAGAGGGAG
CAACGGCCCATAGCCTTGGGGTTGGACATCTCTAGTGTAGCTGCCACATTGATTTTCTATAATCACTTGGGGTT
TGTACATTTTGGGGGGAGAGACACAGATTTTACACTAATATATGGACCTAGCTTGAGGCAATTTAATCCCCT
GCACTAGGCAGGTAATAATAAAGGTTGAGTTTCCAC

2176/6881
FIGURE 2000

CGCTGCTCCAGCCTCTGGGGCGCATTCCAACCTTCCAGCCTGCGACCTGCGGAGAAAAAAATTACTTATTTTCT
TGCCCCATACATACCTTGAGGCGAGCAAAAAAATTAAATTTTAACCATGAGGGAAATCGTGACATCCAGGCTGG
TCAGTGTGGCAACCAGATCGGTGCCAAGTTCTGGGAGGTGATCAGTGATGAACATGGCATCGACCCACCGCTGT
CTTCCGTGGTCGGATGTCCATGAAGGAGGTGATGAGCAGATGCTTAACGTGCAGAACAAAGACAGCAGCTACTT
TGTGGAATGGATCCCCAACAAATGTCAAGACAGCCGTCTGTGACATCCCACCTCGTGGCCTCAAGATGGCAGTCAC
CTTCATTGGCAATAGCACAGCCATCCAGGAGCTCTTCAAGCGCATCTCGGAGCAGTTCAGTGCCATGTTCCGCCG
GAAGGCCTTCCTCCACTGGTACACAGGCGAGGGCATGGACGAGATGGAGTTCACCGAGGCTGAGAGCAACATGAA
CGACCTCGTCTCTGAGTATCAGCAGTACCAGGATGCCACCGCAGAAGAGGAGGAGGATTTCGGTGAGGAGGCCGA
AGAGGAGGCCAAGGCAGAGCCCCATCACCTCAGGCTTCTCAGTTCCCTTAGCCGTCTTACTCAACTGCCCCTT
TCCTCTCCCTCAGAAATTTGTGTTTGCTGCCTCTATCTTGTTTTTGTCTTTTCTTCTGGGGGGGGTCTAGAACAG
TGCCTGGCACATAGTAGGCGCTCAATAAAATACTTGTTTGTGAATGTCTCCTCTCTCTTCCACTCTGGGAAACC
TAGGTTTCTGCCATTCTGG

2177/6881
FIGURE 2001

MMAACDPRHGRYLTVAAVFHGRISMKEVDEQMLNVQNKSSYFVEWIPNNVKTAVCDIPPRGLKMAVTFIGNSSA
IQELFKRILEQFTAMFGRKAFLHWYTGE GMD

2178/6881
FIGURE 2002

ATGGCCCCCTGCACTGCTCCTGATCCCTGCTGCCCTCGCCTCTTTTCATCCTGGCCTTTGGCACCGGAGTGGAGTTC
GTGCGCTTTTACCTCCCTTCGGCCACTTCTTGAGGGGATCCCGGAGTCTGGTGGTCCGGATGCCCGCCAGGGATGG
CTGGCTGCCCTGCAGGACCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTTGTTGGG
CAGCACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCCTTCAGAGGTCACCTG
TATGTGGCCTGCACTGCCCTGGCCTTGACGCTGGTGATGCGGTACTGGGAGCCCATAACCCAAAGGCCCTGTGTTG
TGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCCTCCTCTGCTTTGTGCTCCATGTCATCTCCTGGCTC
CTCATCTTTAGCATCCTTCTCGTCTTTGACTATGCTGAGCTCATGGGCCTCAAACAGGTATACTACCATGTGCTG
GGGCTGGGCGAGCCTCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCCACCTGCGCCACCCAGTGTGT
GTGGAGCTGCTGACAGTGCTGTGGGTGGTGCTACCTGGGCACGGACCGTCTCCTCCTTGCTTTCCTCCTTACC
CTCTACCTGGGCCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCTCCGGGCCCAGCTACAAAGAAAATC
CACCTGCTCTCTCGGCCCCAGGATGGGGAGGCAGAGTGAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCCTCT
CCCGCTGAATTCTAAATCCTTAACATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAAATCCATGGACTGAAGG
AGATGCCCCCTTCTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCCTAAATTCTGAGTTTCAGCCACT
GAACTCCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCCTTCACTGTTTAGAGC
ATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCCCTGACCACTCCCCTGGCACTGTTACTTG
CCTCTGCGCCTCAGGGGTCCCCTTCTGCACCGCTGGCTTCCACTCCAAGAAGGTGGACCAGGGTCTGCAAGTTCA
ACGGTCATAGCTGTCCCTCCAGGCCCAACCTTGCTCACCCTCCCGGCCCTAGTCTCTGCACCTCCTTAGGCC
CTGCCTCTGGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAACTCGATGACTTGGGGCTCCCTGC
TCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAAAGTCAGCCTTTTTCTAC

2179/6881
FIGURE 2003

MAPALLLIPAAALASFILAFGTGVEFVRFTSLRPILLGGIPESGGPDARQGWLAAALQDRSILAPLAWDLGLLLLLFVG
QHSLMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGPVLWEARAEPWATWVPLLCFVLHVISWL
LIFSILLVFDYAELMGLKQVYYHVLGLGEPLALKSPRALRLFSLRHPVCVELLTVLWVVP TLGTDRLLLAFLLT
LYLGLAHGLDQQDLRYLRAQLQRKLHLLSRPQDGEAE

2180/6881
FIGURE 2004A

AGACAAAGCGGTGCGCGCCCCCGCGGCCCTGGTCTCTGTCTCCGTCCCTCCTCCTTTGCTGCCTCTTTCCC
TCCTCCTCTCCCTCCCTCCTCCCTCCCTCCAGTCTCCGATCTCCCTCGGTCCCTCTCTCCTCCTCTCCTCTC
TCTGGACGCGCGGCTCCTCCGCACCCCTCCCCGGGGTCCCGCGGCCTGTGAGTTGACTGAGGGGCTCAGACT
TGGGGAGTGGGTGTCTCCTCGCCCCGTGCTTGTCTCCGTCCCTGGCCCGGACCTTGGCTGTCTCCTCTTTGTGC
CGAGATTGTCACTCTGTGCGGCTACAGCGGGGTGGAGACGGCCGGCTCTGTACGGCTTCATGAGAGCGGGGACG
GGGCGCAGGACTTGCAGGCGCCGGGGAGAAGAGACATGGAGCCGGCCCTTGGCACTCTGGGGTCGCGTGGGGCAG
TCGGTGGGGGAGGCAGGCGGTGGTGACAGGACAGGGTGGGGGTGGACGCCAGGGTTCTGGGAACGCGCTGGCAGC
CCTGACGCCCCGGGTTCGAAAGTCTCGGGGGTGGGTATTTCCCCGACCCGCTCGGGGGCGGAGTGGGGGCGAG
AGGGGTGGGGGCTGGGGAGAGGCGTGGCCCCGAGCGGTGCTGGAAGCGGAGCCGGGACCTTTGGGGCCCGCGCTGA
GACGCGCCCCGGCTGTGCGCGCCGCTCCTTTCCCTCTTCCCTGGTTTCCCTTCTCCTCTAGACCTGTTGCTC
TCCGCCCCCTCCTTGCTCCTCCCAACACCCCTCAGGTCCCGTTCCTCCTGGTCTTTCAGGGATTCTGGTCTCT
CCTTCCACACTAGCCTCCTTGGGGTATCGCTGAGGCAGCCTGGCCTGCACCCAGGTTCCTTCAACCCCTGCCAC
ATTTCTCTCTTCTCCCTCACGCCAACTTTCTTTTCGCCCTTCTCTCTCTTTCTCACATCCTAGAGACGGTCTTT
AATACGCATTAACCTGTGCTGCCACATCTGGCTCCTGCCCTCATTGCCTCCAATCCGGACTCTTCTCTCACAT
CACCCCCACCACCCCAACTTGGGGCTCACAACCTTCTCTTCACTTTTTCCATTTCCCCAGTTCTCTGCCTTCCGTC
TTTCCCTCTGTCTCATCCTTAGCCCCCTCTGCCCTGCTTTGTGTCCCACCTCTCCCCCTCCACTTCTCTCCTCC
CACCTCAGTCTCACCCCCGGGCTGTCTCACTCTCTGGAGCCTCTCCTTCTCTGTCTGTCCCCAGTGCTCCCT
ACCCTCACCTCAAGACGACCATGGCCACCATCCCAGACTGGAAGCTACAGCTGCTAGCCCCGGCGCCGGCAGGAGG
AGGCGTCCGTTTCGAGGCCGAGAGAAAGCAGAACGGGAGCGCCTGTCCAGATGCCAGCCTGGAACGAGGGCTCC
TGGAGCGCCGCCGGGCCAAGCTTGGGGCTGTCCCTGGGGAGCCTAGCCCTGTGCTAGGGACTGTAGAGGCTGGAC
CTCCAGACCCGGATGAGTCTGCGGTCTTCTGGAGGCCATCGGGCCAGTGCACCAGAACCGATTCTATCCGGCAGG
AGCGGCAGCAGCAGCAGCAGCAACAACAACGAGTGAAGAGCTGCTAGCAGAGAGAAAGCCTGGGCCTCTGGAGG
CCCCGGAGCGGAGACCCAGCCCTGGGGAGATGCGGGATCAGAGCCCCAAGGGAAGAGAGTCAAGAGAAGAGAGAC
TAAGTCCGAGGGAGACCAGAGAGAGGAGGCTGGGGATAGGGGGAGCCCAAGAGTTGAGCCTGAGGCCTCTGGAGG
CTCGGGACTGGAGGCAAAGCCCAGGAGAGGTGGGAGACAGGAGCTCCCGACTGTGAGAGGCATGGAAATGGAGGC
TGAGTCTTGAGAACTCCAGAGCGGAGTCTGAGACTAGCAGAGTCTCGAGAGCAAAGCCCCAGGAGAAAAGAGG
TGGAAGTAGACTGAGCCAGGGGAATCTGCCTACCAGAAGTTGGGCCTGACAGAGGCCCATAAATGGAGACCTG
ACTCCAGAGAGTCTCAGGAACAGAGTTTGGTACAACCTGGAGGCAACAGAGTGGAGGCTGAGGTGAGGAGAAGAA
GACAAGACTACTCGGAAGAATGTGGGAGAAAAGAAGAGTGGCCAGTTCCAGGGGTAGCTCCAAAAGAGACTGCAG
AGCTGTCCGAGACCCTGACAAGGGAGGCCCAAGGCAACAGTTCCGCAGGAGTGGAGGCAGCAGAGCAGAGGCCTG
TGGAAGATGGCGAGAGGGGCATGAAGCCAACAGAAGGGTGGAAATGGACCCTGAACTCCGGGAAGGCTCGAGAAT
GGACACCCAGGGACATAGAGGCTCAAACTCAGAACTAGAACCTCCAGAGTCAGCAGAGAAGCTTCTGGAATCTC
CCGGTGTGGAGGCTGGAGAAGGGGAGGCTGAGAAGGAGGAGGCGGGGCTCAGGGCAGGCCTCTGAGAGCCCTGC
AGAACTGCTGCTCTGTGCCCTCCCCCTCCACCAGAGGACGCTGGGACTGGAGGCCTGAGACAGCAGGAAGAGG
AAGCAGTGGAGCTCCAGCCCCCACCACCAGCCCCCTGTGTCTCCCCACCCCCAGCCCCAACTGCCCCCCAACCTC
CTGGGGATCCCCCTCATGAGCCGCTGTTCTATGGGGTGAAGGCAGGGCCAGGGGTGGGGGCCCCCGCCGCAAGT
GACACACCTTCAACGCTCAACCCCCGGCGGTCTGTGCCCTGCGACCCAGCCACCCCAACCTCTCCAGCCACAG
TTGATGCTGCACTCCCGGGGCTGGGAAGAAGCGGTACCCAACCTGCCGAGGAGATCTTGGTTCTGGGGGGCTACC
TCCGTCTCAGCCGAGCTGCCTTGCCAAGGGGTCCCCGAAAGACACCACAAACAGCTTAAGATCTCCTTCAGCG
AGACAGCCCTGGAGACCAGTACCAATACCCCTCCGAGAGTTCCGTACTGGAGGAGCTGGGCCCGGAGCCTGAGG
TCCCCAGTGCCCCCAACCTCCAGCAGCCCCAACCCGACGACGAAGAGGATGAGGAAGAGCTGCTGCTGCTGCAGC
CAGAGCTCCAGGGCGGGCTGCGCACCAAGGCCCTGATTGTGGATGAGTCTGCGCGCGGTGACCATCTTCCAACA
TAGGGATATACCTCCCTCCTTCTTATAACTGAAGATCCTGGAGCCCGGAAGATTAGGGCAGACAGACCCTGATA
ATGAGCCTGGCAGGGAAGGGCAACCAACATCTTGTAACCTTGCTTTCCCCACCCTGTTTCTGGGGGCGAGGCCAAT
TGCCCAATTTCTACCCTAATCCAAAGTCCCTGGTGTGGGTGGGGTTAAACGTGCTGGTGCATCCTAGGTATCCA
AGAGTGAGCGCCAAGTCTGAGAAGGGGCACAGAACTCCCTGGAGGGTGGAGATGGAGCACCTGCCCCCATGGC
AGGGTACACTCTCCCCACAGCCTTCTCCCCACCATCCCGTGGGGACTCTCGGGATTTAAGCACTCGTCTCTCTG
GGAGGCCAGACCCCACTCCATTTATAGGCACATCTCCTTCACTTCTTAGGTCACTGCCCTTTGTTTACAGCTC

2181/6881
FIGURE 2004B

CTGCCTCCTCCCTTGACCACAGCCTGGTTTACAAATTCCATCAGCTCCCAGCCCCACCTGCCAAAAGTCCCAGGTT
TACAAGCCACGCTTACTTGCTGTGTCTGCGTGGAATTCTCTCCTCTGICCCCTCCAGTCTCCTCATTGGAGTGAC
CTGAAGGTGTGGCTTCCTCCACTTTTTCTCAGTATTACTTTGCCTTAGTTTTCCCAAGAGGGAAGGCTGGAAC
CTTAACTCTGTACCCCTTGATAGTTATTTAATTCTGTTTCTCCTAGTGGTTCACAATTGAACTGAATTGAGATGG
TGTCGGGTGGCTAAGGAGACACCTCACCTCTCCTTCCCCATTGTGCCGCCTTTATCAATTGCCTGTTTGTGTTTG
TTTGTTTTTTAACTTTCATAATAAAATGGAGTTCTCTTC

2182/6881
FIGURE 2005

MATIPDWKLQLLARRRQEEASVRGREKAERERLSQMPAWKRGLLERRRAKLGLSPGEPSPVLGTVEAGPPDPDES
AVLLEAIGPVHQNRFIQERQQQQQQQORSEELLAERKPGPLEARERRPSPGEMRDQSPKGRESREERLSPRETR
ERRLGIGGAQELSLRPLEARDWRQSPGEVGDSSRLSEAWKWRLSPGETPERSLRLAESREQSPRRKEVESRLSP
GESAYQKLGLTEAHKWRPDSRESQEQSLVQLEATEWRLRSGEERQDYSEECGRKEEWPVPGVAPKETAESETLT
REAQGNSSAGVEAAEQRPVEDGERGMKPTEGWKWTLSNGKAREWTPRDIEAQTQKLEPPESAEEKLLESPGVEAGE
GEAEKEEAGAQRPLRALQNCCSVPSPLPPEDAGTGGLRQQEEEAVELQPPPPAPLSPPPPAPTAPQPPGDPILMS
RLFYGVKAGPGVGAPRRSGHTFTVNPRRSVPPATPATPTSPATVDAAVPGAGKKRYPTAEELVLGGYLRLSRSC
LAKGSPERHHKQLKISFSETALETYYQYPSESSVLEELGPEPEVPSAPNPPAAQPDDEEDEEELLLLQFELQGGI
RTKALIVDESCRR

2183/6881
FIGURE 2006A

AGGTTTGAATTTTCTCGGAGAAAGACAGGCCGGCCACGAGGAAACAGAAACAAGCCGCAGCAACATCTAAGCCC
TTGAAAGGATCCTGAGAGAGGGGGGAAAGGGAAACAGCAGCCACCAGCCCAACCACTTGTGTCTTCTGCCCTT
CCCACCTATCTTGCCACCCCAACAGCCACGCTGCTTGGGACTTGAAATCTGTGGCCGAAGGACCGTCACTACA
TAACCTTCAAAAATAATCAACCACCTCCCTTCCCAAACCACCCAAATTCATCTATCCAGCGTTTACTTTTTTGAA
TCCACTCAGAACTTTTTTCTGCGACCCCCCTCCCTAAATGGAGTTGGGTGGGGGGGAAATGAATACTGAGTTGGC
CTTTATTTTTTAAAAGACTTTTTGATCCAATGAGGCCCTTAAATAATTGAGTTTTGGGTCTCGTTGGTTGTTT
TATTTTTTTTCTCCAAAATTTTACCCCTCCCTTCCCTGAGCCCGAGGTGCTGACGTCGCAAAAAAATTGGATAAA
ACCACCATCATGGGTTCGGGTCCCATAGACCCCAAAGAACTTCTCAAGGGCCTGGACAGCTTCCTTAACCGAGAT
GGGGAAGTCAAAAGTGTGGATGGGATTTCCAAGATCTTCAGTTTGATGAAGGAAGCACGAAAGATGGTGAGTCGA
TGCACCTACTTGAACATTCTCTGCGACCCGTTTACCAGAAATATTGGTCAAATTTATTGACGTTGGCGGCTAC
AACTTCTTAACAATTGGCTGACGTATTCAAAGACAACCAACAACATTCCCTCCTCCAGCAAATCTACTGACC
CTGCAGCATCTACCGCTCACTGTAGACCATCTCAAGCAGAACAACACAGCTAAACTGGTGAAGCAGCTGAGCAAG
TCAAGTGAGGATGAAGAGCTCCGGAAATTGGCCTCAGTCTTGTGACGCGACTGGATGGCTGTCTCCGCTCTCAG
AGCAGTACCCAGCCTGCTGAGAAAAGATAAGAAGAAACGTAAAGATGAAGGAAAAAGTCAACTACCTTCTGAG
CGACCTTTGACAGAGGTGAAGGCTGAGACCCGGGCTGAGGAGGCCCCAGAGAAGAAGAGGGAGAAGCCCAAGTCT
CTTCGCACCACAGCACCCAGTCATGCCAAGTTCCGTTTCCACTGGACTAGAGCTGGAGACACCATCCTTGGTGCT
GTGAAGAAGAATGCCAGCACAGTGGTGGTTTCTGACAAGTACAACCTTAAACCCATCCCCCTCAAACGTCAGAGC
AACGTAGCTGCTCCAGGAGATGCCACTCCCTTGCAGAGAAGAAATACAAGCCACTCAACACAACACCTAATGCC
ACCAAAGAGATCAAAGTGAAGATCATCCCGCCACAGCCTATGGAGGGCCTGGGCTTTCTGGATGCTCTTAATTCA
GCCCCGTGTTCCAGGCATCAAAATTAAGAAGAAAAAAAAGTACTGTACCTACGGCTGCCAAGCCAAGCCCCCTT
GAAGGGAAAACGAGCACAGAACCAAGCACAGCCAAACCTTCTTCCCCAGAACCAGCACACCTTCTGAGGCAATG
GACGCAGACCGTCCAGGCACCCCGGTTCCCTTGTGAAGTCCCGGAGCTCATGGATACAGCCTCTTTGGAGCCA
GGAGCTCTGGATGCCAAGCCAGTGGAGAGTCTGGAGATCTTAACCAACTGACCCGAAAGGCAGGAAGAGGAAA
AGTGTGACATGGCCTGAGGAAGGCAAACCTGAGAGAATATTTCTATTTTGAATTGGATGAACTGAACGAGTAAAT
GTGAATAAGATCAAGGACTTTGGTGAGGCCGCTAAGCGAGAGATACTGTGACACCGACATGCATTTGAGACAGCG
CGGCGTCTGAGCCATGATAACATGGAGGAGAAGGTGCCCTGGGTGTGCCCCGGCCCCCTGGTTCTGCCCTCACCT
CTTGTACCCCTGGAAGCAATAGTCAGGAGCGATATATCCAGGCTGAGCGGGAGAAGGGAATCCTTCAGGAGCTC
TTCCTGAACAAGGAGAGTCTCATGAGCCTGATCTGAGCCCTACGAGCCCATACCCCTTAACTCATCCCCCTA
GATGAGGAGTGTTCATGGATGAGACTCCGTATGTTGAGACTCTGGAACCTGGGGGGTCAGGTGGCTCACCTGAT
GGGGCAGGAGGCTCCAAGTTGCCTCCAGTTCTGGCCAATCTTATGGGAAGCATGGGTGCTGGAAAGGGCCCCCAA
GGCCCTGGAGGAGGAGGCATTAATGTCCAAGAGATCTCACCTCCATCATGGGTAGCCCAAACAGTCATCCTTCA
GAGGAATACTGAAACAACAGACTATTTCGACAAGATCAAGCAGATGCTGGTGCCACATGGACTCCTAGGCCCT
GGCCCAATAGCCAATGGTTTTCCACCAGGGGGTCTGGGGGGCCCCAAGGGCATGCAGCACTTTCCCCCTGGACCT
GGGGGACCTATGCCAGGTCCCCATGGAGGCCCTGGTGGGCCAGTGGGTCCACGTCTTCTGGGTCTCCACCCCT
CCCCGGGGAGGTGATCCCTTCTGGGATGGCCCGGGCGACCCTATGCGGGGTGGCCCAATGCGGGGGGTCCAGGA
CCAGGTCCTGGACCATAACCATAGAGGCCGAGGTGGCCGAGGAGGAAACGAACCTCCTCCTCCTCCTCCTCCATTC
CGAGGCGCCAGAGGAGGTCGCTCTGGAGGAGGACCCCCAAATGGACGAGGGGGCCCTGGTGGGGGCATGGTTGGA
GGTGGTGGGCATCGTCCTCACGAAGGCCCTGGTGGGGGCATGGGCAACAGCAGTGGACATCGTCCCCACGAAGGC
CCTGGCGGTGGCATGGGAAGTGGGCATCGCCCCATGAAGGCCCTGGTGGTAGCATGGGTGGGGGTGGAGGACAT
CGTCCCCACGAAGGCCCTGGCGGTGGCATCAGTGGTGGCAGTGGCCATCGTCCCCATGAAGGCCCTGGCGGAGGA
ATGGGTGCCGGTGGTGGACATCGCCCCACGAAGGCCCTGGCGGAAGCATGGGTGGAAGTGGTGGACATCGTCCC
CATGAAGGCCCTGGACACGGGGGGCCCCATGGCCACCGGCCTCATGATGTCCCTGGTCACCGAGGCCATGACCAT
CGAGGGCCGCCACCTCATGAGCACCGTGGCCATGATGGTCTGGCCACGGGGGAGGGGGCCACCGAGGGCACGAT
GGAGGCCACAGCCATGGAGGAGACATGTCAAACCGCCCTGTCTGCCGACATTTTATGATGAAGGGCAACTGCCGC
TATGAGAACAACCTGTGCCCTTCTACCACCGGGTGTCAATGGGCCCCCTGCCCTAGGGACCATTGCTGCCCT
GTTACACAACCCCTGTGGACTGCAGCCTCGCTCTTTCCACCCTGTTATGGCTTCTGTGAGGCCCATTTCCTT
TTCCCAGCTGATGAGGAGCCGGCCCCCTCAGTTCCCACTTGCTTGGGTTCCTGGGGGTTTTCTGATCACTGGTG
CGCATTGATGTACATATTTTCTCCAGTCTGGGGAGGAGAGAGACTGGAAACGTTTCTGGACTGCTGAAGAGGAG

2184/6881
FIGURE 2006B

ACCCAGTTGGCTTCACTTTTTGAGAAGATTGCGCCCTGTACCCCAAACCCCTTTCCAGTATTACCCTTAATGCTTG
AGAACCTAAAGCTGGTTATCCTGGCGAACACCCCTACCCTTCTATTGCGGGTCCCCACATGCACACAGAACTCTG
ACACAGGATCAGCTGCACTTAAGAAATCATCCCAACTAAGTTCATTATTCTCATGGGGTGGGGAGATGCTGAAA
GGGGTATTGTATATCCCACTGCACTGAGAGGGCTCAATCAGCTGGATTTGAGTTCTGGAACACACATCATCCCA
CCCCCTCCCCCAGCGTGGGCTCACCATTCTTAGTCCTTTCTCAAGTGGGACCTTCAACTTTCTGTGAACACCCAGT
CTGCGTCCTGGGTCTGCTAGGTTTCGATGATGGCGAACTCGTATCTGCATCCGGTGCAAGTTTTAGCTGGCAGAGG
TGAGACCGGTGGTGTGCTGGTCTGCCTTTGCCAACTATAGCCAGTCTGGAGACTTGATAAAATACTTCAGTGAGACC
AGCTTCTCATCAACTTGGGCCCGGCGTGCTGGGCCTGAAAGTCACACTACATGCACTGCCTTTGGGAGTCAGCTC
ACTCCCTGCTCCACCTGGAACCTTGCCAGCGTGAAGGAGGCTTCAGGTACTTCACCCGTGCAACCACCTCTGA
ATCCCCACCAGGCGCCTTCCTGGGTGGATTCAACAAGATGATTTTGCCCTTTCCAGTTCTCTCCTTCACTTTGG
CATCAGTTGTTTTCTATGAAAACAGTGGATTGGTTGGGTTTTGTGCAGGGTCTTGGGTAGAGCCAAAATGGATT
TGAGGATGAGTATTTTTTTTTTTGGTTTTGTATATTTGTACATTAATAATAAACAGTGGAAAGAGAAGCAGCTT

2185/6881
FIGURE 2007

AACCCAAGCGGGACAAGGACTTTTGGGGGGAGGTCAAAGGGCACGAAGTTGTGCCTACAGCTGTTACCATAGTAA
CCGAGGACCGGATGTGGCGATCTTGGCGGTGCGACAGTCCTCTTCTCAGGCCCTCTGGCCCCGAGAGCCTGTTGAC
TCTGTGACACACTCTGAGGAGCTGGTTGTGGTGTTCAGCGAGGGAAGAAAAGAGTAATTTTTTCAAAGCATT
TATAGAAACGCAGCAAAGGGAAGGTGTGAGGTTGCCGCCATGCCTGGCAGAACGGAGGGAGGCAGTTGGCTCCGG
AATGCGGCCCGCCGAGATGTTCTCCGCAACCTTCCGGAAGTGGAATGGCGGGAGCCTCAGCATTGCTGCCCACCG
ACCCCCCGGAAGCGGAAACAGAATCCCCGCGTGCCCTTCTCTACTACCTTCCAAATCCCGCTGCAGCCATTGCC
GCAGACACGATGCCGAAACGAAAGAAGCAGAATCATCACCAGCCACCGACACAGCAGCAGCCCCGCTGCCCGAG
CGGGAAGAGACTGGAGATGAGGAGGATGGGAGTCCCATCGGACCACCCAGCCTTCTGGGCCCTCCCCCATGGCC
AATGGAAACCTGGCGACCCTAAGTCAGCTCTTACAGAGGTCCTCCAGGATCAAGGGGACCACTGATTCCACCA
CTGCTGAGTCTCCACCTCCTCCTTGGGGTAGAGGCCCAATTTCGAGAGGGGCTTGCCCCAGGTCTAGCCCATAT
GGTCGTGGTTGGTGGGGAGTCAATGCAGAACCTCCTTTTCCGGGGCCAGGCCATGGGGGTCCCACCAGGGGAAGC
TTTCAACAAGGAACAGAGAAACCTCGAAGGCTCAAAGCTGGTCTCTTATCAAGAATACCTGCCCCGCCAAGGAT
GACCCCCAGGTTATGGAAGACAAAATCCGACCGCCCTGTCTGCCGACATTTTGCCAAAAAGGGCCACTGTGATAT
GAGGACCTCTGTGCCTTCTACCATCCAGGCGTCAATGGACCTCCTCTGTGAGACTGTGCCTTCCCATCCAGGCTG
GAAGGAGCTCTCTGTGACCTAGCGGCCATTTATTTCTCTGTAGCCCTATGATGGCTACTGTGAGGCTCTTCTAAC
ACCCTCAGTCAGTGACACACCCATCCCATCCACCACCTCCCCCGTGTGGGGTCCAGAGTGGTGTTGCATCACTGG
TGCGCGGCATACGCGCTTTCTTCTGATCCAGCCTGTAGAGACTCGCCTTTGGGACCCATCTTTGCTTCCTTTAG
TTGCCCTCCTGGATCTTCTTTCCCGTCATCAAATGACTGCTGAACAGGAAACCTCTTTGGTGCTGTTTCTTGTGCA
TCTGTCCACCTGTTCCCCAGTATTGCCCTCAATTCCCTGAGAGCCCTGGAGCGGTTTCCCTACCATTCCCTTCTTTT
AGCTGCTTGTTTTAAGTCCTTTTATGTGACATTCCCTACCCCAATGTTGTCAGCTGCTTGTGAAACTCAGCCA
GGTTGTCTAACCTGGGGTCAAGTTTGGGTGACTGGTGCAGAGTTACTTCCTAAAAGGCCACTCTCCCTGCCTTTG
GATTTCATAGTTTCTCTGTGACGATGATCCCCACCGCTATGGTCTATCTATGATCACCGTGCTTTGTGAAAC
TGTGCATCCCCTTGTAGCCTTTCTCAGTGTCCGTGGCATTGTTGTGACTTCCCAGCACTAGAATAAGTTTTCTTG
CCAAAATGAGTGAGGCGCTTGGTGCCCTCTGGACTTTCCCACTTCCCAACATGGGAGAATTGTGAACTTTCCATC
AGACTGCCTCCCTGGCCCTCCCCATTCTTCTCCTGTTGGTTATTCTGAGTCTGACACAGACCCATGACATGTCTT
ATAAAGCCTCCAATGGCTTTATCCTACCTAGATCCCTTCCAGCCCATTTAATTAGACTATGTCATTGTGAGGCC
ACCAGTCCATTCAATTTGAATCTGTGAATCTCCACCTTGCTATCTTTGGGTAGAAGCTGGACAGTACTGTTGCC
CTCTTCCAATCCTCTTCCCCTACATCCCTGGCACTGGTTGTTTTCTGTGAAAACAGCAGTGAACAGGTTTCACTTT
TGAACCTGGCCCTGAGGAAATGGGTCAGGAGTTGTATTGGCAAGAGGGAGGGGTGAGAGCTGTTGGAGAACTGAGA
ATGAGGTTTTTTTTTTTTTTTTTCTTTTTTAACTTTTTTTATATTAGTAATAAATGCAGTGGAACCAGCATTTTAT
TTAAAAAAA

2186/6881
FIGURE 2008

MPGRTEGGSWLRNAAAADVLRNLPEVEWREPQHCCPPTPRKRKQNPVPLPHYPPNPAAAIAADTMPKRKKQNH
QPPTQQQPPLPEREETGDEEDGSPIGPPSLLGPPPMANGKPGDPKSALHRGPPGSRGPLIPLLSLPPPPWGRGP
IRRGLGPRSSPYGRGWGVNAEPPFPGPGHGGPTRGSFHKEQRNPRRLKSWSLIKNTCPKDDFQVMEDKSDRPV
CRHFAKKGHCRYEDLCAFYHPGVNGPPL

2187/6881
FIGURE 2009

GGGAGCTCGGCGGAGGGCGGGCCAGGTGACTGGTCCGGGGCCATGCCGAGGAAGAAGCCATTACAGCGTGAAGCAGA
AGAAGAAGCAGTTGCAGGACAAACGGGAGCGGAAGAGAGGGCTTCAAGATGGGCTGCGCTCCAGTTCCAACAGCC
GCAGCGGGAGCCGGGAGCGGCGAGAGGAACAGACCGACACCTCGGACGGGGAGTCTGTGACCCATCATATCCGCA
GGCTTAACCAGCAGCCTTCTCAGGGGCTGGGTCCACGAGGCTACGACCCAAATCGATACCGACTGCATTTTGAGA
GAGACAGCAGGGAGGAGGTAGAGAGGAGAAAGAGAGCAGCCCGGGAGCAAGTTCTACAGCCGGTCAGTGCTGAGT
TGTTGGAGCTGGACATCCGGGAGGTGTATCAGCCTGGCTCAGTTCTGGACTTTCCCTCGACGTCCTCCTTGAGCT
ATGAGATGTCCAAGGAGCAACTAATGAGCCAAGAGGAACGGAGCTTCCAAGACTATCTTGGAAGATTTCATGGGG
CTTACTCCTCTGAGAACTCAGCTACTTTGAGCACAATCTGGAGACATGGAGGCAGCTGTGGCGGGTGTAGAGA
TGTCTGACATCGTCCTGCTTATCACTGATATCCGACATCCAGTTGTGAATTTCCCGCCAGCACTTTATGAGTATG
TGACTGGAGAACTTGGAAGTGGCCCTGGTGTCTGGTTTGAACAAGGTGGATCTGGCCCCGCCAGCTCTTGTGGTTG
CCTGGAAGCATTATTTCCATCAACACTATCCCCAGCTCCACGTCGTCCTTTTACCTCTTTTCCCTCGGGACCCCC
GCACCCACAGGATCCTAGTAGTGTCTTGAAGAAGAGTCCGAGGCGGGGAGAGGATGGACTCGGGCCCTGGGGC
CAGAGCAGTTGCTGAGAGCCTGTGAAGCCATCACTGTGGGGAAGTGGACTTGAGCAGCTGGCGGGAGAAGATTG
CTCGGGATGTGGCTGGGGCCACCTGGGGTAATGGCTCTGGGGAGGAGGAGGAAGAGGAGGATGGCCCAGCAGTCC
TGGTGGAGCAGCAGACTGATTACAGCAATGGAGCCAACTGGCCCAACCCAAGAGCGCTACAAGGATGGGGTGGTGA
CCATCGGCTGTGTGGGTTTCCCTAATGTGGGAAAGTCCTCGCTGATCAATGGGCTGGTGGGGCGGAAAGTCGTGA
GTGTCTCCAGAACCCCGGGCCATACCCGATACTTTTACAGCCTACTTTTCTTACCCCCCTCTGTGAAGCTCTGTGACT
GCCCAGGCCTCATCTTCCCATCTCTTCTGCCTAGGCAGTTGCAGGTTCTGGCAGGGATCTACCCTATCGCCCAGA
TCCAGGAGCCCTACACTGCTGTGGGCTACCTGGCCTCCCGAATTCCCGTGCAGGCCCTGCTCCACCTGCGCCACC
CAGAGGCTGAGGACCCCTCAGCGGAACACCCCTGGTGTGCCTGGGACATCTGTGAAGCCTGGGCAGAGAAACGTG
GTTACAAGACAGCCAAGGCGGCTCGGAATGATGTGTACAGAGCAGCCAACAGTCTCTTGCGGCTGGCAGTGGACG
GCCGCCTCAGCCTGTGTTTTTATCCCCAGGCTACAGTGAACAGAAAGGCACCTGGGAGTCCCATCCAGAGACCA
CGGAGCTGGTGGTTTTTGCAGGGCAGGGTGGGGCCAGCAGGTGACGAGGAGGAGGAGGAAGAGGAAGAGCTGAGCA
GCTCCTGTGAGGAGGAGGGAGAGGAGGACCGGGATGCGGATGAGGAGGGAGAAGGGGATGAGGAGACCCCAACCT
CGGCTCCAGGGTCCAGCCTGGCTGGCCGAAACCCCTTATGCCCTGCTGGGTGAGGATGAGTGCTGAGTTCCTCGCC
CAGCGCCATCTTCCCTCCCAGTATCTTTGCTTTTGGACTGACCTGGGGGTATCTCCCCTCTGCCACCCCAATTGT
GAATAAAGATTGTTTGCTTTGTAGCCCTTCCCCAGATGAAGTGAAGTGAAGAGCGGCTGTTCCAGGCTAACAGCT
GTGGGAGGCTTCTCTCCTCTTCTCCCTTCTTTTTT

2188/6881
FIGURE 2010

MPRKKPF SVKQKKKQLQDKRERKRGLQDGLRSSSNSRSGSRERREEQTDTSDGESVTHHIRRLNQQPSQGLGPRG
YDPNRYRLHFERDSREEVERRKRAAREQVLQPVSAELLELDIREVYQPGSVLDFPRPPWSYEMSKEQLMSQEER
SFQDYLGKIHGAYSSEKLSYFEHNLETWRQLWRVLEMSDIVLLITDIRHPVVNFPPALYEYVTGELGLALVLVLN
KVDLAPPALVVAWKHYFHQHYPLHVVLFTSFPRDPRTQPDPSSVLKKSRRRGRGWTRALGPEQLLRACEAITVG
KVDLSSWREKIARDVAGATWGNGSGEEEEEEEDGPAVLVEQQTDSAMEPTGPTQERYKDG VVTIGCVGF PNVGKSS
LINGLVGRKVVSVSRTPGHTRYFQTYFLTPSVKLCDCPGLIFPSLLPRQLQVLAGIYPIAQIQEPYTAVGYLASR
IPVQALLHLRHPEAEDPSAEHPWCAWDICEAWAEKRGYKTAKAARNDEVYRAANSLRLAVDGRLSLCFHPPGYSE
QKGTWESHPETTTELVLVQGRVGPAGDEEEEEEEELSSSCEEEGEEDRDADEEGEGDEETPT SAPGSSLAGRNPYA
LLGEDEC

2189/6881
FIGURE 2011

GGGATCATGGTAGATGGAACCCTCCTTTTACTCCTCTCGGAGGCCCTGGCCCTTACCCAGACCTGGGCGGGCTCC
CACTCCTTGAAGTATTTCCACACTTCCGTGTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCTCTGTGGGCTAC
GTGGACGACACCCAGTTTCGTGCGCTTCGACAACGACGCCGCGAGTCCGAGGATGGTGCCGCGGGCGCCGTGGATG
GAGCAGGAGGGGTCAGAGTATTGGGACCGGGAGACACGGAGCGCCAGGGACACCGCACAGATTTTCCGAGTGAAC
CTGCGGACGCTGCGCGGCTACTACAATCAGAGCGAGGCCGGGTCTCACACCCTGCAGTGGATGCATGGCTGCGAG
CTGGGGCCCCGACAGGCGCTTCCCTCCGCGGGTATGAACAGTTTCGCCTACGACGGCAAGGATTATCTCACCCCTGAAT
GAGGACCTGCGCTCCTGGACCGCGGTGGACACGGCGGCTCAGATCTCCGAGCAAAAGTCAAATGATGCCCTCTGAG
GCGGAGCACCAGAGAGCCTACCTGGAAGACACATGCGTGGAGTGGCTCCACAAATACCTGGAGAAGGGGAAGGAG
ACGCTGCTTACCTGGAGCCCCCAAAGACACACGTGACTCACCACCCCATCTCTGACCATGAGGCCACCCTGAGG
TGCTGGGGCCCTGGGCTTCTACCCTGCGGAGATCACACTGACCTGGCAGCAGGATGGGGAGGGCCATACCCAGGAC
ACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCAGCTGTGGTGGTGCCTTCTGGA
GAGGAGCAGAGATACACGTGCCATGTGCAGCATGAGGGGCTACCCGAGCCCGTCACCCTGAGATGGAAGCCGGCT
TCCCAGCCCACCATCCCCATCGTGGGCATCATTGCTGGCCTGGTTCTCCTTGGATCTGTGGTCTCTGGAGCTGTG
GTTGCTGCTGTGATATGGAGGAAGAAGAGCTCAGGTGGAAGGAGGGAGCTACTCTAAGGCTGAGTGGAGCGAC
AGTGCCCAGGGGTCTGAGTCTCACAGCTTGTAAAGCCTGAGACAGCTGCCTTGTGTGCGACTGAGATGCACAGCT
GCCTTGTGTGCGACTGAGATGCAGGATTTCCCTCACGCCTCCCCTATGTGTCTTAGGGGACTCTGGCTTCTCTTTT
TGCAGGGGCTCTGAATCTGTCTGTGTCCCTGTTAGCACAAATGTGAGGAGGTAGAGAAACAGTCCACCTCTGTGT
CTACCATGACCCCTTCCCTCACACTGACCTGTGTTCCCTGTTCTCTTTTCTATTAAAAATAAGAACCTGGG
CAGAGTGCGGCAGCTCATGCCTGTAATCCCAGCACTTAGGGAGGCCGAGGAGGGCAGATCACGAGGTCAGGAGAT
CGAAACCATCCTGGCTAACACGGTGAACCCCGTCTCTACTAAAAAATACAAAAAATTAGCTGGGCGCAGAGGCA
CGGGCCTGTAGTCCCAGCTACTCAGGAGGCGGAGGCAGGAGAATGGCGTCAACCCGGGAGGCGGAGGTTGCAGTG
AGCCAGGATTGTGCGACTGCACTCCAGCCTGGGTGACAGGGTGAAACGCCATCTCAAAAAATAAAAAATAAAAA
TAAAAAAGAACC

2190/6881
FIGURE 2012

MVDGTL L L L L L S E A L A L T Q T W A G S H S L K Y F H T S V S R P G R G E P R F I S V G Y V D D T Q F V R F D N D A A S P R M V P R A P W M E Q
E G S E Y W D R E T R S A R D T A Q I F R V N L R T L R G Y Y N Q S E A G S H T L Q W M H G C E L G P D R R F L R G Y E Q F A Y D G K D Y L T L N E D
L R S W T A V D T A A Q I S E Q K S N D A S E A E H Q R A Y L E D T C V E W L H K Y L E K G K E T L L H L E P P K T H V T H H P I S D H E A T L R C W
A L G F Y P A E I T L T W Q Q D G E G H T Q D T E L V E T R P A G D G T F Q K W A A V V P S G E E Q R Y T C H V Q H E G L P E P V T L R W K P A S Q
P T I P I V G I I A G L V L L G S V V S G A V V A A V I W R K K S S G G K G G S Y S K A E W S D S A Q G S E S H S L

2191/6881
FIGURE 2013

CCTGAGTCAGACGGGCATGGAGACGCTTCTGGAAGGAACACCGCA**ATG**GCTGCGCAGGGACAGCCCCAGGTCCAG
TTCAAACCTTGATTGGTTGGTGATGGTGGTACTGGAAAAACGACTTTCGTGAAACATCATTTGACTGGTGAATTT
GAGAAGAAGTATGTAGCCACCTTGGGTGTTGAGGTTTCATCCCCTAGTGTTCCATACCAACAGAGGACCTGTAAAG
TTCAATGTATGGGACACAGCCGGCCTGGAGAAATTCAGTGGACTGAGAGATGGCTATTATATCCAAGCCCAGAGT
ACCATCATAGTGTTTGATGTAACATCGAGAGTTACTTACAAGAATGTGCCTAACTGGCATAGAGATCTGGTATGA
GTGTGTGAAAACACCCCCACTGTGTTGAGTGGCAACAAAGTGGATATTAAGGACAGGAAAGTGAAGGCGAAATCC
ATTGCTCTCCACCGAAAGAAGAATCTTCAGTACTACGACATTTCTGCCAAAAGTAACTATAACTTTGAAAAGCCC
TTCCTCTGGCTTGCTAGGAAGCTCATTGGAGACCCTAACTTGAATTTGTTGCCATGCCTGCTCTCGCCCCACCA
GAAGTTGTCATGGACCCAGCTTTGGCAGCACAGTATGAGCAGACTTAGAGGTTGCTCAGACAACCTGCTCTCCCG
GACGAGGATGATGACCTG**TGAGA**ATGAAGCTGGAGCCCAGCGTCAGAAGTCTAGTTTTATAGGCAGCTGTCCTGT
GATGTCAGTTGTGCAGCGTGTGTGCCACCTCATTATTATCTAGCTAAGCGGAACATGTGCTTCATCTGTGGGATG
CTGAAGGAGATGAGTGGGCTTCGCAGTGAATGTGGCAGTTCAAAAAATACCTTCATTGTTTGGACCTGCATATTT
AGCTGTTTTGGAACACAGTTGATTCCCTTGAGTTTCAAATATAGACTGCTACAGTCACATCACAATATTACGCGGT
GAAATCTTGTTTGTTACTGTCATTCCCATTCCTTTTCGTTTAGAATCAGAATAAAGTTGTATTTCAAATATCTAA

2192/6881
FIGURE 2014

MAAQGGPQVQFKLVLVGDGGTGKTTFVKHHLTGEFEKKYVATLGVEVHPLVFHTNRGPVKFNVWDTAGLEKFSGL
RDGYIQAQSTIIIVFDVTSRVTYKNVPNWHRDLVEVCENTPTVLSGNKVDIKDRKVKAKSIVFHRKKNLQYYDIS
AKSNYNFEKPFLLWARKLIGDPNLEFVAMPALAPPEVMDPALAAQYEHDLVAQTTALPDEDDDL

2193/6881
FIGURE 2015

GGAGACGCTTCTGGAAGGAACACCGCAATGGCTGCGCAGGGACAGCCCCAGGTCCAGTTCAAACCTTGTATTGGTT
GGTGATGGTGGTACTGGAAAAACGACTTTTCGTGAAACATCATTGACTGGTGAATTTGAGAAGAAGTATGTAGCC
ACCTTGGGTGTTGAGGTTTCATCCCCTAGTGTTCCATACCAACAGAGGACCTGTTAAGTTCAATGTATGGGACACA
GCCGGCCTGGAGAAATTCAGTGGACTGAGAGATGGCTATTATATCCAAGCCCAGAGTACCATCATAGTGTGTTGAT
GTAACATCGAGAGTTACTTACAAGAATGTGCCTAACTGGCATAGAGATCTGGTATGAGTGTGTGAAAACACCCCC
ACTGTGTTGAGTGGCAACAAAGTGGATATTAAGGACAGGAAAGTGAAGGCGAAATCCATTGTCTTCCACCGAAAG
AAGAATCTTCAGTACTACGACATTTCTGCCAAAAGTAACTATAACTTTGTTGTTGCCATGCCTGCTCTCGCCCCA
CCAGAAGTTGTCATGGACCCAGCTTTGGCAGCACAGTATGAGCACGACTTAGAGGTTGCTCAGACAACTGCTCTC
CCGACGAGGATGATGACCTGTGAGAATGAAGCTGGAGCCCAGCGTCAGAAGTCTAGTTTTATAGGCAGCTGTCC
TGTA

2194/6881
FIGURE 2016

CCCCAGACGCCGAGGATGGCCGTCATGGCGCCCCGAACCTCCTCCTGCTACTCTCGGGGGCCCTGGCCCTGACC
CAGACCTGGGCGGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGGCCGCGGGGAGCCCCGC
TTCATCGCCGTGGGCTACGTGGACGACACGCAGTTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAG
CCGCGGGCGCCGTGGATAGAGCAGGAGGGGGCCGGAGTATTGGGACCAGGAGACACGGAATGTGAAGGCCAGTCA
CAGACTGACCGAGTGGACCTGGGGACCTGCGCGGCTACTACAACCAGAGCGAGGCCGGTTCTCACACCATCCAG
ATAATGTATGGCTGCGACGTGGGGTCGGACGGGCGCTTCCTCCGCGGGTACCGGCAGGACGCCCTACGACGGCAAG
GATTACATCGCCCTGAACGAGGACCTGCGCTCTTGGACCGCGGCGGACATGGCGGCTCAGATCACCAAGCGCAAG
TGGGAGGCGGCCCATGAGGCGGAGCAGTTGAGAGCCTACCTGGATGGCACGTGCGTGGAGTGGCTCCGCAGATAC
CTGGAGAACGGGAAGGAGACGCTGCAGCGCACGGACCCCCCAAGACACATATGACCCACCACCCCATCTCTGAC
CATGAGGCCACCTGAGGTGCTGGGCCCTGGGCTTCTACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGG
GAGGACCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCT
GTGGTGGTGCCTTCTGGAGAGGAGCAGAGATACACCTGCCATGTGCAGCATGAGGGTCTGCCCAAGCCCCTCACC
CTGAGATGGGAGCTGTCTTCCCAGCCCACCATCCCCATCGTGGGCATCATTGCTGGCCTGGTTCTCCTTGGAGCT
GTGATCACTGGAGCTGTGGTCGCTGCCGTGATGTGGAGGAGGAAGAGCTCAGATAGAAAAGGAGGGAGTTACACT
CAGGCTGCAAGCAGTGACAGTGCCAGGGCTCTGATGTGTCCCTCACAGCTTGTAAGTGTGAGACAGCTGCCTT
GTGTGGGACTGAGAGGCAAGAGTTGTTCCCTGCCCTTCCCTTGTGACTTGAAGAACCCTGACTTTGTTTCTGCAA
AGGCACCTGCATGTGTCTGTGTTTCGTGTAGGCATAATGTGAGGAGGTGGGGAGACCACCCACCCCATGTCCAC
CATGACCCTCTTCCACGCTGACCTGTGCTCCCTCCCCAATCATCTTTCTGTTCCAGAGAGGTGGGGCTGAGGT
GTCTCCATCTCTGTCTCAACTTCATGGTGCACCTGAGCTGTAACCTTCTTCCCTTCCCTATTAAATTAGAACCTTAG
TATAAATTTACTTTCTCAAATTCCTTGCCATGAGAGGTTGATGAGTTAATTAAAGGAGAAGATTCCTAAATTTGA
GAGACAAAATAAATGGAAGACATGAGAAC

2195/6881
FIGURE 2017

ATGGCGCCCCGAAGCCTCCTCCTGCTGCTCTCAGGGGCCCTGGCCCTGACCGATACTTGGGCGGGCTCCCACTCC
TTGAGGTATTTT CAGCACCGCTGTGTGTCGCGGCCCGGCCGCGGGGAGCCCCGCTACATCGCCGTGGAGTACGTAGAC
GACACGCAATTCTGCGGTTTCGACAGCGACGCCGCGATTCCGAGGATGGAGCCGCGGGAGCCGTGGGTGGAGCAA
GAGGGGCCGAGTATTGGGAGTGGACCACAGGGTACGCCAAGGCCAACGCACAGACTGACCGAGTGGCCCTGAGG
AACCTGCTCCGCCGCTACAACCAGAGCGAGGCTGGGTCTCACACCCTCCAGGGAATGAATGGCTGCGACATGGGG
CCCGACGGACGCCTCCTCCGCGGGTATCACCAGCACGCGTACGACGGCAAGGATTACATCTCCCTGAACGAGGAC
CTGCGCTCCTGGACCGCGGCGGACACCGTGGCTCAGATCACCCAGCGCTTCTATGAGGCAGAGGAATATGCAGAG
GAGTTCAGGACCTACCTGGAGGGCGAGTGCCTGGAGTTGCTCCGCAGATACTTGAGAAATGGGAAGGAGACGCTA
CAGCGCGCAGATCCTCCAAAGGCACACGTTGCCCACCACCCCATCTCTGACCATGAGGCCACCCTGAGGTGCTGG
GCCCTGGGCTTCTACCTGCGGAGATCACGCTGACCTGGCAGCGGGATGGGGAGGAACAGACCCAGGACACAGAG
CTTGTTGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCCGCTGTGGTGGTGCCTTCTGGAGAGGAA
CAGAGATACACATGCCATGTGCAGCACGAGGGGCTGCCCCAGCCCCCTCATCCTGAGATGGGAGCAGTCTCCCCAG
CCCACCATCCCCATCGTGGGCATCGTTGCTGGCCTTGTTGTCTTGGAGCTGTGGTCACTGGAGCTGTGGTTCGCT
GCTGTGATGTGGAGGAAGAAGAGCTCAGATAGAAACAGAGGGAGCTACTCTCAGGCTGCAGTCACTGACAGTGCC
CAGGGCTCTGGGGTGTCTCTCACAGCTAATAAAGTGTAGACAGCTTCCTTGTGTGGGACTGAGAAGCAAGATAT
CAATGTAGCAGAATTGCACTTGTGCCTCACGAACATACATAAATTTTAAAAATAAAGAATAAA

2196/6881
FIGURE 2018

MAPRSLLLLLSGALALDTWAGSHSLRYFSTAVSRPGRGEPRIAVEYVDDTQFLRFDSDAaiprMEPREPWVEQ
EGPQYWEWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDGKDYISLNE
LSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQRADPPKAHVAAHPI SDHEATLRW
ALGFYPAEITLTWQRDGEEQTQDELVETRPAGDGTQKWAAVVVP SGEEQRYTCHVQHEGLPQFLILRWEQSPQ
PTIPIVGIVAGLVVLGAVVTGAVVAAMWRKKSSDRNRGSYSQAAVTDSAQGSVSLTANKV

2197/6881
FIGURE 2019

GAGAGCAGACGTGCGCGCACCCCTCTCCCCTTGTCCACTGCTGCCGCCTCCTTCTTCTGCCGCTCCTGGTGCTGC
TTGTGTGCTCGTTTGGAGCGGACCTGGTACCTCTTTTGTGAAGCGGCAGCTGAGGAGACTCCGGCGCTCGCCATG
GCCGAAGAAAAGCCCCAAGGAAGGAGTCAAGACTGAGAACAACGATCATATTAATTTGAAGGTGGCGGGGCAGGAT
GGTTCTGTGGTGACGTTTAAAGATTAAGAGGCATACACCACTTAGTAACTAATGAAAGCCTATTGTGAACGACAG
GGATTGTCAATGAGGCAGATCAGATTCCGATTTCGACGGGCAACCAATGAAACAGACACACCTGCACAGTTGGAAA
TGGAGGATGAAGATACAATTGATGTGTTCCAACAGCAGACGGGAGGTGTCTACTGAAAAGGGAACCTGCTTCTTT
ACTCCAGAACTCTGTTCTTTAAAGACCAAGATTACATTCTCAATTAGAAAACCTGCAATTTGCTTCCACCACATCC
TGACTACTACCGTATAGTTTTCTCTATTCTTTCAATTTCCCCCTTCCCCATTCTTTACTGTACATAAAGTAACTG
GTATATGTGCACAAGCATATTACTTTTTTTTTTTTAAACTAAACAGCCAATGGTATGTTTTGATTGACATCAAGT
GGAGACGGGGCGGAAAAATACTGATTCTGTGAAAATACCCCCCTTCTCCATTAGTGGCATGCTCATTGAGCTCTT
ATCTTTATATTCCAGTAAGTTATTTTGCTCTCACTGTTTTAACAACAACAACAAAAACAACAACATAAAAAATC
CTTGCAACCTTGTTCAATTGGAGAATTTTAATGTTTTTCATTTATCATTGTAAAACCAAGGACAATTTTATAAC
TTTTTTGTACTTAGCTGTTACATGCAGAGCAATCTGTCTTTAAGTAGGGATAAATTACTCTAAAACAAAAAAGAA
TCCTAGATAGTTTTCCCTTCAAGTCAAGCGTCTTGTTGTTTAAATAAACTTCTTGTTTAAAA

2198/6881
FIGURE 2020

MAEEKPKKEGVKTENNDHINLKVAGQDGSVVQFKIKRHTPLSKLMKAYCERQGLSMRQIRFRFDGQPMKQTHLHSW
KWRMKIQLMCSNSRREVSTEGTCFFTPELCSLTKITFSIRKLQFASTTS

2199/6881
FIGURE 2021

GCCGCTCCTGGTGCTGCTTGTGTGCTCGTTTGGAGCGGACCTGGTACCTCTTTTGTGAAGCGGCAGCTGAGGAGA
CTCCGGCGCTCGCCATGGCCGAAGAAAAGCCCAAGGAAGGAGTCAAGACTGAGAACAACGATCATATTAATTTGA
AGGTGGCGGGGCAGGATGGTTCGTGGTGCAGTTTAAGATTAAAGAGGCATACACCACTTAGTAAACTAATGAAAG
CCTATTGTGAACGACAGGGATTGTCAATGAGGCAGATCAGATTCCGATTGACGGGCAACCAATGAAACAGACAC
ACCTGCACAGTTGGAAATGGAGGATGAAGATACAATTGATGTGTTCCAACAGCAGACGGGAGGTGTCTACTGAAA
AGGGAACCTGCTTCTTTACTCCAGAACTCTGTTCTTTAAAGACCAAGATTACATTCTCAATTAGTCTTTCATTTC
CCCCTTCCCCATTCTTTACTGTACATTAAAGTAACTGGTATATGTGCACAAGCATATT

2200/6881
FIGURE 2022

MAEEKPKEGVKTENNDHINLKVAGQDGSVVQFKIKRHTPLSKLMKAYCERQGLSMRQIRFRFDGQPMKQTHLHSW
KWRMKIQLMCSNSRREVSTKGTCEFTPELCSLKITFSISLSFPPSPFLYCT

2201/6881
FIGURE 2023

ATGAAGGCCAACTACAGCGCAGAGGAGCGCTTTCTCCTGCTGGGTTTCTCCGACTGGCCTTCCCTGCAGCCGGTC
CTCTTCGCCCTTGTCCTCCTGTGCTACCTCCTGACCTTGACGGGCAACTCGGCGCTGGTGCTGCTGGCGGTGCGC
GACCCGCGCCTGCACACGCCCATGTACTACTTCCTCTGCCACCTGGCCTTGGTAGACGCGGGCTTCACTACTAGC
GTGGTGCCGCCGCTGCTGGCCAACTGCGCGGACCAGCGCTCTGGCTGCCGCGCAGCCACTGCACGGCCCAGCTG
TGCGCATCGCTGGCTCTGGGTTCCGCCGAATGCGTCCTCCTGGCGGTGATGGCTCTGGACCGCGCGCCGCGAGTG
TGCCGCCCCGCTGCGCTATGCGGGGCTCGTCTCCCCGCGCCTATGTCGCACGCTGGCCAGCGCCTCCTGGCTAAGT
GGCCTCACCAACTCGGTTGCGCAAACCGCGCTCCTGGCTGAGCGGCCGCTGTGCGCGCCCCGCTGCTGGACCAC
TTCATCTGTGAGCTGCCGGCGTTGCTCAAGCTGGCCTGCGGAGGCGACGGAGACACTACCGAGAACCAGATGTTT
GCCGCCCCGCTGGTTCATCCTGCTGCTGCCGTTTGCCGTCATCCTGGCCTCCTACGGTGCCGTGGCCCCGAGCTGTC
TGTTGCATGCGGTTTACGCGGAGGCCGGAGGAGGGCGGTGGGCACGTGTGGGTCCCACCTGACAGCCGTCTGCCTG
TTCTACGGCTCGGCCATCTACACCTACCTGCAGCCCGCGCAGCGCTACAACCAGGCACGGGGCAAGTTCGTATCG
CTCTTCTACACCGTGGTCACACCTGCTCTCAACCCGCTCATCTACACCCTCAGGAATAAGAAAGTGAAGGGGGCA
GCGAGGAGGCTGCTGCGGAGTCTGGGGAGAGGCCAGGCTGGGCAGTGA

2202/6881
FIGURE 2024

MEGTQEYDSSMQTVRFQGERRKSPSNATFSPFFWMPHSAKSLVADAGIHSRNQHSYAIASF IKYSQLHFKSRESR
AGARDQPIIWKLKANYSAEERFLLLGFSDWPSLQPVLFALVLLCYLLTLTGNSALVLLAVRDPR LHTPMYYFLCH
LALVDAGFTTSVVP LLANLRGPALWLP RSHCTAQLCASLALGSAECVLLAVMALDRAAAVCRPLRYAGLVSPRL
CRTLASASWLSGLTNSVAQTALLAERPLCAPRLLDHFICELPALLKLACGGDGD TTENQMFAARVVILLLPFAVI
LASYGAVARAVCCMRFSGGRRRAVGTCGSHLTAVCLFYGSAIYTYLQPAQRYNQARGKFVSLFYTVVTPALNPLI
YTLRNKKVKGAARRLLRSLGRGQAGQ

2203/6881
FIGURE 2025

ATGGGGAGAAGGTATGTGAGGAAGGAAAAGAAAAAGGCCAGCAGGTGAAGAAAAAGAAGAAGGTCTGGTGAGGACA
ATGGAGACGGCCAATCGTTCCTTAAAACGGTCTCCTCCTCCTGGTTCCTCTCTCCAAGATGGCAAGGGAGCCTGC
AAATTCGGTCTCCAAGGATCCCTCTGCCCAGAGCAACGAACCTCCCTTTGGCAATATAGGAATAATCTTCATTCTC
CCTGCAATTGTGCACATTAATAGGCTGTTTAATGAAAGTACAGTGTGGAGCTCATTATTGCGAACAGCAGCCCTT
AGAGATCGTAGCTGGCTGGTAAAGGCGGCTTTAGAGCGGACGCCCAGGCTTCTTCATCAGCTTACCAGAAGGTTG
GAGGCAGAAGACCTCCCATTTGCAGATTCATCTCATTTCTCCGCTTATGCTTCCGTTCTTTGAAAGTGAACCACTA
GGTTTCAGAAAGCACCAGGCAGTTAAAACAGAGTTTACTCCCTCGGTCACTGCACTAGAAATCAGGAGGCGAACA
CTGTACCTAAACATAAAACGACATTCTCAAAAAC TGCCCTGCACAGGCTTGTTGGGACTTCACGATCCTTCTTGG
ACCTGCATCCCCCTCTTCTCTGGTACTCGGACCAAATCGAACAATCAAGCAACAAAGTTGGCCTTAAAATTGAG
GCCCCAGAGATGAGGTTACTGAGCGGGTATATGTCACAGAGCCAACTTTCTGCAATGAATTGGAAAAGAACATC
AAGACAGAGGGAGGAGCGCTGGGGGTGAACACCGCCTTGACCTTTGTAACTGCTGCACAAATAAGGAGTGGTG
CTGTGCCAGTTTTCCCTGAAGAGGTGCCTGACCAGCTGGCTCTGTGAATTGGAATACAGTTTTTCAGGCAGGCTCT
GGGAGAGTTTTTGGGGAATCCCGAAAAGACAGCCCAGAGATGCTGGACTGCGAATGCAGGCGCGCTGCAGGCGAGGC
TGGGAGGGCCGCCAGGAGCGCTGCGGGTATCGGGAGACACGCAGAGGGAGGGGCAGGCGGCGGGCTCCGCTTCTT
CGCGTCTTGGCTCTGAAAGCAACCACAGGCCAGCGGGCGGTGCTAGAAAAACACAACCTTCACGGAAGAGTTTT
GAAAAGATTTCCGGCAAGAAAATAATGTTACCAGAGACCGTTGAGGCCCCGCCAGCCTTCAAGATGGATGCCCCT
GCTGGCCGCAAAGTGGGTCTCATTGCTCCCCGCCGACTGGACGTCTCCGGGGAACGAAGACTGTGCAGGAGAAA
GAGAGCTAG

2204/6881
FIGURE 2026

MGRRYVRKERKRPAGEEKEEGLVRTMETANRSLKRSPPPGSSLQDGKGACKFGLQGSLCPEQRTPFGNIGIIFIL
PAIVHINRLEFNESTVWSSLLRTAALRDRSWLVKAALERTPRLHQLTRRLEAEDLPFADSLISPLMLPFFESEPL
GFRKHQAVKTEFTPSVTALEIRRRTLYLNIKRHSQKLPCTGLLGLHDPSWTCIPLFSGTRTKIEQSSNKVGLKIE
APEMRLLSGYMSQSQTFCNELEKNIKTEGGALGVNTALTFTCCTNKEWLLCQFSLKRCLTSWLCEFEYSFQAGS
GRVLGNPERQPRDAGLRMQARCRRGWEGRQERCYRETRRGRGRRRAPLLRVLALKATTGQRGGARKTQPSRKSF
EKISGKKIMLPETVEARPAFKMDAPAGRKVGLIAPRRTGRLRGTKTVQEKES

2205/6881
FIGURE 2027

TACGGCCGTCGTGCCGCTCGTGTCTAGTCAACATGGAGGCAGAGGAATCGGAGAAGGCCGCAACGGAGCAAGAGCC
GCTGGAAGGGACAGAACAGACACTAGATGCGGAGGAGGAGCAGGAGGAATCCGAAGAAGCGGCCTGTGGCAGCAA
GAAGCGGGTAGTGCCAGGTATTGTGTACCTGGGCCATATCCCGCCGCGCTTCCGGCCCCCTGCACGTCCGCAACCT
TCTCAGCGCCTATGGCGAGGTCGGACGCGTCTTCTTTCAGGCTGAGGACCGGTTTCGTGAGACGCAAGAAGAAGGC
AGCAGCAGCTGCCGGAGGAAAAAAGCGGTCCTACACCAAGGACTACACCGAGGGATGGGTGGAGTTCCTGTACAA
GCGCATAGCCAAGCGCGTGGCGGCCAGTCTACACAACACGCCTATGGGTGCCCGCAGGCGCAGCCCCCTTCCGTTA
TGATCTTTGGAACCTCAAGTACTTGCACCGTTTCACCTGGTCCCACCTCAGCGAGCACCTCGCCTTTGAGCGCCA
GGTGCGCAGGCAGCGCTTGAGAGCGGAGGTTGCTCAAGCCAAGCGTGAGACCGACTTCTATCTTCAAAGTGTGGA
ACGGGGACAACGCTTTCTTGCGGCCGATGGGGACCCTGCTCGCCCAGATGGCTCCTGGACATTTGCCACGCGTCC
TACTGAGCAGGAAGTGAAGGGCCCGTAAAGCAGCACGGCCAGGGGGACGTGAACGGGCTCGCCTGGCAACTGCCCA
GGACAAGGCCCGCTCCAACAAAGGGCTCCTGGCCAGGATCTTTGGAGCCCCGCCACCCCTCAGAGAGCATGGAGGG
ACCTTCCCTTGTCTAGGGACTCCTTGAAGGGCCTGGGTGGCCCCCTTCCATTTCTCTGGCCCTGCTCTGCTTCTGTCTA
CCTCATACTAGAATGATCGTGACTACCCGGGCAGACATTTTACTGTGTTTCTCAGACCAAGTGTCTACTGATGGC
CCAAACATGGAGTTTTTGTGGGCTTCCACTGTCCCCACTCCGAACCTCCTGTATGTGCTGGCTGAGTCACCTAATT
CATACTGTCTACTAGCATAATTATGACTATTGCATATGCTTGTTTTGTTTGACTCTTGGCTGCCTACGTCTGTGA
GGTCCCCCTGAAAATCCCCTTCTGCCCCAGAAAGGGCCTTTATTTCCAACCTAGGAGGATAATGCCTAGTCCA
GGCAATCTTTCTCTGTTTAGCAGTACAGGTGAGGGTGGTATTAGCATCTTTTTTATGTAGAAAAAATTGAGTTA
ATGGGGTGGACTGGGTTGGGAAGAAATACATTTCCCTAATGTATTTATAGAAAAATAAAATATTTTTATGTGCCTT
TTTATTTTTGTTGGTGGGGAGGTCATTGGACAAGTTCCAACCTTTCATCTTGTGTTCCCTTCACCTTCATATCCTG
ATCTTAGAGCCCCCTCCCCCTGCCACCCACCTTACTGTTTAACTGGATTTTTTTTTTCTATTTAATTTTTGTCT
AATATCTTAGCCAGTTTATCAATCAGTTATCTTAAGTCAGCATTTTCTAAGCCATTGTTTGAGGAAACAGTGAC
AATAGGTAATAACACATCTTAGTATTAAGAGTTTTACAGGCCACTAGTATAAGATAGGCATCGTGGTAGATGCAT
ATAAAGGGTGGAAATGGGAGCCATGGCAGGTCATAGAGTCTCTCAATGGGAACCTGATTGATGATCACAGTCTTC
AGTGGTGAGTCAGTCCTCACCAAGTTTTCCAGATCATTCTTACAAAGTAACTGGGAGAATAATAAGTCTGAAAG
AGTGTGGAGTGCTCCCACAATTACAAAGAATGCTTCTGGGTGGAGTGTTGAGTTGGAACCATTGTAAAGGTGGG
CAAAGCCTAGTAGAGAACCAGTGCACCTCAGGTGCACTTACATATGGTGGGGCTGAGGCAAAGCAGCCCTGTAGG
CTTCAAAGAATCAGTGTAAGCCACTAAAAGGAACTGAAAACCTAGGTGTCACAATAAACAGTCTACACAGTCTCA
CGTAGACCAAAATTCTGATCATTTTCCAGGCTGTTGCATGAAGTGATAGAGTATGATTATAATTTCTGTTTGCTT
GTGCTGTTTGTGTTTTGTTTTTTCATCTGTCAATGTGATGATCTGTGTTTTATAGGGTAGAGTGGATTTGTCTACTT
TGGCTGTAAATAACCTAATCACATTATGATCTTGACAGGTGCACTTTACTGGGGAGAATAAAAAGGACCATACG
GTAAA

2206/6881
FIGURE 2028

MEAESEKAATEQEPLEGTEQTLDAEEEQEESSEEAACGSKKRVPGIVYLGHIPPRFRPLHVRNLLSAYGEVGRV
FFQAEDRFVRRKKAAAAAGGKKRSYTKDYTEGWVEFRDKRIAKRVAASLHNTPMGARRRSPFRYDLWNLKYLHR
FTWSHLSEHLAFERQVRRQLRAEVAQAKRETD FYLQSV ERGQRFLAADGDPARPDG SWTF AQRPT EQELRARKA
ARPGGRERARLATAQDKARSNKGLLARIFGAPPPSESMEGPSLVRDS

2207/6881
FIGURE 2029

ATTGCTTTCTCTTTTTCTTTCTTCCGGATGAGAGGCTAAGCCATAATAGAAAGAATGGAGAATTATTGATTGA
CCGTCTTTATTCTGTGGGCTCTGATTCTCCAATGGGAATACCAAGGGATGGTTTTCCATACTGGAACCCAAAGGT
AAAGACACTCAAGGACAGACATTTTTTGGCAGAGCATAGATGAAATGGCAAGTTCCCTGGCTTTCCTTCTGCTCA
ACTTTCATGTCTCCCTCCTCTTGGTCCAGCTGCTCACTCCTTGCTCAGCTCAGTTTTCTGTGCTTGACCCCTCTG
GGCCCATCCTGGCCATGGTGGGTGAAGACGCTGATCTGCCCTGTCACCTGTTCCCGACCATGAGTGCAGAGACCA
TGGAGCTGAAGTGGGTAAGTTCCAGCCTAAGGCAGGTGGTGAACGTGTATGCAGATGGAAAGGAAGTGAAGACA
GGCAGAGTGCACCGTATCGAGGGAGAACTTCGATTCTGCGGGATGGCATCACTGCAGGGAAGGCTGCTCTCCGAA
TACACAACGTACAGCCTCTGACAGTGGAAAGTACTTGTGTTATTTCCAAGATGGTGACTTCTATGAAAAAGCCC
TGGTGGAGCTGAAGGTTGCAGCACTGGGTCTAATCTTCACGTCGAAGTGAAGGGTTATGAGGATGGAGGGATCC
ATCTGGAGTGCAGGTCCACCGGCTGGTACCCCCAACCCCAAATACAGTGGAGCAACGCCAAGGGAGAGAACATCC
CAGCTGTGGAAGCACCTGTGGTTGCAGATGGAGTGGGCCTATATGAAGTAGCAGCATCTGTGATCATGAGAGGCG
GCTCCGGGGAGGGTGTATCCTGCATCATCAGAAATTCCTCCTCGGCCTGGAAAAGACAGCCAGCATTTCCATCG
CAGACCCCTTCTTCAGGAGCGCCCAGCCCTGGATCGCAGCCCTGGCAGGGACCCCTGCCTATCTTGCTGCTGCTTC
TCGCCGGAGCCAGTTACTTCTTGTGGAGACAACAGAAGGAAATAACTGCTCTGTCCAGTGAGATAGAAAGTGAGC
AAGAGATGAAAGAAATGGGATATGCTGCAACAGAGCGGGAATAAGCCTAAGAGAGAGCCTCCAGGAGGAACTCA
AGAGGAAAAAATCCAGTACTTGACTCGTGGAGAGGAGTCTTCGTCCGATACCAATAAGTCAGCCTGATGCTCTAA
TGGA AAAATGGCCCTCTTCAAGCCTGGTGAGGAAATGCTTCAGATGAGGCTCCACCTTGTTAAATAAATTGGATG
TATGGAAAAATAGACTGCAGAAAAGGGGAACCTCATTTAGCTCACGAGTGGTCGAGTGAAGATTGAAAATTAACCT
CTGAGGGCCAGCACAGCAGCTCATGCCTGTAATCCTAGCACTTTGGAAGGCTGAGGAGGGCGGATCACAAGGTCA
GGAGATCAAGACCATCCTGGCTAACACGGTGAAACCCCGTCTCTACTAAAAATACAAAAAATAAAAAATTAGCCG
GGCATGGTGACGGGCACCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATGGCATGAACCCGGAAGGCA
GAGCTTGCAGTGAGCCGAGATCACGCCACTGCACTCCAGCCTGGGAGACAGAGCGAGACTCTGTCTCAAGAAAAA
AAAAAAAAAAAAAAAAA

2208/6881
FIGURE 2030

MKMASSLAFLLLNFHVSLLLVLTPCSAQFSVLGPSPILAMVGEDADLPCHLFPTMSAETMELKWVSSSLRQV
VNVYADGKEVEDRQSAPYRGRTSILRDGITAGKAALRIHNVTASDSGKYLCYFQDGDIFYEKALVELKVAALGSNL
HVEVKGIEDGGIHLECRSTGWYPQPQIQWSNAKGENIPAVEAPVVADGVGLYEVAASVIMRGGSGEGVSCIIRNS
LLGLEKTASISIA DPF FRS AQPWIAALAGTLPILL LLLLAGASYFLWRQQKEITALSSEIESEQEMKEMGYAATER
EISLRESLQEELKRKKSST

2209/6881
FIGURE 2031

ATGGACAGGACTGTCATTTCAGAAATACCACACTGTGAATGGCCACAGCTGTGAAGTTAGGAAAGCCCTGTCAAAG
CAAGAGATGGTTAGTGCTTCATCCAGCCAAAGAGGTCTGAAGTGGTTCTGGAAACTTTGCTGGTGGTCTTAGAAGT
GGTTTCAGTGGGAATAACAACCTTTGGTCGTGGAGGAACTTCCGTGGTCGTGGGGCCTTTGGTGGCAGCCGTGGT
GGTGGTGGATATGATGGCAGTGGGGATGGCTATAATGGATATGGCCCAGATAAACAGTCTCCACTTGTTTCAGGAC
TTCAACGGAGATATTCCACTCAGTCCTGCTTATGCCAGACACCTTGCACGAGCCTCTCCCAAGATAGCTAGGACT
CAGGGAACATGCAGGCTGACACAAGCATTGATGATCTATATTAATGCAAGTGTAATATGGAATGGAGAATTTTTA
CAAATGGTGTTCATTACCAGCCATTAATGCCATAGCTTTAATTTGTTTCATTAAAGTTTAGCAGCCAGTTACCTAACA
GGTCATCAAAGGAGGGACACAGAAGAGGCAAGCACTGATAATGAAAGGTCTATATCACAGGTGTGCTCAGAAAAAG
GCAAGCACAGATCACAGTTTCCAGGGCTGCCAGCAGAATGGATTTAATATTGCCACGTGGGAAGAAGAAAAAGCC
ACAGGGTGCAGATATCAGGAATCTGAATTTCCGGGGCATAACGTGTGCACAGATGCAGCTTCAACAGATTTCATCA
TATCATCCCTTCAGAGCTGCTGTGACAGTTTACACCAGATTAACTCTCAGTTTCCAGAAAAAGAGGAAACTCTG
GCCTAG

2210/6881
FIGURE 2032

TTCCCCAGCATTTCGAGAAACTCCTCTCTACTTTAGCACGGTCTCCAGACTCAGCCGAGAGACAGCAAACCTGCAGC
GCGGTGAGAGAGCGAGAGAGAGGGAGAGAGAGACTCTCCAGCCTGGGAACTATAACTCCTCTGCGAGAGGCGGAG
AACTCCTTTCCCCAAATCTTTTGGGGACTTTTCTCTCTTTACCCACCTCCGCCCTGCGAGGAGTTGAGGGGCCAG
TTCGGCCCGCCGCGCGCTTCTCCCGTTTCGGCGTGTGCTTGGCCCGGGGAACCGGGAGGGCCCGGCGATCGCGCGG
CGGCCCGCCGCGAGGGTGTGAGCGCGCTGGGCGCCCGCCGAGCCGAGGCCATGGTGCAGCAAACCAACAATGCCG
AGAACACGGAAGCGCTGCTGGCCGGCGAGAGCTCGGACTCGGGCGCCGGCCTCGAGCTGGGAATCGCCTCCTCCC
CCACGCCCCGGCTCCACCGCCTCCACGGGCGGCAAGGCCGACGACCCGAGCTGGTGCAAGACCCCGAGTGGGCACA
TCAAGCGACCCATGAACGCCTTCATGGTGTGGTTCGAGATCGAGCGGCGCAAGATCATGGAGCAGTCGCCCCGACA
TGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAGCTGCTCAAAGACAGCGACAAGATCCCTTTTCA
TTCGAGAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTACCGGGCCAGGAAGAAGG
TGAAGTCCGGCAACGCCAACTCCAGCTCCTCGGCCCGCGCCTCCTCCAAGCCGGGGGAGAAGGGAGACAAGGTCTG
GTGGCAGTGGCGGGGGCGGCCATGGGGGCGGCGGCGGCGGGGAGCAGCAACGCGGGGGGAGGAGGCGGCGGGT
CGAGTGGCGGCGGCGCCAACCTCAAACCGGCGCAGAAAAAGAGCTGCGGCTCCAAAGTGGCGGGCGGCGCGGGCG
GTGGGGTTAGCAAACCGCACGCCAAGCTCATCTGGCAGGCGGCGGCGGCGGGGAAAGCAGCGGCTGCCGCCG
CCGCCTCCTTCGCCGCCGAACAGGCGGGGGCGCGCCCTGCTGCCCCCTGGGCGCCGCCGCCGACCACCACTCGC
TGTACAAGGCGCGGACTCCCAGCGCCTCGGCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGCAGCGCTCGCGGGCC
CGGGCAAGCACCTGGCGGAGAAGAAGGTGAAGCGCGTCTACCTGTTTCGGCGGCCTGGGCACGTGCTCGTCCGCCG
TGGGCGGCGTGGGCGCGGGAGCCGACCCAGCGACCCCTGGGCCTGTACGAGGAGGAGGGCGCGGGCTGCTCGC
CCGACGCGCCAGCCTGAGCGGCGCGCAGCAGCGCCGCTCGTCCCCCGCCGCCGCGCTCGCCCGCCGACCACC
GCGGCTACGCCAGCCTGCGCGCCGCTCGCCGCCCGCTCCAGCGCGCCCTCGCACGCGTCTCTCTCGGCCTCGT
CCCACTCCTCCTCTTCTCTCTCTCGGGCTCCTCGTCTCCGACGACGAGTTTGAAGACGACCTGCTCGACCTGA
ACCCAGCTCAAACCTTTGAGAGCATGTCCCTGGGCAGCTTCAGTTCTGTCGTCGGCGCTCGACCGGGACCTGGATT
TTAACTTCGAGCCCGGCTCCGGCTCGCACTTCGAGTTCCCGGACTACTGCACGCCCGAGGTGAGCGAGATGATCT
CGGGAGACTGGCTCGAGTCCAGCATCTCCAACCTGGTTTTTACCTACTTGAAGGGCGCGCAGGCAGGGAGAAGGGC
CGGGGGGGGTAGGAGAGGAGAAAAAAAAGTGAAAAAAGAAACGAAAAGGACAGACGAAGAGTTTAAAGAGAAA
AGGGAAAAAAGAAAGAAAAAGTAAGCAGGGCTCGTTCGCCCGCGTTCTCGTCTCGGATCAAGGAGCGCGGCGGC
GTTTTGGACCCGCGCTCCCATCCCCACCTTCCCGGGCCGGGGACCACTCTGCCCAGCCGGAGGGACGCGGAGG
AGGAAGAGGGTAGACAGGGGCGACCTGTGATTGTTGTTATTGATGTTGTTGTTGATGGCAAAAAAAAAAAGCGAC
TTCGAGTTTGCTCCCTTTGCTTGAAGAGACCCCTCCCCCTTCCAACGAGCTTCCGGACTTGTCTGCACCCCCA
GCAAGAAGGCGAGTTAGTTTTCTAGAGACTTGAAGGAGTCTCCCCCTTCTGTCATCACCACCTTGGTTTTGTTTT
ATTTTGCTTCTTGGTCAAGAAAGGAGGGGAGAACCAGCGCACCCCTCCCCCTTTTTTTAAACGCGTGATGAA
GACAGAAGGCTCCGGGGTGACGAATTTGGCCGATGGCAGATGTTTGGGGGAACGCCGGGACTGAGAGACTCCAC
GCAGGCGAATTCCCGTTTGGGGCTTTTTTCTCTCCCTCTTTTCCCTTGCCCCCTCTGCAGCCGGAGGAGGAGA
TGTTGAGGGGAGGAGGCCAGCCAGTGTGACCGGCGCTAGGAAATGACCCGAGAACCCCGTTGGAAGCGCAGCAGC
GGGAGCTAGGGGCGGGGGCGGAGGAGACACGAACTGGAAGGGGGTTACGGTCAAACCTGAAATGGATTGACAG
TTGGGGAGCTGGCGGCGGCGGCTGCTGGGCCTCCGCCTTCTTTTCTACGTGAAATCAGTGAGGTGAGACTTCCCA
GACCCCGAGGCGTGGAGGAGAGGAGACTGTTTGATGTGGTACAGGGGCGAGTCAGTGGAGGGCGAGTGGTTTCG
AAAAAAAAAAGAAAAAAGG

2211/6881
FIGURE 2033

MVQQTNNNAENTEALLAGESSDSGAGLELGIASSPTPGSTASTGGKADDP
SWCKTPSGHIKRP MN AFMVWSQIERR
KIMEQSPDMHNAEISKRLGKRWLLKDSKIPFIREAERLRLKHMADY
PDYKYRPRKKVKSGNANSSSSAAASK
PGEKGDKVGGSGGGGHGGGGGGSSNAGGGGGGASGGGANSKPAQKK
SCGSKVAGGAGGGVSKPHAKLILAGGGG
GGKAAAAAASFAAEQAGAAALLPLGAAADHHS
LYKARTPSASASASSAASASAALAAPGKHLAEKKV
KRVYLFGLGTSSSPVGGVGAGADPSDPLGLYEE
EGAGCSPDAPSLSGRSSAASSPAAGRSPADHR
GYASLRAASPAPSSAPSHASSSASSHSSSSSS
SGSSSSDDEFEDDLLDLNPSSNFESMSLGSFSS
SSSALDRDLDFNFEPGSGSHFEFPDYC
TPEVSEMISSGDWLESSISNLVFTY

2212/6881
FIGURE 2034

GGCCCGCGGCGGCCGAAATCCGCGGTTACAGCATGTCCGCCTCGGCCCTGCTGCGGAGGGGGAGGGGAACCCCC
ACCCAGCCCGCGTCCGAGAAAGAACCCGAAATGCCCGGTCCCAGAGAGGAGCGAGGAGGAAGAGGACGAGGAC
GACGAGGAGGAGGAGGAGGAGGAGGAAAAAGAAAAGAGTCTCATCGTGGAAGGCAAGAGGGAAAAAGAAAAAGTAGAG
AGGTTGACAATGCAAGTCTCTTCCTTACAGAGAGAGCCATTTACAATTGCACAAGGAAAGGGGCAGAACTTTGT
GAAATTGAGAGGATACATTTTTTTCTAAGTAAGAAGAAAACCGATGAACCTAGAAATCTACACAACTGCTTTAC
AACAGGCCAGGCACTGTGTCCTCATTAAGAAGAATGTGGGTCAGTTCAGTGGCTTTCCATTTGAAAAAGGAAGT
GTCCAATATAAAAAGAAGGAAGAAATGTTGAAAAATTTAGAAATGCCATGTTAAAGAGCATCTGTGAGGTTCTT
GATTTGGAGAGATCAGGTGTAAATAGTGAAGTAGTGAAGAGGATCTTGAATTTCTTAATGCATCCAAAGCCTTCT
GGCAAACCATTGCCGAAATCTAAAAAACTTGTAGCAAAGGCAGTAAAAAGGAACGGAACAGTTCTGGAATGGCA
AGGAAGGCTAAGCGAACCAAATGTCCTGAAATTCGTGATGAATCTAGTAGTGATGAAGATGAAAAGAAAAAC
AAGGAAGAGTCTTCAGATGATGAAGATAAAGAAAGTGAAGAGGAGCCACCAAAAAAGACAGCCAAAAGAGAAAAA
CCTAAACAGAAAGCTACTTCTAAAAGTAAAAATCTGTGAAAAGTGCCAATGTTAAGAAAGCAGATAGCAGCACC
ACCAAGAAGAATCAAAACAGTTCAAAAAAGAAAGTGAGTCTGAGGATAGTTTCAGATGATGAACCTTTAATTAA
AAGTTGAAGAAACCCCTACAGATGAAGAGTTAAAGGAAACAATAAAGAAATTAAGTGGCCAGTGCTAAGTTGAA
GAAGTCACAATGAAACAGATTTGCAAAAAGGTCTATGAAAATTATCCTACTTATGATTTAACTGAAAGAAAAGAT
TTCATAAAAACAACGTGAAAAGAGCTAATTTCTTGAGATAGAGGACAGAGAAGATGACTCGTTCCCATAGATTTG
AAGATCTGATTTATACCATATACAGCAAAGAGAATGTATTTCTTTTCTAAATCCTTGTTAAGCAACGTTAGT
AGAACTTACTGCTGACCTTTTTATCTTGAGTGTTATGTGAATTTGAGTTTGCTGTTTTAAATTGCATTTCTATGC
CATTTTTAGTTTTAAATCTTGCATGGCATTAAATTGTTCTTGCTTTTATAGTTGTATTTTGTACATTTTGGATTT
CTTTATATAAGGTCATAGATTCTTGAGCTGTTGTGGTTTTTGTAGTCACTTAATATTAGCTTGCTTAAGGCATACT
TTTAATCAAGTAGAACAAAACTATTATCACCAGGATTTATACATACAGAGATTGTAGTATTTAGTATATGAAAT
ATTTTGAATACACATCTCTGTCAGTGTGAAAATTCAGCGGCAGTGTGTCCATCATATTAATAATATACAAGCTAC
AGTTGTCCAGATCACTGAATTGGAACCTTTCTCCTGCATGTGTATATATGTCAAATTGTCAGCATGACAAAAGTG
ACAGATGTTATTTTXXGTATTTTTTAAAAACAATTGGTTGTATATAAAGTTTTTTTATTTCTTTTGTGCAGATCAC
TTTTTAACTCACATAGGTAGGTATCTTTATAGTTGTAGACTATGGAATGTCAGTGTTCAGCCAAACAGTATGAT
GGAACAGTGAAAGTCAATTCAGTGATGGCAACACTGAAGGAACAGTTACCCTGCTTTGCCTCGAAAGTGTCTCA
ATTTGTAATTTTAGTATTAACCTCTGTAAAAGTGTCTGTAGGTACGTTTTATATTATATAAGGACAGACCAAAAT
CAACCTATCAAAGCTTCAAAAACCTTTGGGAAAGGGTGGGATTAAGTACAAGCACATTTGGCTTACAGTAAATGAA
CTGATTTTTATTAACCTGCTTTTGCCCATATAAAATGCTGATATTTACTGGAAACCTAGCCAGCTTCACGATTATG
ACTAAAGTACCAGATTATAATGCCAGAATATAATGTGCAGGCAATCGTGGATGTCTCTGACAAAAGTGTGTCTCAA
AAATAATATACTTTTTACATTAAAGAAATTTAATGTTTCTCTGGAGTTGGGGCTCTTGGCTTTTACAGATTTGGTTA
ATCAGTGTGATTCTAGATGATCAACATAATGGACCACTCCTGAATGAGACTTAATTTTGTCTTTCAAATTTACT
GTCTTAAATCAGTTTATTAAATCTGAATTTTAAAAACATGCTGTTTATGACACAATGACACATTTGTTGCACCAAT
TAAGTGTTGAAAAATATCTTTGCATCATAGAACAGAAATATATAAAATATATGTTGAATGTTAACAGGTATTTT
CACAGGTTTGTCTTGTAGTTACTCAGACACTAGGGAAAGGTAAATACAAGTGAACAAAATAAGCAACTAAAT
GAGACCTAATAATTGGCCTTCGATTTTAAATATTTGTTCTTATAAACCTTGTCATAAAAAATAAATCTAAATCA

2213/6881
FIGURE 2035

MSASAPAAEGEGTPTQPASEKEPEMPGPREESEEEEEDEDEEEEEEEEEKEKSLIVEGKREKKKVERLTMQVSSLQR
EPFTTIAQGKGQKLCEIERIHFFLSKKKTDELRLNLHKLLYNRP GTVSSLKKNVGQFSGFPFEKGSVQYKKKEEMLK
KFRNAMLKSICEVLDLERSGVNSELVKRILNFLMHPKPSGKPLPKSKKTC SKGSKKERNSSGMARKAKRTKCPEI
LSDESSSDEDEKKNKEESSDDEDKESEEEPPKKTAKREKPKQKATSKSKKSVKSANVKKADSSTTKKNQNSSKKE
SESEDSSDDEPLIKKLKKPPTDEELKETIKKLLASANLEEVMTMQICKKVYENYPTYDLTERKDFIKTTVKELIS

2214/6881
FIGURE 2036A

GGGGGAGGGAAACGGAGCAGTGACAGGTATCCCAGAGGGTGCTGCTGAGGCGACGATGGCCGAGGGGCCCCGAGGA
AGCCCGAGGCCACCCTCCCGGGCAGGACGATGGCGGAGGGGACCACGAGCCCGTCCCTTCCCTGAGAGGCCCTCC
TACCACCGCCGTCCCATGCCCCGCGACGACCCCCAGGCCGAACCCAGGCCCGGGCCGGCCACAGCCCCGGG
CCTCGCGGCTGCCGCGCAGCCGACAAATTGGAGCCGCCGCGCGAGCTCAGGAAGCGCGGGGAGGCGGCCCTCCGG
CTCCGGTGACAGCTGCAGGAGCAGGCGGGCTGCGAGGCGCCGAAGCCGCGGCCACGAGAGAGACCAGCTCG
GCTGAGCGCCCGCGAGTACTCCCGGCAAGTGCACGAGTGCGTGTGGCAGTCTACTGCGGCTACCTCACCTGGCA
CAGCGGCCTGGCCGCTTCCCAGCCTACTGCAGCCCCAGCCCTCCCCGCAGAGCTTCCCTTCGGGCGGCGCTGC
AGTCCCCCAGGCCGCGGCGCCGCCGCCCGCAGCTGGGCTATTACAACCCCTTCTACTTCTGAGCCCCGGGGC
CGCGGGGCTGACCCGCGGACAGCTGCCGGCATCAGCACCCCTGCTCCAGTCGCGGGCCTGGGACCCCCGGGCTCC
TCACGTGCAGGCGTCGGTCCGGGCCACTCCAGTGACGAGGGTAGGATCCGCAGCCCTTTCGCAAGCCCGAGCGA
GACCGGGCGACAGGCAGGCAGAGAATATGTTATTCCATCCTTGGCCCCACAGATTATGGCAGAGATGGTGGATTT
CTTTATTCTCTTCTTTATAAAAGCAACCATTGTCTTAAGCATTATGCACCTCAGTGGGATAAAGGATATCTCTAA
GTTTGCTATGCATTATATAATAGAAGAAATAGATGAAGACACATCAATGGAAGACTTGAGAAAATGATGGTTGT
GGCACTTATATACAGATTATTAGTTTGTCTTATGAGATAATTTGCATTTGGGGAGCAGGTGGAGCTACCCAGG
GAAGTTCCTGCTGGGGCTTCGAGTTGTGACATGTGATACATCAGTGCTTATTGCACCAAGTCGGGTTTTAGTGAT
TCCTTCCTCAAATGTTAGCATTACAACGTCCACTATCCGAGCTTTGATCAAGAATTTTTCAATTGCTTCTTTTTT
CCCTGCTTTCATCACACTGCTGTTTTTTCAGCATAATCGAACAGCTTATGACATTGTAGCAGGAACCATTTGTGGT
AAAAAGAAATGGGGTCAGATGATGCCCCCAAACCCCTGATTTCCACACACTAAGACTAAATTATGTATCAAGGC
CATCAGTATCCCTGGGTTACACTAATTGATGATTTAGAAATTAAGCAGTCACTCCAGTGTGATGCAGGTGACTA
CTCTGAAAGTATTGATTATACTTGAATGCCAAAGAACTTGTCCAGAAGAAAAACCTGTTAAATTCAAGTATTAA
ATTTTTAGATCAAAAAGGCCAAATGATTTTATAACAATGGACAATATATACTTTCTTAAGATCTAAGGTACTTTC
TTAAGATCTAAGAATTTGCTGAAAGCATTTTTCAGCTTTGAAATCTCAAATGAACTTTAAATTTATTTTGGTT
TATCCCAAAATAATGGAAGATGTCCAGTTGTGTTTTGTAAACACCTATGTAACATCTTTTAGTTTACACTTCC
TGGGGAAATTGTCTTTGGTGTTTAGAGGAGGGAATGAGAACACAAATTGGATAATCCACTGTCTCCCATCCCAGG
AGGTGGTGAGTTGGCTACAAGAGAAAGGACAAGTGAGGCAGGCCTAGCAGTTCCTTACCTGAAGTTTTCAAAT
CCATACTGCAGTTCCCTCTCGTAATGATGTAACCTTTACAACATTTCTTAATGCTTGAACATGTATTTAGGGGCAA
GTTTCTCATGATGATGAAAAAGTATCAAGTCATATTGCTATGTTAATTGGTTTTTTTTTTTAAAGGTAAGTTAG
TGATTACTGTTAATGGTGGGGAGTAAGTTTTCTACTGTAAATTGAACTTATAATTTATGTGCAAGTGTTTTCAGT
GCCCTGAATCAAACATAAATGTGGGGAGAAATCACCTCCATCAAACAGTTGCATATTTACTGTAAAGTATTCC
CAGTATGTGTGCAGCATGAAGAAAGTATTAGTGCTTCTCAGTGTTCTCAGTGTAATTTCTATTTATATACAGCAT
ATTCACATACTACTTTCTTATATTTTATATAGTTCTATGACTGTTGAAACATCAAGGAGTTAAAAAATCTTAA
TATTTTCATGATTAACCTCTAAGTACTATTAATTAATAGCTTGCAGAAATATTAGCAATTTTCCCATTATGGACTATT
CTCTCTAAAGCAAGAGAGACTAGCATTCCCAGACATCATTCTAGGGTCTTTAAGCTCATTTTGGGTCTGCTAAAG
TTTGGGGGAAATGTTACGCAAAGTGATACTGTGTATGTTGCCATTTTGCTTTATTCTTCTGTTGAAGCAAAATT
GTGGGGTTTTATTATGTGTGTGTGCTTTTCTAGATGTCCAGTTAGCTGTGCTGAGATATACCTGTACTATTTA
TGGTTTAAGTTTTGATTCTTAGGTATTTTCTCCAGCTCTGACATTGTTTTCCAAAGACACACTAACTGCATTGC
ACAGTTCAAATTTGATTACTTAAGGGATCAATCTAGGTGGTGTCTTGGTCTTAAATTTAACAGCAAACACAGC
ACATATCTATTATCACTATATTAATTTTCAAAGGTTTTTCTTTGACGTTTAAACTGTGACAACAGATATTCACA
TTTGATTATAGAACTTAATGTCTATTAATAATTTTAGTACAAAATTTTATAAACCCTGTTTTTCAAATAAGTT
TATGTCAAATCCAGCTTCCCAGAAACACTAATAATTAAGTACATCAATGTACTAAATAAATCATTAGTTGCACC
CATGGGGAAGATTGTGTTACTGCCCTTCACAGTGAAAAAAGAAAAATCTTTCATTTTTAAATTAGGAGATGTT
ACGTAACCTGGCACTTTAGTAGTGTATACACTAGCATTAGTTTATACACCACTTTTGCCGCTGGGGAATTCAGT
TGAAATGTCCCTCAATCATATAGGTCTGGAATACATCTTTCATTACATAATTTCTGCTCAGATAATTGAATAGTTT
GCCATCGAGATTATTTTCACTTATACTATAAAACAAAGCAAACCTAGTCCAGTTTAATTTTTTGTACTTAGAATA
TTGCACATTTTCTATATATGAGTTATTCAGATTAGTATCTATGTAGGTTTCAGTCAGATCCAACCATGGATTTCGAG
GTATTATACTGTATAACCTACAAAATACATAGAAGTATTATTTGCCTTCATAATAGAACCCAAGAGTCTGTTTC
AATTTATGAATTCAGTATTTGCACCGAGATTTTGATTTCCCAAAGTTTGGAAAAAATGACAAAACAACGAGGGAA
GAAGGAACCAGACCTTAGTGCCACATATTTTCTCTTGGGGTTGTAAGGTAGTCTCCTGCTTTCCAGAACACTTT

2215/6881
FIGURE 2036B

ATTATATTTCACTTATAGACCTGATTTTCTGTGTCAAAGTATAATTCTCATGCTGAAGCTGTAGCCTAAAAAGCC
AAAAGAAAGTTGTCTTCATTGTACAAACATATTCATCACTTTAACAATAAGGGAACAAAATTTAGTATTCAAGCT
GAGTGAGAATACTGTTTCAATGAGCATGTCCCTAAGATAAACAGAAATTGGCAGTTAATTTAGGCGTCTAGAAAA
TCTCAGTTCCCACCAGTAAAATTATCCTGAGTAGCTAATGCACCTTGAGAAAAATCTGGCATACTGAATAAATAA
CATTAACTTGGGAGCCAAGAGCTGGGTAAGCCTTACCTTTAGACTACTCTGTGACTACAGAAATAAAGCCAGCAC
TTTTGGAACTAATAAGCCTTCACTTGTCAGTATCATAAAGAGTATTGCCCAACTGAACTTTGCTCCCACTGGTTT
AATAGTTACTTATTTCTGCCTAAGCACTCACCTTCCGATTTTACCCAAGTATATATATAGGATAGAAAAAATGC
ATTATATTTGAGAGCTACTTCGCCCCAAATTACAAAATGAGTGTTTTTAGATTCAAGTGACAGTAAAAGGATTTGT
TCCCTTCAGTGACTTGAGTGTTTTAGTTATGCATAAGTATTTCTAGCAAAGGAAGGGTAGAAAGGAATTGAAAAT
TAATTTACACTAGTTGCTACTTGGAATAAAGGGCTTTTTGAGGGGGGTATGGATATTAAATGTTTTCGTTATAT
ACTTATCCCTATTAAAACAGGCAGTTGTTTCTTTGAATATGCCTAAATAACAGTATTCCTTAAAATCTGACAGACA
AGTAACATGTCAATTACTTGATATTCCTTGCTCCAGTACCACAGGCCACTCTTGACATCCCATGTTTGCCTGGA
TAAAGTTCCTCATTTCAAACAGTATACATACTTCTTTGCAGTTCATTATAGTAAGGCTTAACCTGTAAACAGTAT
CTGATGGCCACCTATAAATAAAAATTCAGCATTCTATTTTAAATAATTTGTATGCCACCAATTTGTATTATTTGT
CTCAATAAATACTTAGTCATCAATGC

2216/6881
FIGURE 2037

CTCCCCGCGCCGCCCGCCGCGCAGGCGCCCCGCCCCGCCGTCGCCGCCGCCGCGAGCCAGGAGCCGCTGCACCATGC
CCCCGATAGATGCGGACCTCAAGCTCGACTTCAAGGATGTCCTGCTCCGACCTAAGCGGAGCAGCCTCAAGAGCC
GAGCCGAGGTGGATCTTGAACGCACCTTCACGTTTCGAAATTCAAAGCAGACCTACTCAGGGATTCCCATCATCG
TGGCCAACATGGACACTGTGGGCACGTTTGAGATGGCAGCCGTGATGTCACAGCACTCCATGTTTACAGCAATTC
ATAAGCATTACTCCCTGGATGACTGGAAGCTCTTTGCCACAAATCACCCAGAATGCCTGCAGAATGTAGCCGTGA
GTTTACAGGCAGTGGGCAGAATGATCTGGAAGATGACCAGCATCCTGGAAGCTGTGCCACAGGTTAAGTTTATTT
GCCTGGATGTGGCCAATGGGTATTGAGAAATTTTGTGGAATTCGTGAACTTGTCCGTGCCAAATTTCTTGAAC
ACACCATTATGGCAGGGAACGTGGTGACAGGAGAAATGGTAGAAGAGCTTATTCTTTCCGGAGCAGATATCATCA
AAGTGGGAGTTGGACCAGGTTCTGTGTGCACACCCGCACCAAGACGGGAGTGGGGTACCCCCAGCTGAGTGCCG
TCATTGAGTGTGCCGACTCTGCCCATGGCCTGAAGGGCCACATCATCTCTGATGGAGGCTGTACGTGTCCAGGGG
ATGTCGCCAAAGCCTTTGGAGCTGGAGCAGATTTTGTGATGCTGGGAGGAATGTTTTCGGGTCATACGGAGTGTG
CTGGAGAAGTGTTTGAGAGGAACGGACGGAAGCTCAAGCTCTTCTACGGGATGAGCTCTGACACCGCCATGAACA
AGCACGCAGGAGGAGTTGCTGAGTACAGAGCCTCTGAGGGTAAGACTGTGGAAGTTCCCTTACAAAGGAGATGTGG
AAAACACTATCCTGGATATTCTCGGGGGACTGAGGTCCACGTGCACCTACGTGGGGGCCGCCAACTCAAGGAGC
TCAGCAGGAGGGCAACATTCATCCGGGTGACCCAGCAGCACAAACACCGTGTTTACGCTAACCCCTGGGGACAAAGCA
GCGTCTGGCTCGAGTGGAAGCGTCCAAACCTGCTTTTCCCATCTCCCCCAAGTCTGTTCCGTCAGAGCTTCTGG
CTGCTCCTGAATGGTGGAAATGCTGTGTCCTCTCTTCTGTCTCCTGCTGCCTGGAGGCTTCGGGGCTCTCCCGCT
GCCTTCTCGGGGCCCAGACGCAAGGCACCGATTGGGCCAACATCAGAGCCCTGCTGCCAGAATCATAACCTCA
TTGTTCAAACCAACACTTGCACCTTTCTCTTTTCTCTTCTCTCCTTTCTTTGTTTTTCTTTCTTTTTTAA
AAGAAGATGGTTTCACTTTAATATAATGCTATTATCTT

2217/6881
FIGURE 2038

MPRIDADLKLDKDVLLRPKRSSLKSRAEVDLERTFTFRNSKQTYSGIPIIVANMDTVGTFEMA AVMSQHSMFTA
IHKHYSLDDWKLFATNHPECLQNAVSSSGSQNDLEKMTSILEAVPQVKFICLDVANGYSEHFVEFVKLVRAKFP
EHTIMAGNVVTGEMVEELILSGADI IKVGVGP GSVCTTRTKTG VGY PQLSAVIECADSAHGLKGHI ISDGGCTCP
GDVAKAFGAGADFVMLGGMFSGHTECAGEVFERNRKLKLFYGMSSDTAMNKHAGGVAEYRASEGKTVEVPYKGD
VENTILDILGGLRSTCTYVGA AKLKELSRRAFIRVTQQHNTVFS

2218/6881
FIGURE 2039A

GTTTTACTAAAGTGAATTTTTTTTTTGTTCGTTTCGTTCTTTGGCTCTTTTTTTTTTCTTCCCAATTTTCGGAT
TTATTTCAAGGCGAATCTGGCTTTGGGGGAAGAGGAAGAAAAGTCGGATTACAAGATCAACCACCACCAACAACA
ATAAAAACCACCAGGATATTTTTTTGCAAATTTCTGACGGCTTTAAATTCATGAAGCAATTGTCCCCTTTTGCAA
TCAGCATTTGGATCTCAGAAATGAGCAAGGAAAGACCCAAGAGGAATATCATTGAGAAGAAATACGATGACAGTGA
TGGGATTCGGTGGTCAGAAGAACGGGTGGTACGTAAAGTCCTTTATTTGTCTCTGAAGGAGTTCAAGAATTTCCCA
GAAGAGGCAGCATGCGGAAGGCATTGCTGGGAGCCTGAAAAGTGTGAATGGGCTCCTTGGTAATGACCAGTCTAA
GGGATTAGGACCAGCATCAGAACAGTCAGAGAATGAAAAGGACGATGCATCCCAAGTGTCTTCCACTAGCAACGA
TGTTAGTTCTTCAGATTTTGAAGAAGGGCCGTCGAGGAAAAGGCCAGGCTGCAAGCACAAAGGAAGTTTGCTCA
GTCTCAGCCGAATAGTCCCAGCACAACTCCAGTAAAGATAGTGGAGCCATTGCTACCCCTCCAGCTACTCAGAT
ATCAGACCTCTCTAAAAGGAAGCCTAAGACAGAAGATTTTCTTACCTTTCTCTGCCTTCGAGGTTCTCCTGCGCT
GCCAACAGCATGGTGTATTTTGGAAGCTCTCAGGATGAGGAGGAAGTCGAGGAGGAAGATGATGAGACAGAAGA
CGTCAAAACAGCCACCAACAATGCTTCATCTTCATGCCAGTCGACCCCCAGGAAAGGAAAAACCCACAAAACATGT
TCACAACGGGCATGTTTTCAATGGTTCCAGCAGGTCAACACGGGAGAAGGAACCTGTTCAAAAACACAAAAGCAA
AGAGGCCACTCCCGCAAAGGAGAAGCACAGCGATCACCGGGCTGACAGCCGCCGGGAGCAGGCTTCAGCTAACCA
CCCCGCAGCGGCCCTCCACGGGTTTCTCGGCCAAGGGGCTTGCTGCCACCCATCACACCCCCCTCTGCATCG
GTCGGCTCAGGACTTACGGAAACAGGTTTCTAAGGTAAACGGAGTCACTCGAATGTCATCTCTGGGTGCAGGTGT
AACCAGTGCCAAAAGATGCGCGAGGTGAGACCTTCACCATCCAAAAGTGTGAAGTACACTGCCACGGTGACGAA
GGGGGCTGTACATACACCAAAGCCAAGAGAGAACTGGTCAAGGACACCAAACCAATCACACAAGCCCAGTTC
CGCTGTCAACCACACAATCTCAGGGAAGAACTGAAAGTAGCAATGCAAAAACCCGCAAACAGGTGCTATCCCTCGG
GGGGGCGTCCAAGTCCACTGGGCCCGCCGTCATGGCCTCAAGGTGAGTGGCAGGTTGAACCCAAAGTCATGCAC
TAAGGAGGTGGGGGGGCGGCAGCTGCGGGAGGGCCTGCAGCTGCGGGAGGGGCTGCGGAAGTCCAAGAGGAGACT
GGAAGAGGCACACCAGGCGGAGAAGCCGAGTCGCCCCCAAGAAGATGAAAGGGGCGGCTGGCCCCGCGGAAGG
CCCTGGCAAGAAGGCCCGGCCGAGAGAGGTCTGCTGAACGGACACGTGAAGAAGGAAGTGCCGGAGCGCAGTCT
GGAGAGGAATCGGCCGAAGCGGGCCACGGCCGGGAAGAGCACGCCAGGCAGACAAGCACATGGCAAGGCGGACAG
CGCCTCCTGTGAAAATCGTTCTACCTCGCAACCGGAGTCCGTGCACAAGCCGAGGACTCGGGCAAGGCCGAGAA
GGGCGGCGGCAAGGCCGGGTGGGCGGCCATGGACGAGATCCCCGTCTCAGGCCCTCCGCCAAGGAGTTCCACGA
TCCGCTCATCTACATCGAGTCGGTCCGCGCTCAGGTGGAGAAGTTCGGGATGTGCAGGGTGATCCCCCTCCGGA
CTGGCGGCCCGAGTGCAAGCTCAACGATGAGATGCGGTTTGTACGCAGATTGAGCACATCCACAAGCTGGGCCG
GCGCTGGGGCCCCAACGTGCAGCGGCTGGCCTGCATCAAGAAGCACCTCAAATCTCAGGGCATCACCATGGACGA
GCTCCCGCTCATAGGGGGCTGTGAGCTCGACCTGGCCTGCTTTTTCCGGCTGATTAATGAGATGGGCGGCATGCA
GCAAGTGACTGACCTCAAAAAATGGAACAACTAGCAGACATGCTGCGCATCCCCAGAAGTGGCCAGGACCGGCT
GGCCAAGCTGCAGGAGGCCTACTGCCAGTACCTACTCTCCTACGACTCCCTGTCCCCAGAGGAGCACCGGCCGGCT
GGAGAAGGAGGTGCTGATGGAGAAGGAGATCCTGGAGAAGCGCAAGGGGCGGCTGGAAGGCCACACAGAGAACGA
CCACCACAAGTTCCACCCCTCTGCCCCGCTTCGAGCCCAAGAATGGGCTCATCCACGGCGTGGCCCCCAGGAACGG
CTTCCGCAGCAAGCTCAAGGAGGTGGGCCAGGCCAGTTGAAGACTGGCCGGCGGCGACTCTTCGCTCAGGAAAA
AGAAGTGGTCAAGGAAGAGGAGGAGGACAAAGGCGTCTCAATGACTTCCACAAGTGCATCTATAAGGGAAGGTC
TGTTTCTCTAACAACCTTTTTATCGAACAGCGAGGAATATCATGAGCATGTGTTTCAGCAAGGAGCCTGCCCCAGC
CGAAATCGAGCAAGAGTACTGGAGGCTAGTGGAAGAGAAGGACTGCCACGTGGCAGTGCATGCGGCAAGGTGGA
CACCACACTCACGGCAGTGGATTCCCAGTAGGAAAATCAGAACCCCTTTTCGAGGCATGGATGGAACCTCACCGT
CCTCCCCAATAACACAGGGTCCATCCTGCGTCACCTCGGTGCTGTGCCTGGAGTGAATTTCCCTGGCTAAATAT
TGGCATGGTCTTTTCTACCTCATGCTGGTCTCGAGACCAAAATCACCTTCCATACATTGACTACTTACACACTGG
TGCTGACTGCATTTGGTATTGCATTCCTGCTGAGGAGGAGAACAAGCTGGAAGATGTGGTCCACACCCTGCTGCA
AGCCAATGGCACCCCGGGCTGCAGATGCTGGAAAGCAACGTGATGATCTCCCCGGAGGTGCTGTGCAAAGAGGG
GATCAAGGTGCACAGGACCGTGCAGCAGAGTGGCCAGTTTGTGCTGCTGCTTCCCGGGATCCTTTGTGTCAAAGT
GTGCTGTGGGTACAGCGTGTCTGAAACCGTGACTTTGCTACCACCCAGTGGACAAGTATGGGCTTTGAGACCGC
CAAGGAAATGAAGCGTCGCCATATAGCTAAGCCATTCTCCATGGAGAAGTTACTCTACCAGATTGCACAAGCAGA
AGCAAAAAAAGAAAACGGTCCCACTCTCAGTACCATCTCAGCCCTCCTGGATGAGCTCAGGGATACAGAGCTGCG
GCAGCGCAGGCAGCTGTTTCGAGGCTGGCCTCCACTCCTCCGCACGCTATGGCAGCCACGATGGCAGCAGCACGGT

2219/6881
FIGURE 2039B

GGCGGACGGGAAGAAAAAGCCTCGAAAGTGGCTGCAGTTGGAGACGTCAGAGAGGAGGTGTCAGATCTGCCAGCA
CCTGTGCTACCTGTCCATGGTGGTACAAGAGAACGAAAACGTCGTGTTCTGTCTGGAGTGTGCTCTGCGCCACGT
GGAGAAACAGAAGTCCTGCCGAGGGCTGAAGTTGATGTACCGCTACGATGAGGAACAGATTATCAGTCTGGTCAA
TCAGATCTGCGGCAAAAGTGTCTGGTAAAAACGGCAGCATTGAGAACTGTCTCAGTAAACCCACACCAAAAAGAGG
TCCCCGCAAGAGAGCGACAGTGGACGTGCCCCCTCCCGTCTGTCAGCCTCCAGTTCATCCAAAAGTGCTTCGAG
CTCATCATGAAGATGCCAACGCCCCGTGGTCGATTTATATATATTTTTTTGTAAATTATTATATTCTAGTTTGGAGT
ACTTGCTGTAGGATTCAAGCTGTCTTTGCACTAGCTCTAAAGAAGATTTTCTTCTGGTTTTAGAGAACTAATTTT
GTTTTAGCATTAAACTGTTGAACTTTTTTTTGTACTTAGAAAACTAGATACTGCAGTCAGATTTTGGAACTGC
CGTATAGTCACTGTTTTAAAAACCCCGAGGGGCTGTATTAATTTGTATTGCCCCATGGCTGACAAAAGCCTTTT
TTTTTGGTTTTGATTTTTTTTTTTTTTTGTAAGTGTGGGGGAAAAAGGCTTTTTTAACCCATTTTTGAAGAGGGTG
AAGTTTGGAGAACAAATTTAAAAACCATCAGTCATGTGAGCAGATTTTTTAGAAGGGATAGGAGACACACGCGCA
CACACACACACACAGAACTTGAAATGGCTTTTGCTTTGGCTGTGCTCTTCTGCCGTGTGCCAGATGAGCTTGTG
ATCTGGGAAGCCGGGGCACCCCGTTTTGTTTCTCTGGGCGGTTGTGGCAGCTGAAGGCGGACGTTGTTTCCATA
CCATAGGTGGAACGAGGAGACGGGAGCGAGTGGGCTCTCCACCAGCACATCACTATGCATCTGTTCCAGGAAAGA
AGAAAAGCGAGCGAGGAAGACGGAAAAGACTGCCTGCCTTGGAGGGGTCACATGAGGGAGACCTGTGCCTGATTT
CATTAGGAAATCCATTCTGTTATTTTTTGGTGTCTGTTGGCTACTTTATCAAAAAACCTTCAATAGCATCCTTAA
GATTTAAAAAAGGAAAAAAGTGAATGGAAGCCGTAAGTGCTTCTTTGTCATCGACGTGCA
ATCTTTCTAACATTCCATCTCCATCTCACCGCTTCTTGTGTTGACACCTTCACAAGTCAGCATTAACTTTCTTTT
AAAACCTGTTTCATTTATGATCATGTAGAGAGCCACTAGGAGGCCTGCAGTTATTTTTGAATGTGAAAATGCATT
TGCGTTTCATCTTGTCTATTTTTTCTCTTCATGTTGTAACAAAAAGGAAAAAAGAAAAAATCCCATCCCTTTT
GTACATATGCCTGTAAATTGTTTTAAATACTTGAGCCTTTTTCTCGGTGGGGGGTGGGGAGGGGGGTGAGAAGAC
AAGATGAAGAAAAGCCTTACATTTAGTTTCTTCATCGGTTGGATTGGATGCTTACAGGGTTTTTCTTGTAACAT
TTATAAGTGCTGCTTACATCACTGAACAACAACAAAAAATAATAATGGAGTAGCTGTTGCCCTTCTCCGGTTGT
GTGTACAGTATGTGTGGAATAAAAAAGGGAACTGTTTTACAAGCTGTTCTTTGTTTCATAATTGGATTTCATCA
ATCCCGTAGCTACCCATATTGCACTGAGCTTGCCAGTGGTGAAGTGCAGGAACGTCCTATGATCCACTTTGTTGG
TTGTTGTTGCAGAAGACTGAACTGTTTTGGAATATTTAACAATTACAGAAACAGTCAAGTGTGTTTCCAATGTGGT
TGTCGGTTTTCTATGGCCTTGCTGTGTACTTTCCCTCTTTTTGACAGTAACTTCTGCCTATGGCTTACAGTTTG
ACATTTAATTTATTAGCGCTGCTCTGCACCCCTCCCTTGGGAGGGAGACTTCATGTGGTTTATTGCGAGTTTTTT
GTTTACTTTTTAGGTTTGTACTACAAGTTTAATAATAAAAAACAAAGTTTTTTGGA

2220/6881
FIGURE 2040

MSKERPKRNI IQKKYDDSDGIPWSEERVVRKVLYLSLKEFKNSQKRQHAEGIAGSLKTVNGLLGNDQSKGLGPAS
EQSENEKDDASQVSSTSDVSSSDFEEGSPSRKRPRQLQAQRKFAQSQPNSPSTTPVKIVEPLLPPTATQISDLSKR
KPKTEDFLTFCLRGSPALPNSMVYFGSSQDEEEVEEEDDEDEDVKTATNNASSSCQSTPRKGKTHKHVHNGHVF
NGSSRSTREKEPVQKHKSKEATPAKEKHSDDRADSRRREQASANHPAAAPSTGSSAKGLAATHHHHPPLHRS AQDLR
KQVSKVNGVTRMSSLGAGVTSAKKMREVVRPSPSKTVKYTATVTKGAVTYTKAKRELVKDTKPNHHKPSSAVNHTI
SGKTESSNAKTRKQVLSLGGASKSTGPAVNGLKVSGRLNPKSCTKEVGGRLREGLQLREGLRNSKRRLEEAHQA
EKPQSPPKKMKGAAGPAEGPGKKAPAERGLLNHGHVKKEVPERSLERNRPKRATAGKSTPGRQAHGKADSASCENR
STSQPESVHKPQDSGKAKEGGGKAGWAAMDEIPVLRPSAKEFHDPLIYIESVRAQVEKFGMCRVIPPPDWRPECK
LNDEMRFVTQIQHIHKLGRRWGPNVQRLACIKKHLKSQGITMDELPLIGGCELDLACFFRLINEMGGMQQVTDLK
KWNKLADMLRIPRTAQDRLAKLQEAYCQYLLSYDSLSP EHRRLKEVLEMEKEILEKRKGPLEGHTENDHHKFHP
LPRFEFPKNGLIHGVAPRNGFRSKLKEVGQAQLKTGRRRLFAQEKEVVKEEEDKGVLENDFHKCIYKGRSVSLTTF
YRTARNIMSMCFSEKAPAEIEQEYWRLVEEKDCHVAVHCGKVDTNTHGSGFPVGKSEPF SRHGWNLT VLPNNTG
SILRHLGAVPGVTIPWLNIGMVFSTSCWSRDQNHLPYIDYLHTGADC IWYCIPAEENKLEDVVHTLLQANGTPG
LQMLESNVMISPEVLCKEGIKVHRTVQSGQFVVCFPGSFVSKVCCGYSVSETVHFATTQWTSMGFETAKEMKRR
HIAKPF SMEKLLYQIAQAEAKKENGPTLSTISALLDEL RDTELRRQLFEAGLHSSARYGSHDGSSTVADGKKK
PRKWLQLET SERRCQICQHLCYLSMVVQENENVVFCLECALRHVEKQKSCRG LKLMYRYDEEQIISLVNQICGKV
SGKNGSIENCLSKPTPKRGRPRKRATVDVPPSRLSASSSSKSASSSS

2221/6881
FIGURE 2041

GCCCATGCCCCGCCCCCGCGTAGACGCTGTGGTGTGTACGGCCGCAGCGGGGCAGGGGGTCTCCGAGGCCGCTGCG
GCACGTAATCAGAGAGCTTTCAAAGCATCACTCATGAAACTGACTTGTTTAGAGCCCTCCCCTGCTCCCTGCGC
TGCACTGACAATGCCATCTATACCCCTCAGCATGACCCAGGAGGAACATATTTTCATTCAATCACTCTTGGAAG
GCACCCAGAATTGCTAACCAAATTCTGGCTCCCTTTGAAATGAGGCCTGTATTTGTGGAGGTCACGGGACATACA
GGTGTTACATCATCCTCTGTGAGATGAAGAAGAGTTGCATGCAGCAGTTCATTAAGATCGATGGCAAGGTCCGA
ACTGACAAAACCTACCCTGCTGGATTTCATGGATGTCATCAGCATTGACAAGATGGGAGAGAATTTTGTCTGATC
TATGACACCAAGGGTCACTTTGCTGTACATTGTATTACACCTGAGGAAGCCAAAATTGGTGTGATCACCAACAGA
GAGAGGCACCCTGGATCTTTTGACGTGTTTCACATGAAAGATGCCAATGGCCACAGCTTTGCCACTCAACTTTCC
AACATTTTTGTTATTGGCAAGGGCAACAAACCATGGATTCTCTTCCCTGA

2222/6881
FIGURE 2042

CCTTTCCGTCTGGCGGCAGCCATCAGGTAAGCCAAGATGGGTGCATACAAGTACATCCAGGAGCTATGGAGAAAG
AAGCAGTCTGATGTCATGCGCTTTCTTCTGAGGGTCCGCTGCTGGCAGTACCGCCAGCTCTCTGCTCTCCACAGG
GCTCCCCGCCCCACCCGGCCTGATAAAGCGCGCCGACTGGGCTACAAGGCCAAGCAAGGTTACGTTATATATAGG
ATTCGTGTTGCGCGTGGTGGCCGTAACCAGCTAAAGTTTGCTCGAAGCCTTCAGTCCGTTGCAGAGGAGCGAGTT
GGACGCCACTGTGGGGCTCTGAGGGTCCTGAATTCTTACTGGGTTGGTGAAGATTCCACATACAAATTTTTTGAG
GTTATCCTCATTGATCCATTCCATAAAGCTATCAGAAGAAATCCTGACACCCAGTGGATCACCAAACCAAGTCCAC
AAGCACAGGGAGATGCGTGGGCTGACATCTGCAGGCCGAAAGAGCCGTGGCCTTGGAAGGGCCATAAGTTCAC
CACACTATTGGTGGCTCTCGCCGGGCAGCTTGGAGAAGGCGCAATACTCTCCAGCTCCACCGTTACCGCTAATAT
AAGTAAAGTCTGTAAATTCATACTTAATAAA

2223/6881
FIGURE 2043

MGAYKYIQELWRKKQSDVMRFLLRVRCWQYRQLSALHRAPRPTRPDKARRLG YKAKQGYVIYRIRVRRGGRNQLK
FARSLQSVAEERVGRHCGALRVLSYWVGEDSTYKFFEVLIDPFHKAIRRNPDTQWITKPVHKKHREMRGLTSAG
RKSRLGKGHKFHHTIGGSRRAAWRRRNTLQLHRYR

2224/6881
FIGURE 2044A

CCGACCAACACCAACACCCAGCTCCGACGCAGCTCCTCTGCGCCCTTGCCGCCCTCCGAGCCACAGCTTTCCTCC
CGCTCCTGCCCCCGGCCCGTTCGCCGTCTCCGCGCTCGCAGCGCCTCGGGAGGGCCAGGTAGCGAGCAGCGACC
TCGCGAGCCTTCCGCACTCCCGCCCGGTTCCCGGCCGTCCGCCTATCCTTGCCCCCTCCGCTTTCTCCGCGCC
GGCCCGCCTCGCTTATGCCTCGGCGCTGAGCCGCTCTCCCGATTGCCCGCCGACATGAGCTGCAACGGAGGCTCC
CACCCGCGGATCAACACTCTGGGCGCATGATCCGCGCCGAGTCTGGCCCGGACCTGCGCTACGAGGTGACCAGC
GGCGGCGGGGACACCAGCAGGATGTACTATTCTCGGCGCGGCGTGATCACCGACCAGAACTCGGACGGCTACTGT
CAAACCGGCACGATGTCCAGGCACCAGAACCAGAACACCATCCAGGAGCTGCTGCAGAACTGCTCCGACTGCTTG
ATGCGAGCAGAGCTCATCGTGACGCTGAATTGAAGTATGGAGATGGAATACAACCTGACTCGGAGTCGAGAAATTG
GATGAGTGTTCCTGCCCAGGCCAATGACCAATGGAAATCCTCGACAGCTTGATCAGAGAGATGCGGCAGATGGGC
CAGCCCTGTGATGCTTACCAGAAAAGGCTTCTTCAGCTCCAAGAGCAAATGCGAGCCCTTTATAAAGCCATCAGT
GTCCCTCGAGTCCGCGAGGGCCAGCTCCAAGGGTGGTGGAGGCTACACTTGTGAGAGTGGCTCTGGCTGGGATGAG
TTCACCAAACATGTCAACAGTGAATGTTTGGGGTGGATGAGGCAGCAAAGGGCGGAGATGGACATGGTGGCCCTGG
GGTGTGGACCTGGCCTCAGTGGAGCAGCACATTAACAGCCACCGGGGCATCCACAACCTCCATCGGCGACTATCGC
TGGCAGCTGGACAAAATCAAAGCCGACCTGCGCGAGAAATCTGCTATCTACCAGTTGGAGGAGGAGTATGAAAAC
CTGCTGAAAGCGTCCTTTGAGAGGATGGATCACCTGCGACAGCTGCAGAACATCATTACAGGCCACGTCCAGGGAG
ATCATGTGGATCAATGACTGCGAGGAGGAGGAGCTGCTGTACGACTGGAGCGACAAGAACACCAACATCGCTCAG
AAACAGGAGGCCTTCTCCATACGCATGAGTCAACTGGAAGTTAAAGAAAAAGAGCTCAATAAGCTGAAACAAGAA
AGTGACCAACTTGTCTCAATCAGCATCCAGCTTCAGACAAAATTGAGGCCATATATGGACACTCTGCAGACGCAG
TGGAGTTGGATTCTTCAGATCACCAAGTGCATTGATGTTTCATCTGAAAGAAAATGCTGCCTACTTTTCAGTTTTTT
GAAGAGGCGCAGTCTACTGAAGCATACCTGAAGGGCTCCAGGACTCCATCAGGAAGAAGTACCCCTGCGACAAG
AACATGCCCCCTGCAGCACCTGCTGGAACAGATCAAGGAGCTGGAGAAAGAACGAGAGAAAATCCTTGAATACAAG
CGTCAGGTGCAGAACTTGGTAAACAAGTCTAAGAAGATTGTACAGCTGAAGCCTCGTAACCCAGACTACAGAAGC
AATAAACCCATTATTCTCAGAGCTCTCTGTGACTACAAACAAGATCAGAAAATCGTGCATAAGGGGGATGAGTGT
ATCCTGAAGGACAACAACGAGCGCAGCAAGTGGTACGTGACGGGCCCCGGAGGCGTTGACATGCTTGTTCCCTCT
GTGGGGCTGATCATCCCTCCTCCGAACCCACTGGCCGTGGACCTCTCTTGCAAGATTGAGCAGTACTACGAAGCC
ATCTTGCTCTGTGGAACCAGCTCTACATCAACATGAAGAGCCTGGTGTCTGGCACTACTGCATGATTGACATA
GAGAAGATCAGGGCCATGACAATCGCCAAGCTGAAAACAATGCGGCAGGAAGATTACATGAAGACGATAGCCGAC
CTTGAGTTACATTACCAAGAGTTTCATCAGAAATAGCCAAGGCTCAGAGATGTTTGGAGATGATGACAAGCGGAAA
ATACAGTCTCAGTTACCCGATGCCCAGAAGCATTACCAGACCCTGGTCAATCAGCTCCCTGGCTATCCCCAGCAC
CAGACAGTGACCACAACCTGAAATCACTCATGGAACCTGCCAAGATGTCAACCATAATAAAGTAATTGAAACC
AACAGAGAAAATGACAAGCAAGAAACATGGATGCTGATGGAGCTGCAGAAAGATTGCGCAGGCAGATAGAGCACTGC
GAGGGCAGGATGACTCTCAAAAACCTCCCTCTAGCAGACCAGGGATCTTCTCACCACATCACAGTGAATAATTAAC
GAGCTTAAGAGTGTGAGAATGATTCACAAGCAATTGCTGAGGTTCTCAACCAGCTTAAAGATATGCTTGCCAAC
TTCAGAGGTTCTGAAAAGTACTGCTATTTACAGAATGAAGTATTTGGACTATTTTCAGAACTGGAATAATCAAT
GGTGTACAGATGGCTACTTAAATAGCTTATGCACAGTAAGGGCACTGCTCCAGGCTATTCTCCAAACAGAAGAC
ATGTTAAAGGTTTATGAAGCCAGGCTCACTGAGGAGGAAACTGTCTGCCTGGACCTGGATAAAGTGGAAGCTTAC
CGCTGTGGACTGAAGAAAATAAAAAATGACTTGAACCTGAAGAAGTCGTTGTTGGCCACTATGAAGACAGAACTA
CAGAAAAGCCCAGCAGATCCACTCTCAGACTTCACAGCAGTATCCACTTTATGATCTGGACTTGGGCAAGTTCCGT
GAAAAAGTCACACAGCTGACAGACCGCTGGCAAAGGATAGATAAACAGATCGACTTTAGGTTATGGGACCTGGAG
AAACAAAATCAAGCAATTGAGGAATTATCGTGATAACTATCAGGCTTTCTGCAAGTGGCTCTATGATGCTAAACGC
CGCCAGGATTCTTAGAATCCATGAAATTTGGAGATTCCAACACAGTCATGCGGTTTTTGAATGAGCAGAAGAAC
TTGCACAGTGAAATATCTGGCAAACGAGACAAATCAGAGGAAGTACAAAAAATTGCTGAACCTTTCGCCAATTCA
ATTAAGGATTATGAGCTCCAGCTGGCCTCATACCTCAGGACTGGAAACTCTGCTGAACATACCTATCAAGAGG
ACCATGATTCAGTCCCTTCTGGGGTGATTCTGCAAGAGGCTGCAGATGTTTCATGCTCGGTACATTGAACTACTT
ACAAGATCTGGAGACTATTACAGGTTCTTAAGTGAGATGCTGAAGAGTTTGGAAAGATCTGAAGCTGAAAAATACC
AAGATCGAAGTTTTGGAAGAGGAGCTCAGACTGGCCCGAGATGCCAACTCGGAAAACCTGTAATAAGAACAAATTC
CTGGATCAGAACCTGCAGAAATACCAGGCAGAGTGTTCCAGTTCAAAGCGAAGCTTGCGAGCCTGGAGGAGCTG
AAGAGACAGGCTGAGCTGGATGGGAAGTCGGCTAAGCAAAATCTAGACAAGTGCTACGGCCAAAATAAAGAAGCTC

2225/6881
FIGURE 2044B

AATGAGAAGATCACCCGACTGACTTATGAGATTGAAGATGAAAAGAGAAGAAGAAAATCTGTGGAAGACAGATTT
GACCAACAGAAGAATGACTATGACCAACTGCAGAAAGCAAGGCAATGTGAAAAGGAGAACCTTGGTTGGCAGAAA
TTAGAGTCTGAGAAAGCCATCAAGGAGAAGGAGTACGAGATTGAAAGGTTGAGGGTTCTACTGCAGGAAGAAGGC
ACCCGGAAGAGAGAATATGAAAATGAGCTGGCAAAGGTAAGAAACCACTATAATGAGGAGATGAGTAATTTAAGG
AACAAGTATGAAACAGAGATTAACTTACGAAGACCACCATCAAGGAGATATCCATGCAAAAAGAGGATGATTCC
AAAAATCTTAGAAACCAGCTTGATAGACTTTCAAGGGAAAATCGAGATCTGAAGGATGAAATTGTCAGGCTCAAT
GACAGCATCTTGCAAGGCACTGAGCAGCGAAGGCGAGCTGAAGAAAACGCCCTTCAGCAAAAAGGCCTGTGGCTCT
GAGATAATGCAGAAAGAAGCAGCATCTGGAGATAGAAGTGAAGCAGGTCATGCAGCAGCGCTCTGAGGACAATGCC
CGGCACAAGCAGTCCCTGGAGGAGGCTGCCAAGACCATTGAGGACAAAATAAGGAGATCGAGAGACTCAAAGCT
GAGTTTCAGGAGGAGGCCAAGCGCCGCTGGGAATATGAAAATGAACTGAGTAAGGTAAGAAACAATTATGATGAG
GAGATCATTAGCTTAAAAAATCAGTTTGAGACCGAGATCAACATCACCAAGACCACCATCCACCAGCTCACCATG
CAGAAGGAAGAGGATACCAAGTGGCTACCGGGCTCAGATAGACAATCTCACCCGAGAAAACAGGAGCTTATCTGAA
GAAATAAGAGGGCTGAAGAACACTCTAACCAGACCACAGAGAATCTCAGGAGGGTGGAAGAAGACATCCAACAG
CAAAAGGCCACTGGCTCTGAGGTGTCTCAGAGGAAACAGCAGCTGGAGGTTGAGCTGAGACAAGTCACTCAGATG
CGAACAGAGGAGAGCGTAAGATATAAGCAATCTCTTGATGATGCTGCCAAAACCATCCAGGATAAAAACAAGGAG
ATAGAAAGGTTAAAACAAGTATCGACAAAGAAACAAATGACCGGAAATGCCTGGAAGATGAAAACGCGAGATTA
CAAAGGGTCCAGTATGACCTGCAGAAAGCAAACAGTAGTGCGACGGAGACAATAAACAACTGAAGGTTGAGGAG
CAAGAACTGACACGCTGAGGATCGACTATGAAAGGGTTCCAGGAGAGGACTGTGAAGGACCAGGATATCACG
CGGTTCCAGAAGCTCTCTGAAAGAGCTGCAGCTGCAGAAGCAGAAGGTGGAAGAGGAGCTGAATCGGCTGAAGAGG
ACCGCGTCAGAAGACTCCTGCAAGAGGAAGAAGCTGGAGGAAGAGCTGGAAGGCATGAGGAGGTCGCTGAAGGAG
CAAGCCATCAAAATCACCAACCTGACCCAGCAGCTGGAGCAGGCATCCATTGTTAAGAAGAGGAGTGAGGATGAC
CTCCGGCAGCAGAGGGACGTGCTGGATGGCCACCTGAGGGAAAAGCAGAGGACCCAGGAAGAGCTGAGGAGGCTC
TCTTCTGAGGTGAGGCGCTGAGGCGGAGTTACTCCAGGAACAGGAAAGTGTCAAACAAGCTCACTTGAGGAAT
GAGCATTTCAGAAAGGCGATAGAAGATAAAAGCAGAAGCTTAAATGAAAGCAAATAGAAATTGAGAGGCTGCAG
TCTCTCACAGAGAACCTGACCAAGGAGCACTTGATGTTAGAAGAAGAACTGCGGAACCTGAGGCTGGAGTACGAT
GACCTGAGGAGAGGACGAAGCGAAGCGGACAGTGATAAAAATGCAACCATCTTGGAAGTAAAGGAGCCAGCTGCAG
ATCAGCAACAACCGGACCCTGGAAGTGCAGGGGCTGATTAATGATTTACAGAGAGAGAGGGAAAATTTGAGACAG
GAAATTGAGAAATTCCAAAAGCAGGCTTTAGAGGCATCTAATAGGATTCAGGAATCAAAGAATCAGTGTAAGTCA
GTGGTACAGGAAAGAGAGAGCCTTCTGGTGAAAATCAAAGTCTGAGGCAAGACAAGGCAAGGCTGCAGAGGCTG
GAGGATGAGCTGAATCGTGCAAAATCAACTCTAGAGGCAGAAAACAGGGTGAAACAGCGCCTGGAGTGTGAGAAA
CAGCAAATTCAGAATGACCTGAATCAGTGGAAGACTCAATATTCCCGCAAGGAGGAGGCTATTAGGAAGATAGAA
TCGGAAAGAGAAAAGAGTGAGAGAGAGAAGAACAGTCTTAGGAGTGAGATCGAAAGACTCCAAGCAGAGATCAAG
AGAATTGAAGAGAGGTGCAGGCGTAAGCTGGAGGATTCTACCAGGGAGACACAGTCACAGTTAGAAACAGAACGC
TCCCGATATCAGAGGGAGATTGATAAACTCAGACAGCGCCCATATGGGTCCCATCGAGAGACCCAGACTGAGTGT
GAGTGGACCGTTGACACCTCCAAGCTGGTGTTTGATGGGCTGAGGAAGAAGGTGACAGCAATGCAGCTCTATGAG
TGTCAGCTGATCGACAAAACAACCTTGACAAAACCTATTGAAGGGGAAGAAGTCAGTGGAAGAAGTTGCTTCTGAA
ATCCAGCCATTCTTCGGGGTGCAAGGATCTATCGCTGGAGCATCTGCTTCTCCTAAGGAAAAATACTCTTTGGTA
GAGGCCAAGAGAAAAGAAATTAATCAGCCCAGAATCCACAGTCATGCTTCTGGAGGCCCAGGCAGCTACAGGTGGT
ATAATTGATCCCCATCGGAATGAGAAGCTGACTGTGACAGTGCCATAGCTCGGGACCTCATTGACTTCGATGAC
CGTCAGCAGATATATGCAGCAGAAAAGCTATCACTGGTTTTGATGATCCATTTTTCAGGCAAGACAGTATCTGTT
TCAGAAGCCATCAAGAAAAATTTGATTGATAGAGAAAACCGGAATGCGCCTGCTGGAAGCCCAGATTGCTTCAGGG
GGTGTAGTAGACCTGTGAACAGTGTCTTTTTGCCAAAAGATGTGCGCTGGCCCCGGGGGCTGATTGATAGAGAT
TTGTATCGATCCCTGAATGATCCCCGAGATAGTCAGAAAAACTTTGTGGATCCAGTCACCAAAAAGAAGGTCAGT
TACGTGCAGCTGAAGGAACGGTGCAGAAICGAACCACATACTGGTCTGCTCTTGCTTTCAGTACAGAAGAGAAGC
ATGTCCTTCCAAGGAATCAGACAACCTGTGACCGTCACTGAGCTAGTAGATTCTGGTATATTGAGACCGTCCACT
GTCAATGAACTGGAATCTGGTCAGATTTCTTATGACGAGGTTGGTGAGAGAATTAAGGACTTCCTCCAGGGTTCA
AGCTGCATAGCAGGCATATACAATGAGACCACAAAACAGAAGCTTGGCATTTATGAGGCCATGAAAATTGGCTTA
GTCCGACCTGGTACTGCTCTGGAGTTGCTGGAAGCCCAAGCAGCTACTGGCTTTATAGTGGATCCTGTTAGCAAC

2226/6881
FIGURE 2044C

TTGAGGTTACCACTGGAGGAAGCCTACAAGAGAGGCTCTGGTGGGCATTGAGTTCAAAGAGAAGCTCCTGTCTGCA
GAACGAGCTGTCACTGGGTATAATGATCCTGAAACAGGAAACATCATCTCTTTGTTCCAAGCCATGAATAAGGAA
CTCATCGAAAAGGGCCACGGTATTTCGCTTATTAGAAGCACAGATCGCAACCGGGGGGATCATTGACCCAAAGGAG
AGCCATCGTTTACCAGTTGACATAGCATATAAGAGGGGCTATTTCAATGAGGAACTCAGTGAGATTCTCTCAGAT
CCAAGTGATGATACCAAAGGATTTTTTGACCCCAACACTGAAGAAAATCTTACCTATCTGCAACTAAAAGAAAGA
TGCATTAAGGATGAGGAAACAGGGCTCTGTCTTCTGCCTCTGAAAGAAAAGAAGAAACAGGTGCAGACATCACAA
AAGAATACCTCAGGAAGCGTAGAGTGGTCATAGTTGACCCAGAAACCAATAAAGAAATGTCTGTTGAGGAGGCC
TACAAGAAGGGCCTAATTGATTATGAAACCTTCAAAGAACTGTGTGAGCAGGAATGTGAATGGGAAGAAATAACC
ATCACGGGATCAGATGGCTCCACCAGGGTGGTCTCTGGTAGATAGAAAGACAGGCAGTCAGTATGATATTCAGAT
GCTATTGACAAGGGCCTTGTTGACAGGAAGTTCTTTGATCAGTACCGATCCGGCAGCCTCAGCCTCACTCAATTT
GCTGACATGATCTCCTTGAAAAATGGTGTCCGCCACCAGCAGCAGCATGGGCAGTGGTGTGAGCGATGATGTTTTT
AGCAGCTCCCGACATGAATCAGTAAGTAAGATTTCCACCATATCCAGCGTCAGGAATTTAACCATAAGGAGCAGC
TCTTTTTTCAGACACCTTGGAAGAATCGAGCCCCATTGCAGCCATCTTTGACACAGAAAACCTGGAGAAAAATCTCC
ATTACAGAAGGTATAGAGCGGGGCATCGTTGACAGCATCACGGGTCAGAGGCTTCTGGAGGCTCAGGCCTGCACA
GGTGGCATCATCCACCAACCACGGGCCAGAAGCTGTCACTTCAGGACGCAGTCTCCCAGGGTGTGATTGACCAA
GACATGGCCACCAGGCTGAAGCCTGCTCAGAAAGCCTTCATAGGCTTCGAGGGTGTGAAGGGAAAGAAGAAGATG
TCAGCAGCAGAGGCAGTGAAAGAAAAATGGCTCCCGTATGAGGCTGGCCAGCGCTTCCTGGAGTTCCAGTACCTC
ACGGGAGGTCTTGTTGACCCGGAAGTGCATGGGAGGATAAGCACCGAAGAAGCCATCCGGAAGGGGTTTCATAGAT
GGCCGCGCCGCACAGAGGCTGCAAGACACCAGCAGCTATGCCAAAATCCTGACCTGCCCCAAAACCAAATTAATA
ATATCCTATAAGGATGCCATAAATCGCTCCATGGTAGAAGATATCACTGGGCTGCGCTTCTGGAAGCCGCCTCC
GTGTCGTCCAAGGGCTTACCCAGCCCTTACAACATGTCTTCGGCTCCGGGGTCCCGCTCCGGCTCCCGCTCGGGA
TCTCGCTCCGGATCTCGCTCCGGGTCCCGCAGTGGGTCCCGGAGAGGAAGCTTTGACGCCACAGGGAATTCTTCC
TACTCTTATTCTACTCATTTAGCAGTAGTTCTATTGGGCACTAGTAGTCAGTTGGGAGTGGTTGCTATACCTTG
ACTTCATTTATATGAATTTCCACTTTATTAAATAATAGAAAAGAAAATCCCGGTGCTTGCAGTAGAGTGATAGGA
CATTCTATGCTTACAGAAAATATAGCCATGATTGAAATCAAATAGTAAAGGCTGTTCTGGCTTTTTATCTTCTTA
GCTCATCTTAAATAAGCAGTACACTTGGATGCAGTGCCTCTGAAGTGCTAATCAGTTGTAACAATAGCACAAATC
GAACTTAGGATTTGTTTCTTCTTCTGTGTTTTGATTTTTGATCAATTCTTTAATTTTGGAAGCCTATAATACA
GTTTTCTATTCTTGAGATAAAAATTAAATGGATCACTGATATTTTAGTCATTCTGCTTCTCATCTAAATATTTT
CATATTCTGTATTAGGAGAAAATTACCCTCCAGCACCAGCCCCCTCTCAAACCCCAACCCAAAACCAAGCAT
TTTGGAATGAGTCTCCTTTAGTTTCAGAGTGTGGATTGTATAACCCATATACTCTTCGATGTACTTGTTTGGTTT
GGTATTAATTTGACTGTGCATGACAGCGGCAATCTTTCTTTGGTCAAAGTTTTCTGTTTATTTTGCTTGTCTATA
TTCGATGTACTTTAAGGTGTCTTTATGAAGTTTGCTATTCTGGCAATAAACTTTTAGACTTTT

2227/6881
FIGURE 2045

TCCAAGAAGAGGAAGTTTGTCACTGATGGCATCTTCTAAGCTGAAATGAATGAGTTTCTTACTCAGGAGCTGGCT
GAAGATGGCTACTCTGGAGTTGAGATGCGAGTTACACCAACCAGGACAGAAATCATTGTCTTAGCCACCAGAACA
CAGAATGTTCTTGGTGAGAAGGGCCGGCGGATTTCGGGAAGTGAAGTGTAGTTTCAGAAGAGGTTTGGCTCTCCA
GAGGGCAGTGTAGAGCTTTATGCTGAAGAGGTGGCCACTAGGGGTCTGTGTGCCATTGCCCAGGCAGAGTCTCTG
CCTTACAAACTCCTAGGAGGGCTTGCTGTGCGGAGGGCCTGCTATGGTGTGTGCGGGTTCATCATGGAAACTGGG
GCCAAAGGCTGTGAGGTCGTGGTGTCTGGGAAACTCTGAGAGACAGAGAGCTAAATCCATGAAGTTTGTGGACGGC
CTGATGATCCACAGCAGAGACCCTGTAACTACTACGTTGACACTGCTGTGCGCCATGTGTTGCTCAGACAGAGT
GTGCTGGGCATCAAGGTGAAGATCATGCTGCCCTGGGACCCAAAGATGAGATAACTGCCCACCACCCCATCTCA
GAACAGAAGGGTGGA

2228/6881
FIGURE 2046

MNEFLTQELAEDGYSGVEMRVTPTRTEIIVLATRTQNVLGEKGRRIRELTAVVQKRFGSPEGSVELYAEVATRG
LCAIAQAESLPYKLLGGLAVRRACYGVSRFIMETGAKGCEVVVSGKL

2229/6881
FIGURE 2047

ATGACCAGGTTTCATCATCGCCTCTCTCCTCCCCCTCTACCTTTCTCCCTGGTTTCCATAGAGCAGAAATCTGGGTC
AAGGTGGAGTGCATTGGATCAAGAGTTGCTATGATTTGGGAAAAGCTCTGCAGGATAAGTCGAATAAAATCAGAC
CTTGCAGAAACTCAATCTGGCCCCCTGGGAACCTCTCCGGTGTGGAGCTGGAGGAAAAACCAGTACAGTACTCTCTC
AGGAAAAACAAGCTCAGAGGCGGAATCAACAAGACAGCTGACGAACACATCCTCTTCAAGAGAGGCCAGGGTCTCA
AGCTCAAGTGGCCAAGGCAAGACGGGTCAAAGTCAGAGTGGTGGTCACAGTCCTGGAGGTGGCAAGAAGGATGAC
AAGGACAAGAAAAAGAAATATGAACCTCCTGTACCAACTGGAGTGGGAAAAAGAAGAAAAACAAAAGGATCAGAT
GTTGCCAGCAAACCTGCCACTGGAATCGGGAACAAATGGAACCATTAGAAGAAAAGCAAGAGGAGGAAAGATCAAA
GGTGGACGATCTGAGGGGACCCCGATGTGAGTAGGAACCTTGGGAAGAGATCAATGACAGTCATGCCATCGTGTCT
ACATCTGTGGGCTCAGGACACTACGCCAACATTCTTTTCATTTGTAGACAAGGATCTGCTGGCAACTGGCTGCTCA
GTCCTGCTCAATCACAAGGTGCATGCCATGAGAGGGGTGCTGATGGATGACGTGGATCCCCCTGGTCACAGTGATG
AAGGTGGAAAAGGTCCCCCAGGAGACCTATGCCAATACTGGGAGGTTGGATAATCAAATTCAGGAAATTAAGGAA
TCTGTGGAGCTTCCTCTCACCCATGCTGAACATTATGAAGAGATGGGTATAAAGCCTCCTAAGGGGGTCAATTCTC
TATGGTCCACCTGGCATAGTTAAACCTTGCTAGCCAAAGCGGTAGCAAACCAAACCTCAGCCACTTTCTTGAAA
GTGGTTGGCTCTGAACTTATTCAGAAGTACCTAGGTGATGGGCCCAAACCTTGACGGGAATTGTTTCAAGTTGCT
GGAGAACATGCACCATCCATCGTGTCTTACTGATGAAACTGACGCCATTGGGACAAAAAGATATGACTCAAATTCT
GGTGAAGCTGGTCTGATGGCCTTAAGAGAACGTAGAATGAAAGCAACAAATGAAGACTTCAAAAAATCTAAAGAA
AATGTTCTTTATAAGAAACAGGAAGGCACCCCTGAGGGGCTGTCTCTCTAG

2230/6881
FIGURE 2048

MSVGTLEEINDSHAIVSTSVGSGHYANILSFVDKDLLATGCSVLLNHKVHAMRGVLMDDVDPLVTVMKVEKVPQE
TYANTGRLDNQIQEIKESVELPLTHAEHYEEMGIKPPKGVILYGPPGIVKTLLAKAVANQTSATFLKVVGSELIQ
KYLGDGPKLVRELFQVAGEHAPSIVFTDETDAGTKRYDSNSGEAGLMAIRERRMKATNEDFKKSKENVLYKKQE
GTPEGLSL

2231/6881
FIGURE 2049

GGGGGGCTCGGGCTGGGGGCGCGGCCTGTGCCGGCCGCCACCCCTCCTTGCATAAAAGCCGGAGCCCGCGGGGC
CGGCGCTCTCAGCCCGTCGGTTCCCGAGCGCCTTCCCGGTGACCCCGCAGTGGGTGTGTGAGGGGAGGACGGACA
GACCCAGACGCCCGCGGACCAGGAGGACGCTGACGAGGCACCATGCGTGAGATCGTGCACATCCAGGCGGGCCAG
TGCGGCAACCAGATCGGCGCCAAGTTTTGGGAGGTCATCAGTGATGAGCATGGGATTGACCCCACTGGCAGTTAC
CATGGAGACAGTGATTTGCAGCTGGAGAGAATCAATGTTTACTACAATGAAGCCACTGGTAACAAATATGTTTCCT
CGGGCCATCCTCGTGGAATCTGGAGCCAGGCACGATGGATTCCGGTTAGGTCTGGACCATTCCGGCCAGATCTTCAGA
CCAGACAATTTCTGTGTTTGGCCAGAGTGGAGCCGGGAATAACTGGGCCAAGGGCCACTACACAGAGGGAGCCGAG
CTGGTCGACTCGGTCCCTGGATGTGGTGAGGAAGGAGTCAGAGAGCTGTGACTGTCTCCAGGGCTTCCAGCTGACC
CACTCTCTGGGGGGCGGCACGGGGTCCGGGATGGGCACCCCTGCTCATCAGCAAGATCCGGGAAGAGTACCCAGAC
CGCATCATGAACACCTTCAGCGTCATGCCCTCACCCAAGGTGTCAGACACGGTGGTGGAGCCCTACAACGCCACC
CTCTCGGTCCACCAGCTGGTGGAAAACACAGATGAAACCTACTGCATTGACAACGAGGGCCCTGTATGACATCTGC
TTCCGCACCCCTGAAGCTGACCACCCCCACCTACGGGGACCTCAACCACCTGGTGTGCGCCACCATGAGCGGGGT
ACCACCTGCCTGCGCTTCCCGGGCCAGCTGAACGCAGACCTGCGCAAGCTGGCGGTGAACATGGTGCCCTTCCCT
CGCCTGCACTTCTTCATGCCCGGCTTCGCGCCCCCTGACCAGCCGGGGCAGCCAGCAGTACCGGGCGCTCACGGTG
CCCGAGCTCACCCAGCAGATGTTGACTCCAAGAACATGATGGCCGCTGCGACCCGCGCCACGGCCGCTACCTG
ACGGTGGCTGCCATCTTCCGGGGCCGCATGTCCATGAAGGAGGTGGACGAGCAGATGCTCAACGTGCAGAACAAG
AACAGCAGCTACTTCGTGGAGTGGATCCCCAACAACGTGAAGACGGCCGTGTGCGACATCCCGCCCCGCGGCCTG
AAGATGTGCGCCACCTTCATCGGCAACAGCACGGCCATCCAGGAGCTGTTCAAGCGCATCTCCGAGCAGTTCACG
GCCATGTTCCGGCGCAAGGCCTTCTGCACTGGTACACGGGCGAGGGCATGGACGAGATGGAGTTCACCGAGGCC
GAGAGCAACATGAACGACCTGGTGTCCGAGTACCAGCAGTACCAGGACGCCACGGCCGACGAACAAGGGGAGTTC
GAGGAGGAGGAGGGCGAGGACGAGGCGTAGATGCCCCCGGAGACGGGTTAGGGAAAGCGGAGGAGGAAAGCGAG
GGGTGGGGGGCTTCCCGGGACGATAACCTGGCAGTGGAAGGAAAGAAGCATGGTCTACTTTAGGTGTGCGCTGG
GTCTCTGGTGCTCTTCACTGTTGCCTGTCACTTTTTTTTTTCTTTTTTTGTAATATTGATGACATCAATGTAACAT
TTGAGATATTTCTGAATTACTGTTGTAATGGCTAAAATCACATAAACGTTTGTGTCGG

2232/6881
FIGURE 2050

GCCCCCGGTCCACGCCGCGCACCGCTCCGAGGGCCAGCGCCACCCGCTCCGCAGCCGGCACCATGCGCGAGATC
GTGCACATCCAGGCGGGGCCAGTGCGGCAACCAGATCGGCGCCAAGTTTTGGGAGGTCATCAGCGATGAGCATGGG
ATCGACCCACAGGCAGTTACCATGGAGACAGTGACTTGCAGCTGGAGAGAATCAACGTGTACTACAATGAGGCT
GCTGGTAACAAATATGTACCTCGGGCCATCCTGGTGGATCTGGAGCCTGGCACCATGGACTCTGTCAGGTCTGGA
CCCTTCGGCCAGATCTTCAGACCAGACAACCTTCGTGTTTCGGCCAGAGTGGAGCCGGGAATAACTGGGCCAAGGGC
CACTACACAGAGGGAGCCGAGCTGGTGCAGCTCGGTCTGGATGTGGTGAGGAAGGAGTCAGAGAGCTGTGACTGT
CTCCAGGGCTTCAGCTGACCCACTCTCTGGGGGGCGGCACGGGGTCCGGGATGGGCACCCTGCTCATCAGCAAG
ATCCGGGAAGAGTACCCAGACCGCATCATGAACACCTTCAGCGTCATGCCCTCACCCAAGGTGTCAGACACGGTG
GTGGAGCCCTACAACGCCACCCTCTCGGTCCACCAGCTGGTGGAAAACACAGATGAAACCTACTCCATTGATAAC
GAGGCCCTGTATGACATCTGCTTCGCGACCCTGAAGCTGACCACCCCCACCTACGGGGACCTCAACCACCTGGTG
TCGGCCACCATGAGCGGGGTCACCACCTGCCTGCGCTTCCCGGGCCAGCTGAACGCAGACCTGCGCAAGCTGGCG
GTGAACATGGTGCCCTTCCTCGCTGCACTTCTTCATGCCCGGCTTCGCGCCCCTGACCAGCCGGGGCAGCCAG
CAGTACCGGGCGCTCACGGTGCCCGAGCTCACCCAGCAGATGTTGCACTCCAAGAACATGATGGCCGCCTGCGAC
CCGCGCCACGGCCGCTACCTGACGGTGGCTGCCATCTTCGGGGCCGCATGTCCATGAAGGAGGTGGACGAGCAG
ATGCTCAACGTGCAGAACAAAGAACAGCAGCTACTTCGTGGAGTGGATCCCCAACACGTGAAGACGGCCGTGTGC
GACATCCCGCCCCGCGGCTGAAGATGTGCGCCACCTTCATCGGCAACAGCACGGCCATCCAGGAGCTGTTCAAG
CGCATCTCCGAGCAGTTCACGGCCATGTTCCGGCGCAAGGCCTTCCTGCACTGGTACACGGGCGAGGGCATGGAC
GAGATGGAGTTCACCGAGGCCGAGAGCAACATGAACGACCTGGTGTCCGAGTACCAGCAGTACCAGGACGCCACG
GCCGACGAACAAGGGGAGTTCGAGGAGGAGGAGGGCGAGGACGAGGCTTAAAAACTTCTCAGATCAATCGTGCAT
CCTTAGTGAACCTTCTGTTGTCTCAAGCATGGTCTTTCTACTTGTAAGTATGGTGCTCAGTTTTGCCTCTGTTA
GAAATTCACACTGTTGATGTAATGATGTGGAACCTCTCTAAAAATTACAGTATTGTCTGTGAAGGTATCTATACT
AATAAAAAAGCATGTGTAG

2233/6881
FIGURE 2051

MREIVHIQAGQCGNQIGAKFWEVISDEHGIDPTGSYHGSDSLQLERINVYYNEAAGNKYVPRAILVDLEPGTMDS
VRSGPFGQIFRPDNFVFGQSGAGNNWAKGHYTEGAELVDSVLDVVRKESESCDCLQGFQLTHSLGGGTGSGMGT
LISKIREEYPDRIMNTFSVMPSPKVSDTVVEPYNATLSVHQLVENTIDETYSIDNEALYDICFRTLKLTTPTYGDL
NHLVSATMSGVTTCLRFPGLNADLRKLAVNMVFPRLHFFMPGFAPLTSRGSQQYRALTVPELTQQMFDSKNMM
AACDPRHGRLTVAAIFRGRMSMKEVDEQMLNVQKNSSYFVEWIPNNVKTAVCDIPPRGLKMSATFIGNSTAIQ
ELFKRISEQFTAMFRRKAFLHWYTGECMDEMETFTEAESNMNDLVSEYQQYQDATADEQGEFEEEEGEDEA

2234/6881
FIGURE 2052

CCGCGTTCCCTGCCGGCACCGCGCCTGCCCTCTGCCGCGCTCCGCCCTGCCGCCGACCGCACGCCCCGCCGCGGGAC
ATGGCACACGCACCGGCACGCTGCCCCAGCGCCCGGGGCTCCGGGGACGGCGAGATGGGCAAGCCCAGGAACGTG
GCGCTCATCACCGGTATCACAGGCCAGGATGGTTCCCTACCTGGCTGAGTTCCTGCTGGAGAAAGGCTATGAGGTC
CATGGAATTGTACGGCGGTCCAGTTCATTTAATACGGGTGGAATTGAGCATCTGTATAAGAATCCCCAGGCTCAC
ATTGAAGGAAACATGAAGTTGCACTATGGCGATCTCACTGACAGTACCTGCCTTGTGAAGATCATTAAATGAAGTA
AAGCCCACAGAGATCTACAACCTTGGAGCCCAGAGCCACGTCAAAATTTCCCTTGACCTCGCTGAGTACACTGCG
GACGTTGACGGAGTTGGCACTCTACGACTTCTAGATGCAGTTAAGACTTGTGGCCTTATCAACTCTGTGAAGTTC
TACCAAGCCTCAACAAGTGAACTTTATGGGAAAGTGCAGGAAATACCCCAGAAGGAGACCACCCCTTTCTATCCC
CGGTCACCCTATGGGGCAGCAAACTCTATGCCTATTGGATTGTGGTGAACCTCCGTGAGGCGTATAATCTCTTT
GCAGTGAACGGCATTCTCTTCAATCATGAGAGTCCCAGAAGAGGAGCTAATTTTCGTTACTCGAAAAATTAGCCGG
TCAGTAGCTAAGATTTACCTTGGACAACTGGAATGTTTCAGTTTGGGAAATCTGGATGCCAAACGAGATTGGGGC
CATGCCAAGGACTATGTGGAGGCTATGTGGTTGATGTTGCAGAAATGATGAGCCGGAGGACTTCGTTATAGCTACT
GGGAGGTCCATAGTGTCGGGAATTTGTGAGAAATCATTCTTGACATTGGAAAAACCATTGTGTGGGAAGGA
AAGAATGAAAATGAAGTGGGCAGATGTAAAGAGACCGGCAAAAGTTCACGTGACTGTGGATCTCAAGTACTACCGG
CCAAGTGAAGTGGACTTTCTGCAGGGCGACTGCACCAAAGCGAAACAGAAGCTGAAGTGAAGCCCCGGGTGCGT
TTCGATGAGCTGGTGAGGGAGATGGTGCACGCCGACGTGGAGCTCATGAGGACAAACCCCAATGCCTGAGCAGCG
CCTCGAGCCCCGGCCCCGCCCTCCGGCTACAATCCCCGAGAGTCTCCGGTGCAGACGCGCTGCGGGGATGGGGAG
CGGCGTGCCAATCTGCGGGTCCCCTGCGGCCCTGCTGCCGCTGCGCTGTCCCGCCGCAAGAGCGGGGCCGCC
CGCCGAGGTTTGTAGCAGCCGGGATGTGACCCTCCAGGGTTTGGGTGCTTTGCGTTTGTGCAAGCCTCCTCTGA
ATGGCTTTGTGAAATCAAGATGTTTTAATCACATTCACCTTTACTTGAAATTATGTTGTTACACAACAAATTGTGG
GGCCTTCAAATTGTTTTTCC

2235/6881
FIGURE 2053

MAHAPARCP SARGSGDGEMGKPRNVALITGITGQDGSYLAEFLLKGYEVHGIVRRSSSFNTGRIEHLYKNPQAH
IEGNMKLHYGDLTDSTCLVKIINEVKPTEIYNLGAQSHVKISFDLAEYTADV DGVGTLRLLD AVKTCGLINSVKF
YQASTSELYGKVQEIPQKETTPFYPRSPYGA AKLYAYWIVVN FREAYNLFAVNGILFNHESPRRGANFVTRKISR
SVAKIYLGQLECFSLGNLDAKRDWGHAKDYVEAMWMLQNDPEDFVIATGEVHSVREFVEKSFLHIGKTIVWEG
KNENEVGRCKETGKVHVTVDLKYRPT EVDFLQGDCTKAKQKLNWKPRVAFDELVREMVHADVELMRTNPNA

2236/6881
FIGURE 2054A

CGCCGCGGCCCGGTACCAACGGGTGGTCTCGCCGAGGGAGCTGTCGTGCCTCGTGGTCCCGGGACTGCAGTGGTG
TGCGCTCTCGGCGCGTGGCGCTAGGCATGGCGATGGATCAAGTAAACGCGCTGTGCGAGCAGCTGGTGAAAGCGG
TGACGGTCATGATGGACCCCAACTCCACCCAGCGCTACCGGCTGGAAGCCCTCAAGTTTTGTGAGGAGTTTAAAG
AAAAGTGTCTATCTGTGTCCCTGTGGCTTGAGGTTGGCTGAGAAAACACAAGTTGCCATCGTCAGACATTTTG
GCCTTCAGATCCTGGAACACGTTGTCAAGTTTCGGTGGAACGGCATGTCTCGATTGGAGAAGGTGTATCTGAAGA
ACAGTGTGATGGAGCTGATTGCAAATGGAACATTGAACATTTTGGAGAGGAGAACCATATTAAAGATGCTCTGT
CTCGAATTGTAGTGGAATGATCAAGCGAGAGTGGCCACAGCATTGGCCTGACATGCTAATAGAATTGGACACTC
TTTCCAAACAAGGGGAAACACAGACAGAATTGGTGTATGTTTATCCTTTTGGCGACTGGCAGAGGATGTAGTGA
TTCAGACACTTCCCCCTCAAAGAAGAAGGGACATCCAGCAAAACATTAACCCAGAACATGGAAAGGATCTTCAGT
TTCTGCTTAACACACTTCAAGAAAATGTAAACAAGTATCAGCAAGTGAAGACAGATACTTCTCAGGAGTCAAAGG
CGCAAGCAAACCTGTGAGTAGGAGTTGCAGCACTGAATACTCTAGCAGGCTATATTGACTGGGTGTCTATGAGTC
ACATCACTGCTGAAAACCTGTAAACCTCTGGAGATACTGTGTTTGTCTGTTGAATGAACAGGAACCTTCAGTTGGGAG
CCGCTGAGTGTCTTCTCATTGTCAGTCAGCAGAAAAGGCAAGTTGGAAGACCGGAAGCCCTTGATGGTCTTATTTG
GAGATGTTGCCATGCATTATATACTCTCCGCCGCACAGACTGCTGATGGAGGAGGTTTGGTAGAAAAACACTACG
TCTTTCTGAAGAGGCTCTGTGAGGTGTTGTGTGCGCTGGGCAATCAGCTGTGTGCATTGCTGGGTGCAGATTCTG
ATGTAGAAACACCATCAAACCTTGGAAAATACCTGGAATCTTTTCTTGTCTTCAACCCATCCAAGTCAGTTTC
TACGCTCTTCAACTCAGATGACTTGGGGAGCCCTCTTCAGGCATGAAATCCTGTCCCGTGATCCTTTGCTATTAG
CAATAATACCAAAATATCTTCGTGCTTCCATGACTAAGTTGGTCAAGATGGGCTTTCCTTCTAAACAGACAGCC
CTAGCTGTGAATATTCTCGGTTTGATTTTGATAGCGATGAGGACTTCAATGCTTCTTCAACTCCTCCCGAGCAC
AACAGGAGAGGTGATGAGGTTGGCATGTGCTTTGGATCCCAAACTAGCTTCCAGATGGCTGGGGAGTGGCTAA
AGTATCAACTATCAACCTTTTCTTGATGCTGGTTCTGTGAATCTTGTCTGCAGTTGGAACCTGGAGAAGGAAGCC
TCTGTTCCGCTCTTCTCACCTTCATTCTGTCAGTGGGAAGCCATGACTCTTTTTTTGGAAAGTGTATACCCAGA
TGTTTCGAACACTAAATAGAGAAGAAATTCCTGTTAATGATGGAATAGAGCTATTGCAGATGGTTCTGAACCTTG
ATACCAAGGATCCCCTCATCCTGTCTGCTCCTTACTAATGTCTCTGCACTCTTCCATTGTGTACCTACAGAC
CAGAGTTCCTGCCCCAGGTCTTCTTAAGCTATTTTCATCTGTCACTTTTGAACTGTTGAAGAAAGTAAGGCC
CCAGAACCCGGGCAGTGAGGAATGTGAGGAGGCATGCTTGTTCCTCCATCATCAAGATGTGTGCTGACTACCCCC
AGCTTGTGCTGCCCAATTTTGACATGCTTTATAACCATGTGAAGCAACTCCTCTCCAATGAGCTACTCCTGACAC
AAATGGAGAAGTGTGCCCTCATGGAAGCCCTGGTTCTCATTAGCAACCAATTTAAGAACTACGAGCGTCAGAAGG
TGTTCTTAGAGGAGCTGATGGCACCAGTGGCCAGCATCTGGCTTTCTCAAGACATGCACAGAGTGTGTGATG
TTGATGCTTTTCATTGCGTATGTGGGTACAGATCAGAAGAGCTGTGACCCAGGCCTGGAGGATCCGTGTGGCTTAA
ACCGTGCACGAATGAGCTTTTGTGTATACAGCATTCTGGGTGTGGTGAAACGAACTTGCTGGCCCACTGACCTAG
AAGAGGCCAAAGCTGGGGGATTTGTGGTGGGTATACATCCAGTGGAAATCCAATCTTCCGTAACCCCTGCACAG
AGCAGATTCTGAAACTTCTTGACAATTTGCTTGGCCTTATAAGAACCACATAACATTATATGCACCAGAAATGC
TAGCCAAAATGGCAGAGCCTTTACCAAGGCTCTGGATATGCTTGACGCGGAAAAATCTGCTATATTAGGATTAC
CTCAACCTCTCTTGGAACCTCAATGACTCTCCTGTCTTCAAACCGTCTTGGAAGAATGCAGCGTTTCTTCTCTA
CCCTCTATGAAAACCTGTTTTTCATATCCTAGGGAAGGCAGGCCCTTCCATGCAGCAAGACTTCTATACTGTGGAGG
ACCTTGCTACCCAGCTTCTCAGCTCAGCCTTTGTCAACTTGAACAATATTCCTGACTACCGACTCAGACCCATGC
TTGGGGTCTTTGTAAAGCCTCTGGTGCTCTTCTGTCCCCCAGAGCACTATGAAGCCCTGGTATCCCCCATCCTCG
GACCTCTTTTACCTACCTCCATATGAGGCTTTCTCAGAAATGGCAAGTTATCAACCAAAGGAGCCTGCTGTGTG
GAGAAGATGAGGCTGCAGATGAAAACCCAGAGTCTCAAGAGATGCTGGAGGAGCAACTGGTGAGGATGTTAACC
GAGAAGTCATGGACCTAATCACGGTTTGCTGTGTTTCAAAGAAGGGTGTGACCACAGTAGTGCTCCCCCAGCAG
ATGGAGACGATGAAGAAATGATGGCCACAGAGGTCACCCCTCAGCTATGGCAGAGCTTACAGACCTGGGCAAAT
GTCTGATGAAGCATGAGGATGTTTGTACAGCGCTATTAATTACAGCCTTCAATTCCCTGGCCTGGAAGATACTC
TGTCCTGCCAGAGGACAACCTCACAGCTCTGCTGGCCTCTCTCAAACAAGTGTGTGACGGGACACTGCTCGCAG
ATGCAGTTACGTGGCTTTTACCAGTGTGCTGAAAGGCTTACAGATGCACGGGCAGCACGACGGGTGCATGGCTT
CCCTGGTCCATCTGGCCTTCCAGATATACGAGGCACTGCGCCCCAGGTACCTGGAGATAAGAGCTGTAATGGAGC
AAATCCCTGAAATACAGAAGGACTCACTGGACCAGTTTGAAGTCAAGCTTTTAAACCCCTCCCTGCAGAAAGTGG
CTGACAAGCGCCGAAAGGACCAATTCAAACGCCTCATTGCTGGTTGCATTGGGAACCCCTTGGGAGAGCAGTTCC

2237/6881
FIGURE 2054B

GAAAAGAAGTTCACATTAAGAATCTTCCCTCACTTTTCAAAAAACAAAGCCAATGCTGGAGACGGAGGTGCTGG
ACAATGATGGGGGTGGCCTGGCCACCATCTTTGAACCCTGAATCAAGCTTTTGGGCATCCTTCCTCGGCCTTTCT
TGTCATCTCTTCTTTCCCTTTGTAGCCGATCTCTAGGCCCTTCTTGCACTGCCACCTCACTTTCCACCACTGTCA
GCCTGGAAAGAGATCCAGGTCTGGAGCTGGAGAGAACAGGCCCTGTGCAGGACCAGAAGTAATTATACTAAAGTA
TCAAGAAAGGGAGTTAGGGCTTAAACTATTCTGTCTAGATGTCCCAGATAGTTCCCATTCTACTTTGGAGATTTGG
CTTTTCCAAGAAAAGCTAGAGCAGAGCAGCCCTTCTCCCACAAGCCCTCCCACCCCGTGCAGCCACATACCTGT
ACAGAATGGTAACATAAGGGTGTGTGCCAACCCCTGCGACTAGCAAGGCTCGCAGCAAGAGCACAGCCCTCAACT
ACTTGTGCCAGAGTTTCTCTTGGACCACTCCAACCTCCCACTGAGCCCTTTTGCTGCTGGGCTGGCAGGAACTTT
CCCCACTCCCTAAGGGGCATGTCTGGGTAGGTGCTAAGTGCTGAAGAGAACTTGGTCAGTTCTCTCAACTTTGC
TTTGGGCAAGAATCTGGTCACCTGATGGGATCCATGGTACAGGCTACTGCTAAACTTGGCACAGTATCAAGTATA
GTACCTCCAAGGACCAGGGCTGGGCAGTCTTTAGTGCTAACATCCCTTTAGAGTTCACACATCTTGCCCTTCCA
TGAATGACCCCTCAGTCTGGCCTCCCCAGCCTCAAGGTCCACTCAGGCACAAGAGCCACAGTACCCTAGATAGTG
TCACATGACACCGTTGTCTATCCAAGGATAATACAGACCAACTAGGCTACATCTGTGATGAGCAGCTAGCAAAGCC
GCTGGTCTTCTCCTAGGACTAAGTCCAGGTGCCTTCCACAATCTCATGGTCTTTCAGGTCCCTGGTTACTTTTCT
CAAAGGCCATTTCCAAAAGAATACATGCCTTCACATCACAACTGTACTGTGAGTCCATTCTAGAGGTCACTGAA
AGGCCCTGTAAAGAGAGGACATGGATACGGGACCTGGCCCTGAGGTTATTACTGGCCGTAAGGCAGAGTTAATCC
ATACAGAAACCAGTGTGTCCATGTGCTCTGCACAAAAACAGACCTGTTGTCCATCCAGTCCACTGACAAGAGGGT
TTCCCCGAGAGCCGAAGTGGACTGAAGCTACAGTTTTTTAGCTGGTGCGGGCCACAGGCAGGGTCAGATTGAGAAG
AAGCAAAGCTGGGGAAAGCAGAAGTTGGGAGTCTTGTGTTGCTCCCTCTTCCTGTGTGGTGCTCTGGGTTTCTGTG
GATCGTGAAGGCGATCTCAAGAGTGTTCCTCCAAACCTGATAGCTGCCTATTCCTGTCTGGTTGGGGCTGTGG
AGGATGTAGTTGTATTTATTGCATTGTAATATTTTTAACATCCTGTGACTTCATGCTAGAAATTTTCTATTGTTT
ATAGAAACTTTTTGTAGAAACATTAACCTCTAAAGCACATCTGCATGTCAGTAAAAATCTCAGTTTCGTACAG

2238/6881
FIGURE 2055

MAMDQVNALCEQLVKAVTVMMDPNSTQRYRLEALKFCEEFFKEKCPICVPCGLRLAEKTQVAIVRHFGGLQILEHV
KFRWNGMSRLEKVKYLNKNSVMELIANGTLNILEEENHIKDALSRIVVEMIKREWPQHWPDMLEIDTILSKQGETQT
ELVMFILLRLAEDVVTFTQTLPPQRRRDIQQTLTQNMERIFSFLNLTQENVNKYQQVKTDTSQESKAQANCRVGV
AALNTLAGYIDWVSMHITAENCKLLEILCLLLNEQELQLGAAECLLIASRKGLKLEDRKPLMVLFGDVAMHYIL
SAAQTADGGGLVEKHVFLKRLCQVLCALGNQLCALLGADSDVETPSNFGKYLESFLLAFTTHPSQFLRSSTQMTW
GALFRHEILSRDPLLLAIIPKYLRASMTNLVKMGFPSTKDSPSCEYSRFDSDSDDFNAFFNSSRAQQOGEVMRLA
CRLDPKTSFQMGAEWLKYQLSTFLDAGSVNSCSAVGTGEGSLCSVFSFVQWEAMTLFLESVITQMFRTLNREE
IPVNDGIELLQMVLFNFDTKDPLILSCVLTNVSALEFPFVTYRPEFLPQVFSKLFSSVTFETVEESKAPRTRAVRNV
RRHACSSIIKMCRDYPQLVLPNFDMLYNHVKQLLSNELLLTQMEKCALMEALVLISNQFKNYERQKVFLEELMAP
VASIWLSDMHRVLSVDVAFIAYVGTQKSCDPGLEDPGLNRRMSFCVYSILGVVKRTCWPTDLEEAKAGGFV
VGYTSSGNPIFRNPCTEQILKLLDNLLALIRTHNTLYAPEMLAKMAEPFTKALDMLDAEKSAILGLPQPLLELND
SPVFKTVLERMQRFFSTLYENCFHILGKAGPSMQQDFYTVEDLATQLLSSAFVNLNNIPDYRLRPMHLHVFKPLV
LFCPPEHYEALVSPILGPLFTYLHMRSLQKWQVINQRSLLCGEDEAADENPESQEMLEEQLVRMLTREVMDLITV
CCVSKKGADHSSAPPADGDDEEMMATEVTPSAMAELTDLGKCLMKHEDVCTALLITAFNSLAWKDTLSCQRTTSQ
LCWPLLKQVLSGTLLADAVTWLFTSVLKGLQMHGQHDGCMASLVHLAFQIYEALRPRYLEIRAVMEQIPEIQKDS
LDQFDCKLLNPSLQKVADKRRKDQFKRLIAGCIGKPLGEQFRKEVHIKNLPSLFKKTCPMLETEVLNDGGGLAT
IFEP

2239/6881
FIGURE 2056

AAAACACCAAATGGCGGATGACGCCGGTGCAGTGGGGGGCCCTGGAGGCCCTGGTGGCCCTGGGATGGGGAACCG
CGGTGGCTTCCGCAGAGGTTTCGCCAGTGGCATCCGGGGCCGGGGTCGCAGCCGTGGACCGGGCCGGGGCTGAGG
CCGCGGAGCTCGCGGAGGCAAGGCCAAAGATAAGGAGTGGATGCCCGTCACCAAGCTGGGCCGCTTGGTCAAGGA
CATGAAGATCAAGTCCCTGGAGGAGATCTATCTCTTCTCCCTGCCCATTAAGGAATCAGAGATCATTGACTTTTT
CCTGGGGGCCTCTCTCAAGGATGAGGTTTTGAAGATTATGCCAGTGCAGAAGCAGACCCGTGCTGGCCAGCGCAC
CAGGTTCAAGGCGTTTGTGCTATCGGGGACTACAGTGGCCACGTCGGTCTGGGTGTTAAGTGCTCCAAGGAGGT
GGCCACCGCCACCCGTGGGGCCATCATCTGGCCAAGCTCTCCATTGTCCCGTGCACAGAGGCTACTAGGGGAA
CAAGATCGGCAAGCCCCACACCGTCCCCTGCAAGGTGACAGGCCGCCGTGGCTCTGTGCTGGTGCGCCTCATCCC
TGCACCCAGGGGCACTGGCATTGTCTCCGCACCTGTGCCCAAGAAGCTGCTCATGATGGCTGGTATCGATGACTG
CTACACCTCAGCCCAGGGCTGCACTGCCACCCTGGGCAACTTCGCCAAGGCCACCTTTGATGCCATTTCTAAGAC
CTACAGCTACCTGACCCCCGACCTCTGGAAGGAGACTGTATTTACCAAGTCTCCCTATCAGGAATTCACTGACCA
CCTCGTCAAGACCCACACCAGAGTCTCTGTGCAGCAGACCCAGGCTCCAGCTGTGGCTACAACATAGGGTTTTTA
TACAAGAAAAATAAAGTGAATTAAGCGTG

2240/6881
FIGURE 2057

GGGCTGCGCTCTCCAGCTGTGGCTATGGCCCCAGCCCCGAGATGAGGAGGGAGAGAACTAGGGGCCCCGAGGCCT
GGGAATTTCCGTCCCCACCAAGTCCGGATGCTCACTCCAAAGTCTCAGCAGGCCCCCTGAGGGAGGGAGCTGTCA
GCCAGGGAAAACCGAGAACACCATCACCATGACAACCAGTCACCAGCCTCAGGACAGATACAAAGCTGTCTGGCT
TATCTTCTTCATGCTGGGTCTGGGAACGCTGCTCCCGTGGAAATTTTTTCATGACGGCCACTCAGTATTTACAAA
CCGCCTGGACATGTCCAGAAATGTGTCCTTGGTCACTGCTGAACTGAGCAAGGACGCCCAGGCGTCAGCCGCCCC
TGCAGCACCCCTTGCTGAGCGGAACCTCTCTCAGTGCCATCTTCAACAATGTCATGACCCTATGTGCCATGCTGCC
CCTGCTGTTATTACCTACCTCAACTCCTTCCTGCATCAGAGGATCCCCAGTCCGTACGGATCCTGGGCAGCCT
GGTGGCCATCCTGCTGGTGTCTTGATCACTGCCATCCTGGTGAAGGTGCAGCTGGATGCTCTGCCCTTCTTTGT
CATCACCATGATCAAGATCGTGCTCATTAATTCATTTGGTGCCATCCTGCAGGGCAGCCTGTTTGGTCTGGCTGG
CCTTCTGCCTGCCAGCTACACGGCCCCCATCATGAGTGGCCAGGGCCTAGCAGGCTTCTTTGCCCTCCGTGGCCAT
GATCTGCGCTATTGCCAGTGGCTCGGAGCTATCAGAAAGTGCCCTTCGGCTACTTTATCACAGCCTGTGCTGTTAT
CATTTTGACCATCATCTGTTACCTGGGCCTGCCCCGCTGGAAATCTACCGCTACTACCAGCAGCTCAAGCTTGA
AGGACCCGGGGAGCAGGAGACCAAGTTGGACCTCATTAGCAAAGGAGAGGAGCCAAGAGCAGGCAAAGAGGAATC
TGGAGTTTCAGTCTCCAACCTCTCAGCCCACCAATGAAAGCCACTCTATCAAAGCCATCCTGAAAAATATCTCAGT
CCTGGCTTTCTCTGCTGCTTCATCTTCACTATCACCATTGGGATGTTTCCAGCCGTGACTGTTGAGGTCAAGTC
CAGCATCGCAGGCAGCAGCACCTGGGAACGTTACTTCATTCCCTGTGTCTGTTTCTTGACTTTCAATATCTTTGA
CTGGTTGGGCGGAGCCTCACAGCTGTATTATGTGGCCTGGGAAGGACAGCCGCTGGCTGCCAAGCCTGGTGCT
GGCCCGGCTGGTGTGTTGTGCCACTGCTGCTGTGTGCAACATTAAGCCCCGCCGCTACCTGACTGTGGTCTTCGA
GCACGATGCCTGGTTTCATCTTCTTCATGGCTGCCTTTGCCTTCTCCAACGGCTACCTCGCCAGCCTCTGCATGTG
CTTCGGGCCCAAGAAAGTGAACACAGCTGAAGCAAAAACCGCAGGAGCCATCATGGCCTCCTTCCTGTGTCTGGG
TCTGGCACTGGGGGCTGTTTTCTCCTTCCTGTTCCGGGCAATTGTGTGACAAAGGATGGACAGAAGGACTGCCTG
CCTCCCTCCCTGTCTGCCCTCCTGCCCTTCCTTCTGCCAGGGGTGATCTTGAGTGGTCTGGCGGTTTTTTCTTCT
AACTGACTTCTGCTTTCCACGGCGTGTGCTGGGCCCCGATCTCCAGGCCCTGGGGAGGGAGCCTCTGGACGGACA
GTGGGGACATTGTGGGTTTGGGGCTCAGAGTCGAGGGACGGGGTGTAGCCTCGGCATTTGCTTGAGTTTCTCCAC
TCTTGGCTCTGACTGATCCCTGCTTGTGCAGGCCAGTGGAGGCTCTTGGGCTTGGAGAACACGTGTGTCTCTGTG
TATGTGTCTGTGTGTCTGCGTCCGTGTCTGTGCACTGTCTGCCTGTCTGGGTGGCTAGGAGCTGGGTCTGAC
CGTTGTATGGTTTGACCTGATATACTCCATTCTCCCCTGCGCCTCCTCCTCTGTGTTCTCTCCATGTCCCCCTCC
CAACTCCCCATGCCCAGTTCTTACCCATCATGCACCCTGTACAGTTGCCACGTTACTGCCTTTTTTAAAAATATA
TTTGACAGAAACCAGGTGCCTTCAGAGGCTCTCTGATTTAAATAAACCTTTCTTGTTTTTTT

2241/6881
FIGURE 2058

GC GCGGC ACTTCCGCTGGCCGCTGGCTCGCTGGCCGCTCCTGGAGGCGGCGGGAGCGCAGGGGGCGCGCGGC
CCGGGGACTCGCATTCCCCGTTCCCCCTCCACCCACGCGGCCTGGACCATGGACGCCAGATGGTGGGCAGTGG
TGGTGTCTGGCTGCGTTCCCCCTCCCTAGGGGCAGGTGGGGAGACTCCCGAAGCCCCTCCGGAGTCATGGACCCAGC
TATGGTTCTTCCGATTTGTGGTGAATGCTGTGGCTATGCCAGCTTTATGGTACCTGGCTACCTCATGGTGCAGT
ACTTCAGGCGGAAGAACTACCTGGAGACCGGTAGGGGCTCTGCTTTCCCCTGGTGAAGCTTGTGTGTTTGGCA
ATGAGCCCAAGGCCTCTGATGAGGTTCCCCTGGCGCCCCGAACAGAGGCGGCAGAGACCACCCCGATGTGGCAGG
CCCTGAAGCTGCTCTTCTGTGCCACAGGGCTCCAGGTGTCTTATCTGACTTGGGGTGTGCTGCAGGAAAGAGTGA
TGACCCGCAGCTATGGGGCCACAGCCACATCACCGGTGAGCGCTTTACGGACTCGCAGTTCCTGGTGCTAATGA
ACCGAGTGCTGGCACTGATTGTGGCTGGCCTCTCCTGTGTTCTCTGCAAGCAGCCCCGGCATGGGGCACCCATGT
ACCGGTACTCCTTTGCCAGCCTGTCCAATGTGCTTAGCAGCTGGTGCCAATACGAAGCTCTTAAGTTTCGTACAGT
TCCCCACCCAGGTGCTGGCCAAGGCCTCTAAGGTGATCCCTGTCTATGCTGATGGGAAAGCTTGTGTCTCGGCGCA
GCTACGAACACTGGGAGTACCTGACAGCCACCCTCATCTCCATTGGGGTTCAGCATGTTTCTGTCTATCCAGCGGAC
CAGAGCCCCGCAGCTCCCCAGCCACCACACTCTCAGGCCTCATCTTACTGGCAGGTTATATTGCTTTTGACAGCT
TCACCTCAAACCTGGCAGGATGCCCTGTTTGCCTATAAGATGTTCATCGGTGCAGATGATGTTTGGGGTCAATTTCT
TCTCCTGCCTCTTACAGTGGGCTCACTGCTAGAACAGGGGGCCCTACTGGAGGGAACCCGCTTCATGGGGCGAC
ACAGTGAGTTTGCTGCCCCATGCCCTGCTACTCTCCATCTGCTCCGCATGTGGCCAGCTCTTCATCTTTTACACCA
TTGGGCAGTTTGGGGCTGCCGTCTTACCATCATCATGACCCCTCCGCCAGGCCTTTGCCATCCTTCTTTCTGCTG
TTCTCTATGGCCACACTGTCACTGTGGTGGGAGGGCTGGGGGTGGCTGTGGTCTTTGCTGCCCTCCTGCTCAGAG
TCTACGCGCGGGGCCGTCTAAAGCAACGGGGAAGAAGGCTGTGCCTGTTGAGTCTCCTGTGCAGAAGGTTTGAG
GGTGGAAGGGCCTGAGGGGTGAAGTGAAATAGGACCCTCCACCATCCCCTTCTGCTGTAACCTCTGAGGGAGC
TGGCTGAAAGGGCAAAATGCAGGTGTTTTCTCAGTATCACAGACCAGCTCTGCAGCAGGGGATTGGGGAGCCAG
GAGGCAGCCTTCCCTTTTGCCTTAAGTCAACCATCTTCCAGTAAGCAGTTTATTCTGAGCCCCGGGGGTAGACAG
TCCTCAGTGAGGGGTTTTGGGGAGTTTGGGGTCAAGAGAGCATAGGTAGGTTCCACAGTTACTCTTCCCACAAGT
TCCCTTAAGTCTTGCCCTAGCTGTGCTCTGCCACCTTCCAGACTCACTCCCCTCTGCAAATACCTGCATTTCTTA
CCCTGGTGAGAAAAGCACAAAGCGGTGTAGGCTCCAATGCTGCTTTCCAGGAGGGTGAAGATGGTGTGCTGTGCTGA
GGAAAGGGGATGCAGAGCCCTGCCAGCACCACCACCTCCTATGCTCCTGGATCCCTAGGCTCTGTTCCATGAGC
CTGTTGCAGGTTTTGGTACTTTAGAAATGTAACTTTTTGCTCTTATAATTTTATTTTATTAAATTAAATTACTGC

A

2242/6881
FIGURE 2059

CAGAATCGGTAGACATTGCGAACCAGGTTATGAAGTGCAAGGCTGCAGTTGCTTGGGAGGCTGGAAAGCCTCTCT
CCATAGAGGAGATAGAGGTGGCACCCCCAAAGGCTCATGAAGTTCGAATCAAGATCATTGCCACTGCGGTTTGCC
ACACCGACGCCTATACCCTGAGGGGAGCTGATCCTGAGGGTTGTTTTCCAGTGATCTTGGGACATGAAGGTGCCG
GAATTGAGGAAAGTGTTGGCGAGGGAGTTACTAAGCTGAAGGCGGGTGACACTGTCATCCCACTTTACATCCCAC
AGTGTGGAGAATGCAAATTTTGTCTATATCCTAAACTAACCTTTGCCAGAAGATAAGAGTCACTCAAGGGAAAG
GATTAATGCCAGATGGTACCAGCAGATTTACTTGCAAAGGAAAGACAATTTTGCGTTACATGGGAACCAGCACAT
TTTCTGAATACACAGTTGTAGCTGATATCTCTGTTGCTAAAATAGATCCTTTAGCACCTTTGGATAAACTCTGCC
TTCTAGGTTGTGGCATTTCAGCTGGTGATGGTGCTGCTGTGAACACTGCCAAGGTGGAACCTGGCTCTGTTTGTG
CCGTCTTTGGTCTGGGAGGAGTTGGATTGGCAGTTATCAAGGGCTGTAAAGTGGCTGGTGATCCCGGATCATTG
GTGTGGACATCAATAAAGATAAAATTTGCAAGGGCCAAAGAGTTTGGAGCCACTGAATGTATTAACCTCAGGGTT
TTAGTAAACCCATCCAGGAAGGGCTCATTGAGACGACTGATGGAGGAGTGGACTATTCTTTGAATGTATTGGTA
ATGTGAAGGTCATGAGAGCAGCACTTGAGGCTTATCACAAGGGCTGGGGAGTCAGCGTGGTGGTTGGAGTAGCTG
CTTCAGGTGAAGAAATTGCCACTCGTCCATTCCAGCTGGTAACAGGTGCGACATGGAAAGGAACTGCCCTTTGGAG
GATGGAAGAGTGTAGAAAGTGTCCCAAAGTTGGTGTCTGAATATATGTCCAAAAAATAAAAGTTGATGAATTTG
TGAATCACAATCTGTCTTTTGGTGAAATTAACAAAGCCTTTCAACTGATGCATTCTGGAAAGAGCATTCGAACCTG
TTGTAAAGATTTAATTCAAAGAGAAAAATAATGTCCAACCTGTCGTGATGTGATGGGAGCAGCTTAACAGGCAG
GGAGAAGCGCCTCCAAACTCACAGCCTCGTAGAGCTTCGCAGCTACCCAGAGAATAGTGTTATGAGTGTAAATC
ATGAATCTCTATAATCAACGACAAGGATAATTCAGTCATGGACCTGTTTTCTGGACGCTCCTCCACATAAATAAT
TGCTAGCTTATTAAGGAATATTTTAACATAATAAAAGTAATTTCTACATTTGTGTAGAAATTGTCTTTGTTTTAT
GCTGTAATCATTGTCTATGTTTTGTCTGCCATTATCTTCATTCTGTAAGGGAAATGTAAAGGAAGCAGGGCAGTG
GTGGGTGTCTGAAACCTCAGAAACATTCGTTGAAGTTTAAAGGTCTCAGTCCCGTTGATTGAAGAACAGATCCT
AGCCATCAGTGACAAAGTTAATCAGGAGCCAAGTCTGCTTCTGTGATATTATCTTGAAGGGAGGTACTGTGCCTT
GTTTCGTGCCTGTACCCCAAATTCCTAGTATGGCATCTGCCCCTCAGGGGACACTAAAATGTATTATTGAAACAGC
ATTCTGGACTTAAATAGGTGTATGTGTGTGTTGGTTGTGGCTGTACTATTTCTAGTATAGTGAATTACATACTGA
ATATCCAAGTTCTCAGCACCTACTTTTGTCAAATCTTAACATTTTGCCACTTCCACATCACATTGCCATTCCTCC
CCTCCAGAGGTAACAATTATCCAAAATTTGATGTTTGTCAATTCCTGTGTTGTTGTACTTTTACTGTGTATAACCT
AAACCATCTACTCTTTAGTACTGTTTTATATATTTTTAAGCCTTATACTTGCTCATTCTACAGCTTTTCTTTTTT
TCACTCATTATTGTATAATTATATGTGAAGCTTTTCATTCATTAATTTTAGTACTGTGTAGCAGTATTCAATTACG
CGAACTATCTTAATTCATCTGTTCTCCAGTTGAAGGCATGAAGTTGTTGCCAGTTTCTGTATTACAACACTGTAG
TGGAACATTCTTCTGCATTGGGCTCACTACATTAGTTACTTAAGATGTGTATCACAGAATAAACACATTTAGCCT
TATAGACATTGCCAAATTTATCTTCAAAGTAAATGTGAGTTTTTGTGAATTACGTGAGTGTAGAATGGTGTTTTA
TTATGAGTTTAGTTTGCATTTTCCACAA

2243/6881
FIGURE 2060

ATGATCAAGGGTGTTACACTAGGCTTCCATTACAAGATGAGATCTGTGTATGCTCACTTCCCCATCAACGTCGTT
ATCCAGGAGAATGGGTCTCTTGTTGAAATCCGAAATTTCTTGGGTAAAAAATACATCCGCAGGGTTTGGATGAGA
GCAGGTGTTGTTTGTTTCAGTATCTCAAGCCCAGAAAGATGAATTAATCCTTGAAGGAAATGACATTGAGCTTGTT
TCAAATTCAGCGGCTTTGATTCAACAAGCCACAACAGTTAAAAAGAAGGATATCAGGGAATTTTGGATGGTATC
TATGTCTCTGAAAAAGGAAGTGGTCAGCAGGCTGATGAATAA

2244/6881
FIGURE 2061

MIKGVTLGFHYKMRSVYAHFPINVVIQENGLVEIRNFLGKKYIRRVWMRAGVVCSVSQAQKDELILEGNDIELV
SNSAALIQQATTVKKKDIREFLDGIYVSEKGTGQQADE

2245/6881
FIGURE 2062

GCTGTCGGTCCACGCCGCCGCTCGCGCTGCCCGCCCGCTCGGCGTCGGCCGCCGCC**ATG**GGAGTGCACGTGGAAA
CCATCTCCCCAGGAGACTGGCGCACCTTCCCGAAGCGCAGCCAGACCTGCGTGATGCACTACACGGGGATGCTTG
AAGATGGAAAGAAATTTGATTCTCCCGGGACAGAAACAAGCCCTTTAAGTTTATGCTAGGCAAGCAGGAGGTGA
TCCGAGGCTGGGAAGAAGGGGTTGTCCAGATGAGTGTGGGTCAGAGAGCCAAACTGACTATATCTCCAGATTATG
CCTATGGTGCCACTGGGCACCCAGGCATCATCCACCACATGCCACTCTCGTCTTCGATGTGGAGCTTCTAAAC
TGGAAT**TGA**CAGGAATGGCCTCCTCCCTTAGCTCCCTGTTCTTGGATCTGCCATGGAGGGATCTGGTGCCTCCAGA
CGTGTGCACATAAATCCATATGGAGCTTTTCCTGATGTTCCACTCCACTTTGTATAGACATCTGCCCCAACTGAA
TTATTCTCCAAGTTGAGAGATGTCCTTGGGTAAATTAAAAGCCCTACCTAAAACCTGAGGTGGGGATGGGGAGAG
GCTTTGCC

2246/6881
FIGURE 2063

MGVHVETISPGDWRTFPKRSQTCVMHYTGMLDGGKKFDSSRDNRNPFKFM LGKQEVIRGWEEGVVQMSVGQRAKL
TISPDYAYGATGHPGIIPPHATLVFDVELLKLE

2247/6881
FIGURE 2064

CGCCTTGGCCATTTGCCAGCCACACAACCCAGGACCTCCAATGGGGACGCCCACTGAGGATCCTAGTGGTTGCTC
TTTTCCCTTGCTCTTTCTTTCCCCCAGTCTTTCTTGTTCTATCATGGGCAATTTCCCGCCTTCCATCCCTCTT
TCTTCTGTCTGGCTTGTGTCCTCAGAAACCTCAAACCTCTTCACCTTGCACCCAATCTAAAGGCTAAACGTCTAA
TTTTTTTCTGTAACACGTCCTGGCCCCAGTATAAATTAGAAAAATGGCGCTCAGTGGCCAGAAAACAGCACTTCCA
ATTTCTCTATTTTGTGGGACTTAGACAACCTTCTATGGAAAAATGGGCAAATGGGTCTGAGGTACCCTACTTCCAG
GCATTTTTTACATACGATCTCTCCCTAGCCTATGCTTCCAATGTAATCCATCCCCAATTTTCCTTATTTCCCTTC
TGTCTACCCCTCCTTCTTCCACTGGCGATGCTGACTCCTCTTTGTCTGTTGACCCCTCCGATCTTTCTCCCCCAG
CACCTATCCGAACCTGCTTCTAATTCTCCCCCAGAACCTATTTCTACCCACAATCCACCCTCTTATGCCCCCTCCC
ATTACCACCCCTTCTCACATCCTCTATGGCTTACAGTTTGGGCCTGCGACCAACCCCCAGGCCCTGCCTAGCAA
TTTCCCCTCGGAGAGGTGGCAGGAACCAAAGGAATAGTTCGGGTTCAGGTCCCTTTCTCCCTGTTTCGACCTTTCC
CAAATTAGTGAACATCTAGGCTCTTTCCCATCTGACCCCCACCAAAATATACGAGAATTCCAATACTTAACCCAG
TCCTATAATCTTACTTGGAATGACTTAAATGTCATCCTTACCTCTACCCCTCGCTCCTGAGGAGTGAGAGTGGGT
TGGATCCTAGCTCAATCTTAGGCTGATAACCGCCGGTGCCGTAAGCCTGGCCTCCAGTAAGGTGCTAGGGCAGTA
CCCTGTGAAGACCCCGGATGGACTTACCAGGCCCTGGGACCCATGCATAGCCAGGCGGGACTACATGATCTCTTG
CCTAGTTAAAGGGCTTCAGAAGGCTGCAIATAAAGCCGTCAATTATGACAAACTAAAAAACAAAAACAAAAACAA
AAAAAACCACTCAGAACAAAGATAAAAAATCCAGCTCAGTTTATGGCCTGTCTACCTGCCACCCTCAGGCGATATA
CAGCACTAGACCCTGAAGGGATAGAAGGCCGCTTATTCTTAACATGCATTTTATTACCCAGTCAGTTTCTGACA
GTAGAAAGAACTTCAAAAAATTAGAGTCTGGCTCTCAGATCCCACAACAGGAATTAATCAACCTCGCCTTCAAGG
TGTTCAATAATAGGGAAGAGACTGCCCGGCGACAGCGCATTTCAGAACTACAGATGCTTGCCTCCGCCATAAGAC
AAACCCAGCTGCACTGCCTACCTGCAAGAACTTCAAGGCATCTAAACGCAACATCCAACAGCCCCTCTGGGACT
TTGCTTCAAGCGATGAAAACCTGGCCACTGGGCAAGGAATGCCTGCAGCCTGGGATTCTCTAAGCCATGCCCC
GCCTGTGCGTCCCTCACTGGAAGTCTGACTGCCCCGACTCTCATCGCCACTTCCGGAGCTCCTGGAGCTCAAACCC
AAAGCTCCCCACCGACTCCTTCCCAGATCTCCTCGGCTTGGCGGCTGAAGACTGACGCTGCCCGAACGTCTCGGA
GGCCCCTTAGACAATCGCGGATGCCGAGCTTCGGGTAACTCTTAGGGTGGAGGCATAAAAAGACAGGAATGTAAG
GTCCTCTGAGCAGGCGGCGCCATGGTCAAGCCATCGTGACCCCTGTGACTCACACGTACACATCCAGAAGGTCTC
CTGGAGCCAGAAAGTCTGGGACGACAGGAAAACCACAAAAGAAGAAAAA

2248/6881
FIGURE 2065

GGGCCTGGACGCTTTGGCAACCGCTACTCCCGGGGGTGCTTTTTCTGCAGGGACGAAGTGCCACCTATGCTAGTG
GCGGGTCTGGAAGCCTAGAGGGGAACCAGGCTGCAGAGCCGGGCCAAGGGATTAGCGGCGGGCGGCGGGCATGGC
CTGGACTGCGCGGGACCGCGGGGCCCTGGGGCTGCTGCTGTTGGGGCTCTGCTTGTGCGCGGCTCAAAGAGGTCC
CCCGGGTGAGCAGGGTCCTCCCGGGCCTCCGGGCCCCCTGGAGTTCCAGGCATCGATGGCATCGACGGTGACCG
AGGTCCCTAAGGGCCCCCGGGCCCCCGGGTCTGTCAGGTGAACCGGGAAAGCCAGGAGCTCCAGGCAAGCCTGG
CACACCTGGCGCTGATGGATTAAACAGGACCTGATGGATCCCCTGGCTCCATTGGGTCAAAGGGACAAAAAGGAGA
ACCTGGTGTGCTGGATCGCGTGGATTTCCAGGCCGTGGTATTCCTGGACCCCCTGGTCTCTGGGACAGCAGG
ACTCCCTGGAGAGCTTGGCCGTGTAGGACCTGTTGGTGACCCTGGGAGAAGAGGACCACCTGGCCCCCTGGCCC
CCCAGGACCCAGAGGAACAATTGGCTTTCATGATGGAGATCCATTGTGTCCCAATGCCTGTCCACCAGGTCGCTC
AGGATATCCAGGCCCTACCAGGCATGAGGGGTCATAAAGGGGCTAAAGGAGAAAATTGGTGAACCAGGAAGACAAGG
ACACAAGGGTGAAGAAGGTGACCAGGGAGAACTCGGAGAAAGTTGGAGCTCAAGGACCTCCAGGAGCCCAGGGTTT
GCGAGGCATCACCGGCATAGTTGGGGACAAAGGGGAAAAAGGTGCTCGGGGCTTAGATGGTGAACCTGGGCCTCA
GGGTCTTCCTGGTGACCTGGTGTATCAAGGACAGCGAGGACCTCCAGGAGAAGCAGGTCCCAAAGGAGATAGAGG
GGCTGAAGGTGCTAGAGGAATTCCTGGTCTCCCTGGGCCCCAAAGGAGACACGGGTTTGCCAGGTGTGGATGGCCG
TGATGGGATCCCTGGAATGCCTGGAACAAAGGGTGAACCAGGAAAACCTGGGCCTCCTGGTGTATGCAGGATTGCA
GGGGTTACCAGGTGTACCTGGAATTCCTGGTGCAAAGGGTGTGTGCTGGTGAAGGGGTAGCACAGGTGCTCCAGG
GAAGCCTGGTTCAGATGGGAAATTCAGGCAAACCGGGCCAACAGGGGCCCTCCAGGAGAGGTGGGACCCCCGAGGACC
CCAGGGGCTTCCTGGCAGTAGAGGAGAATTAGGACCAGTGGGATCCCCAGGCCTACCAGGTAAACTGGGTTCTCT
GGGTAGCCCTGGCCTCCCTGGCTTGCTGGGCCCCCTGGACTTCCTGGAATGAAAGGTGACAGGGGTGTAGTTCGG
TGAACCGGGTCCAAAGGGTGAACAGGGTGCCTCTGGTGAAGAAGGTGAAGCAGGAGAAAGGGGGGAACCTGGAGA
TATAGGATTACCTGGCCCCAAAGGGATCTGCAGGTAATCCTGGGGAACCTGGCTTGAGAGGGCCTGAGGGAAGTCG
GGGGCTTCCTGGAGTGGAAGGACCAAGAGGACCACCTGGACCCCGGGGTGTGCAGGGAGAACAGGGTGCCACCGG
CCTGCCTGGTGTCCAGGGCCCTCCGGGTAGAGCACCGACAGATCAGCACATTAAGCAGGTTTGCATGAGAGTCAT
ACAAGAACATTTTGCTGAGATGGCTGCCAGTCTTAAGCGTCCAGACTCAGGTGCCACTGGGCTTCCTGGAAGGCC
TGGCCCTCCTGGTCCCCCGGGCCCTCCTGGAGAGAATGGTTTCCCAGGCCAGATGGGAATTCGTGGCCTTCCGGG
CATTAAAGGGGCCCCCTGGTGTCTTGGTTTGAGGGGACCTAAAGGTGACTTGGGAGAAAAGGGGGAGCGTGGCCC
TCCAGGAAGAGGTCCCAACGTTTTGCTGGAGCTATAGGTCTCCCAGGTGACCCAGGCCCTGCCAGCTATGGCAG
AAATGGCCGAGACGGTGAGCGAGGCCCCCCAGGGGTGGCAGGAATTCCTGGAGTGCCTGGACCCCGGGACCTCC
TGGGCTTCCCGGTTTCTGTGAGCCAGCCTCCTGCACCATGCAGGCTGGTCAGCGAGCATTTAACAAAGGGCCTGA
CCCTTGAAAGGCTTACTGCTGCATGGCTGTCTGCATGAACCACGCCTGGTGAAGGAGCCTGGGTGAGAAACACCA
TCCAAAGCTGGGGCAAAGATGATTACCTTCAGCATGATTACAATGTATTACCTTCAGTATGATTACAGAAGTCCT
ACTTGACAATCACATATAGAAGAACGGTGCTATTTCAGTAAGTTCTCTTTCCCTTTCCCTTGGAGGGAAGACAGCAG
AGTCATCAGTTAAAAAAGAAAACCAAACACCTCCCTTGAATAAATTTATACTCCTGTTCCCAGGATCT
TGAGCTTTAGTGTGCTATACCTATGTGTCTTATCGTGGGCCACTGTGCCAATAAACAAAAACAACCTGTTTGGTTT
ACCTC

2249/6881
FIGURE 2066

GGCCGCGCCCTGCAGATTGTCTCTTGTGCGTAAGTTTTTTTTGACCGTCACTCGTGTGAGCTTCAAAGTCAGATA
GATTTTTCTCCAGCATGTTTCTACTTCCGAGGCTGTGGCCGTTGGGTGCGGGTTTCCTTACCAAGCAGCAATTT
CCGTTGGCACGGTTGAGCAGTGACAGCGCGCGCCCGGACTCCGCACTTCGACGTGATAGTCATTGGTGGAGGA
CATGCCGGGACTGAGGCAGCCACCGCCGCCGCTCGGTGCGGCTCTCGGACTCTGCTCCTCACTCACCGCGTGGAC
ACGATCGGTGAGATGTGATGTAATCCTTCTTGGTGGCATCGGAAAGGGACATTTAATGAGGGAAAGTAGATGCC
TTGGATGGCCTGTGTTCTCGCATCTGTGACCAGTCTGGTGTACATTATAAAGTATTAAACCGGCGTAAGGGACCA
GCTGTGTGGGGTCTGAGAGCTCAGATTGATAGGAACTCTACAAACAGAACATGCAGAAAGAAATCTTGAATACA
CCACTGCTTACTGTTTCTGAGAGGGAGCTGTAGAAGATCTTATTCTTACAGAACCAGAGCCTGAACACACTGGGAAA
TGCCGTGTGAGTGGGGTTGTTTTGGTGGATGGAAGCACAGTATATGCAGAGAGTGTGATTCTGACTACTGGGACA
TTTCTGAGAGGCATGATTGTAATTGGATTGGAGACGCATCCAGCAGGACGTTTAGGGGATCAGCCTTCTATAGGA
TTGGCTCAGACACTGGAGAAGTTAGGGTTTGTGGTGGGAAGGTTGAAGACTGGGACTCCACCCCGAATTGCCAAA
GAGTCCATTAATTTTCACTATTCTAAACAAGCATATACCGGACAATCCATCCATACCATTACAGCTTTACCAATGAG
ACAGTATGGATTAAAGCCAGAAGATCAGCTGCCATGTTACTTGACTCACACCAACCCTAGAGTGGATGAGATTGTC
CTTAAGAACCCTTACCTTAATAGTCATGTTAAAGAAAACGACAAGAGGACCTCGATACTGTCCCTCCATTGAATCA
AAAGTTTTGCGTTTTTCAAACCGTCTACATCAGGTTTTGGTTGGAACCTGAAGGAATGGATTCTGACCTTATCTAC
CCACAGGGGTTATCTATGACGCTACCAGCTGAGTTACAAGAGAAAATGATCACATGCATCAGAGGCTTGGAGAAA
GCTAAAGTGATTGAGCCAGACGGAGTTTTGCTCTTGTGCCCAGGATGGAGTGCAATGGTGCATCTCGGCTCAC
CACAACCTCCCCCTGCCAGGCTACGGTGTTCAGTATGATTACTTAGATCCCCGTCAGATCACCCCTTCTTGGAG
ACTCATTTGGTTCAACGACTCTTCTTTGCTGGACAGATCAATGGCACCCTGTTTATGAGGAAGCTGCAGCTCAA
GGTGTGATAGCCGAATCAACGCCAGTCTTCGGGTGAGTCGCAAGCCTCCCTTTGTGGTTAGCCGAACAGAAGGT
TACATAGGAGTCTTGATTGATGACCTCACTACTCTGGGCACCAGTGAACCATAACGCATGTTTACCAGCCGAGTA
GAGTTCCGTTTGTCACTGCGCCCTGATAATGCTGACAGCCGGCTCACACTGCGAGGGTATAAAGACGCTGGCTGT
GTGTCCCAACAACGATATGAAAGAGCTTGTGGATGAAGTCTTCTTTAGAAGAAGGCATTTCTGTGTTGAAATCT
ATTGAGTTTTTGTGCTCTAAATGGAAAAAATTAATCCAGAGGCTTCTATAAGTACTAGTAGAAGTCTGCCTGTC
AGAGCTCTCGATGTTCTGAAGTATGAGGAAGTTGACATGGATTCAATTAGCCAAGGCTGTTCCAGAGCCCTTGAAG
AAGTATACTAAATGTAGAGAGCTGGCTGAAAGACTGAAAATAGAAGCCACTTATGAATCAGTGTGTTCCATCAA
CTACAAGAAATAAAGGGAGTTCAGCAAGATGAAGCTCTCCAACGCCAAAAGACCTAGATTATTTGACTATCAGG
GATGTGTCTTTGTCCCATGAAGTTCGAGAGAACTACATTTTAGTCGTCCACAGACGATCGGGGCTGCTAGTCGC
ATACCCGGAGTAACACCTGCCGCCATCATCAATCTGCTGAGATTTGTGAAGACCACTCAACGAAGACAGTCGGCT
ATGAATGAATCATCCAAGACTGATCAATACTTATGTGATGCAGACAGACTTCAAGAGAGAGAGTTATAGCTTTTCA
ATTCATAAAAGATTTTTAAAGAGCATATAAATAATTTGATCAATACAACAGTATAGATAAAAGAATTATTTAGCA
CATGTTAAATAGCTTTATTAGGTTACTATGGGTTTGCCATTAATTTCTGAGTGGGACAGAAATTATAATTGTGC
TTTTTCGTGTATATGAAAAAAGTGTGTAACAATTTGTACTCTTTCTTTAAGGAGCTGTAATACAAATAAATTT
TGTGCAAGTGTTCATCAAAAGAGAGAGACAGTGAACCTAAAAGTGAACCTGGAATAAAACTCAACATGCAGATTGTC
CTACTCATAGGGACTTTGCCATTAAAGTCTACCAAATTAAGTCTTATCATTACAGCGTGTGTTTGGAGGTTAATA
ATCTTTTGCTTGGTTATACTAGGCTAGGAAGCAATATCAAAGCCCTTAAATTTCTCAAGACTAAAGACTTGAGATT
ATATAAAATTATCCAGAATCATTACAGCTAATACTATTGGAATATAGTATGTAGGGTGAAAGTTGACAGAAATCTG
TACTTCTTCAGGAAATCCTCACTGGTAATTGTTTTGAACATTAATGAAAGCCCTATAAAATAGAAAGATTGGAAA
TCACCATTTGTTTCTATTATCCACAGTGTGGATGGATACTTATTTGGTGACCTAGTTATGGGAGAATTGAGTAAC
GTTAGTTATTTTATATCATACCATAAAAATATTTTC

2250/6881
FIGURE 2067

MFYFRGCGRWVAVSFTKQFPLARLSSDSAAPRTPHFDVIVIGGGHAGTEAATAAARCGSRTLLLTTHRVDITIGQM
SCNPSFGGIGKGHLMREVDALDGLCSRICDQSGVHYKVLNRRKGPAVWGLRAQIDRKLYKQNMQKEILNTPLLT
QEGAVEDLILTEPEPEHTGKCRVSGVVLVDGSTVYAESVILTTGTFLRGMIVIGLETHPAGRLGDQPSIGLAQTL
EKLGFVVGRKLTGTPPRIAKESINF SILNKHIPDNPSIFFSFTNETVWIKPEDQLPCYLTHTNPRVDEIVLKNLH
LNSHVKETTRGPRYCPSIESKVLRFNRLHQVWLEPEGMDSDLIYPQGLSMTLPAELQEKMITCIRGLEKAKVIQ
PDGVLLLLPRMECNGAISAHNLPLPGYGVQYDYLDPQITPSLETHLVQRLFFAGQINGTTGYEAAAAQGVIA
INASLRVSRKPPFVVSRTGYIGVLIDDLTTLGTSEPYRMFTSRVEFRLSLRPDNADSRLTLRGYKDAGCVSQQ
YERACWMKSSLEEGISVLKSIEFLSSKWKLIPEASISTSRSLPVRALDVLKYEEVDMDSLAKAVPEPLKKYTK
RELAERLKIEATYESVLFHQLEIKGVQQDEALQLPKDLDYLTIRDVSLSHEVREKLHFSRPQTIGAASRIPGVT
PAAIINLLRFVKTQRRQSAMNESSKTDQYLCADRLQEREL

2251/6881
FIGURE 2068

CTCATTTAAC TTTTTTAATGGGTCTCAAAATTCTGTGACAAATTTTTGGTCAAGTTGTTTCCATTAAAAAGTACT
GATTTTAAAACTAATAACTTAAACTGCCACACGCAAAAAGAAAACCAAAGTGGTCCACAAAACATTCTCCTT
TCCTTCTGAAGGTTTTACGATGCATTGTTATCATTAAACAGTCTTTTACTACTAAACTTAAATGGCCAATTGAAA
CAAACAGTTCTGAGACCGTTCTTCCACCACTGATTAAGAGTGGGGTGGCAGGTATTAGGGATAATATTCAATTAG
CCTTCTGAGCTTTCTGGGCAGACTTGGTGACCTTGCCAGCTCCAGCAGCCTTCTTGTCCTACTGCTTTGATGACAC
CCACCGCAACTGTCTGTCTCATATCACGAACAGCAAAGCGACCCAAAGGTGGATAGTCTGAGAAGCTCTCAACAC
ACATGGGCTTGCCAGGAACCATATCAACAATGGCAGCATCACCAGACTTCAAGAATTTAGGGCCATCTTCCAGCT
TTTTACCAGAACGGCGATCAATCTTTTCCTTCAGCTCAGCAAACCTGTCATGCAATGTGAGCCGTGTGGCAATCCA
ATACAGGGGCATAGCCGGCGCTTATTTGGCCTGGATGGTTTCCAGGATAATCACCTGAGCAGTGAAGCCAGCTGCTT
CCATTGGTGGGTCAATTTTTGCTGTCACCAGCAACGTTGCCACGACGAACATCCTTGACAGACACATTCTTGACAT
TGAAGCCCACATTGTCCCCAGGAAGAGCTTCACTCAAAGCTTCATGGTGCAATTCGACAGATTTTACTTCCGTTG
TAACGTTGACTGGAGCAAAGGTGACCACCATAACGGGTTTGAGAACACCAGTCTCCACTCGGCCAACAGGAACAG
TACCAATACCACCAATTTTGTAGACATCCTGGAGAGGCAGGCGCAAGGGCTTGTGAGTTGGACGAGTTGGTGGTA
GGATGCAGTCCAGAGCCTCAAGCAGCGTGGTTCCACTGGCATTGCCATCCTTACGGGTGACTTTCCATCCCTTGA
ACCAAGGCATGTTAGCACTTGGCTCCAGCATGTTGTACCATTTCCAACCAGAAATTGGCACAATGCTACTGTGT
CGGGGTTGTAGCCAATTTTCTTAATGTAAGTGCTGACTTCCTTAACAATTTCTTCATATCTCTTCTGGCTGTAGG
GTGGCTCAGTGAATCCATTTTGTAAACACCGACAATTAGTTGTTTTCACACCCAGTGTGTAAGCCAGAAGGGCAT
GCTCTCGGGTCTGCCCATTCTTGGAGATACCAGCTTCAAATTCACCAACACCAGCAGCAACAATCAGGACAGCAC
AGTCAACCTGAGATGTCCCTGTAATCATGTTTTTGATAAAGTCTCTGTGTCCTGGGGCATCAATGATAGTCACAT
AGTACTTGCTGGTCTCAAATTTCCACAAGGAGATATCAATGGTGATACCACGTTACGCTCAGCTTTTCAAGTTTAT
CCAAGACCCAGGCATACTTGAAGGAGCCCTTTCCATCTCAGCAGCCTCCTTCTCAAATTTTTTCAATGGTTCTTT
TGTCGATGCCACCGCATTTATAGATCAGATGGCCAGTAGTGGTGGACTTGCCCGAATCTACGTGTCCAATGACGA
CAATGTTGATATGAGTCTTTTCTTTCCATTTTGGCTTTTAGGGGTAGTTTTACGACACCTGTGTTCTGGCGG
CAAACCCG

2252/6881
FIGURE 2069

ACGGGTTTGCCGCCAGAACACAGGTGTCGTGAAACTACCCCTAAAAGCCAAAATGGGAAAGGAAAAGACTCATA
TCAACATTGTCGTCATTGGACACGTAGATTTCGGGCAAGTCCACCACTACTGGCCATCTGATCTATAAATGCGGTG
GCATCGACAAAAGAACCATTGAAAAATTTGAGAAGGAGGCTGCTGAGATGGGAAAGGGCTCCTTCAAGTATGCCT
GGGTCTTGGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTGTGGAAATTTGAGACCA
GCAAGTACTATGTGACTATCATTGATGCCCCAGGACACAGAGACTTTATCAAAAACATGATTACAGGGACATCTC
AGGCTGACTGTGCTGTCCTGATTGTTGCTGCTGGTGTGGTGAATTTGAAGCTGGTATCTCCAAGAATGGGCAGA
CCCGAGAGCATGCCCTTCTGGCTTACACACTGGGTGTGAAACAATAATTGTCGGTGTAAACAAAATGGATTCCA
CTGAGCCACCCTACAGCCAGAAGAGATATGAGGAAATTGTTAAGGAAGTCAGCACTTACATTAAGAAAATTGGCT
ACAACCCCGACACAGTAGCATTGTGCCAATTTCTGGTTGGAATGGTGACAACATGCTGGAGCCAAGTGCTAACA
TGCCTTGGTTCAAGGGATGGAAAGTCACCCGTAAGGATGGCAATGCCAGTGAACACGCTGCTTGAGGCTCTGG
ACTGCATCCTACCACCAACTCGTCCAAGTACAAGCCCTTGCGCCTGCCTCTCCAGGATGTCTACAAAATTGGTG
GTATTGGTACTGTTCTGTTGGCCGAGTGGAGACTGGTGTCTCAAAACCCGGTATGGTGGTCACCTTTGCTCCAG
TCAACGTTACAACGGAAGTAAAATCTGTGAAATGCACCATGAAGCTTTGAGTGAAGCTCTTCTGGGGACAATG
TGGGCTTCAATGTCAAGAATGTGTCTGTCAAGGATGTTTCGTGCTGGCAACGTTGCTGGTGACAGCAAAAATGACC
CACCAATGGAAGCAGCTGGCTTCACTGCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCCGGCTATG
CCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCGTT
CTGGTAAAAAGCTGGAAGATGGCCCTAAATTCCTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCTGGCA
AGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTGCTGTTTCGTGATATGAGACAGACAG
TTGCGGTGGGTGTGATCAAAAGCAGTGGACAAGAAGGCTGCTGGAGCTGGCAAGGTCACCAAGTCTGCCAGAAAAG
CTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGAAGAACGGTCTCAG
AACTGT

2253/6881
FIGURE 2070

CCGGCTCGCGCCCTCCGGGCCCAGCCTCCCGAGCCTTCGGAGCGGGCGCCGTCCCAGCCCAGCTCCGGGGAAACG
CGAGCCGCGATGCCTGGGGGGTGCTCCCGGGGCCCCGCCGCCGGGGACGGGCGTCTGCGGCTGGCGCGACTAGCG
CTGGTACTCCTGGGCTGGGTCTCCTCGTCTTCTCCACCTCCTCGGCATCCTCCTTCTCCTCCTCGGCGCCGTTT
CTGGCTTCCGCCGTGTCCGCCCAGCCCCGCTGCCGGACCAGTGCCCCGCGCTGTGCGAGTGCTCCGAGGCAGCG
CGCACAGTCAAGTGCCTTAACCGCAATCTGACCGAGGTGCCACGGACCTGCCCGCCTACGTGCGCAACCTCTTC
CTTACCGGCAACCAGCTGGCCGTGCTCCCTGCCGGCGCCTTCGCCCGCCGGCCGCGCTGGCGGAGCTGGCCGCG
CTCAACCTCAGCGGCAGCCGCTGGACGAGGTGCGCGCGGGCGCCTTCGAGCATCTGCCAGCCTGCGCCAGCTC
GACCTCAGCCACAACCCACTGGCCGACCTCAGTCCCTTCGCTTTCTCGGGCAGCAATGCCAGCGTCTCGGCCCCC
AGTCCCCCTGTGGAAGTATCCTGAACCACATCGTGCCCCCTGAAGATGAGCGGCAGAACCCGAGCTTCGAGGGC
ATGGTGGTGGCGGCCCTGCTGGCGGGCCGTGCACTGCAGGGGCTCCGCCGCTTGAGAGCTGGCCAGCAACCACTTC
CTTTACCTGCCGCGGGATGTGCTGGCCCAACTGCCCAGCCTCAGGCACCTGGACTTAAGTAATAATTGCTGGTG
AGCCTGACCTACGTGTCTTCCGCAACCTGACACATCTAGAAAGCCTCCACCTGGAGGACAATGCCCTCAAGGTC
CTTCACAATGGCACCCCTGGCTGAGTTGCAAGGTCTACCCACATTAGGGTTTTCTGGACAACAATCCCTGGGTC
TGCGACTGCCACATGGCAGACATGGTGACCTGGCTCAAGGAAACAGAGGTAGTGACGGGCAAAGACCGGCTCACC
TGTGCATATCCGGAAAAAATGAGGAATCGGGTCCCTCTTGGAAGTCAACAGTGCTGACCTGGACTGTGACCCGATT
CTTCCCCCATCCCTGCAAACCTCTTATGTCTTCCCTGGGTATTGTTTTAGCCCTGATAGGCGCTATTTTCCTCCTG
GTTTTGTATTTGAACCGCAAGGGGATAAAAAAGTGGATGCATAACATCAGAGATGCCTGCAGGGATCACATGGAA
GGGTATCATTACAGATATGAAATCAATGCGGACCCAGATTAAACAAACCTCAGTTCTAACTCGGATGTCTGAGAA
ATATTAGAGGACAGACCAAGGACAACCTCTGCATGAGATGTAGACTTAAGCTTTATCCCTACTAGGCTTGCTCCAC
TTTCATCCTCCACTATAGATAACAACGGACTTTGACTAAAAGCAGTGAAGGGGATTTGCTTCCTTGTTATGTAAAG
TTTCTCGGTGTGTTCTGTTAATGTAAGACGATGAACAGTTGTGTATAGTGTTTTACCCTCTTCTTTTTCTTGAA
CTCCTCAACACGTATGGAGGGATTTTTAGGTTTTCAGCATGAACATGGGCTTCTTGCTGTCTGTCTCTCTCAG
TACAGTTCAAGGTGTAGCAAGTGTACCCACACAGATAGCATTCAACAAAAGCTGCCCTCAACTTTTTCGAGAAAAA
TACTTTATTCATAAATATCAGTTTTATTCTCATGTACCTAAGTTGTGGAGAAAATAATTGCATCCTATAAACTGC
CTGCAGACGTTAGCAGGCTCTTCAAAATAACTCCATGGTGCACAGGAGCACCTGCATCCAAGAGCATGCTTACAT
TTTACTGTTCTGCATATTACAAAAATAACTTGCAACTTCATAACTTCTTTGACAAAGTAAATTACTTTTTTGAT
TGCAGTTTATATGAAAATGTACTGATTTTTTTTTTAATAAACTGCATCGAGATCCAACCGACTGAATTGTTAAAAA
AAAAAAAAAATAAAGATTCTTAAAAGAA

2254/6881
FIGURE 2071

MPGGCSRGPAAAGDGRRLRLARLALVLLGWVSSSSPTSSASSFSSSAPFLASAVSAQPPLPDQCPALCECSEAARTV
KCVNRNLTEVPTDLPAYVRNLFLTGNQLAVLPAGAFARRPPLAELAALNLSGSRLDEVRAAGAFEHLPSLRQIDLS
HNPLADLSPFAFSGSNASVSAPSPLVELILNHIVPPEDERQNRSFEGMVVAALLAGRALQGLRRLELASNHFLYL
PRDVLAQLPSLRHLDLSNNSLVSLTYVSFRNLTHLESLHLEDNALKVLHNGTLAELQGLPHIRVFLDNNPWVDC
HMADMVTWLKETEVVQGDRLTCAYPEKMNRNVLELNSADLDCDPILPPSLQTSYVFLGIVLALIGAIFLLVLY
LNRKGIKKWMHNIRDACRDHMEGYHYRYEINADPRLTNLSSNSDV

2255/6881
FIGURE 2072

CCTGGAGGCCGGCTTGGCGGCCAGGCGCAAGTTCGCGACGTCACCCGATCCGACCCCTGGTACCCGGAGCGGCCCT
GGCGCGGCTGTCGGCTGGCACCAGCTCCCTGCAGGAAGAGTGGAGAGGTTGTTCCCGCGGGGAGCGGGTACCGG
CCGCATCCCGGCCGGACCAGGGAGCCTGGGCGCCGGCAGTTCGGCTGCTGGTGTTTAATGTGTGTTTTTGGTCTT
CTCCCCAAGCAATGGAACAGAGTTGCTGCTTCAGTGGTAGTAGTACTTGCAATTCAAGTAACACTAACTTAAAA
TCTACTTTAGACACAGTGGGCGATAGTATGAAAGAACCAAGAAGGATTTCCGGCTGTCCTGGAGCTGATAATGCTG
CAAACAAGCCATGATGAGATGTTCTCCACATTTACAAAATCCGGGAGACTGCGGATGGGCTGTGCCTGGAGGTG
GAGGGGAAATTGGTAAGTAGGACAGAGGGTAACATTGATGACTTGCTCATTGGTGGAATGCCTCCGCTGAAGGC
ACTGAAAGCGAAGGCAAACCTTGAAGAACAGAGACCAGAAAGAGTAAACCTTTTATGACAGGGGCTGCAGAACAA
ATCAAACACATCCTTGCTAATTTCAAAGCTACCACTTCTTTATTGGTGAAAACATGAATCCAGATGGCATGGTT
GCTCCACAGGACTACCAAATAGAAGTTCAAGCTTCGGATGACACTGAAAGGTGTTTCAGGAGATTTTGGTTCCACT
AGAAATAATGAAAATTTATGCCAAGAATAG

2256/6881
FIGURE 2073

MCVFGLLPKQWKQSCCFSGSSTCNSSNTNLKSTLDTVGDSMKEPRRISAVLELIMLQTSHEMFSHIYKIRETAD
GLCLEVEGKLVSRTEGNIDDLIGGNASAEGTESEGKLEEQRPERVKPFMTGAAEQIKHILANFKSYHFFIGENM
NPDGMVAPQDYQIEVQASDDTERCSGDFGSTRNNENLCQE

2257/6881
FIGURE 2074

AGAGAGGAGCCGACTCGGCAGGGACTGGGGGACCGGGCCGAGAGTGCAGAGCGAGCGAGGGAGGGAGTGAGGGAGC
GTGCGAGCCAGAAGGGGAAAGGCGGCCACTCGTGCCTGAGCGACCGCAGAGGGGAGTGGGAGCAGTGGGGTAAAG
GAGCGGGGGGCGGGAATAAGAAAGGCCGAGAGAAGGCGGACAGAGGCTAGTGGTGGTGGTGGTGGTAGGGGGAGA
AGGAGGAGCTGGAGGAGGGCAGGGGCTGAGGGAGTGAGTGAAGCGGACGCGCGAGGGAGGGGAGGGAAGGGAAGG
GAAGGGAAGGGGGGGTACGCGGGGGCGCGCGCGCACCGGGAGCGCGCTCGGAGGCGAGTGGAACCTGGATCGG
GTTTGCTGCCAGCGGCGTGAGCTTCGGCCGCCATTTTACAACAGCTCCACTCGCGCCGGACACAGGGAGCAGCGA
GCACGCGTTTCCCGCAACCCGATACCATCGGACAGGATTTCTCCGCCCTCAGCCCAACGGGGAGATCTCTGGAAAC
ATGGCTACAGAACATGTTAATGGAATGGTACTGAAGAGCCCATGGATACTACTTCTGCAGTTATCCATTCAGAA
AATTTTCAGACATTGCTTGATGCTGGTTTACCACAGAAAGTTGCTGAAAACTAGATGAAATTTACGTTGCAGGG
CTAGTTGCACATAGTGATTTAGATGAAAGAGCTATTGAAGCTTTAAAAGAATTCAATGAAGACGGTGCATTGGCA
GTTCTTCAACAGTTTAAAGACAGTGATCTCTCTCATGTTCAGAACAAAAGTGCCTTTTTATGTGGAGTCATGAAG
ACTTACAGGCAGAGAGAAAAACAAGGGACCAAAGTAGCAGATTCTAGTAAAGGACCAGATGAGGCAAAAAATTAAG
GCACTCTTGGAAGAACAGGCTACACACTTGATGTGACCACTGGACAGAGGAAGTATGGAGGACCACCTCCAGAT
TCCGTTTATTTCAGGTCAGCAGCCTTCTGTTGGCACTGAGATATTTGTGGGAAAGATCCCAAGAGATCTATTTGAG
GATGAACTTGTTCCATTATTTGAGAAAGCTGGACCTATATGGGATCTTCGTCTAATGATGGATCCACTCACTGGT
CTCAATAGAGGTTATGCGTTTGTCACTTTTTGTACAAAAGAAGCAGCTCAGGAGGCTGTTAAACTGTATAATAAT
CATGAAATTCGTTCTGGAAAACATATTGGTGTCTGCATCTCAGTTGCCAACAAATAGGCTTTTTGTGGGCTCTATT
CCTAAGAGTAAAACCAAGGAACAGATTCTTGAAGAATTTAGCAAAGTAACAGAGGGTCTTACAGACGTCATTTTA
TACCACCAACCGGATGACAAGAAAAAAACAGAGGCTTTTGCTTCTTGAATATGAAGATCACAAAACAGCTGCC
CAGGCAAGGCGTAGGTTAATGAGTGGTAAAGTCAAGGTCTGGGGGAATGTTGGAAGTGTGAAATGGGCTGATCCT
ATAGAAGATCCTGATCCTGAGGTTATGGCAAAGGTAAAGTGCTGTTTGTACGCAACCTTGCCAATACTGTAAACA
GAAGAGATTTTAGAAAAGGCATTTAGTCAGTTTGGGAAACTGGAACGAGTGAAGAAGTTAAAAGATTATGCGTTC
ATTCATTTTGATGAGCGAGAIGGTGCTGTCAAGGCTATGGAAGAAATGAATGGCAAAGACTTGGAGGGAGAAAAAT
ATTGAAATTGTTTTTGCCAAAGCCACCAGATCAGAAAAGGAAAGAAAGAAAGCTCAGAGGCAAGCAGCAAAAAAT
CAAATGTATGACGATTACTACTATTATGGTCCACCTCATATGCCCCCTCCAACAAGAGGTCGAGGGCGTGGAGGT
AGAGGTGGTTATGGATATCCTCCAGATTATTATGGATATGAAGATTATTATGATTATTATGGTTATGATTACCAT
AACTATCGTGGTGGATATGAAGATCCATACTATGGTTATGAAGATTTTCAAGTTGGAGCTAGAGGAAGGGGTGGT
AGAGGAGCAAGGGGTGCTGCTCCATCCAGAGGTCGTGGGGCTGCTCCTCCCCGCGGTAGAGCCGTTATTTCACAG
AGAGGAGGTCCTGGATCAGCAAGAGGCGTTTCAGGTGCGAGAGGAGGTGCCCAACAACAAAGAGGCCGCGGGGTA
CGTGGTGCGAGGGGTGGCCGCGGTGGAAATGTAGGAGGAAAGCGCAAAGCTGATGGGTACAACCAGCCAGATTCC
AAGCGGCGCCAGACCAATAATCAGAACTGGGGCTCCCAACCCATTGCTCAGCAACCGCTCCAAGGTGGTGATCAT
TCTGGTAACTATGGTTACAAATCTGAAAACCAGGAGTTTTATCAGGATACTTTTGGGCAACAGTGGAAGTAGAAA
CAGTAGGGCCTCTGTAAAATTGGAGACTGATAGGTTGATCAGAACTCACCTAAATCTGAACGGGTGCCGCTAT
AATTTGTGACATCTGGCAAGATTTCCCTTTATGTATATATTTTAAACAATCCGCTTGGACACGAACAAAGCCACAC
TTCTAACTGCTTCTGGCGAACTGATTTTATTTTTTAATTTTTTTCAATAAAGATATTCTTAGATACTGAAAGAAAT
AGTTAATGAGTTTGCATTTGTGCTTGAGAAAATTTGGCTCAAGTCCATTTGGCTGTAGTGTCAACGATGTTTCCA
GTAGTGTTTAGATTTGGTGTCTTCAAAGGTAGTTGATTAAAACCAAGTGTGTCTTTAATATCTTGTATCAGAATA
ACTTTGTATGTTACCAACTTAAATTGCTAGAATAAGGTAAATTGATACAACTGCTATTTTTTAATTTAGAACTT
TGACCTAATTTGGGTTTTCAAACCAATTTGGCTACTTGTATTCTTTATGCTGTTGTTTATTTCAATAAAAAATT
CACACCT

2258/6881

FIGURE 2075

ATGGCGTGCGGCTTTTCGCCGCGCTATTGCTTGCCAGCTTTCCAGAGTGTTGAATCTTCCACCAGAAAACCTTGATC
ACATCAATATCTGCAGTTCCAATTTCCCAAAAAGAAGAAGTAGCTGATTTTCAGCTTTCTGTGGATTCTTTATTG
GAAAAAGACAATGACCATTCAAGACCAGATATTCAAGTTCAAGCCAAGAGACTAGCAGAGAAGCTAAGATGTGAT
ACAGTGGTGAGTGAAATCAGTACTGGTCAAAGGACTGTAAATTTCAAATAAACAGAGAGCTCTTAACAAAGACA
GTGCTACAACAAGTAATTGAAGATGGCTCAAAATATGGATTAAAAAGTGAACCTTTCTCTGGACTTCCCCAGAAG
AAGATTGTGGTTGAATTCAGTTACCTAATGTTGCCAAAAAATTTTCATGTTGGACATTTGCGTTCTACCATCATA
GGAAATTTTATAGCAAATCTCAAAGAAGCTTTAGGACATCAAGTAATAAGAATAAATTACCTTGCGGATTGGGGC
ATGCAGTTTGGTCTTCTGGGAACTGGCTTCCAGCTGTTTGGCTATGAGGAAAACTGCAGTCCAATCCTCTACAG
CATCTCTTTGAAGTTTATGTACAAGTTAATAAAGAAGCAGCAGATGATAAAAGTGTAGCAAAAGCAGCACAGGAG
TTCTTCCAACGATTGGAACCTGGGCGATGTGCAAGCACTTTCCTGTGGCAAAAATTCGGGACTTGAGCATTGAA
GAGTACATTCGGGTTTACAAGCGTCTGGGAGTATATTTTGATGAATATTCAGGAGAATCATTTTATCGTGAAAAA
TCTCAAGAGGTCTTAAAGTTGCTGGAGAGTAAAGGACTCCTACTGAGAACAATAAAAGGAACGGCTGTAGTAGAT
CTCTCTGGGAATGGCGACCCCTCCTCAATTTGTACTGTAATGCGAAGTGATGGGACTTCTCTCTATGCAACCAGA
GATCTTGCAGCTGCTATAGATCGAATGGACAAGTATAATTTTGATACAATGATATATGTGACAGATAAAGGACAA
AAAAAGCATTTTCAGCAAGTATTCCAAATGCTGAAGATCATGGGATATGACTGGGCAGAAAGGTGCCAGCACGTG
CCCTTTGGAGTAGTACAGGGAATGAAGACTCGAAGAGGAGATGTCACTTTTCTGGAAGATGTTTTAAATGAGATT
CAATTAAGGATGCTACAGAACATGGCTTCAATTAAGACAACCTAAAGAACTCAAGAACCCACAAGAGACTGCAGAG
AGGGTCGGGCTCGCAGCACTCATTATTCAAGACTTCAAAGGTTTACTCTTATCTGACTACAAGTTTCACTGGGAT
CGTGTTTTCCAGAGTCGCGGGGACACAGGAGTCTTCTACAGTACACACACGCCCGCTCCACAGTTTGAAGAG
ACTTTTGGATGTGGGTACCTGAATGACTTCAACACTGCTTGTTTACAAGAGCCACAGTCTGTTTCAATTCTTCAG
CATCTTCTCAGGTTTCGACGAGGTGCTTTATAAATCATCTCAGGACTTTCACCCAGGCATATCGTCAGTTACCTT
CTAACTTTAAGTCATCTTGCAGCTGTGGCACACAAAACACTACAAATAAAAGATAGTCCTCCTGAAGTGGCTGGG
GCCAGACTTCATCTTTTCAAAGCTGTCCGTTCTGTCTAGCCAATGGAATGAACTTCTTGGAATAACACCTGTA
TGTAGGATGTAA

2259/6881
FIGURE 2076

MACGFRRRAIACQLSRVLNLPENLITSISAVPISQKEEVADFQLSVDSLLEKDNDHSRPDIQVQAKRLAEKLRC
TVVSEISTGQRTVNFKINRELLTKTVLQQVIEDGSKYGLKSELFSGLPQKKIVVEFSSPNVAKKFHVGHRLRSTII
GNFIANLKEALGHQVIRINYLGDWGMQFGLLGTGFQLFGYEEKLQSNPLQHLFEVYVQVNKEAADDKSVAKAAQE
FFQRLLELGDVQALSLWQKFRDLSIEEYIRVYKRLGVYFDEYSGESFYREKSQEVCLKLLESKGLLLRTIKGTAVD
LSGNGDPSSICTVMRSDGTSLYATRDIAAIDRMDKYNFDTMIYVTDKGQKKHFQQVFQMLKIMGYDWAERCQHV
PFGVVQGMKTRRGDVTFLLEDVLNEIQLRMLQNMASIKTTKELKNPQETAERVGLAALI IQDFKGLLLSDYKFSWD
RVFQSRGDTGVFLQYTHARLHSLEETFCCGYLNDFNTACLQEPQSVSILQHLLRFDEVLYKSSQDFQPRHIVSYL
LTLSHLA AVAHKTLQIKDSPPEVAGARLHLFKAVRSVLANGMKLLGITPVCRM

2260/6881
FIGURE 2077

TTTTTTTTTTTTTTTGTTCCTGAATTATTTAAGTTTCTTATAGATTCTGGATATTAGACCTTTCTTAGATGCATA
GCTTATGAATATTTTCTCCATTATTTAGGTTGTAGGGAAAGGGAGAGCTTTTGATTTTTTTTAAGCATTACAGA
TAATGTTGAAGTCACTGATATATATTTGTTTGACTGCATTCCCTACCCTGCTTCCCTAGAGAGAAGTATCTCAT
GATGCAAATGATTTATTTTACGAATCAGTTGCTTTGTGTTTGTTCCTTTGTTTTGTATTTTTTTTTCACCTAC
CCAGTGAAAAGGATAAATGGCATTGTCCATCTCTTAATGAACACTAGTGTGAAGAAGAATATCTCTTTTT
CTCATGTTGAACTCAAATTACAACATTTAAAAAATATGTCATTTGGAGGTCAGTGGAGAGGTTTGAATTAGAAG
CATGTATTTGGAGTAGTAGAGGAAGCATTGTAGAAGAGGTAAAGAGACCTGGGCTTTTTTCTCAGTCTGTTTTT
TTTGCAGTAGGATTTTAAAGGAGACATTTAGCTTGCCAGACATCAGTTTTTCATGTCTATAAAATAAGGTGGCTAG
TATAAGAGGAAGAATTTTTTGAGACTAGGCTTGCTCTGTCACCCAGACTGGAGTGCAGTGGCATGATCTCGGCT
CACTGCAACCTCTGCCTCCTGGGTTCAGCAATTTCTCGTGCCTAAGCCTCCCGAGTAGCTGGGCTTACGGGCACA
TGCCACCACGCCTGGCTAATTTTTTGATTTTTTAGTAGAGATGGGGTTTTTCCATGTTGGCCAGGCTGGTCTCAA
CTCCTGACCTTAAGTGGTCCACTTGCTCGGCCTCCCAAAGTGCTGGGATCTGTGCCCAGACAGAAGAGGAAGAA
TTTTATAAGATGATAAGAAAAACATTCTGAATAAATACTAGGTTATTTCTCATTTTCTTGCTTTTAATTTTGTTT
TTTATTTATTTATTTTATTTTATTTTACTTTTTTGAGACAGAGTTTCGCTCTTGTCACCCAGGCTGGAGTGCAGTG
GCACAATCTTGACTCGCTGCAGTCTCCACCTCCAGGATTCAAGCGATTCCCCTGCCTCAGTCTCCCAAGCAGCTG
GGATTGTAGGTACACACCACCATGCTGGCTAATTTTTGTGTGTGTGTGTATTTTTTAGTAGAGATGGGGTTTT
ACCATGTGGCCAGGCTGGTCTAGAACTCAACCTCAGGTGATCCGCCTGCCTTAGCCTCCCAAAGTGCTGGGATTA
CAGGCATGAGCCACCGCTCTCGGCCCCCTTGCTTTTAATTTTGAAAGTACACATAACACCTTCTTCTGGTAAAGG
TATGTCTCAATGGAGAACTCATAGTGATTAGTCTTTGTTTAAACAATAATGCTTTTAAGGTAACAGTTCTATCTC
GTTTCGATGTCTGTCTTTAGAGAAGTAGCTGATTTTCAGCTTTCTGTGGATTCTTTATTGGAAAAAGACAATGAC
CATTCAAGACCAGATATTCAAGTTCAAGCCAAGAGACTAGCAGAGAAGGTACGTTAGCACTATTATCTCTTTTTG
ACATTGTAATAAACTTGTTATTAAAAAAGTACTTTGCAGGCTATCTCAGCCATAATAGTGAATTTAATAGTGTT
TCTTTGAGGCATCTTGTAATAATAAATTTAAATTCATTTTAGCCATGTACTATAAGGTTATAATGATTTTTTCA
TTAGTTATAAAGCACTCCTCTTGAGCTGACATTGTTCAATTTTTTGATTAACCACTTACAGGAAGACTGAAGTGT
TAATTAAATTTACAGATTGAAGCTGG

2261/6881
FIGURE 2078

MPFRLANFCIFSRDGVFPCWPGWSQTPDLKWSTCLGLPKCWDLCPPDRRGRIL

2262/6881
FIGURE 2079A

GATTGCCCCCTGTGGGTCACCTTCTCAGTCATTTTGTAGCTCAGCCTAATCAAAGACTGAGGTTATGAAGTCGATC
CTAGATGGCCTTGCAGATACCACCTTCCGCACCATCACCCTGACCTCCTGTACGTGGGCTCAAATGACATTTCAG
TACGAAGACATCAAAGGTGACATGGCATCCAAATTAGGGTACTTCCCACAGAAATTCCTTTAACTTCCTTTAGG
GGAAGTCCCTTCCAAGAGAAGATGACTGCGGGAGACAACCCCCAGCTAGTCCCAGCAGACCAGGTGAACATTACA
GAATTTTACAACAAGTCTCTCTCGTCCCTCAAGGAGAATGAGGAGAACATCCAGTGTGGGGGAGAACTTCATGGAC
ATAGAGTGTTCATGGTCCTGAACCCCAGCCAGCAGCTGGCCATTGCAGTCCTGTCCCTCACGCTGGGCACCTTC
ACGGTCCTGGAGAACCTCCTGGTGTGTGCGTCATCTCCACTCCCGCAGCCTCCGCTGCAGGCCTTCCTACCAC
TTCATCGGCAGCCTGGCGGTGGCAGACCTCCTGGGGAGTGTCAATTTTGTCTACAGCTTCATTGACTTCCACGTG
TTCCACCGCAAAGATAGCCGCAACGTGTTTCTGTTCAAACCTGGGTGGGGTCACGGCCTCCTTCACTGCCTCCGTG
GGCAGCCTGTTCTCACAGCCATCGACAGGTACATATCCATTACAGGCCCTGGCCTATAAGAGGATTGTCACC
AGGCCCAAGGCCGTGGTGGCGTTTTGCCTGATGTGGACCATAGCCATTGTGATCGCCGTGCTGCCTCTCCTGGGC
TGGAAGTGGGAGAACTGCAATCTGTTTGCTCAGACATTTTCCCACACATTGATGAAACCTACCTGATGTTCTGG
ATCGGGGTCAACAGCGTACTGCTTCTGTTTCATCGTGTATGCGTACATGTATATTCTCTGGAAGGCTCACAGCCAC
GCCGTCCGCATGATTACAGCGTGGCAGCCAGAGAGCATCATCATCCACACGTCTGAGGATGGGAAGGTACAGGTG
ACCCGGCCAGACCAAGCCCGCATGGACATTAGGTTAGCCAAAGACCCTGGTCCTGATCCTGGTGGTGTGATCATC
TGCTGGGGCCCTCTGCTTGCAATCATGGTGTATGATGTCTTTGGGAAGATGAACAAGCTCATTAAAGACGGTGT
GCATTCTGCAGTATGCTCTGCCTGCTGAACCTCCACCGTGAACCCCATCATCTATGCTCTGAGGAGTAAGGACCTG
CGACACGCTTTCCGGAGCATGTTTCCCTCTTGTGAAGGCACTGCGCAGCCTCTGGATAACAGCATGGGGGACTCG
GACTGCCTGCACAAACACGCAAACAATGCAGCCAGTGTTCACAGGGCCGCAGAAAGCTGCATCAAGAGCACGGTC
AAGATTGCCAAGGTAACCATGTCTGTGTCCACAGACACGTCTGCCGAGGCTCTGTGAGCCTGATGCCTCCCTGGC
AGCACAGGAAAAGAATTTTTTTTTTTAAGCTCAAATCTAGAAGAGTCTATTGTCTCCTTGGTTATATTTTTTA
ACTTTACCATGCTCAATGAAAAGGTGATTGTCAACCATGATCACTTATCAGTTTGCTAATGTTTCCATAGTTTAGG
TACTCAAACCTCCATTCTCCAGGGGTTTACAGTGAAGAAAGCCTGTTGTTTAAAGTACTGAACGATCCTTCAAAGT
CTCAATGAAATAGGAGGGAAACCTTTGGCTACACAATTGGAAGTCTAAGAACCCATGGAAAAATGCCATCAAATG
AATAATGCCTTTGTAACCACAACCTTTCACTATAATGTGAAATGTAAGTGTCCGTAGTATCAGAGATGTCCATTTT
TACAAGTTATAGTACTAGAGATATTTTGTAAATGTATTATGTCTGTGAGATGTGTATCAGTGTATATGTGCTA
TTAATATTTGTTTAGTTTACAGCAAACTGAAAGGTAGACTTTTATGAGAACAATGGACAAGCAGTGGATACGTGTC
AATGTGTGCACTTTTTTCTATATTATTGCCCATGATATAACTTTAGAAATAAACCTTAATATTTCTTCAAATAT
CTCTATTTAATTTTGACACTGAAATAACCGTAAAGGTTTATTTTTCTGTTACCTCAACAAGAAGAATTTGAAGAC
TTCAAATATTGAGCAGAATTCATTCTACTTAAAAATTTATTAGCCCTGCATTTTCATAGGAAGACACATTATC
TTCTGGACTATAGCTGTTCTAATGGATTATAATCAGAATGGAAGAGAGAAAAGCATATTGACTTTTTTTGAGCGAC
ATCTCTGACTTTCTTTAGTCTTTAGCTATTACTGGATCTCTTAAGACAGCATGTGTTAATCTTAATGTATATCGT
TATCACTGTGCAGTTGCTGTTTACTTGAATAGTATTGTGTTCTATATTCCAGGTTTAAAGTAGATTTTCATGCCTG
GGTGGCCAAACAACAGTCTTCATTTTTTTTTAATTGAAAAGAAGTAGTGTCTGGATCAGTAAAATTATACTGTGTG
TGAGTGTGAATATAAATGTGTGTATGTGTGTTTCTGTCTGTAACTGTTACAGTAATGTCATAAAGTGAGAAAAC
TGTGACCAAGTATAAACTTTTACCACCTTGCTGCACCTCTTGACATGGATTTCAGTTTCTAAAATTGAGTTCTTCCT
GTAATCTTGTTGATAAAAAATACTGACTCCAACCATTCAAATTTTCAACCCATCCCTCCTTAAGAGATTGGATCA
AGTATTACTAAATTGACCTTTAGGTATTACACAAGACCAGTGTCTTAGCAAAAAATAATGACAGGCATCCAAGGAA
GGGATGTATTTGTAGTGTATTGCGCAGGAAAGGAGAGTACTTTGGTTTCTGAGCACCGAATATTGAGCAATATGT
CAGTCACTAAAAGGAAGACAGTTCTACAGAAAAACAATGGTAACATTTTCAATAGCGTGTGTAGATAGTATGCA
CTATATACATCACGTTAAAGTAGGACTATCACACCCAGCCCATGTGGCTAAAAAGCTGAATCAGACAGTGGATG
AGACACACAACGGCAGTGAAGAACCGATACACTTGGCATTGACGTCTAGCTATGCTGTATCTGTGCTTTGCCAC
ATGCCCTTGGTGACAGCTGAGCACCCAGCTCTGTCTTGGTAGGTTTGGGCTAAGGAACAAATCTCTCCTTTGCTC
GTGGTTAGCAAGATACACTCAAGCATGAAGATAAACACAGCTGCTTTCTTCTTACACCCCGGTCTCATGCTCCTT
AATGGCGCCATGGGTGCTTGTGGGCCTTTTCCAGTAAGGAATGATATTGCTGAAGAATCTACTTAACCTTGAC
AAATTTTAATTATAATCTCTTCTTATACAGATAAAACATGACTCCTACAAGGCCCAAGGTTTACATAGTCTGAA
GTGAAGTACAGAGCTGGCATCTATCTGGTGATTCTTAGCTCTCGAGATACCCAAGCAGCCTGATGGGGCAGTTCC
CCTTCTTACGGTTCACGCTCTAAGGCAGGATGTGGCTTATGAGATACTTTGCATTGTCTGTCTGCACACCTTGAA

2263/6881
FIGURE 2079B

TCTGCCTGCTGGCTCCCTTACTTTACCTCTCTGTTCATGTGCAGATGAAGGCTCAGGGTGCTAGAGGATTAGTAAG
ATCTCTTTCTAAAGACAGGAGAGATTATTTACAAGAAGAACTCACCAGGGTTTAGTTTGCATTTAAGAATTGCCA
GTCTTTTGTCTGCATCATCTTGAACATTAAATCCACATGTTTCAGAGCTCACCAGGCAGTACCAATGCTCTTTTC
ACAGCTATGAAGAGCTAGAGAAATTCTTGTTATGGTAGAAAAATTCACGATTCATTTTTGAAACTGCATTTGTG
CGTATGCAGTGTAGATTTTATAGTGTGTTGTGCTTTCAAGATCTAAATCATATATAATAAATTAAGGGACAATGG
GGCTGACAGCACTAAACTTGGTGCTTATTGATATTCTAAGAAATATCTGTGAAATATCATCACGTATGTTATACA
ACCTTCATTTAAAAAGGTTTAAACTAGTTAGATTCACTTTGACACTTTTCATATCATTTCCTTAACCCAAGTGAC
GAAAACATTGTCCCAATGAATATACTCATTAGAATTACCATTTGTTAATATCACTCATTAAATTAACCCCAAT
TAGATCCATTAATTTAAATGATTTAAATTTAAGTAAGTTTATAAGGCTGACATCAGAGGTATCTTACTTTCCCT
CTGAGGATGATGTACTTGCCCTGACCATGCATTTTACCATCACACATGTTTCAGAAAGGGCCAAATTTCCCAACCTG
CTCATTTTTTTTTTATCAGAGTCATGATGAATCAGTCCTAGAATGTTTCATTTGCACAAGTAGGGCTGCCCTCCAA
GAGGAACCTCTGATTTATTTTGTATGAAATATATGTGAAAGGATATGAATCTGAGAGATGCTGTAGACATCTGTC
CTACACTTGAGATGATTTCCAAGCCTCTCTGGCACTTTGAGTTAAGTCTATCTGGTATTAAATGCCAAGGACCTT
TTGCTGCCTAAATCCACTCTGCAGGAAATAGGCCCAACCACCAGATGAGAATTAGGCCCTGGATGAGTAGCGCTA
TAGTTACTGTCCTGTTGATTAATTTCTGCCATTTTCATGTCCATAAAAGAGACCACCCATATCATGCACACAATTA
GATTTCTCACACTCTAACTGTATATTTGTATGATATTTTAAATCTCCTAAATGCTGGGCAATGGCTATTAAACAA
TTAATTGTCTTGCACCTGGCCTTCTGATGAAATGTTAACAATGCCTATTGTAATATAGAAAAAACATTCTATCTA
CTGATTTGGGCTGAATGTATGTAAATAGGTTTCTAAAAAGTCAGATGTTTGAGCAGTGGCCTACAAATCAGTAAT
TTTCGGATGGGAGAGTTTCTTTACATTGCCGTGGCATCTTAAAAGCTATCTTCATGTAAATTGACTGTACTAGGC
CTACTGGGGATCAGAGTTCCAAGAAAGGAAACCTTTTCTTGATCTGGATTCAAATTTATTTCCAATGTTTCAA
GCGGGAACATGACTCTTTATTGTCTGTAAATCTAACATTATTACTTTTCTCTTAGAAGAATATTGTATTGTTA
GATGTTTGTGAGCTGGTAACATCGTTGCAACCACTGCAATATCTTCGTTAGTAATCTGTATAATACTTTGTATA
CAAGTACTGGTAAGATTGTTATTAAATGTAGCTTCAGTCATTAAATTACTATAGCAAAGTAGTACTTCTTCTGTA
ATATTTACAATGTATTAAGCCACAGTATATTTTATTTCAATGTAATTAACTGTTAACTTATTCAAAGAGAAAA
CATCTCATCATGTCTATTGTCCAAAGTTACCTGGAATCAAATAAAAATTCTAGATTACCATGAAGAACATA

2264/6881
FIGURE 2080

GAGCGCGGTTACCGGACGGGCTGGGTCTATGGTCGCTCCGCGGGCCGCTCCGCCGGCTGGTGCTTTTTTATCAGG
GCAAGCTGTGTTCCATGGCAGGGAACCTTTTGGCAGAGCTCCCACTATTTGCAATGGATTTTGGATAAACAAGATC
TGTTGAAGGAGCGCCAAAAGGATTTAAAGTTTCTCTCAGAGGAAGAATATTGGAAGTTACAAATATTTTTTACAA
ATGTTATCCAAGCATTAGGTGAACATCTTAAATTAAGACAACAAGTTATTGCCACTGCTACGGTATATTTCAAGA
GATTCTATGCCAGGTATTCTCTGAAAAGTATAGATCCTGTATTAATGGCTCCTACATGTGTGTTTTTGGCATCCA
AAGTAGAGGAATTTGGAGTAGTTTCAAATACAAGATTGATTGCTGCTGCTACTTCTGTATTAAAACTAGATTTT
CATATGCCTTTCCAAAGGAATTTCTTATAGGATGAATCATATATTAGAATGTGAATTCTATCTGTTAGAACTAA
TGGATTGTTGCTTGATAGTGTATCATCCTTATAGACCTTTGCTCCAGTATGTGCAGGACATGGGCCAAGAAGACA
TGTTGCTTCCCTTGTCATGGAGGATAGTGAATGATACCTACAGAACGGATCTTGCCTACTGTATCCTCCTTTCA
TGATAGCTTTAGCTTGCCTACATGTAGCCTGTGTTGTACAGCAGAAAAGATGCCAGGCAATGGTTTGCTGAGCTTT
CTGTGGATATGGAAAAGATTTTGGAAATAATCAGGGTTATTTTAAACTATATGAGCAGTGAAGAATTTTCGATG
AGAGAAAAGAGATGGCAACCATTCTTAGTAAGATGCCAAAACCAAACCTCCAAACAGTGAAGGAGAGCAGG
GTCCAAATGGAAGTCAGAACTCTAGCTACAGCCAATCTTAAACATTCCGAAGAATTCCATAGTGGACCACCTTGG
AAATAAACCATTTGGACAGATTTTCAAGTAATGTCTTCAGTGGAAACACAAATGAAAATGAATAGCTTGTTTCTGTCAA
GCATATTGGAAAAGTGATTTTATTTTTGCAAATAAGTTTTTCTTTAATATGATTCTAGTACATAATTGATTAAAA
TCTCTTGATTATAAATGTTTGGAAAGGTTCTAAGGGGACCTACAGACAGACATACATAGACATTTCAAAATTAAT
AGCTTTTGATTAGTATAATATTTCTTAATTTGGATAATAAAAAATTGTAGCTTTTTTATTAAGCCAGGAAACATGAA
GCATAATTTGTTTAAAAATTTCTTTTGGTCATTGAGGGACCAAAAAAGGACGTAAATTTTACAGTCAATCTATGAG
GGTTTTTTTTCCCTCCATAAGTTTAACTTTAAACTGTATTTAAGGAATCAAATCTTACAAAATCCTGGAAGATTT
TGGTAATGATGTTGATAATTTTCAAGGAAATTAATCAAGTACCTATATTGATTTAAAAGTGATTTTATTTCAGTAG
TTTGAGG

2265/6881
FIGURE 2081

AGTCTCCCCAGGTTGTAGACGCTGCGGCCCGGCCCGGGTAAATAACAGATGCGGGTGAAAGATCCAACATAAA
GCTTTACCTGAGAAAAGCCAAAAGAAGTAAAAGGCCTACTGTACCTCATGATGAAGACTCTTCAGATGATATTGCT
GTAGGTTTAACTTGCCAACATGTAAGTCATGCTATCAGCGTGAATCATGTAAAGAGAGCAATAGCTGAGAATCTG
TGGTCAGTTTGCTCAGAATGTTTAGAAGAAAGAAGATTCTATGATGGGCAGCTAGTACTTACTTCTGATATTG
TTGTGCCTCAAGTGTGGCTTCCAGGGATGTGGTAAAACTCAGAAAGCCAACATTCATTGAAGCACTTTAAGAGT
TCCAGAACAGAGCCCCATTGTATTATAATTAATCTGAGCACATGGATTATATGGTGTATGAATGTGATGAAAAA
TTATCAACGCATTGTAATAAGAAGGTTTTGGCTCAGATAGTTGATTTTCTCCAGAAACATGCTTCTAAACACAA
ACAAGTGCATTTTCTAGAATCATGAACTTTGTGAAGAAAAATGTGAAACAGATGAAATACAGAAGGGAGGAAAA
TGCAGAAATTTATCTGTAAGAGGAATTACAAATTTAGGAAATACTTGCTTTTTTAATGCAGTCATGCAGAACTTG
GCACAGACTTATACTCTTACTGATCTGATGAATGAGATCAAAGAAAGTAGTACAAACTCAAGATTTTTCTTCC
TCAGACTCTCAGCTGGACCCATTGGTGGTGGAACTTTCAAGGCCTGGACCACTGACCTCAGCCTTGTTCTGTTT
CTTCACAGCATGAAGGAGACTGAAAAAGGACCACCTTCTCCTAAAGTTCTTTTTAATCAGCTTTGTGAGAAGCGG
GTGCATCTACATTTAATATAAAATAATTATGAGTTACAAAATACTAATGTATTTCATCATTTAACATGAATAGTCGT
TTTTACTGTAACTTTGCTCTTATTGCCCTGACTATGAAGAGAACTAAAAATTTGTTACAGCTCTATGCTTTATGAA
AATTATATCTCAGTCCTCAGAAGAAGCAGCTTATCCTCATATATAAGGAAATGGAGACACAGAAATTAAATGGCT
CACCTAGTCTGAGTGAAAAGCTGAGAATCAAATGGAGATCTGTCTGACTTGATGCCTATGTTGTAATACCATA
AAGTGAGAAAACCATAGAGTTGTAAAACTAGAAAGTACCGTAAGATAACATCTAATCTAGCTTTCTTATTTTAA
AAGATGAGCTGTGAGGCAATAGAGTTTAAAGTGAATTTCTCAAGGTATTACAGTATGTTTAAAAACCAATCCTT
ATGTGCCTGGAAATAAACACATAAAGGATCTGACTTGTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

2266/6881
FIGURE 2082

MRVKDPTKALPEKAKRSKRPTVPHDEDSSDDIAVGLTCQHVS HAISVNHVKRAIAENLWSVCSECLEERRFYDGQ
LVLTSDIWLCLKCGFQCGKNSSEQHSLKHFKSSRTEPHCIIINLSTWIIWCYECDEKLSTHCNKKVLAQIVDFL
QKHASKTQTSAFSRIMKLCEEK CETDEIQGGKCRNLSVRGITNLGNTCFFNAV MQNLAQTYTLTDL MNEIKES
TKLKIFPSSDSQLDPLVVELSRPGPLTSALFLFLHSMKETEKGPLSPKVLFNQLCQKRVHLHLI

2267/6881
FIGURE 2083

AGTTTGTTGCTCCCACCGAGTTCTGAAGAACGCCAGCAGCTCGCTGCTTAAAATTAAACCACAGGGTTCCATGAT
GGGTCAACTTGATGGGAAAGTCATCATCCTGACAGCCGCTGCTCAGGGGATTGGCCAAGCAGCTGCCTTAGCTTT
TGTAAGAGAAGGTGCCAAAGTCATAGCCACAGACATTAATGTGTCCAACTTCAGGAACTGGAAAAGTACCTGGG
TATTCAAACTCGTGTCCTTGATGTCACAAAGAAGAAACAAATTGATCAGTTCGCCAATGAAGTTGAGAGACTTGA
TGTTCTCTTTAATGTTGCTGGTTTTGTCCATCATGGAAGTGTCTGGATTGTGAGGAGAAAGACTGGGACTTCTC
GATGAATCTCAATGTGCGCAGCACGTACCTGATGATCAAGGCATTCCTTCCTAAAATGCTTGCTCAAAAATCTGG
CAATATTATCACCATGTTTTCTGTGGTTTTCCAGCATCAAAGGAGTTGTGAACAGATGTGTGTACAGCACAAACCA
GGCAGCCGTGATTGGCCTCACAAAATCTGTGGCTGCAGATTTTCATCCAGCAGGGCATCAGGTGCAACTGTGTGTG
CCCAGGAACGGTTGATACGCCATCTCTACAAGAAAGAATACAAGCCAGAGGAAATCCTGAAGAGGCACGGAAATGA
TTTCCTGAAGAGACAAAAGATGGGACGATTTGCAACTGCAGAAGAAATAGCCATGCTCTGCGTGTATGTGGCTTC
TGATGAATCTGCTTATGTAAGTGGTAACCCTGTCATCATTGATGGAGGATGGAGCTTGTGATTTTAGGATCTCCA
TGGTGGGAAGGAAGGCAGGCTCTTCCTATCCACAGTGAACCTGGCTATGAAGAAACTCACCAATCATCTCCTTC
CTGCTAATCACATGTTAATGAACTAAGCCCTTTTTTAACAATGTCACTGTTTGCAAGAGTCTGATTCTTTAAGTA
TATTAATCTCTTTGTAATCTCTTCTGAAATCATTGTAAAGAAATAAAAATATTGAACTCACAGCAAGAGAATAGT
TTTTAAATAAATCTCAATTTGTAAGC

2268/6881
FIGURE 2084

MGQLDGKVIILTAAAQGIGQAAALAFVREGAKVIATDINVSKLQELEKYLGIQTRVLDVTKKKQIDQFANEVERL
DVLFNVAGFVHHGTVLDCEEKDWDFSMNLNVRSTYLMIKAFLPKMLAQKSGNIITMFSVVSSIKGVVNRCVYSTT
KAAVIGLTKSVAADFIQQGIRCNCVCPGTVDTPSLQERIQARGNPPEARNDFLKRQKMGRFATAEEIAMLVCVYVA
SDESAYVTGNPVIIDGGWSL

2269/6881
FIGURE 2085

ATGAATGCTATAAAGAGATTTCAGGATGGAAAATTAGTACAGAACAAAGCCTACTGTGGAGAATCAACACCACAG
CATTTCACAGGCCTGCAGCCTTATGTGGTTAGCATGGATGAGGGTTCTTCAGGTTTCATGAGAATAGGCTATGAA
CACTGGGTTTTGGTCTTCTTGATTCTCAGTGCCTGGATACCAGAAAAAGAGAAATATGAGATTGCAGAGCAGCCC
AAGATTGATCAGAAAGCTGTGGACTCACAAATTTTACCAAAAATCAAAAAGTATTCCTCAGCTCCAGTGCTACCTG
CGATCTGTGTTTGCTCTGACGAATGGAATTTATCCTCACAAATTGGTGTTTTAA

2270/6881
FIGURE 2086

MNAIKRFQDGKLVQNKAYCGESTPQHFTGLQPYVVSMDGSSGFMRIGYEHWVLVFLILSAWIPEKEKEYEIAEQP
KIDQKAVDSQILPKIKSIPQLQCYLRSVFALTNGIYPHKLVF

2271/6881
FIGURE 2087

ACAATCCAGCCAATGGCAGAAGACTGCCGGAATGTAGAAGAGTTAAGTGTGTGTCCTATGCGTTCTACCTCAAT
GCAGATATCAGAGTCCCTTTGAGCTCCCTGAAGAATATACTCACACCAAAGTATTACCTGCACATAGCTGCTCCC
TTCCACCTCGCGGCAGTTCAAAATGAAGCTGTTGTCATTTCTGGAAGGAACTAGCCCAGCAGATCAAGCAGAAA
GTGCGGCAGGAGGTGGAAGAGTGGGTGGCCTCAGGCAACAAACCTGAGCATGATCCTGTACCTGCTGCTATAGTT
CCAGCAAAAAAGATGACTTCTTGCAAGCAAGAAGGCTCCAGCCCAGAAGGTTCCCTGCCCAGAAAGCCACAGGCTA
GAGGCAGTGCCTCCTCTGAAAGCTCAGAAGTTTCAAAGCAACGTGCCCAGAAAGCATGTTGTCCAAAAGCATCT
GGCAAGAAAGCGTTAAGAGGCTATTATAAAAGTAGTAAAGGGTCCAACAACCTCAAGGACAAGAATGATGTATTT
TCATCACTTGTGACTTCCGGTTTCCTAGACCAGATTTGCGGTGCGGTCTGACCAGGTGCAGCCCCATCCTAGCAGC
AGATTGCTTGTTCTCAGCATTCCTCATGGAAGAATCTTAGTGTGGTGGGAGGCTTGGGAAATACCGTTTTCAAA
GACCAGTGGATTAGTAGCCTGAAAACTCGCCAGCAGTTGCCTGCTTTTGTTCATCTTCCTGTCTCTGGAAGAGCAC
CTGATCCTCACTACCAAAAACTTAA

2272/6881
FIGURE 2088

MAEDCRKCRRVKCVSYAFYLNADIRVPLSSLKNILTPKYYLHIAAPFHAAVQNEAVVISGRKLAQQIKQKVRQE
VEEWVASGNKPEHDPVPAAIVPAKKMTSCRQEGSSPEGSCPESHRL EAVPPLKAQKFQKQRAQKACCPKASGKKA
LRGYKSSKGSNNFKDKNDVFSSLVTSGFLDQISGRSDQVQPHPSRLLVLSIPIMENLSVVGGLGNTVFKDQWI
SSLKTRQQLPAFVIFLSLEEHLILT TKN

2273/6881
FIGURE 2089

ACCTGATGGAGATCCAAGTGTTTGGGCAGGATGAGATGATCGACGTCATTGGGGTGACCAAGGGCAAAGGCTACA
AAGGGGTCACCAGTCGTTGGCACACCAAGAAGCTGCCCTGCAAGACCCACCGAGGCCTGTGCAAGGTGGCCTGTA
TTGGGGCATGGCATCCTGCTCGTGTGGCCTTCTCTGTGGCACGTGCTGGGGAGAAAGGCTACCGTCACCGCACTG
AGATCAACAAGAAGATCTATAAGATTGGCCAGGGCTACCTTATCAAGGATGGCAAGCTGATCAAGAACAATGCCT
CCACTGACTCTGACCTGTCTGACAAGAGCACCAATCCTCTGGGTGGCTTTGTCCACTATGGTGAAGTGACCAATG
ACCTTGTCATGCTGAAAGGCTGTGTGGTGGGAACCAAGAAGCGGGTGCTCACCTCCACGAGTCCTTGCTGGTGC
AGATGAAACGGCAGGCTCTGGAGAAGATTGACCTTAAGTTCATTGACACCACCTCCAAGTTTGGCCATGGCTGCT
TCCAGACCATGGAGCAGAAGAAAGCATTATGGGACCACTCAAGAAAGACGGAATTGCAAAGGAAGAAGGAGCTT
AATGCCAGGAACAGATTTTCGACGCTGGTGTGGTCTCAATAAAAGTTATTTTCCACTGGGAAAAAAAAA

2274/6881
FIGURE 2090

GCGTGATGTCTCACAGAAAGTTTTCTGCTCCCAGACATGGGTCCCTCGGCTTCCTGCCTCAGAAGCGCAGCAGCA
GGCATCGTGGGAAGGTGAAGAGCTTCCCTAAGGATGATCCGTCCAAGCCGGTCCACCTCACAGCCTTCCTGGGAT
ACAAAGCTGGCATGACCCACATCATGAGGGCTCTGGAGAAGATTGACCTTAAGTTCATTGACACCACCTCCAAGT
TTGGCCATGGCTGCTTCCAGACCATGGAGCAGAAGAAAGCATTTCATGGGACCACTCAAGAAAGACGGAATTGCAA
AGGAAGAAGGAGCTTAATGCCAGGAACAGATTTTCGCAGCTGGTGTGGTCTCAATAAAAGTTATTTTCCACTG

2275/6881
FIGURE 2091

AACAGGAAGGACGGCCCTCCGGCTTCGGAGGCGCGCCACACTCATCTCTGCCAGCTGCTGCCCTCCCCAGGAGGC
 CTCCATGGCTTACCTACCTCCACCAACCCAGCGCATGCCACTTTGAGAGCTTCTGCGAGGCCAGCTGTGCCA
 GGACGTGCTGAGCAGCTTCCAGGAGCTGTGTGGGGCCCTGGGGCTGGAACCCGGTGGGGGGCTGCCCCAGTACCA
 CAAGATCAAGGACCAGCTCAACTACTGGAGCGCCAAGTCACTGTGGACCAAGCTGGACAAGCGAGCAGGCCAGCC
 TGTCTACCAGCAGGGCCGGGCTGCACCAGCACCAAGTGCCTGGTGGTGGTGTGTTGACCTTGC GG GCTGCGGGT
 CGCTGTGGAGCTGGCGCTGCTGGGGGCCGAGTGGTGTGTTGGTGGAAAAGCGCACCAAGTTCTCTCGCCACAACGT
 GCTCCACCTCTGGCCCTTACCATCCACGACCTGCGGGCACTCGGTGCTAAGAAGTTCTACGGGCGCTTCTGCAC
 CGGCACCCTGGACCACATCAGCATCAGGCAGCTCCAGCTGCTTCTGCTGAAGGTAGCATTGCTGCTGGGGGTGGA
 AATTCACTGGGGTGTCACTTTCACTGGCCTCCAGCCCCCTCCTAGGAAGGGGAGTGGCTGGCGTGCCAGCTCCA
 ACCCAACCCCCCTGCCAGCTGGCCAACATATGAATTTGACGTCTTATATCTCGGTGCAGGAGGTAAATTTCGTCCC
 TGAAGGCTTCAAAGTTTCGAGAAATGCGAGGCAAACCTGGCCATTGGCATCACAGCCAACCTTTGTGAATGGACGCAC
 CGTGGAGGAGACACAGGTGCCGGAGATCAGTGGTGTAGCCAGGATCTACAACCAGAGCTTCTTCCAGAGCCTTCT
 CAAAGCCACAGGCATTGATCTGGAGAACATTGTGTACTACAAGGACGACACCCACTACTTTGTGATGACAGCCAA
 GAAGCAGTGCCTGCTGCGGTGGGGGTGCTGCGCCAGGACTGGCCAGACACCAATCGGTGCTGGGCAGTGCCAA
 TGTGGTGCCCCGAGGCTCTGCAGCGCTTTACCCGGGCAGCTGCTGACTTTGCCACCCATGGCAAGCTCGGGAACT
 AGAGTTTGGCCAGGATGCCCATGGGCAGCCTGATGTCTCTGCCTTTGACTTACAGAGCATGATGCGGGCAGAGAG
 TTCTGCTCGTGTGCAAGAGAAGCATGGCGCCCGCTGCTGCTGGGACTGGTGGGGGACTGCCTGGTGGAGCCCTT
 CTGGCCCCCTGGGCAGTGGAGTGGCACGGGGCTTCTGGCAGCCTTTGATGCAGCCTGGATGGTGAAGCGGTGGGC
 AGAGGGCGCTGAGTCCCTAGAGGTGTTGGCTGAGCGTGAGAGCCTGTACCAGCTTCTGTACAGACATCCCCAGA
 AAACATGCATCGCAATGTGGCCAGTATGGGCTGGACCCAGCCACCCGCTACCCCAACCTGAACCTCCGGGCAGT
 GACCCCCAATCAGGTACGAGACCTGTATGATGTGCTAGCCAAGGAGCCTGTGCAGAGGAACAACGACAAGACAGA
 TACAGGGATGCCAGCCACCGGGTCGGCAGGCACCCAGGAGGAGCTGCTACGCTGGTGCCAGGAGCAGACAGCTGG
 GTACCCGGGAGTCCACGTCTCCGATTTGTCTTCTCCTGGGCTGATGGGCTAGCTCTGTGTGCCCTGGTGTACCG
 GCTGCAGCCTGGCCTGCTGGAACCCCTCAGAGCTGCAGGGGCTGGGAGCTCTGGAAGCAACTGCTTGGGCATAAA
 GGTGGCAGAGAATGAGCTGGGCATCACACCGGTGGTGTCTGCACAGGCCGTGGTAGCAGGGAGTGACCCACTGGG
 CCTCATTGCCTACCTCAGCCACTTCCACAGTGCCTTCAAGAGCATGGCCACAGCCCAGGCCCTGTCCAGCCAGGC
 CTCCCCAGGGACCTCCAGTGTGTATTATTCTTAGTAACTTTCAGAGGACCTGCAGCGATCCCGGGCCAAGGA
 AAATGCAGAGGATGCTGGTGGCAAGAAGCTGCGCTTGGAGATGGAGGCCGAGACCCCAAGTACTGAGGTGCCACC
 TGACCCAGAGCCTGGTGTACCCCTGACACCCCCATCCCAACACCAGGAGGCCGGTGTGTTGGGACCTGTGTGCACT
 TTGTGGGGAACACCTCTATGTCTTGGAAAGCCTCTGTGTCAACGGCCATTTCTTCCACCGAGCTGCTTCCGCTG
 CCATACCTGTGAGGCCACACTGTGGCCAGGTGGCTACGAGCAGCACCCAGGAGATGGACATTTCTACTGCTTCCA
 GCACCTGCCCCAGACAGACCACAAAGCGGAAGGCAGCGATAGAGGCCCTGAGAGTCCGGAGCTCCCCACACCAAG
 TGAGAATAGCATGCCACCAGGCCTCTCAACTCCCACAGCCTCGCAGGAGGGGGCCGGTCTGTGTCCAGATCCCAG
 CCAGCCCACCCGTCGGCAGATCCGCCTCTCCAGCCCCGAGCGCCAGCGGTTGTCTCCCTTAACCTTACCCCTGA
 CCGGAAATGGAGCCTCCACCCAAGCCTCCCCGCAGCTGCTCCGCCTTGGCCCCGCCACGCCCTGGAGCAGCTT
 TGTGGGCTGGGGCCTGCCAGTCCAGAGCCCTCAAGCTCTTGTGGCCATGGAGAAGGAGGAAAAAGAGAGTCCCTT
 CTCCAGTGAAGAGGAAGAAGAAGATGTGCCTTTGGACTCAGATGTGGAACAGGCCCTGCAGACCTTTGCCAAGAC
 CTCAGGCACCATGAATAACTACCCAACATGGCGTCGGACTCTGCTGCGCCGTGCGAAGGAGGAGGAGATGAAGAG
 GTTCTGCAAGGCCAGACCATCCAACGGCGACTAAATGAGATTGAGGCTGCCTTGAGGGAGCTAGAGGCCAGGG
 CGTGAAGCTGGAGCTGGCCTTGAGGCGCCAGAGCAGTTCCCCAGAACAGCAAAAGAACTATGGGTAGGACAGCT
 GCTACAGCTCGTTGACAAGAAAAACAGCCTGGTGGCTGAGGAGGCCGAGCTCATGATCAGGTGCAGGAATTGAA
 TCTGGAGGAGAAACAGTGGCAGCTGGACCAGGAGCTACGAGGCTACATGAACCGGGAAGAAAACCTAAAGACAGC
 TGCTGATCGGCAGGCTGAGGACCAGGTCTGAGGAAGCTGGTGGATTGTGTCACCCAGAGAGATGCCCTCATCCG
 CTTCAGGAGGAGCGCAGGCTCAGCGAGCTGGCCTTGGGGACAGGGGCCAGGGCTAGACGAGGGTGGGCCGTCT
 GCTTTCGTTCCCAAAAGAAAGCACCTACCCACGACAGTGCCACCCCTGTTATCTGGGCTGCCTGGCAGAGA
 GCCTTGCTGTTTACAATTAATAATGTTTCTGCCAC

2276/6881
FIGURE 2092

GTTCCGGCGCACGTAATCGCCGAGGGCACGTGCATGCCCCCTGGTTAAGAGTTGCAGGTAGCGGTAGCGGATGGAC
ACTCTGGATCGAGTAGTAAAGCCCCAAAACGAAAAGAGCCAAGAGATTCCTTGAGAAGAGAGAACCGAAACTCAAT
GAAAATATTAAAAATGCCATGCTGATTAAAGGGGGAAATGCAAATGCAACAGTGACAAAAGTACTTAAAGATGTG
TATGCACTGAAAAAACCATAACGGTGTACTATATAAAAAGAAAAATATTACAAGACCTTTTGAGGATCAGACATCA
CTGGAATTCTTTTCAAAGAAGTCAGATTGTTCTTTATTCATGTTTGGCTCCCATATAATAAGAAGCGGCCAAATAAT
CTAGTAATAGGTCGTATGTATGACTACCATGTGCTGGATATGATTGAATTAGGTATTGAGAATTTTGTCTCTCTA
AAAGACATTAAAGAACAGTAAATGTCTGAGGGAAACAAAACCCATGCTGATATTTGCTGGCGATGATTTTCGATGTA
ACAGAAGATTATAGAAGACTAAAAAGTCTTCTTATTGATTTCTTCAGAGGCCCCACAGTATCAAATATCCGCCTG
GCTGGATTAGAGTATGTTCTGCACTTCACTGCACTGAATGGGAAGATTTACTTTTGAAGCTATAAGTTGCTGTTG
AAGAAATCTGGTTGCAGAACACCACGGATTGAATTGGAAGAGATGGGACCCTCATTGGATCTGGTTCTGAGGAGG
ACACACCTGGCATCGGATGACCTTTATAAATTATCTATGAAAATGCCAAAAGCTCTCAAGCCAAAGAAGAAGAA
AATATTTCCCATGATACTTTTGGTACAACCTTATGGAAGGATTCATATGCAGAAGCAAGACCTAAGCAAACCTACAA
ACCAGGAAAATGAAGGGGTTGAAGAAGCGACCTGCAGAAAGGATAACAGAAGACCACGAGAAAAAGTCAAAAAGA
ATTAAAAAAAATTGATGGAACCTTAGCCAGCCACTACTGTTTCATTGTGTTCTACTTAAGAGAATTATCAAGCGTC
AATCCATTCAGAGTTTCTTATAAGATCTTATTATATATTTTTATAACATGATAATTTTACGATATATTATTATGA
ACAGTAATATACTAGTATTAAGTGTAAGTAAGCCTTTTATTTGAGACATTACACCCTGGTGTGCCATTTTCTCT
TGTGATATCCCCTGCCCTCCACAAATCTTCTTTCTCATTGGGTGGATGGATGGGTGAGGAGGGATCTCCATAAC
CATTGGGATTTTTTTGAATTTCTGGCCTTAGCTAAAGAAAGCCACAGAAAGCCGGACCCGCAGGAGCTGTGTAAA
CAATCTCAGTATGAATTACCTGGAAAGTTAACCTCCTCTCCCAACATGGATCTACATTCTGATTTTTATTTTCTA
CTTTTATTTTGCCTGAAATCCTACTCGTTGACATTTGAGATTTTAAGCTTTGTGGCTGAAAATATATAGATCTCT
GAG

2277/6881
FIGURE 2093

MDTIDRVVKPKTKRAKRFLEKREPKNENIKNAMLIKGGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQ
TSLEFFSKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFVSLKDIKNSKCPEGTKPMLIFAGDDF
DVTEDYRRLKSLIDFFRGPTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLKKS GCRTPRIELEEMGPSIDLVL
RRTHLASDDLYKLSMKMPKALKPKKKKNISHDTFGTTYGRIHMQDLSKLQTRKMKGLKKRPAERITEDHEKKS
KRIKKN

2278/6881
FIGURE 2094

ATGGAAACAGTACATCTGTAAAAGGACAAGTGATGGCATCTACATCATAAATCTGAAGAGGACCTGGGAGAAGCTT
CTGCTGGCAGCTCATGCCATTGCTGCCATTGAAAACCTGCAGATGTCAGTGTTATATCCTCCAGGAATATTGGC
CAGAGGGCTGTGCTGAAGTTTGTGCTGCCACTGGAGCCACTCCAATTGCTGGCCGCTTCACTCCTGGAACCTTC
ACTAACCAGATCCAGGCAGCTTTCTGGGAGCCACGGCTTCTTGTGGTTACTGACCCAGGGCTGACCACCAGCCT
CTCAGGAGGCATCTTATGTTAACCTACCTACCATTGCTCTATTCTCCTTGTGCTATGTGGACATTGCCATCGCA
TGCAACAACAAGGGAGCTCACTCGGTGGGTTTGATGTGGTGGACACCGGCTCGGGAAGTTCTGCGCATGCGTGGC
ACCATTTCTGCGAACACCCGTGGGAGGTCATGCCTGATCTCTACTTCTACAGAGATCCTGAAGAGATTGAAAAA
GAAGAGCAGGCTGCTGCTAAAAAAGCTGTGACCAAGAAAGAATTCAGGGTGAATGGACTGCTTCAGCTCCTGAG
TTCCTGCTACTCAGCCTGAGGTTGCAGACTGGTCTGAAGGCATGCAGGCCACCGAATGGGTAAAAGCAATCACT
GAATGGGTAGAAGCAACCGCTGAATGGTCTTAA

2279/6881
FIGURE 2095

MEQYICKRTSDGIYIINLKRTWEKLLLAHAIAAIENPADVSVISSRNIGQRAVLKFAAATGATPIAGRFTPGETF
TNQIQAAFWEPRLLVVTDPRAHQPLTEASYVNLPTIALFSLCYVDIAIACNNKGAHSVGLMWWTPAREVLRMRG
TISCHEPWEVMPDLYFYRDPEEIEKEEQAAAKKAVTKKEFQGEWTASAPFTATQPEVADWSEGMQATEWVKAIT
EWVEATAEWS

2280/6881
FIGURE 2096

ATGGCAAAGGAAGATAACAGAAGACCCTCCAGAGAGTGGAATCCTGAAAATCAAGGAACATTTCTGTATACTCAA
GTGAATGGGAAAGTGGAATATTTCTGAAGTGGAAGGGATTTACAGATGCTGACAATACTTGGGAACCTGAAGAA
AATTTAGATTGTCCAGAATTGATTGAAGCATTTCTTAGCTCTCAGAAAGCTGGCAAACAAAAAGATGACAGCAGT
GGAGAATTGATGTTTCTCATGAAATGGAAAGATTCAGATGAGGCAGACTTGGTGCTGGCAAAAGAAGCAAGTATG
AAGTGTCCCTCAAATTGTAATTGCTTTTTATGAAGAGAGACTAACTTGGCATTCTTGTCCAGAAGATGAAGCTCAA
TAA

2281/6881
FIGURE 2097

MAKEDNRRRPSREWNPENQGTFLYTQVNGKVEYFLKWKGFTDADNTWEPEENLDCPELIEAFLSSQKAGKQKDDSS
GELMFLMKWKDSDEADLVLAKEASMKCPQIVIAFYEERLTWHSCPEDEAQ

2282/6881
FIGURE 2098

CTCTTCCGGTTCTAGGCACTTCGGGAGCCGCGGCTTATGGTGCAGACATGGCCAAGTCCAAGAACCACACCACAC
ACAACCAGTCCCGAAAATGGCACAGAAATGGTATCAAGAAACCCCGATCACAAAGATACGAATCTCTTAAGGGGG
TGGACCCCAAGTTCCTGAGGAACATGCGCTTTGCCAAGAAGCACAACAAAAGGGCCTAAAGAAGATGCAGGCCA
ACAATGCCAAGGCCATGAGTGCACGTGCCGAGGCTATCAAGGCCCTCGTAAAGCCCAAGGAGGTTAAGCCCAAGA
TCCCAAAGGGAGTCAGCTGCAAGCTCGATCGACATGCCTACGTTGCCACCCCAAGCTTGGGAAGCGTGCTCTTG
CCCGTATTGCCAAGGGGCTCAGGCTGTGCCGGCCAAAGGCCAAGGCCAAGGCCAAGGATCAAA¹CCAAGGCCCAGG
CTGCAGCTCCAGCTTCAGTTCCAGCTCAGGCTCCCAAAGGTACCCAGGCCCTACAAAGGCTTCAGAGTAGATAT
CTCTGCCAACATGAGGACAGAAGGACTGGTGCACCCCCACCCCCACCCCTGGGCTATCATCTGCATGGGGCTG
GGGTCCCTCCTGTGCTATTTGTACAAATAAACCTGAGGCAGG

2283/6881
FIGURE 2099

ACAAAAAAGCTTTTACGAGGTATCAGCACTTTTCTTTCATTAGGGGGAAGGCGTGAGGAAAAGTACCAAACAGCAG
CGGAGTTTTAACTTTAAATAGACAGGTCTGAGTGCCTGAACTTGCCTTTTTCATTTTACTTCATCCTCCAAGGAG
TTCAATCACTTGCGGTGACTTCACTACTTTTAAAGCAAAAGAGTGGTGCCAGGCAACATGGGTGACTGGAGCGCC
TTAGGCAAACTCCTTGACAAGGTTCAAGCCTACTCAACTGCTGGAGGGAAGGTGTGGCTGTGCTAGTACTTTTCATT
TTCCGAATCCTGCTGCTGGGGACAGCGGTTGAGTCAGCCTGGGGAGATGAGCAGTCTGCCTTTCGTTGTAACACT
CAGCAACCTGGTTGTGAAAATGTCTGCTATGACAAGTCTTCCCAATCTCTCATGTGCGCTTCTGGGTCTGCGAG
ATCATATTTGTGTCTGTACCCACACTCTTGTACCTGGCTCATGTGTTCTATGTGATGCGAAAGGAAGAGAACTG
AACAAGAAAAGAGGAAGAACTCAAGGTTGCCCAACTGATGGTGTCAATGTGGACATGCACCTGAAGCAGATTGAG
ATAAAGAAGTTCAAGTACGGTATTGAAGAGCATGGTAAGGTGAAAATGCGAGGGGGGTTGCTGCGAACCTACATC
ATCAGTATCCTCTTCAAGTCTATCTTTGAGGTGGCCTTCTTGCTGATCCAGTGGTACATCTATGGATTTCAGCTTG
AGTGCTGTTTACACTTGCAAAAGAGATCCCTGCCACATCAGGTGGACTGTTTCTCTCTCGCCCCACGGAGAAA
ACCATCTTCATCATCTTCATGCTGGTGGTGTCTTGGTGTCCCTGGCCTTGAATATCATTGAACTCTTCTATGTT
TTCTTCAAGGGCGTTAAGGATCGGGTTAAGGGAAAGAGCGACCTTACCATGCGACCAGTGGTGGCTGAGCCCT
GCCAAAGACTGTGGGTCTCAAAAATATGCTTATTTCAATGGCTGCTCCTCACCACCGCTCCCCTCTCGCCTATG
TCTCTCCTGGGTACAAGCTGGTTACTGGCGACAGAAACAATTCTTCTTGCCGCAATTACAACAAGCAAGCAAGT
GAGCAAACTGGGCTAATTACAGTGCAGAACAAAATCGAATGGGGCAGGCGGGAAGCACCATCTCTAACTCCCAT
GCACAGCCTTTTGATTTCCCCGATGATAACCAGAATTCTAAAAAACTAGCTGCTGGACATGAATTACAGCCACTA
GCCATTGTGGACCAGCGACCTTCAAGCAGAGCCAGCAGTCGTGCCAGCAGCAGACCTCGGCCTGATGACCTGGAG
ATCTAGATACAGGCTTGAAAGCATCAAGATTCCACTCAATTGTGGAGAAGAAAAAAGGTGCTGTAGAAAGTGCAC
CAGGTGTTAATTTTGATCCGGTGGAGGTGGTACTCAACAGCCTTATTCATGAGGCTTAGAAAACACAAAGACATT
AGAATACCTAGGTTCACTGGGGGTGTATGGGGTAGATGGGTGGAGAGGGAGGGGATAAGAGAGGTGCATGTTGGT
ATTTAAAGTAGTGGATTCAAAGAAGCTTAGATTATAAATAAGAGTTCCATTAGGTGATACATAGATAAGGGCTTTT
TCTCCCCGAAACACCCCTAAGAATGGTTCGTGTATGTGAATGAGCGGGTGGTAATTGTGGCTAAATATTTTG
TTTTACCAAGAACTGAAATAATTCTGGCCAGGAATAAATACTTCCCTGAACATCTTAGGTCTTTTCAACAAGAAA
AAGACAGAGGATTGTCCTTAAGTCCCTGCTAAAACATTCCATTGTTAAAATTTGCACTTTGAAGGTAAGCTTTCT
AGGCTGACCCTCCAGGTGTCAATGGACTTGTGCTACTATATTTTTTTTATTCTTGGTATCAGTTTAAAATTCAGA
CAAGGCCACAGAATAAGATTTTCCATGCATTTGCAAATACGTATATTCTTTTCCATCCACTTGCACAATATCA
TTACCATCACTTTTTTCATCATTCCTCAGCTACTACTCACATTCAATTAATGGTTTCTGTAAACATTTTTAAGACA
GTTGGGATGTCACCTTAACATTTTTTTTTTTTGTAGCTAAAGTCAGGGAATCAAGCCATGCTTAATATTTAACAATC
ACTTATATGTGTGTCGAAGAGTTTGTGTTTGTGTCATGTATTGGTACAAGCAGATACAGTATAAACTCACAAAC
ACAGATTTGAAAATAATGCACATATGGTGTTCAAATTTGAACCTTTCTCATGGATTTTTGTGGTGTGGGCAATA
TGGTGTTTACATTATATAATTCCTGCTGTGGCAAGTAAAGCACACTTTTTTTTTCTCCTAAAATGTTTTTCCCTG
TGTATCCTATTATGGATACTGGTTTTGTTAATTATGATTCTTTATTTTCTCTCCTTTTTTTAGGATATAGCAGTA
ATGCTATTACTGAAATGAATTTCCTTTTTCTGAAATGTAATCATTGATGCTTGAATGATAGAATTTTAGTACTGT
AAACAGGCTTTAGTCATTAATGTGAGAGACTTAGAAAAAATGCTTAGAGTGGACTATTAAATGTGCCTAAATGAA
TTTTGCAGTAACTGGTATTCTTGGGTTTTCTTACTTAATACACAGTAATTCAGAACTTGTTATTCTATTATGAGTT
TAGCAGTCTTTTGGAGTGACCAGCAACTTTGATGTTTGCCTAAGATTTTATTTGGAATGCAAGAGAGGTTGAAA
GAGGATTCAGTAGTACACATACAACTAATTTATTTGAACTATATGTTGAAGACATCTACCAGTTTCTCCAAATGC
CTTTTTTAAACTCATCACAGAAGATTGGTGAAAATGCTGAGTATGACACTTTTCTTCTGATGCATGTCAGCT
ACATAAACAGTTTTGTACAATGAAAATTACTAATTTGTTTGACATTCCATGTTAAACTACGGTCATGTTTCAGCTT
CATTGATGTAATGTAGACCTAGTCCATCAGATCATGTGTTCTGGAGAGTGTCTTTATTCAATAAAGTTTTAAT
TTAGTATAAACAT

2284/6881
FIGURE 2100

MGDWSALGKLLDKVQAYSTAGGKVWLSVLFIFRILLLLGTAVESAWGDEQSAFRCNTQQPGCENVCYDKSFPISHV
RFWVLQIIFVSVPTLLYLAHVFYVMRKEEKLNKKEEELKVAQTDGVNVDMLKQIEIKKFKYGIEEHGKVKMRGG
LLRTYIISILFKSIFEVAFLLIQWYIYGFSLSAVYTCKRDPCPHQVDCFLSRPTEKTIFIIIFMLVVSLVSLALNI
IELFYVFFKGVKDRVKGKSDPYHATSGALSPAKDCGSQKYAYFNGCSSPTAPLSPMSPPGYKLVTGDRNNSSCRN
YNKQASEQNWANYSAEQNRMGOAGSTISNSHAQPFDFPDDNQNSKKLAAGHELQPLAIVDQRPSSRASSRASSRP
RPDDLEI

2285/6881
FIGURE 2101

GCTGTGCGTCCGGAAGTGTCTCGCAGATAGTAAATAATCTCGGAAAGGCGAGAAAGAAGCTGTCTCCATCTTGTC
TGTATCCGCTGCTCTTGTTGTGACGTTGTGGAGATGGGGAGCGTCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCA
TGTTTGTGTGGAAGTGCCCGTGTTTGCTATGCCGATGCTGTCTAGTGGAACAACCTCCACTGTAACTAGATTG
ATCTATGCACTTTTCTTGCTTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAACCTG
AATAAGATTCTTGGAATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATTTTGGTTGGCTATAAAGCTGTA
TATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGT
GATCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCA
TTCTTCATTCCAGAAGGAACTTTTACAACCTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTC
ATACAACCTAGTCTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGGTGAAAAAATGGAAGAAGGGAAC
TCGAGATGTTGGTATGCAGCCTTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTAGTTGCTATCGTCTTG
TTCTTTGTCTACTACATCATCCAGCCAGTTGTTTCAAGAAACAAGGCGTTTATCAGTGTCAACATGCTCCTCTGC
GTTGGTGCTTCTGTAATGTCTATACTGCCAAAAATCCAAGAATCACAACCAAGATCTGGTTTGTACAGTCTTCA
GTAATTACAGTCTACACAATGTATTTGACATGGTCAGCTATGACCAATGAACCAGAAACAAATTGCAACCCAAGT
CTACTAAGCATAATTGGCTACAATAACAAGCACTGTCCCAAAGGAAGGCGAGTCAGTCCAGTGGTGGCATGCT
CAAGGAATTATAGGACTAATTCTCTTTTTGTTGTGTGTATTTTATCCAGCATCCGTACTTCAAACAATAGTCAG
GTTAATAAACTGACTCTAACAAGTGATGAATCTACATTAATAGAAGATGGTGGAGCTAGAAGTGATGGATCACTG
GAGGATGGGGACGATGTTTACCGAGCTGTAGATAATGAAAGGGATGGTGTCACTTACAGTTATTCTCTCTTTCAC
TTCATGCTTTTCTGGCTTCACTTTATATCATGATGACCCTTACCAACTGGTACAGGTATGAACCTCTCTGAG
ATGAAAAGTCAGTGGACAGCTGTCTGGGTGAAAAATCTCTTCCAGTTGGATTGGCATCGTGTGTATGTTTGGACA
CTCGTGGCACCCTTGTCTTACAAATCGTGATTTTGACTGAGTGAGACTTCTAGCATGAAAAGTCCCACTTTGAT
TATTGCTTATTTGAAAACAGTATTCCCACTTTTGTAAGTTGTGTATGTTTTTGCTTCCCATGTAACCTTCTCCA
GTGTTCTGGCATGAATTAGATTTTACTGCTTGTCATTTTGTTATTTTCTTACCAAGTGCATTGATATGTGAAGTA
GAATGAATTGCAGAGGAAAGTTTTATGAATATGGTGATGAGTTAGTAAAAGTGGCCATTATTGGGCTTATTCTCT
GCTCTATAGTTGTGAAATGAAGAGTAAAAACAAATTTGTTTGACTATTTTAAAATTATATTAGACCTTAAGCTGT
TTTAGCAAGCATTAAAGCAAATGTATGGCTGCCTTTTGAAATATTTGATGTGTGCTTGGCAGGATACTGCAAG
AACATGGTTTATTTTAAAATTTATAAACAAGTCACTTAAATGCCAGTTGTCTGAAAAATCTTATAAGGTTTTACC
CTTGATACGGAATTTACACAGGTAGGGAGTGTTTAGTGGACAATAGTGTAGGTTATGGATGGAGGTGTCGGTACT
AAATTGAATAACGAGTAAATAATCTTACTTGGGTAGAGATGGCCTTTGCCAACAAGTGAAGTGTGTTGGTTGTT
TTAAACTCATGAAGTATGGGTTTCACTGGAATGTTTGGAACTCTGAAGGATTTAGACAAGGTTTTGAAAAGGATA
ATCATGGGTTAGAAGGAAGTGTGTTGAAAGTCACTTTGAAAGTTAGTTTTGGGCCAGCACGGTAGCTCACCTTGT
AATCCCAGCACTTTGGGAGGCTGAGGTGGGTAGATTACTTGAGCCAGGAATCAAGACCAGCCTGGGCAACATG
GTGAAACCTGTTTCTATAAAAAATAATCTGGGCTTTGTAGCATATGCCTGTGGTCCCAGCTACTGAGGAGGCTG
AGGTGGGAGGATTGCTTGAGCCAGGAGGCAGAGGTGTCAGTGAGCCAAGGTACGTCAGTCACTCTAGCCTGG
GCAACAGAGTAAGACAAAAAATATATATATATTGAAAATCAAAGGAGGCAAAATTTTGACAGGGAAGGAAGTAA
CTGCAAAACACTAGGCTTTAGTAGGTACTTATATAAAATCTAGTCCAGTTCTCTCATTTAAAAAATGAAGACAC
TGAAATACAGACTTAAATAGCTCAGATAGCTAATTAGGAAATTTCAAGTTGGCCAATAATAGCATTCTCTCTGAC
ATTTAAAAATAATTTCTATTCAAAATACATGCATAATTGATTTTACACCTCATTACTGGTGGATAATTTATGTGA
TGTGGATTGCTGGTGTCCAGCATGACCCATAAACAGGTGAGAAGAATGATGGAATGTTTTAGAATAAACTCCTGC
TTATAGTATACTACACAGTTCAAAAGATGTTTAAATGCTTTTGTATTTACTGCCATGTAATTGAAATATATAGA
TTATTGTAACCTTTCAACCTGAAAATCAAGCAGTATGAGAGTTTAGTTATTTGTATGTGTCACTAGTGTCTAATG
AAGCTTTTAAATCTACAATTTCTCTTTAAAAATATTTATTAATGTGAATGGAATATAACAATTCAGCTTAATT
CCCCAACCTTATTCTGTGTGTAGACATTGTATTCCACAATTTTGAATGGCTGTGTTTTACCTCTAAATAAATGAA
TTCAGAG

2286/6881
FIGURE 2102

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGMEEQLNKIPGFCENE
KGVVPCNILVGKYKAVYRLCFGLAMFYLLLSLLMIKVKSSSDPRAAVHNGFWFFKFAAAIAIIIGAFFIPEGTFIT
VWFYVGMAGAFCFILIQLVLLIDFAHSWNESWVEKMEEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPAS
CSENKAFISVNMLLCVGASVMSILPKIQESQPRSGLLQSSVITVYTMylTWSAMTNEPETNCNPSLLSIIGYNTT
STVPKEGQSVQWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVHRAV
DNERDGVITYSYFFHFMLFLASLYIMMTLINWYRYEPSREMKSQWTAVWVKISSSWIGIVLYVWTLVAPLVLTNR
DFD

2287/6881
FIGURE 2103

GGGGACCCCTCTCCTGACGCTGCGCTCTCTGCGAGGCAACCTTTACGTCCATCGCTTGTTCATCTTAGGATCCCCA
TGTTATTTTATAGCCCAGATTGGCTAGTTCTGGGGAGGCAGCATGGTGGGACGATTCTGTCCCGAGTCCCCGCCAGG
CTTTGTTTCGGGTCGCCGCTACCAGCGCGGTCTCCCTAGATCCTCCATCCGGGGAACCTCGCCCCGGGTGCGGGTA
CCCCGGGCGCGCAGCGCTGCCTCGAGGGTGTATGGATGCACCGCGCCGCGGAGAGAGACCGGGGGCTGGGCCTG
GGAGACCCCTAGCGGGGGCGGGGGCGAAGAAGAGATTATTCAGTGAAACAACAACCTGGAACCTCAAGTAACCTC
TCCCAGAGTACTTCCAACCTCTGGGTTGGCCCCAAATCCAATAATGCCACCACCAAGGCGGCTGGTGGTGCCCTG
CAGTCAACAGCCAGTCTCTTCGTGGTCTCACTCTCTCTCTGTCATCTCTACTCTTAAGAGACTCAGGCCAAGAAA
CGTCTTCTAAATTTCCCATCTTCTAAACCCAATCCAATGGCGTCTGGAAGTCCAATGTGGCAAGGAAAAACAG
GTCTTCATCGAATCTACTAATTCCACACCTTTTATTGACACAGAAAATGTTGAGAATCCCAAATTTGATTGATTT
GAAGAACATGTGAGAGGTTTGACTAGATGATGGATGCCAATATTAAATCTGCTGGAGTTTCATGTACAAGATGAA
GGAGAGGCAACATCCAAAATAGTTAAGACATGATTTCCCTGAATGTGGCTTGAGAAATATGGACACTTAATACTA
CCTTGAAAAATAAGAATAGAAATAAAGGATGGGATTGTGGAATGGAGATTGAGTTTTCATTTGGTTCATTAATTCT
ATAAGGCCATAAACAGGTAATATAAAAAGCTTCCATGATTCTATTTATATGTACATGAGAAGGAACTTCCAGGT
GTTACTGTAAATCCTCAACGTATTGTTTTGACAGCACTAATTTAATGCCGATATACTCTAGATGAAGTTTTACAT
TGTTGAGCTATTGCTGTTCTCTTGGGAACTGAACTCACTTTCCCTCCTGAGGCTTTGGATTGACATTGCATTTGA
CCTTTTATGTAGTAATTGACATGTGCCAGGGCAATGATGAATGAGAATCTACCCCCAGATCCAAGCATCCTGAGC
AACTCTTGATTATCCATATTGAGTCAAATGGTAGGCATTTCCCTATCACCTGTTTCCATTCAACAAGAGCACTACA
TTCATTTAGCTAAACGGATTCCAAAGAGTAGAATTGCATTGACCACGACTAATTTCAAAATGCTTTTTATTATTA
TTATTTTTTAGACAGTCTCACTTTGTGCGCCAGGCCGAGTGCAGTGGTGCATCTCAGATCAGTGTACCATTG
CCTCCCGGGCTCAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGATTACAGGCACCTGCCACCATGCCCG
GCTAATTTTTGTAAATTTTAGTAGAGACAGGGTTTTACCATGTTGCCAGGCTGGTTTTCGAACTCCTGACCTCAGG
TGATCCACCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCTTGAGCCCCCGCGCCCAGCCATCAAAATGCTT
TTTATTTCTGCATATGTTGAATACTTTTTACAATTTAAAAAATGATCTGTTTTGAAGGCAAAATTGCAAATCTT
GAAATTAAGAAGGCAAAAATGTAAAGGAGTCAAACTATAAATCAAGTATTTGGGAAGTGAAGACTGGAAGCTAA
TTTGCAATTAATTCACAACTTTTATACTCTTCTGTATATACATTTTTTTCTTTAAAAAACAACCTATGGATCA
GAATAGCCACATTTAGAACACTTTTTGTTATCAGTCAATATTTTATAGATAGTTAGAACCTGGTCTTAAGCCTAAA
AGTGGGCTTGATTCTGCAGTAAATCTTTTACAACGCTCGACACACATAAACCTTTTTAAAAATAGACACTCCC
CGAAGTCTTTTGTTCGCATGGTCACACACTGATGCTTAGATGTTCCAGTAATCTAATATGGCCACAGTAGTCTTG
ATGACCAAAGTCCTTTTTTTCCATCTTTAGAAAACATGGAACAAACAGATCGAACAGTTTGAAGCTACTG
TGTGTGTGAATGAACACTCTTGCTTTATCCAGAATGCTGTACATCTATTTTGGATTGTATATTGTGTTTGTGTA
TTTACGCTTTGATTCATAGTAACCTTCTTATGGAATTGATTGTCATTGAACACAACTGTAAATAAAAAGAAA

2288/6881
FIGURE 2104

CAGAAGCGGCTAGTGGCGGCTGCCTGCGTCCCCAACCCCTCCGCGCAGCGCTCGCGACACGCGTGCCAGGAGTG
GGAGCGAGCGGCGGGGCCAGCTGCGTTCTGAGCCTGGGCGCAGCTGCCATCTGCTCTGGGAAGCACCAGGGTGTC
CCCGCCGCCCTCAGCTCGAAGTCAGCCACCATGGAGGCGCAGGCACAAGGTTTGTTGGAGACTGAACCGTTGCAA
GGAACAGACGAAGATGCAGTAGCCAGTGCTGACTTCTCTAGCATGCTCTCTGAGGAGGAAAAGGAAGAGTTAAAA
GCAGAGTTAGTTCAGCTAGAAGACGAAATTACAACACTACGACAAGTTTTGTCAGCGAAAGAAAAGGCATCTAGTT
GAGATAAAACAAAACTCGGCATGAACCTGATGAATGAATTAAACAGAACTTCAGCAAAAGCTGGCATGACATG
CAGACTACCACTGCCTACAAGAAAACACATGAAACCTGAGTCACGCAGGGCAAAAGGCAACTGCAGCTTTTCAGC
AACGTTGGAACGGCCATCAGCAAGAAGTTCGGAGACATGAGTTACTCCATTGCGCATTCCATAAGTATGCCTGCT
ATGAGGAATTCTCCTACTTTCAAATCATTTGAGGAGAGGGTTGAGACAACCTGTCACAAGCCTCAAGACGAAAGTA
GGCGGTACGAACCCTAATGGAGGCAGTTTTGAGGAGGTCTCAGCTCCACGGCCCATGCCAGTGCCAGAGCTTG
GCAGGAGGCTCCCGGCGGACCAAGGAGGAGGAGCTGCAGTGCTTAAGTCCAGCCAGCGTGTCAGCTGCATCCAGAAA
CCGGCCACTACCCAGCCCATCTCTGCCTGTGCTTATCCAGATAAGAAGACCAAAATCCCGCTGGGAAAAACCCAG
GCCTTGACATTGTTATTCAAATGGCCCCCTCCAGAAAGTTTAATGATTTCCATTTGTATTTGTGTTGATGATGGAC
CACTTGACCATCACATTTTCAGTATTCATAGATGACTGTCACATTTTAAATGTTCCCACTTGAGCAGGTACACAA
CTGGTCATAATTCTGTCTGTGTAATTCGATGTATATTTTCCAAACATGTAGCTATTGTTTGCTTTGATTTTTG
CTTGGCCTCCTTTATGATGTGCATGTCCTTGAAGGCTGAATGAACAGTCCCTTTCAGTTCAGCAGATCAACAGGA
TGGAGCTCTTCATGACTGTCTCCAGCAATAGGATGATTTACTATAAATTTTCATCCAACACTACTTGTGATCTCTCTC
ACCTACATCAATTATGTATGTTAATTTTCAGCAATTAAAGAATTGATTTT

2289/6881
FIGURE 2105

MEAAQAGLLETEPLQGTDEDAVASADFSSMLSEEEKEELKAEIVQLEDEITTLRQVLSAKERHLVEIKQKLG MNL
MNELKQNF SKSWHDMQTTTAYKKTHETLSHAGQKATAAF SNVGTAI SKKFGDMSYSIRHSI SMPAMRNSPTFKSF
EERVETTVTSLKTKVGGTNPNGGSFEEVLSSTAHASAQSLAGGSRRRTKEEELQC

2290/6881
FIGURE 2106

GGAGTTGGAAGGGGAGGAGGAAGAGGGGGAGCAGGAAGAGGGGCAGAAGGAAGAAGAAGAGGGGGAGGAGAAAGA
GATAGAAGAGTAAGAGGAGGGGGAAGAAAGACAAGGGGAAGGGGAGGAGGAGGAGGACGGGGAGGAGCTTCGCCG
CGGCCTGCTCCGCCCAGCCGGGGTCGGTGGCCGCATGGCTTCGGTCTCCTCTGCGACCTTCTCGGGCCACGGGGC
TCGGTCCCTACTGCAGTTCCCTGCGGCTGGTAGGGCAGCTCAAGAGAGTCCCACGAACCTGGCTGGGTATACAGAAA
TGTCAGAGGCGGAGAGCGTTTCAGATCACATGTACCGGATGGCAGTTATGGCTATGGTGATCAAAGATGACCG
TCTTAACAAAGACCGATGTGTACGCCTAGCCCTGGTTCATGATATGGCAGAATGCATCGTTGGGGACATAGCACC
AGCAGATAACATCCCCAAAGAAGAAAAACATAGGCGAGAAGAGGAAGCTATGAAGCAGATAACCCAGCTCCTACC
AGAGGACCTCAGAAAGGAGCTCTATGAACTTTGGGAAGAGTACGAGACCCAATCTAGTGCAGAAGCCAAATTTGT
GAAGCAGCTAGACCAATGTGAAATGATTCTTCAAGCATCTGAATATGAAGACCTTGAACACAAACCTGGGAGACT
GCAAGACTTCTATGATTCCACAGCAGGAAAATTCATCACCCTGAGATAGTCCAGCTTGTTTCTGAACTTGAGGC
AGAAAGAAGCACTAACATAGCTGCAGCTGCCAGTGAGCCACACTCCTGAGACACTCTCTAAATTGCTGCACTCCT
GTAACAAACATTATTTTTCCATTTTCATTGTATTGTGTTTTGCCATTGTTGGTCTGTTGATTTCCCTAGATGTGAG
TCTGTTTGTTCATTTGTCTGAACTTCAGCAAGAAATGTGATACAACCTTGGGCACTAAAAGAAGCCACAGAACA
GGAAGCGGTCATGAAAGTGCCATGGATGAACACTGGAGGTGGCAGTGCCCTGTTTATGAACTAAATAAATAAATAT
TAAACACCTAAAATATTAGAATATTTATTGGAGATTTAAATCATCTTATTCTGACTTAATTACCGATATCCCCG
AAGGCTAGGTTTCATTGAATAATAGAAAATTTTCATTATGATTGCTTTTTAAGAACAGATTCTTCAGCTGATTTAGTG
ATAAGAATCCAGAAAAGAAAATGTACTAGTGATGTATTCTCTCCCCAGATGAAATTGCTGCCTTATTCAGATTTA
CTCTCTTGAGCCAGATTTTGAATTCACCTGCAGACTGCTTCAGACTTCTAATCATAGGCTTGTAACCTACTAAT
AGGCTCTGCCCCCTCTTCCCAATACTTTTTGTGCTTTAGAGATATAAACCGGGGCATATAAAAATGCAACTTGTAT
TCCTTTGTATATTTTTCCCTGTCTGACTTATAAATCTTGAGACCTTTATTGTAAAAGCATGTATCATCAGGTGAG
AAATATAAATAGGAAGTGGGGTCATTGAGCCTCAGGTAGGGAATATATCAACCCGATTTCTTCCTCTCTTTTCCC
TTTTATAGGATAAATAATCC

2291/6881
FIGURE 2107

GACGGCAGCCGCCCCGGCCGACAGCCCCGAGACGACAGCCCGGCGCGTCCCGGTCCCCACCTCCGACCACCGCCA
GCGCTCCAGGCCCCGCGCTCCCCGCTCGCCGCCACCGCGCCCTCCGCTCCGCCCCGAGTGCCAACCATGACCGC
CGCCAGTATGGGCCCCGTCCGCGTGCCTTCGTGGTCCTCCTCGCCCTCTGCAGCCGGCCGGCCGTTCGGCCAGAA
CTGCAGCGGGCCGTGCCCGGTGCCCGGACGAGCCGGCGCCGCGCTGCCCGGCGGGCGTGAGCCTCGTGCTGGACGG
CTGCGGCTGCTGCCGCGTCTGCGCCAAGCAGCTGGGCGAGCTGTGCACCGAGCGCGACCCATGCGACCCGCACAA
GGGCCTATTCTGTCACTTCGGCTCCCCGGCCAACCGCAAGATCGGCGTGTGCACCGCCAAAGATGGTGCTCCCTG
CATCTTCGGTGGTACGGTGTACCGCAGCGGAGAGTCCTTCCAGAGCAGCTGCAAGTACCAGTGCACGTGCCTGGA
CGGGGCGGTGGGCTGCATGCCCCCTGTGCAGCATGGACGTTTCGTCTGCCCAGCCCTGACTGCCCCCTTCCCGAGGAG
GGTCAAGCTGCCCCGGGAAATGCTGCGAGGAGTGGGTGTGTGACGAGCCCCAAGGACCAAACCGTGGTTGGGCCTGC
CCTCGCGGCTTACCGACTGGAAGACACGTTTGGCCCAGACCCAACTATGATTAGAGCCAACTGCCTGGTCCAGAC
CACAGAGTGGAGCGCCTGTTCCAAGACCTGTGGGATGGGCATCTCCACCCGGGTTACCAATGACAACGCCTCCTG
CAGGCTAGAGAAGCAGAGCCGCTGTGCATGGTCAGGCCTTGCGAAGCTGACCTGGAAGAGAACATTAAGAAGGG
CAAAAAGTGCATCCGTACTCCCAAAATCTCCAAGCCTATCAAGTTTGAGCTTTCTGGCTGCACCAGCATGAAGAC
ATACCGAGCTAAATTCTGTGGAGTATGTACCGACGGCCGATGCTGCACCCCCACAGAACCACCACCCTGCCGGT
GGAGTTCAAGTGCCCTGACGGCGAGGTCATGAAGAAGAACATGATGTTTCATCAAGACCTGTGCCTGCCATTACAA
CTGTCCCGGAGACAATGACATCTTTGAATCGCTGTACTACAGGAAGATGTACGGAGACATGGCATGAAGCCAGAG
AGTGAGAGACATTAACCTATTAGACTGGAACCTGAAGTATTACATCTCATTTTTCCGTAAAAATGATTTTCAGT
AGCACAAGTTATTTAAATCTGTTTTTCTAACTGGGGGAAAAGATTCCACCCAATTCAAAACATTGTGCCATGTC
AAACAAATAGTCTATCAACCCCAGACACTGGTTTGAAGAATGTTAAGACTTGACAGTGGAACCTACATTAGTACAC
AGCACCAGAATGTATATTAAGGTGTGGCTTTAGGAGCAGTGGGAGGGTACCAGCAGAAAGGTTAGTATCATCAGA
TAGCATCTTATACGAGTAATATGCCTGCTATTTGAAGTGAATTGAGAAGGAAAAATTTAGCGTGCTCACTGACC
TGCCTGTAGCCCCAGTGACAGCTAGGATGTGCATTCTCCAGCCATCAAGAGACTGAGTCAAGTTGTTTCCTTAAGT
CAGAACAGCAGACTCAGCTCTGACATTCTGATTCTGAATGACACTGTTCAGGAATCGGAATCCTGTCGATTAGACT
GGACAGCTTGTGGCAAGTGAATTTGCCTGTAACAAGCCAGATTTTTTAAATTTATATTGTAAATATTGTGTGTG
TGTGTGTGTGTATATATATATATATGTACAGTTATCTAAGTTAATTTAAAGTTGTTTGTGCCTTTTTATTTTT
GTTTTTAATGCTTTGATATTTCAATGTTAGCCTCAATTTCTGAACACCATAGGTAGAATGTAAAGCTTGTCTGAT
CGTTCAAAGCATGAAATGGATACTTATATGGAAATTCTGCTCAGATAGAATGACAGTCCGTCAAAACAGATTGTT
TGCAAAGGGGAGGCATCAGTGTCTTGGCAGGCTGATTTCTAGGTAGGAAATGTGGTAGCCTCACTTTTAATGAA
CAAATGGCCTTTATTAAAACTGAGTGACTCTATATAGCTGATCAGTTTTTTTACCTGGAAGCATTTGTTTCTAC
TTTGATATGACTGTTTTTCGGACAGTTTATTTGTTGAGAGTGTGACCAAAAGTTACATGTTTGCACCTTTCTAGT
TGAAAATAAAGTGTATATTTTTTCTATAAA

2292/6881
FIGURE 2108

CACTGCTGACATAACTCCCTTGGTCTTCAATTTAATAGTTGTTAAGTTTTTGCCACATTGCATATGCCTTTCAT
TTATAATTTATTTACCCCTGCTTGACTTAGTTTTGGGAATTCGTAAATTTAAAGGTGTGTGATTCTGTTTGCATC
TCCCTGTCACTGTGACACACCTAGATGTGTGTTACTTCAATTTAAATTCTCAAATTTAATTTTGATTGCTTCAG
CAGGGAAAATATTCTCAATAATGTAAAATAATTAAGGTCTATACATGGGTGTGATTTTTCTGGTTCACAACAGCA
CAAAGTGTCTTTTCATTTTTTTGTTGGTTTTCTTTTAAGATCTTTTTTACCCTGAAGTCGGTGAATACTTTTCTAG
TTTATTTGATACTCTTTCTGTGTATATATTAAGCTTTTGCTGTAGATTGCCTAGTAAATTTACTAAGGATAGGTT
GTTTTTACATATGGTCTATTTAAGTCTGATGTTTACGGGGGAAAGTGTAGTTACTAAAAATGTTTAACATAATTT
GGAAGAAGAGTATGAACAACCAATACCAATACCTATTGCGTTTGGATTCTTAAGACCCCAAGTTTGTTATTTCCACT
AAACTAGTTAICTTAACCATATCATCTGGTTTTGTGGGCCATTATTTACCTTCCCTTATGCTTTATAGAATAATG
GTTAATATTTTTAGGTCAAAATTACTTTTGGAAAGTAACTTTCCCAATAAATGTTTTTGAGCACCTGACAAA
ATTTAGTGTTTACCTTGCGTGCCATTTTGTGTATCCTTCATTAAAAAGCAATTGGAGGTTTGCCAGTTATCTC
ACTTCCCTTTTTAAATCAATGTTGTTTTAATGCACTAATCTGAATTTCTGTAAAGAGGATTATCTTAGTTTATACT
TTGTATTTTATAATGTTCTTGTATAGCAGCTCGGTACTGAAGGCGGTGTTTAACTTGCAAGCTCTGAGACTTCA
AATGGGAACAAATAGTAAGTAGCTAAGTAAACCACATCTTTGCAACCAAAAATAAAGATGAGTTAAAAGGTATCTG
GTTAGGCCTATTTTCATGAGGACTATGCTCTGGTGGGACCACAGGTACCTGATACTTAGTGCTGTGCTGCCTGAA
ACCTCAGCATGGAGACATCACCACATGCCTGTGGCCATTACAGCATCTTTCTGGAGCACCAGTTCACCTCCAGGTT
TTTATTTTAGGGTGTGATCGATTTTACCTACTTTGTGCACTGGTAGAAGTTGCTTTGCATATCAGAAAACTCC
ATTTTTTTCCACAAAAGGGATTACAGAAAACCTCTTTTGTGAGTGAGTGATTGGAACCTTAGAGACTCCTGTTGCCA
GAATCAGACTGCCCTAGAACAGAATGGACAATGCAGGGAGGAGAATTCACACAAACAGCACCTGTTCTGAGGCCT
GTGCCAGCCCACCAGGCCTGCTCAAATGTGGTCTTTACTTCAAGTGCACAGAGGCACATGAGGTTTTCTGGTGATA
AACCAGCGTCTTACCGCTGTTTTAAAGTCCCATCCCCATGGCTTTCACAATCAGTTCGGTTTTTTTTTGCTGTACT
TGATAAAATGTTTATTCTCATAACAGGTCAAGTACATTTACTTCTATTACAGTGAGTACCCAATAACAACAAAAG
CGCTTACAAATTTGGGGGGCGTGATTTTAGTACCTTTATTTGAAGTGTAATCATTTTAAATTATTATTATTTTAA
CTGGGGCAGTTATCAGTGGTTTTAAACAGGAACCTTTAGTGGCTTCAATTTGTTTAAAGAAACATATTAAGTTTGAGG
GAAAAATTTCCCATGAAATATTTGGAACGTAAGAGTAGTATTGATTAGAGAAAATTAATAAGAAACATAGTATG
GTAGCCAAATTTTTTAAAAAATCTTGAACTTTTCTGTAGGTCAGTTTTAGAACTGCTGTGAAAAGTGAAGGTTGC
CCTGTGGAGATTAAAATTAGAGTTGTTTTCACTAAGTACAGCATGGTGAATCCATTTGAGTCAAAGTGAAGAATT
TCCTCATCAAGTGACTATACATTTGTTTTTGTGTGCTCAAAAGAAATACTCAAACACAGACTGATATTAACCAGC
CAGGTAAATTGAACGACAATGTGGCAATTAGGTATTTGGCTGTTTTATTGGTCGTTAAATACTATGGTTTTGCAATA
TGATTGATGGTAAAAGAGTGATGTCATATTGATACTAGAGTAGCTTGTTTTTTTAGTAGGTGTGGGACCATCTCT
TTTACAAGTGCAACTCAGTCTAGGACAGCCATGGATGCAGTGTCTGGAGTTGGACCCTCTGAGCCCCTGGCTGC
CCCAGTAGCATCTGCATTGGTGACCAAGGACACTGCATTTGAAGAGGTCGCCACTGGGTTATTTAGTGTCTTCA
CTGCTTTTTGTTAAAAAATTGTAAAATTTGTACACAAAAAGTTGTGTTTTTGAATATCAATTGTTTAGACACACCT
ACAATGATAAATAAGTGCCTTTAAAGGCCCTCTTTCCATGAAATACATCTGTGGTTTAGCAAGGAAAGTACAAA
ATAGTTTATGTAGTTGGTATAATTTTTATTTGTGTCTTCATGTAGAAAAATGAATGTCATAATAAAATATAAAA
CTTACGTAAAG

2293/6881
FIGURE 2109

MDNAGRRIHTNSTCSEACASPPGLLKCGLYFKCTEAHEVSGDKPASRYCFKVPSPWLSQSVPFLLYLIKCLFSY
RSSTFTSIHSEYPITTKALTNLGGVILVPLFEV

2294/6881
FIGURE 2110

GTGACTGCTTAGAAAACTGCACAGCATCTGATGAAATTAGCGAATAAGAACATCAACCATGTCTTACACTCCAGG
AGTTGGTGGTGACCCCGCCAGTTGGCCAGAGGATCTCTTCTAACATCCAGAAGATCACACAGTGTTCTGTGGA
AATACAAAGAACTCTGAATCAACTTGGAACACCTCAAGATTCACCTGAATTGAGGCAACAGTTGCAACAGAAGCA
GCAGTATACTAACCAGCTTGCCAAAGAAACAGATAAGTACATTAAAGAGTTTGGATCTCTGCCCACCACCCCCAG
TGAACAGCGTCAAAGGAAAATACAGAAGGATCGCTTAGTGGCAGAGTTCACAACATCACTGACAAACTTCCAGAA
GGTCCAGAGGCAGGCTGCTGAGCGAGAGAAAGAGTTTGTGCTCGAGTAAGAGCCAGTTCCAGAGTGCTGTGGCAG
TTTTCTGAGGACAGCTCAAAGAAAGGAATCTTGTATCCTGGGAAAGCCAAACTCAACCTCAAGTGCAGGTGCA
GGATGAAGAAATTACAGAGGATGACCTCCGTCTTATTCATGAGAGAGAATCTTCTATCAGGCAACTTGAAGCTGA
TATTATGGATATTAATGAAATATTTAAAGATTTGGGAATGATGATTCATGAACAAGGAGATGTAATAGATAGCAT
AGAAGCCAATGTGGAAAATGCAGAGGTGCACGTTTCAGCAAGCAAATCAGCAGCTGTCAAGGGCAGCAGATTATCA
GCGCAAATCCAGAAAAACCCTGTGCATCATCATTCTTATCCTTGTCATTGGAGTTGCGATTATCAGTCTCATCAT
ATGGGGATTGAACCACTGAAGTTATAAAGGAGCACACTGTGCGACTACATTGTCTAAATTATGTAGGAAGATTCC
TGTAATCATGTTTTTTTAAATTATTATTTTAAAGCTATTGTATAAAGGATGGTTCCCATACTTTGTTATTTTTATT
GGGGGGGTTGGGGTGGTTCCTTTGGATTAAATCTGATATTTTCTAATACTGAAAGATTTTCTAAATGTCAGTGCT
GACATAACTCCCTTGGTCTTCAATTTAATAGTTGTTAAGTTTTTGCCACATTGCATATGCCTTTCATTTATAAT
TTATTTACCCTGCTTGACTTAGTTTTGGGAATTCGTAAATTTAAAGGTGTGTGTATTCTGTTTGCATCTCCCTGT
CACTGTGACACACCTAGATGTGTGTTACTTCAATTAAATTCTCAAATTTAATTTTGATTTGCTTCAGCAGGGAA
AATATTCTCAATAATGTAAAATAATTAAGGTCTATACATGGGTTGTATTTTTCTGGTTCACAACAGCACAAAGTG
TCTTTCATTTTTTTTGTGGTTTTCTTTTAAGATCTTTTTTACCCTGAAGTCGGTGAATACTTTTCTAGTTTATTT
GATACTCTTCTGTGTATATATTAAGCTTTTGCTGTAGATTGCCTAGTAAAATTACTAAGGATAGGTTGTTTTTA
CATATGGTCTATTTAAGTCTGATGTTTACGGGGGAAAGTGTAGTTACTAAAAATGTTTAACATAATTTGGAAGAA
GAGTATGAACA

2295/6881

FIGURE 2111

CTTTCCCTGCCGCCGCCGAGTCGCGCGGAGGCGGAGGCTTGGGTGCGTTCAAGATTCAGCTTCACCCGTAACCCA
CCGCCATGGCCGAGGAAGGCATTGCTGCTGGAGGTGTAATGGACGTTAATACTGCTTTACAAGAGGTTCTGAAGA
CTGCCCTCATCCACGATGGCCTAGCACGTGGAATTCGCGAAGCTGCCAAAGCCTTAGACAAGCGCCAAGCCCATC
TTTGTGTGCTTGCATCCAACCTGTGATGAGCCTATGTATGTCAAGTTGGTGGAGGCCCTTTGTGCTGAACACCAAA
TCAACCTAATTAAGGTTGATGACAACAAGAACTAGGAGAATGGGTAGGCCTTTGTAAAATTGACAGAGAGGGGA
AACCCCGTAAAGTGGTTGGTTGCAGTTGTGTAGTAGTTAAGGACTATGGCAAGGAGTCTCAGGCCAAGGATGTCA
TTGAAGAGTATTTCAAATGCAAGAATCAAAGAAATAAATCTTTGGCTCACAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAA

2296/6881
FIGURE 2112

MAEEGIAAGGVMDVNTALQEVLTALIHDLARGIREAAKALDKRQAHLCVLASNCDEPMYVKLVEALCAEHQIN
LIKVDDNKKLGEWVGLCKIDREGKPRKVVGCSVVVKDYGKESQAKDVIEEYFKCKK

2297/6881
FIGURE 2113

GGCCGCCTCGCACCCGGAACAACAAAGCAAGGAAGACGGAGTCCGAGCCTCGGGGGCTCCTAGCAACGGGCGGG
GCGGGAGTTCCATGGAGACTGGGGAGCGCGCCCGTCTCATCCTCATCCTTGTCTCCAGCTTCTCCTTCGCATCC
GACGCAACCGGCAGCAGCGCTGCCGCCGCGTCCTCAGCCACCGCTCCCTCTTCCCACGGATGTGATCTTCGTGGT
GGAAAGCTAAATTTTAAAACACCCCAATGGATGCAGACAGTGATGTTGCATTGGACATTCTAATTACAAATGTA
GTCTGTGTTTTTAGAACAAGATGTCATTTAAACTTAAGGAAGATTGCTTTGGAAGGAGCAAATGTAATTTATAAA
CGTGATGTTGGAGTAATATTAATGAAGCTTAGAAAACCTAGAATTACAGCTACAATTTGGTCCTCAGGAAAAATT
ATTTGCACTGGAGCAACAAGTGAAGAAGAAGCTAAATTTGGTGCCAGACGCTTAGCCCGTAGTCTGCAGAACTA
GGTTTTTCAGGTAATATTTACAGATTTTAAGGTTGTTAACGTTCTGGCAGTGTGTAACATGCCATTTGAAATCCGT
TTGCCAGAATTCACAAAGAACAATAGACCTCATGCCAGTTACGAACCTGAACTTCATCCTGCTGTGTGCTATCGG
ATAAAATCTCTAAGAGCTACATTACAGATTTTTTCAACAGGAAGTATCACAGTAACAGGGCCCAATGTAAAGGCT
GTTGCTACTGCTGTGGAACAGATTTACCCATTTGTGTTTGAAAGCAGGAAAGAAATTTTATAATTCACCACTTAA
TTGGTTAGAATCTCTAACTGAGCACCTTTTAAACCTGCTGCACATTGGACTCAAAAGGAAAACCTGGACCAACAAT
AATTGAGGAAATAGACTCTTTTTATTCAATTCACGGCTACAGTGTAAGCTCCAGTCCCTTTGGATTTTATTCCAAAC
CTTGCTGTAATATAAAAGGAAGTTTACAAGACATGATATTGCTGCTTTTACAAAAGGACATTCTATTTATTTTCG
CAGTAATTCCTCATGTCCCCATAAGCAGAGCTGTCACAGTGTGCACTACCTTAGATTGTTTTATTGTCGTCATTGT
TATTTTTTTCCATTTTGAGCTAATGTGTTTTATTTGTGAATAGTCTTTTACATTTTGTATGCTGAATATGGGCA
CCAAAGAACCTGTAAAAGTTATCTTTTCAATTGAATGTGCACAAATAAAAGTTTGGA

2298/6881
FIGURE 2114

GCCGGGGAGGGACGCAGGCAGGCGGGCGGGCAGCGGGAGGCGGCAGCCCCGGTGCGGTCCCCGCGGCTCTCGGCGGA
GCCCCGCGCCCCGCCGCGCCATGGCCCCGAAGACCCCGGCACAGCATATATAGCAGTGACGAGGATGATGAGGACTT
TGAGATGTGTGACCATGACTATGATGGGCTGCTTCCCAAGTCTGGAAAGCGTCACTTGGGGAAAACAAGGTGGAC
CCGGGAAGAGGATGAAAACTGAAGAAGCTGGTGGAAACAGAATGGAACAGATGACTGGAAAGTTATTGCCAATTA
TCTCCCGAATCGAACAGATGTGCAGTGCCAGCACCGATGGCAGAAAGTACTAAACCCTGAGCTCATCAAGGGTCC
TTGGACCAAAGAAGAAGATCAGAGAGTGATAGAGCTTGTACAGAAATACGGTCCGAAACGTTGGTCTGTTATTGC
CAAGCACTTAAAGGGGAGAATTGGAAAACAATGTAGGGAGAGGTGGCATAACCACTTGAATCCAGAAGTTAAGAA
AACCTCCTGGACAGAAGAGGAAGACAGAATTATTTACCAGGCACACAAGAGACTGGGGAACAGATGGGCAGAAAT
CGCAAAGCTACTGCCTGGACGAACGATAATGCTATCAAGAACCCTGGAATTCTACAATGCGTCGGAAGGTCTGA
ACAGGAAGGTTATCTGCAGGAGTCTTCAAAGCCAGCCAGCCAGCAGTGCCACAAGCTTCCAGAAGAACAGTCA
TTTGATGGGTTTTTGCTCAGGCTCCGCCTACAGCTCAACTCCCTGCCACTGGCCAGCCCACTGTAAACAACGACTA
TTCCTATTACCACATTTCTGAAGCACAAAATGTCTCCAGTCATGTTCCATACCCTGTAGCGTTACATGTAAATAT
AGTCAATGTCCCTCAGCCAGCTGCCGCAGCCATTAGAGACACTATAATGATGAAGACCCTGAGAAGGAAAAGCG
AATAAAGGAATTAGAATTGCTCCTAATGTCAACCGAGAATGAGCTAAAAGGACAGCAGGTGCTACCAACACAGAA
CCACACATGCAGCTACCCCGGGTGGCACAGCACCACCATTGCCGACCACACCAGACCTCATGGAGACAGTGCACC
TGTTTCCTGTTTGGGAGAAACACCACTCCACTCCATCTCTGCCAGCGGATCCTGGCTCCCTACCTGAAGAAAGCGC
CTGCCAGCAAGGTGCATGATCGTCCACCAGGGCACCATTCTGGATAATGTTAAGAACCTCTTAGAATTTGCAGA
AACACTCCAATTTATAGATTCTTTCTTAAACACTTCCAGTAACCATGAAAACCTCAGACTTGGAATGCCTTCTTT
AATTCCACCCCCCTCATTGGTCACAAATTGACTGTTACAACACCATTTTCATAGAGACCAGACTGTGAAAACCTCA
AAAGGAAAATACTGTTTTTTAGAACCCAGCTATCAAAGGTCAATCTTAGAAAGCTCTCCAAGAACTCCTACACC
ATTCAAACATGCACTTGCAGCTCAAGAAATTAATACGGTCCCCTGAAGATGCTACCTCAGACACCCTCTCATCT
AGTAGAAGATCTGCAGGATGTGATCAAACAGGAATCTGATGAATCTGGAATTGTTGCTGAGTTTCAAGAAAATGG
ACCACCCTTACTGAAGAAAATCAAACAAGAGGTGGAATCTCCAACCTGATAAATCAGGAACTTCTTCTGCTCACA
CCACTGGGAAGGGGACAGTCTGAATACCCAACCTGTTACGCAGACCTCGCCTGTGGCAGATGCACCGAATATTCT
TACAAGCTCCGTTTTTAATGGCACCAGCATCAGAAGATGAAGACAATGTTCTCAAAGCATTTACAGTACCTAAAAA
CAGGTCCCTGGCGAGCCCCCTTGACGCTTGTAGCAGTACCTGGGAACCTGCATCCTGTGGAAAGATGGAGGAGCA
GATGACATCTTCCAGTCAAGCTCGTAAATACGTGAATGCATTCTCAGCCCGACGCTGGTCACTGAGACATTTTC
CAGAAAAGCATTATGGTTTTTCAGAACACTTCAAGTTGACTTGGGATATATCATTCTCAACATGAACTTTTCAT
GAATGGGAGAAGAACCTATTTTTGTTGTGGTACAACAGTTGAGAGCAGCACCAAGTGCATTTAGTTGAATGAAGT
CTTCTTGGATTTACCCAACTAAAAGGATTTTTAAAAATAAATAACAGTCTTACCTAAATTATTAGGTAATGAAT
TGTAGCCAGTTGTTAATATCTTAATGCAGATTTTTTTAAAAAAAACATAAAATGATTTATCTGTATTTTAAAGGA
TCCAACAGATCAGTATTTTTTCTGTGATGGGTTTTTTGAAATTTGACACATTAAGGTAAGTACTCCAGTATTTTAC
TTTTCTCGATCACTAAACATATGCATATATTTTTAAAAATCAGTAAAAGCATTACTCTAAGTGTAGACTTAATAC
CATGTGACATTTAATCCAGATTGTAAATGCTCATTTATGGTTAATGACATTGAAGGTACATTTATTGTACCAAAC
CATTTTATGAGTTTTCTGTTAGCTTGCTTTAAAAATTATTACTGTAAGAAATAGTTTTATAAAAAATTATATTTT
TATTCAGTAATTTAATTTTGTAAATGCCAAATGAAAAACGTTTTTTTGCTGCTATGGTCTTAGCCTGTAGACATGC
TGCTAGTATCAGAGGGGCAGTAGAGCTTGGACAGAAAAGAAAAGAACTTGGTGTTAGGTAATTGACTATGCACTA
GTATTTTACAGACTTTTTTAATTTTATATATATATACATTTTTTTTTCTTCTGCAATACATTTGAAAACCTGTTTGGG
AGACTCTGCATTTTTTTATTGIGGTTTTTTTGTTATTGTTGGTTTATACAAGCATGCGTTGCACTTCTTTTTTGGG
AGATGTGTGTTGTTGATGTTCTATGTTTTGTTTTGAGTGTAGCCTGACTGTTTTATAATTTGGGAGTTCTGCATT
TGATCCGCATCCCCTGTGGTTTTCTAAGTGTATGGTCTCAGAACTGTTGCATGGATCCTGTGTTTGCAACTGGGGA
GACAGAACTGTGGTTGATAGCCAGTCACTGCCTTAAGAACATTTGATGCAAGATGGCCAGCACTGAACTTTTGA
GATATGACGGTGTACTTACTGCCTTGTAGCAAAATAAAGATGTGCCCTTATTTT

2299/6881
FIGURE 2115

MARRPRHSIYSSDEDDDFEMCDHDYDGLLPKSGKRHLGKTRWTREEDKLLKLLVEQNGTDDWKVIANYLPNRTD
VQCQHRWQKVLNPELIKGPWTKEEDQRVIELVQKYGPKRWSVIAKHLKGRIGKQCRERWHNHLNPEVKKTSWTEE
EDRIIYQAHKRLGNRWAEIAKLLPGRTDNAIKNHWNSTMRRKVEQEGYLQESSKASQPAVATSFQKNSHLMGFAQ
APPTAQLPATGQPTVNNDYSYYHISEAQNVSSHVPYPVALHVNIVNVPQAAAAIQRHYNDEDPEKEKRIKELEL
LLMSTENELKGQQVLPTQNHTCSYPGWHSTTIADHTRPHGDSAPVSCLEHHSTPSLPADPGSLPEESASPARCM
IVHOGTILDNVKNLLEFAETLQFIDSFLNTSSNHENS DLEMP SLTSTPLIGHKLTVTTPFHRDQTVKTQKENTVF
RTPAIKRSILESSPRTPTPFKHALAAQEIKYGPLKMLPQTPSHLVEDLQDVIKQESDESGIVAEFQENGPPLLKK
IKQEVESPTDKSGNFFCSHHWEGDSLNTQLFTQTSPVADAPNILTSSVLMAPASEDEDNVLKAFTVPKNRSLASP
LQPCSSTWEPASCGKMEEQMTSSSQARKYVNAFSARTLVM

2300/6881
FIGURE 2116

CTCCCTGTCGCCGCGGAGGGGCGGGGCGAGGACGCGCAACTCCGGCCGGAGCTGTCCGGGGTCGTGAGCCGGGCC
CGCCTTGGTGGCGGCGCCCCCTCGCGGTCCAGAGGCAGACGCATCGGGTGGGCTCGGGTCTCCAGCCCGGCCGGG
AGGAGGGACCGGGTCTGCGGAGCGGGGACTCGGGGCCTCGGCGGGGCGCGCACACGCAGGCGGGGCGGCCCGGG
TGCGGGGCCTCTGCGCGGCTGACCAGGCTCCCAGAGCGTCAGCGCCGCCCATGGCCGAGCCGCTCCAGCCAGACC
CCGGGGCGGCCGAGGACGCGGCGGCCCAAGCTGTGGAGACGCCGGGCTGGAAGGCCCCGGAGGACGCCGGCCCC
AGCCCGGAAGTTATGAGATCCGACACTATGGACCAGCCAAGTGGGTCAGCACGTCCGTGGAGTCTATGGACTGGG
ATTCAGCCATCCAGACGGGCTTTACGAACTGAACAGCTACATTCAAGGCAAAAACGAGAAAGAGATGAAAATAA
AGATGACAGCTCCAGTGACAAGCTACGTGGAGCCTGGTTCAGGTCCTTTTAGTGAGTCTACCATTACCATTTCCC
TGTATATTCCCTCTGAACAGCAATTTGATCCACCCAGGCCTTTAGAGTCAGATGTCTTCATTGAAGATAGAGCCG
AAATGACTGTGTTTGTACGGTCTTTTCGATGGATTTTCTAGTGCCCAAAAGAATCAAGAACAACCTTTTGACATTAG
CAAGCATTTTAAGGGAAGATGGAAGTTTTTCGATGAGAAGGTTTACTACACTGCAGGCTACAACAGTCCTGTCA
AATTGCTTAATAGAAATAATGAAGTGTGGTTGATTCAAAAAAATGAACCCACCAAAGAAAACGAATTGAGAAAAAT
GAAAGGAAGTTCTGCTGTCAGAGGCAAAACATCTGTTTATCATAGACATCAACATGACCTATAAGTAAAGTGCCT
GTCTAGTGTCTTCTATTGAGAGTACTACTATTAATTAAGCTTATTTCCAATGTGCCTTTTTAATGCTTGAAGTTT
TATCTACATACACAGGTAACAGAGGACAGTAGTCTGTAAACATATAAATCGGTCATAACTATCGTGGTCTTTATT
TCTGTGAGGATC

2301/6881
FIGURE 2117

MAEPLQDPFGAAEDAAAQAVETPGWKAPEDAGPQPGSYEIRHYGPAKWVSTSVESMDWDSAIQTGFTKLNSYIQG
KNEKEMKIKMTAPVTSYVEPGSGPFSESTITISLYIPSEQQFDPPRPLESDVFIEDRAEMTVFVRSFDGFSSAQK
NQEQLLTLASILREDGKVFDEKVYYTAGYNPVKLLNRNNEVWLIQKNEPTKENE

2302/6881
FIGURE 2118

AGAACCACCACAACAAATAACCAGCCTGGCAGTCAATTCTTCCTATGGACTGGTGGTTTTTGGCAATTGCAATGG
CATTGCTATGGTTGACTACCTCCAGAAAGCAGTGCTGCTCAACCTGGGCACTATTGAATTATATGGCTCTAATGA
TCCTTATCGGAGAGAACCCCGATCTCCTCGTAAATCTCGACAGCCTTCAGGAGCCGGTCTGTGTGATATTAGTGA
AGGGACTGTTGTTCCAGAGGATCGCTGCAAATCTCCAACCTCTGCAAAGATGTCAAGGAAGTTAAGCTTACCTAC
TGACCTAAAGCCTGATTTAGATGTAAAGGATAACTCCTTTAGCCGATCACGGAGTTCAAGTGTAAACAAGCATTGA
CAAAGAATCCCGAGAAGCGATCTCCGCTCTTCATTTCTGTGAAACGTTTACTCGAAAGACGGACTCGTCCCTTC
CCCTTGTCTATGGGTGGAACAACGCTAGGAACAGTGCTTGTTCATTGCACTGAACCTTCCCCCAGGGGGAGAGCA
AAGACTTCTTCAGCCAGTAATTGTGTCTCCAAGTGGTACTATATTGAGGTTAAAAGGTGCAATCTTGAGAATGGC
ATTTCTGGATACCACAGGCTGCTTAATACCACCTGCGTATGAACCTTGGAGAGAGCACAATGTTCTTGAAGAAAA
AGACGAAAAGGAGAAATTGAAAAACGGCGGCCTGTCTCAGTATCCCCCTCCTCTTCTCAGGAAATTAGTGAAAA
CCAGTATGCAGTGATATGTTCTGAAAAGCAAGCAAAAGTAATCTCACTGCCAACCCAGAACTGTGCTTATAAGCA
AAATATTACAGAGACCTCGTTTTGTGCTTCGTGGAGATATTGTAGCATTGAGTAACAGTATCTGCCTTGCCTGTTT
CTGTGCCAATGGACATATAATGACTTTTAGTTTGCCAGTTTAAAGACCTCTGTTGGATGTGTATTACTTGCCCT
TACCAATATGCGGATAGCCAGAAGCTTGCTTTTACCAACAATGGACAAGCATTATACCTTGTTCACCTACAGA
AATCCAGAGACTTACTTATAGTCAAGAGACCTGTGAAAATCTTCAGGAAATGTTGGGTGAACTCTTCACTCCTGT
AGAAACACCTGAAGCACCAAAACAGGGGATTCTTTAAAGGCTTATTTGGAGGTGGTGCACAAATCTCTTGACAGAGA
AGAACTATTTGGAGAATCGTCTCAGGAAAAGGCTTCAAGGAGCCTTGACAGCATATTCTTGGCCCTGGTGGCAT
TGAAGGCGTAAAAGGGGCAGCATCTGGAGTTGTTGGTGAATTAGCACGAGCCAGGCTGGCACTAGATGAAAGAGG
GCAGAACTTGGCGATCTGGAAGAAAGAACTGCGGCCATGTTATCAAGTGCAGAGTCATTTTCTAAACATGCTCA
TGAGATTATGTTGAAATACAAAGATAAGAAGTGGTACCAGTTCTGACAACCAGAATCCAATAAGTCCAACCTTCAG
CCAGAAGGAAAAAAGTTTTCCATTTTTATTACATTCTTTAGGAAAGTTAACGTTAAAGGGATGTTCTGTCCTGAA
TACTGTTCTTTCTTAGCACAGTCATGCACTGTTTTACCTCAGTCATGTGGCTTTAACTGAGGAGTGTTACACGC
ACTCGAAATGGAGTATATGGTGTGTGCCAGTTATGAGTTGACCATTTGGGAATTAAACAGGTCACACGTGACAGA
TGAAGAAACCAAGGGGGCTGCTGAGGAGACCTGGTGCAGGGACTAATCCTGGATCATTCTGTATTAACTTTCA
TATGCCAAAAGGGTTTTGTGCCGTTTTATCTGCCATCAGTGTTTGACCTGTTTAGGGCAGAGGCAATAAGTCAGAA
GTCTTGAAAGTTGAAATAGTTATATGTGTGTCATTGGACTGGATTATAAACAGCTGTCTTGACTTTCCCTCTCTT
AACACTGACTGGTCATCAGTATCATTAGTGAAAAAGAAACAAATTGTTTGTTATCATCTCTTTAGACAGATAAGC
TGAATGGTGGGCTTTAAATAATAAAAAACATACACATAGTTGACTTGTGTATGAGCTACTCTTGGATTCTTGTTAT
TATAGACTTGTTAGTTTCATATTTGTCAAAAGCAAAACAAGAAGATACATCACTTTTCATTGAAAAGAAAAG
TGTAAGCATGACTGAATTGCTCATCATTCTGGGAGTTTCCATGTAGTGGCTATGCAGTGTGAAAGTGAGAAAA
ACCTCCATTGTGGTGAGGAGAATACTTCAATGTCCCTTGTCTTGTCTCATTAAATTCAGCTAAAGGTGGATTTG
ACCAAAAATAATGCTGGTTAAATTTGTAGAAATGTTGAAATTGGCTGTGTTTTAAATTTTGCTTGAATTTTTATAA
AATGTTTAACCAATGTACCTTTGCATTCTTTAATTAAAATTGCTT

2303/6881
FIGURE 2119

TTTTTCGTCTGGGCTGCCAACATGCCATCCAGACTGAGGAAGACCCGGAACTTAGGGGGCCACGTGAGCCACCGC
CACGGCCGCATAGGCAAGCACCGGAAGCACCCCGGCGGCCGCGGTAATGCTGGTGGTCTGCATCACCACCGGATC
AACTTCGACAAATACCACCCAGGCTACTTTGGGAAAGTTGGTATGAAGCATTACCACTTAAAGAGGAACCAGAGC
TTCTGCCCAACTGTCAACCTTGACAAATTGTGGACTTTGGTCAGTGAACAGACACGGGTGAATGCTGCTAAAAAC
AAGACTGGGGCTGCTCCCATCATTGATGTGGTGCGATCTGGCTACTACAAAGTTCTGGGAAAGGGAAAGCTCCCC
AAGCAGGCTGTCACCGTGCAGGCCAAATTCTTCAGCAGAAGAGCTGAGGAGAAGATTAAGAGTGTGGGGGGGCC
TGTGTCCTGGTGGCTTGAAGCCGCATGGAGGGAGTTTCATTAAATGCTAACTACTTAAAAAAAAAAAAAGAAGAA
GAAGAAGAAGAAAA

2304/6881
FIGURE 2120

MPSRLRKTRKLRGHVSHRHGRIGKHKHPGGRGNAGGLHHHRINF¹DKYHPGYFGKVGMMKHYHLKRNQSF²CPTVNL
DKLWTLVSEQTRVNAAKNKTGAAP³IIDVVRSGYYKVLGKGKLPKQAVTVQAKFF⁴SRRAEEKIKSVGGACVLVA

2305/6881
FIGURE 2121

ATGCGGTCCCGGGTTCTGTGGGGCGCTGCCCGGTGGCTCTGGCCCCGCCGGGCCGTTGGCCCCAGCCCGCCGGCCC
CTGAGCTCCGGTAGCCCGCCGCTGGAGGAGCTGTTACCCGGGGCGGGCCCTTGCGGACCTTCCTCGAGCGCCAG
GCGGGGTCTGAAGCCCATTGAAGGTCAGGAGGCCCCGAGTTGCTGGCGGTGATCAAACCTGCTGAACGAGAAGGAG
CGGGAGCTGCGGGAGACTGAGCACTTGCTGCACGGTAAGGGTCGGGCCCGGGGGAGAGGCGTCAGAGCACATTCT
TGA CTCTTCGTTTGA CTTTTCCACTGCCCACACTACCCGAGTTTGAACTCTTTACTCACTTGCAGCCGTTTTTA
TTTTGGATCAGAGGTCAGGACATCATTACGTGCTGTGATCCCATCCTCTCCTGTGGGCTCTCTGTGCTCCTTG
CCACGGCGCTCTGCCGCCTTTTACATGCTTATTAGTTGTGGACTCGGGCAAGAGCTCATTAGCTCAGCAAGGATA
AATAAGGCACTGTCCCTGTGATGGGCTCCACAGCGGTGTTTCTCAAAGTGTGGTGTGGAGACCCATTGCACTAG
TATCAGGGCAGTGCTTGTTAATAGCAGACTTAGGACTCAGAATCTCAGACCTATACGTGGGTAAAGGTACTAAAT
TGGGAAATTCAGTATGGCCTAAGTATAGAATAGGTGGGAGATGATGTCATAGAAACATGAAGCCAGAAAAATAGT
TAAGAACCCTTGCAAGACAAAGAATTTGGATTTATTTTTTATAGACCATGGAAAGTTAGCAAATGTTTTTAAGCAG
AGAATTCACGTCTTTGTAAAGAAAAGTTAATGGTGGCATGCGCTGAGGATAAATTGGAGTATTCTCCAGAAACGC
TGGTGGCTGACAGGCCAGGGAGGAGGCAGTTGAAACAATCCAAAGAAGAAATGGTGATAGGCATAGTTCTGACTC
ACAAAACATTTTGAGAAACAAGTTAGGATTTAGTGGCTTATGCCCTGAGAAGGATGAGGGAGAGAGTTAGTTCTA
AGAAAAGTCTTAGGTTTCTGGCTTCAGCACGAGTGCTACTGTTAATTAAGATGAAAGTATAAAAAGTTGGACCGAA
TTTTTTAAAAAGATGAGTTTTGCATTGAATGCCATATTAAGTTAAAAATACCTGTGAAAAGGAATTCCAATAAAG
ATATCTGTACTAGTCTAGGAGAAAAAATTACTGACATAGGAGAAAAATTGAGCCCAAATAATCATATGAGAGCTC
TCGAGATATACAGTACGTGGTAAATTAAACCTTAGAAGTAGATGAGAACACTCAGGGAAAAATGTGTTAAGATAGA
AACAGTCTAACAGGCCAGAAATACACAGTATTTGAGGAGCAGGCAGAGAAGAAGGCTATAAAAGGTCAAGAAA
AAAACAGCCAGAGCTTTGTGACCCTGAAGTAGATAAATAAATGAAGCTGTAGAAGCCAATAGAAAATTTCAAGAA
GTAAGAGATCCTTGCCAGGCGTGGTGGCTCACGCCTCTAATTCAGCACTTTGAGAGGCTCAGGTGGGCCGATC
ACTTGAGCCCAGGAGTTTCGAGACCAGCCTGGGTAAACATGGCAAACCTGTCTCTACAAACAATGCAAAATTAGC
TGGGCATGGTGGTGCCTGTGGTCCCAGCTACTTGAGAGGCTGAGGTGGGAGAATCGCTTGAACCCGGGAGG
TGGAGGTTGCAGTGAGCCAAGATGGTGCCACTGCATTCCAGCCTGGGTGACAGCGCAAGACCCCTGCCTC

2306/6881
FIGURE 2122

ATGCGGTCCCGGGTTCTGTGGGGCGCTGCCCCGGTGGCTCTGGCCCCGCCGGGCCGTTGGCCCAGCCCGCCGGCCC
CTGAGCTCCGGTAGCCCGCCGCTGGAGGAGCTGTTACCCGGGGCGGGCCCTTGCGGACCTTCCTCGAGCGCCAG
GCGGGGTCTGAAGCCCATTTGAAGGTCAGGAGGCCCGAGTTGCTGGCGGTGATCAAACCTGCTGAACGAGAAGGAG
CGGGAGCTGCGGGAGACTGAGCACTTGCTGCACGATGAGAATGAAGATTTAAGGAACTTGCAAGAGAATGAAATC
ACTTTGTGTCAAAAAGAAATAACTCAGCTGAAGCATCAGATTATCTTACTTTTGGTTCCCTCAGAAGAAACAGAT
GAAAATGATTTGATCCTGGAAGTAACTGCAGGAGTTGGAGGTCAGGAGGCAATGTTGTTTACATCAGAGATATTT
GATATGTATCAGCAATATGCTGCATTTAAAAGATGGCATTTTGAAACCCTGGAATATTTTCCAAGTGAAGTAGGT
GGCCTTAGACATGCATCTGCCAGCATTGGGGGTTTCAAGCCTATAGGCACATGAAATTTGAAGGAGGTGTTTAC
AGAGTACAAAGAGTGCCAAAGACAGAAAAGCAAGGCCGCGTCCATACTAGCACCATGACTGTAGCAATATTACCC
CAGCCTACTGAGATTAATCTGGTGATTAATCCGAAAGATTTGAGAATTGACACTAAGCGAGCCAGTGGAGCTGGG
GGGCAGCATGTAAATACCACGGACAGTGCTGTCCGGATAGTTTATCTTCCAACAGGTGTTGTTTCTGAATGTCAA
CAAGAGAGATCTCAGCTGAAAAATAAAGAGCTGGCTATGACAAAGTTACGTGCAAAACTGTACAGCATGCATCTA
GAAGAAGAAATAAATAAAAGACAGAATGCTAGAAAAATTCAGATTGGAAGTAAAGGAAGATCAGAGAAAATAAGA
ACATATAATTTTCCACAGAACCGGGTCACAGATCACAGAATAACAAGACGCTGCATGATCTTGAACTTTTATG
CAAGGAGATTATCTACTGGATGAACTTGTACAGTCATTGAAGGAATACGCCGATTATGAATCTTTAGTAGAAATT
ATTTCCCAAAAAGTTTAA

2307/6881
FIGURE 2123A

CAAAAATCAGTCTGATCTCGGGAAACCTGGAGAAATTTATTTTCTGTACTCTAATGTTCTTTTCATTTTGGTGACC
ATCAAGGTGCTGGGAGAGGAATTAGATGGCTGTAATTCAAAGTTAATGGAATTAGATGCAGCAGTACAGAAATTC
TTGGAACAGAATGGCCAACTGGGTAAGCCACTGGCCAAGAAGATAGGAAAACCTGACTGAACTTCACCAGCAGACC
ATTAGACAAGCTGAGAATCGGCTCTCCAAGCTCAATCAGGCAGCATCACATTTAGAAGAATACAATGAAATGCTT
GAATTAATTTTGAAGTGGATTGAAAAAGCTAAAGTCTTGGCTCATGGAACTATTGCATGGAATTCTGCAAGCCAG
CTTCGGGGAACAATATATTTTGCATCAGACCCTGCTAGAAGAATCCAAAGAAATTGACAGTGAGCTGGAAGCAATG
ACTGAGAAAATTACAGTACCTCACTAGCGTGACTGTACAGAAAAAATGTCTCAGCAAGTGGCAGAACTGGGACGG
GAGACTGAGGAGTTGCGACAGATGATCAAAATTCGTTTGCAGAACCTCCAAGATGCAGCTAAGGATATGAAAAAA
TTTGAAGCAGAGTTGAAAAAGTTACAAGCTGCCTTGGAGCAAGCCCAGGCAACACTGACTTCTCCAGAAGTTGGA
CGTCTCAGTCTCAAGGAGCAGCTCTCTCATCGGCAGCATTGTTGTCTGAGATGGAGTCACTGAAGCCGAAGGTG
CAAGCAGTGCAGCTCTGCCAGAGTGCCCTCCGGATCCCCGAGGATGTGGTTGCCAGCTTACCTCTCTGTATGCT
GCTCTGCGGCTGCAGGAAGAGGCCAGCCGGCTGCAGCACACCGCCATCCAGCAGTGTAACATCATGCAGGAAGCT
GTGGTACAATATGAACAATATGAGCAAGAAATGAAACATCTCCAGCAACTGATAGAAGGAGCTCACAGAGAGATT
GAGGATAAACCTGTTGCCACCAGTAACATACAGGAGCTGCAGGCTCAGATTTCTCGGCATGAGGAGCTGGCGCAG
AAAATTAAGGGCTACCAGGAGCAGATCGCTTCTTTGAATTCCAAGTGCAAGATGCTGACGATGAAAGCCAAGCAC
GCCACCATGCTGCTGACGGTGACCGAGGTGAGGGGCTGGCGGAAGGGACAGAGGACCTGGATGGGGAGCTCCTC
CCCACGCCTTCGGCCCCACCCCTCTGTGGTCATGATGACTGCAGGTCGCTGTACACTTTGCTGTACCCGGTCACT
GAGGAGTCTGGGGAGGAGGGAACCAACAGTGAGATTTCTCTCCACCTGCCTGTGCTCCCCTTCACCTGTGGCT
AATACAGATGCTTCTGTTAACCAGGACATTGCATATTACCAAGCCTTGTCTGCTGAGAGGTTGCAGACAGATGCT
GCAAAAATTCACCCAGCACATCCGCATCCCAGGAGTTCTATGAACCGGGATTGGAGCCATCCGCTACTGCCAAA
CTGGGTGATTTGCAGCGTTCTTGGGAAACCTTAAAGAATGTGATCAGTGAGAAGCAGCGCACACTCTATGAAGCT
TTGGAACGCCAGCAGAAGTACCAGGACTCCCTCCAGTCCATCTCTACGAAGATGGAGGCCATTGAGCTGAAACTC
AGTGAGAGCCCAGAGCCTGGCAGGAGTCCAGAAAGCCAGATGGCTGAACATCAGGCATTGATGGATGAGATTCTC
ATGCTCCAGGATGAAATCAATGAGCTCCAGTCCCTCTCTCGCAGAGGAGCTGGTATCCGAGTCTTGTGAGGCCGAC
CCTGCGGAGCAGCTGGCCTTGCAGTCCACGCTCACTGTCTTAGCCGAGCGAATGTCCACCATCAGGATGAAAGCC
TCGGGGAAACGGCAGCTTTTGGAGGAGAAGTTGAATGATCAGCTGGAGGAACAAAGGCAGGAACAGGCCCTGCAG
AGGTATCGCTGTGAAGCCGATGAGCTGGACAGCTGGCTCTTGAGTACCAAGGCCACTCTGGACACTGCGCTGAGT
CCACCCAAGGAGCCCATGGACATGGAGGCCAGCTTATGGACTGCCAGAATATGCTGGTGGAAATAGAGCAGAAG
GTGGTGGCTTTATCAGAACTGTCACTCCACAATGAGAACCTGCTGCTGGAGGGCAAAGCTCACACCAAGGACGAG
GCCGAGCAGCTGGCTGGAAAGCTGAGAAGGCTCAAGGGGAGCCTGCTGGAGCTGCAGAGAGCCCTGCATGATAAG
CAGCTCAACATGCAGGGAACAGCACAGGAGAAGGAGGAGAGCGATGTTGACCTAACAGCCACGCAGAGCCCCGGC
GTCCAGGAATGGCTGGCCCAAGCTCGCACCACATGGACCCAGCAGCGGCAGAGCAGTCTCCAGCAACAAAAGAG
TTAGAACAGGAATTAGCCGAGCAGAAGAGTCTCCTTCGCTCAGTAGCCAGTCGTGGAGAGGAGATTCTAATTCAA
CATTCGGCGGCAGAGACCTCTGGTGATGCTGGCGAAAAACCTGATGTGTTATCCCAGGAGTTGGGGATGGAAGGG
GAGAAATCATCCGCTGAAGACCAGATGAGAATGAAATGGGAAAGCCTACATCAAGAATTTAGTACCAAGCAGAAA
CTACTACAGAATGTTCTGGAACAGGAACAAGAGCAAGTGCTTTATAGCAGGCCAAATCGACTCTTGTCTGGTGTG
CCACTGTACAAAGGGGACGTGCCAACCACAGATAAATCTGCAGTTACATCTTTGCTGGATGGACTGAACCAAGCC
TTCGAGGAGGTTTATCCCAGAGTGGAGGGGCAAAGAGGAGAGTATACACTTGGAGCAGAAGTTGTATGATGGA
GTCTCAGCCACCTCTACTTGGTTGGATGACGTTGAAGAACGTTTATTTGTTGCCACAGCACTTTTACCAGAAGAA
ACAGAGACTTGTCTCTTCAACCAAGAGATTCTTGCCAAAGACATTAAGGAAATGTCTGAAGAAATGGATAAGAAC
AAAACTTGTTTTCCCAAGCTTTTCCAGAGAATGGTGATAATCGAGATGTTATTGAAGATACTTTGGGTTGTCTT
TTGGGCAGGTTATCCTTGCTAGACTCAGTAGTGAATCAACGATGTCATCAGATGAAAGAAAGACTTCAGCAAATA
CTAAATTTCCAGAATGATCTGAAAGTGCTGTTTACATCACTGGCTGACAACAAATACATCATTCTGCAAAAACCTG
GCAATGTGTTTGAACAGCCGTAGCAGAACAAATAGAGGCAATACAACAGGCTGAAGATGGACTCAAAGAATTT
GATGCAGGAATCATTGAATTAAGAGGCGTGGTGACAAGCTACAGGTCGAGCAGCCGTCCATGCAAGAACTCTCC
AAGCTCCAGGACATGTATGATGAGCTGATGATGATCATTGGCTCCCGGAGGAGTGGTCTGAATCAGAACCTTACA
CTCAAGAGTCAGTATGAGAGGGCCCTACAAGATCTGGCTGACCTGCTAGAACTGGTCAGGAGAAGATGGCAGGA
GACCAGAAAATCATCGTGTCTTCCAAAGAGGAAATCCAGCAACTACTTGACAAACATAAGGAATACTTTTCAGGGC

2308/6881
FIGURE 2123B

CTGGAATCTCATATGATCTTGACTGAAACACTCTTCAGAAAGATAATCAGCTTTGCAGTCCAAAAGGAAACCCAG
TTCCATACAGAGCTGATGGCTCAGGCTTCTGCTGTACTGAAACGGGCTCACAAGAGGGGTGTGGAGCTGGAGTAC
ATTCTAGAGACGTGGTCCCCTCTGGATGAGGACCAGCAGGAGCTCAGCAGACAGCTGGAGGTGGTGGAAAGCAGC
ATCCCAAGCGTGGGTCTGGTGGAGGAGAACGAGGACAGGCTTATTGACCGCATAAACTCTACCAGCATTTAAAA
TCTAGCCTTAATGAATACCAGCCCAAATTATATCAAGTATTAGATGATGGGAAACGACTTCTGATATCCATCAGC
TGCTCAGATCTAGAAAGCCAACTAAATCAACTTGGAGAGTGCTGGCTAAGTAACACCAATAAAATGTCTAAGGAA
CTTCACAGACTGGAAACAATATTGAAACACTGGACCAGATATCAAAGTGAATCTGCAGATCTAATTCAGTGGTTA
CAATCTGCAAAAGACCGGCTAGAATTTTGGACTCAGCAATCTGTGACAGTCCCACAAGAGCTGGAAATGGTCCGT
GATCATCTAAATGCTTTCCCTGGAGTTTTCTAAAGAAGTGGATGCCCAATCTTCCCTGAAATCATCTGTTCTGAGT
ACTGGAAATCAGCTCCTTCGACTAAAAAAGGTGGACACAGCCACGCTGCGCTCTGAGCTGTGCGCATTGATAGC
CAGTGGACTGACCTGCTAACCAATATCCCAGCCGTCCAGGAGAAGCTCCACCAGCTCCAGATGGATAAACTGCCT
TCCCGCCATGCCATTTCTGAAGTCATGAGTTGGATTTCTCTAATGGAAAATGTTATTGAGAAGGATGAAGATAAT
ATTAAAAATTCCATAGGTTACAAGGCAATTCATGAATACCTTCAGAAATATAAGGGTTTTAAGATAGACATTAAAC
TGTAACAGCTGACAGTGGATTTTGTGAACAGTCCGTGCTACAAATCAGCAGTCAGGATGTGGAAAGTAAGCGT
AGTGATAAGACTGATTTTGTCTGAGCAACTTGGAGCAATGAATAAAAGTTGGCAAATCTGCAAGGTCTAGTAACT
GAGAAGATCCAGCTGTTGGAAGGCTTATTGGAATCTTGGTCAGAAATATGAAAATAATGTACAATGTCTGAAAACA
TGGTTTGAACCCAGGAAAAGAGACTAAAACAACAGCATCGAATTGGAGATCAGGCTTCTGTTCAAATGCACTG
AAAGACTGTCAGGATCTGGAAGATTTGATTAAAGCAAAAGAAAAAGAAGTAGAGAAAATTGAGCAGAATGGACTT
GCTTTGATTGAGAACAAAGAAAGAACGCTCTCTAGCATTGTCTATGAGCACACTGCGAGAGCTCGGCCAAACCTGG
GCAAATTTAGATCACATGGTTGGACAATTAAAGATACTGCTGAAATCAGTGCTTGACCAATGGAGTAGTCACAAA
GTGGCCTTTGACAAGATAAACAGTTACCTCATGGAGGCCAGATACTCTCTTTCCCGATTCCGTCTGCTGACTGGC
TCCTTAGAAGCTGTGCAAGTTTCAGGTGGACAATCTTCAGAAATCTCCAAGATGATCTGGAAAACAGGAAAGGAGC
TTACAGAAATTTGGCTCTATCACCAACCAATTATTAAGAGAGTGTACCCACCCGTGACAGAACTCTTACCAAT
ACACTGAAAGAAGTCAACATGAGATGGAATAACTTGCTGGAAGAGATTGCTGAGCAGCTACAGTCCAGCAAGGCC
CTACTTCAGCTTTGGCAAAGATACAAGGACTACTCCAACAGTGTGCTTCGACAGTTCAGCAGCAGGAGGATCGA
ACCAATGAGCTGTTGAAGGCAGCCACAAACAAGGACATTGCCGATGATGAGGTTGCCACATGGATTCAAGATTGC
AACGACCTCCTCAAAGGACTGGGCACAGTTAAAGATTCCCTCTTTTTTCTCCATGAGCTGGGAGAGCAACTGAAG
CAACAAGTGGATGCTTCCGCAGCATCAGCTATTCAATCGGATCAACTCTCTTTGAGTCAACACTTGTGTGCCCTG
GAGCAAGCTCTCTGCAAACAGCAGACTTCATTACAGGCTGGAGTTCTTGATTATGAAACCTTTGCCAAGAGTTTA
GAAGCTTTGGAGGCCTGGATAGTGAAGCTGAAGAAATACTACAAGGGCAGGACCCTAGCCACTCATCTGACCTC
TCCACAATCCAGGAAAGGATGGAAGAACTTAAGGGACAGATGTTAAAATTCAGCAGCATGGCTCCAGATTTAGAC
CGTCTAAATGAGCTTGATATAGGTTACCTTGAATGATAAGGAAATCAAAAGAAATGCAGAATCTGAACCGCCAT
TGGTCTCTGATCTCCTCTCAGACTACAGAAAGATTAGCAAGTTGCAGTCATTTTTGCTACAACATCAGACTTTC
TTGGAAAAATGTGAAACATGGATGGAATTCCTAGTTAGACAGAAACAAAAGTTAGCAGTAGAGATTTAGGAAAT
TATCAGCACCTTTTGAACAGCAGAGAGCACACGAGTTGTTTCAAGCCGAGATGTTTCAGTCGTCAGCAGATTTTG
CACTCAATCATTATTGATGGGCAACGTCTTCTAGAACAAGGTCAAGTTGATGACAGGGATGAATTCAACCTGAAA
TTGACACTCCTCAGTAATCAATGGCAGGGAGTGATTGCGAGGGCCAGCAGAGGCGGGGATCATTGACAGCCAG
ATTGCGCCAGTGGCAGCGCTATAGGGAGATGGCAGAAAAGCTTCGTAAATGGTTGGTTGAAGTGCCTACCTCCCC
ATGAGTGGTCTCGGAAGTGTTTCTATACCACTGCAACAAGCAAGGACCCTCTTTGATGAAGTGCAGTTCAAAGAA
AAAGTGTTTTCTGCGGCAACAAGGCAGCTACATCCTGACTGTGGAGGCTGGCAAGCAACTCCTTCTCTCGGCGGAC
AGTGGCGCTGAGGCCGCTTGCAGGCCGAACCTCGCTGAAATCCAAGAGAAATGGAAATCAGCCAGCATGCGGCTG
GAAGAACAGAAGAAAAAACTAGCCTTCTTGTGAAAGACTGGGAAAAATGTGAGAAAGGAATAGCAGATTCCTTG
GAGAACTACGAACCTTTCAAAAAGAAGCTTTTCGAGTCTCTCCCGGATCACCATGAAGAGCTCCATGCAGAACAA
ATGCGTTGCAAGGAATTAGAAAATGCAGTTGGGAGCTGGACAGATGACTTGACCCAGTTGAGCCTGCTGAAGGAC
ACCCTCTCTGCCTATATCAGTGCTGATGATATCTCCATTCTTAATGAACGCGTAGAGCTTCTGCAAAGGCAGTGG
GAAGAACTATGCCACCAGCTCTCCTTAAGGCGGCAGCAATAGGTGAAAGATTGAATGAATGGGCAGTCTTCAGT
GAAAAGAACAAAGGAATCTGTGAGTGGTTGACTCAAATGGAAAGCAAAGTTTCTCAGAATGGAGACATTCTCATT
GAAGAAATGATAGAGAAGCTCAAGAAGGATTATCAAGAGGAAATTGCTATTGCTCAAGAGAACAAAATACAGCTC

2309/6881
FIGURE 2123C

CAACAAATGGGAGAACGACTTGCTAAAGCCAGCCATGAAAGCAAAGCATCTGAGATTGAATACAAGCTGGGAAAG
GTCAACGACCGGTGGCAGCATCTCCTGGACCTCATTGCAGCCAGGGTGAAGAAGCTGAAGGAGACCCTGGTAGCC
GTGCAGCAGCTTGATAAGAACATGAGCAGCCTGAGGACCTGGCTCGCTCACATCGAGTCAGAGCTGGCCAAGCCA
ATAGTCTACGATTCCCTGTAACTCGGAAGAAATACAGAGAAAGCTTAATGAGCAGCAGGAGCTTCAGAGAGACATA
GAGAAGCACAGTACAGGTGTTGCATCTGTCTCAACCTGTGTGAAGTCCTGCTGCACGACTGTGACGCCTGTGCC
ACTGATGCCGAGTGTGACTCTATACAGCAGGCTACGAGAAACCTGGACCGGCGGTGGAGAAACATTTGTGCTATG
TCCATGGAAAGGAGGCTGAAAATCGAAGAGACGTGGCGATTGTGGCAGAAATTTCTGGATGACTATTCACGTTTT
GAAGATTGGCTGAAGTCTTCAGAAAGGACAGCTGCTTTTCCCAGCTCTTCTGGGGTGATCTATACAGTTGCCAAG
GAAGAACTAAAGAAATTTGAGGCTTTCCAGCGACAGGTCCACGAGTGCCTGACGCAGCTGGAACTGATCAACAAG
CAGTACCGCCCGCTGGCCAGGGAGAACCGCACTGATTACGCATGTAGCCTCAAACAGATGGTTTCACGAAGGCAAC
CAGAGATGGGACAACCTGCAAAAGCGTGTACCTCCATCTTGCGCAGACTCAAGCATTTTATTGGCCAGCGTGAG
GAGTTTGAGACTGCGCGGGACAGCATTCTGGTCTGGCTCACAGAGATGGATCTGCAGCTCACTAATATTGAACAT
TTTTCTGAGTGTGATGTTCAAGCTAAAATAAAGCAACTCAAGGCCTTCAGCAGGAAATTTCACTGAACCACAAT
AAGATTGAGCAGATAATTGCCCAAGGAGAACAGCTGATAGAAAAGAGTGAGCCCTTGGATGCAGCGATCATCGAG
GAGGAACTAGATGAGCTCCGACGGTACTGCCAGGAGGTCTTCGGGCGTGTGGAAAGATACCATAAGAAACTGATC
CGCCTGCCTCTCCCAGACGATGAGCACGACCTCTCAGACAGGGAGCTGGAGCTGGAAGACTCTGCAGCTCTGTCTG
GACCTGCACTGGCAGCAGCCGCTCTGCAGACAGCCTGCTTTCTCCACAGCCTTCTCCAATCTCTCCCTCTCGCTC
GCTCAGCCCCCTCCGGAGCGAGCGGTGAGGACGAGACACCCCGGCTAGTGTGGACTCCATCCCCCTGGAGTGGGAT
CACGACTATGACCTCAGTCGGGACCTGGAGTCTGCAATGTCCAGAGCTCTGCCCTCTGAGGATGAAGAAGGTCAG
GATGACAAAGATTTCTACCTCCGGGGAGCTGTTGGCTTATCAGGGGACCACAGTGCCCTAGAGTCACAGATCCGA
CAACTGGGCAAAGCCCTGGATGATAGCCGTTTTTCAGATACAGCAAACCGAAAATATCATTGCGAGCAAAACTCCC
ACGGGGCCGGAGCTAGACACCAGCTACAAAGGCTACATGAAACTGCTGGGCGAATGCAGTAGCAGTATAGACTCC
GTGAAGAGACTGGAGCACAACTGAAGGAGGAAGAGGAGAGCCTTCTGGCTTTGTTAACCTGCATAGTACCGAA
ACCCAAACGGCTGGTGTGATTGACCGATGGGAGCTTCTCCAGGCCCAGGCATTGAGCAAGGAGTTGAGGATGAAG
CAGAACCTCCAGAAGTGGCAGCAGTTTAACTCAGACTTGAACAGCATCTGGGCCTGGCTGGGGGACACGGAGGAG
GAGTTGGAACAGCTCCAGCGTCTGGAACCTCAGCACTGACATCCAGACCATCGAGCTCCAGATCAAAAAGCTCAAG
GAGCTCCAGAAAGCTGTGGACCACCGCAAAGCCATCATCCTCTCCATCAATCTCTGCAGCCCTGAGTTCACCCAG
GCTGACAGCAAGGAGAGCCGGGACCTGCAGGATCGCTTGTGCGCAGATGAATGGGCGCTGGGACCGAGTGTGCTCT
CTGCTGGAGGAGTGGCGGGGCTGCTGCAGGATGCCCTGATGCAGTGCCAGGGTTTCCATGAAATGAGCCATGGT
TTGCTTCTTATGCTGGAGAACATTGACAGAAGGAAAAATGAAATTGTCCCTATTGATTCTAACCTTGATGCAGAG
ATACTTCAGGACCATCACAAACAGCTTATGCAAATAAAGCATGAGCTGTTGGAATCCCAACTCAGAGTAGCCTCT
TTGCAAGACATGTCTTGCCAACCTACTGGTGAATGCTGAAGGAACAGACTGTTTAGAAGCCAAAGAAAAAGTCCAT
GTTATTGGAATCGGCTCAAACCTCTCTTGAAGGAGGTGAGTCGTCATATCAAGGAAGTGGAGAAGTTATTAGAC
GTGTCAAGTAGTCAGCAGGATTTGTCTTCTGGTCTTCTGCTGATGAACTGGACACCTCAGGGTCTGTGAGTCCC
ACATCAGGAAGGAGCACCCCAAACAGACAGAAAACGCCACGAGGCAAGTGTAGTCTCTCACAGCCTGGACCCCTCT
GTCAGCAGTCCACATAGCAGGTCCACAAAAGGTGGCTCCGATTCTCCCTTTCTGAGCCAGGGCCAGGTCCGTCC
GGCCGCGGCTTCTGTTCAGAGTCTTCCGAGCAGCTCTTCCCTTCAGCTTCTCCTGCTCCTCCTCATCGGGCTT
GCCTGCCTTGTACCAATGTCAGAGGAAGACTACAGCTGTGCCCTCTCCAACAACCTTGGCCGGTCATTCCACCCC
ATGCTCAGATACACGAATGGCCCTCCTCCACTCTGAACTAAGCAGATGCCATCTGCAGAAGTGTGGTAGCATAA
GGAGGATCGGGTCATAAGCAATCCCAAACCTACCAACAAGAGGACCTTGATCTTGCGGAAAGCCCTCGGTGTGGCA
GCTTTAGCCCTCCTCCAGATCACATGTGTGCAAATTATGGCTTCAGAGGTGGAAGATAAACAGTGACGGGGGAAC
AAACAGACAACAAGAAGGTTTGGAAGAAATCTGGTTTGAGACTCTGAACCTTAGCACTAAGGAGATTGAGTAAGG
ACCTCCAAAGTTCCCCGGACTCATGAATTCTGGGCCCTTGGCCCATCTGTGCACAGCCAAGGACTTCAGTAGAC
CATCTGGGCAGCTTTCCCATGGTGCTGCTCCAACCATCAGATAAATGACCCTCCCAAGCACCATGTCAGTGTGCT
ACAATCTACCAACCAACCAGTGCTGAAGAGATTTTAGAACCTTGTAACATACAATTTTAAAGAGCTTATATGGCA
GCTTCCTTTTTACCTTGTTTTTCTTTGGGGCATGATGTTTTAACCTTTGCTTTAGAAGCACAAGCTGTAAATCTA
AAAGGCACTTTTTTTTAGAGGTATAAAGAAAACTAGATGTAATAAATAAGATCATGGAAGGCTTTATGTGAAAA
AAGTTGAATGTTATAGT

2310/6881
FIGURE 2124A

GCAGAGTCTGAGTCCCACCTCCGCACCCCCACCCCTCTGTCTGGTACAGCTTACCAAACCAAAGTGCCCCAAAGCCGTG
ACATCCCGGCCGGCGGCTCGCAGGCCCCCGCCCTCCGCACGTACAGGCCGCCGGGTGCAGTGCCCCCTAGGGGCC
CCTGGGACGAGGAGGAAGCGCCAGGTCTTCCCGCCGCCGCCGCCGCCGCCCGCTGCTCCCTTGGCACGCGC
CCCGCCGCCCTCGGCAGCCGCAGCTCCGTGTCCCTGAGAACCAGCCGTCCCGCGCCATGGGCACGCGTCTGCCG
CTCGTCCCTGCGCCAGCTCCGCCGCCGCCGCCAGCCCCGGGCCCTCCGCGCCGCCCTCCGTGTGCCCTGTGCGCT
AGCAGCGGCGGCGGCGGAGGCGGCGGCGGTGGCCGGGAGGGCCTGCTTGGACAGCGGCGGCCGAGGATGGCCAG
GCCCGGAGCAGCTGCAGCCCCGGCGGCCGAACGCCCGCGGCGCGGGACTCCATCGTCAGAGAAGTCATTCAAGAT
TCAAAAGAAGTTCTAAGTTTATTGCAAGAAAAAACCTGCCTTCAAGCCGGTTCTTGCAATTATCCAGGCAGGT
GACGACAACCTTGATGCAGGAAATCAACCAGAAATTTGGCTGAGGAGGCTGGTCTGAACATCACTCACATTTGCCTC
CCTCCAGATAGCAGTGAAGCCGAGATTATAGATGAAATCTTAAAGATCAATGAAGATACCAGAGTACATGGCCTT
GCCCTTCAGATCTCTGAGAACTTGTTTAGCAACAAAGTCTCAATGCCTTGAAACCAGAAAAAGATGTGGATGGA
GTAACAGACATAAACCTGGGGAAGCTGGTSCGAGGGGATGCCCATGAATGTTTTGTTTACCTGTTGCCAAAGCT
GTAATTGAACCTTCTTGAAAAATCAGTAGGTGTCAACCTAGATGGAAAGAAGATTTGGTAGTGGGGGCCATGGG
TCTTTGGAAGCTGCTCTACAATGCCTGTTCCAGAGAAAAGGGTCCATGACAATGAGCATCCAGTGGAAAACACGC
CAGCTTCAAAGCAAGCTTCACGAGGCTGACATTGTGGTCTTAGGCTCACCTAAGCCAGAAGAGATTTCCCTTACT
TGGATACAACCAGGAACCTACTGTTCTCAACTGCTCCCATGACTTCCTGTGAGGGAAGGTTGGGTGTGGCTCTCCA
AGAATACATTTTGGTGGACTCATTGAGGAAGATGATGTGATTCTCCTTGCTGCAGCTCTGCGAATTCAGAACATG
GTCAGTAGTGGAAGGAGATGGCTTCGTGAACAGCAGCACAGGCGGTGGAGACTTCACTGCTTGAAACTTCAGCCT
CTCTCCCTGTGCCAAGTGACATTGAGATTTCAAGAGGACAAACTCCAAAAGCTGTGGATGTCTTGCCAAGGAG
ATTGGATTGCTTGACAGATGAAATTGAAATCTATGGCAAAGCAAAGCCAAAGTACGTTTGTCCGTGCTAGAAAAGG
TTAAAGGATCAAGCAGATGGAAAATACGTCTTAGTTGCTGGGATCACACCCACCCCTCTTGAGAAGGGAAGAGC
ACAGTCACCATCGGGCTTGTGCAGGCTCTGACCGCACACCTGAATGTCAACTCCTTTGCCTGCTTGAGGCAGCCT
TCCCAAGGACCGACGTTTGGAGTGAAAGGAGGAGCCGCGGGTGGTGGATATGCCAGGTATCCCATGGAGGAG
TTCAACCTTCACTTGACTGGAGACATCCACGCCATCACCGCTGCCAATAACTTGCTGGCTGCCGCCATCGACACG
AGGATTCTTCATGAAAACACGCAAACAGATAAGGCTCTGTATAATCGGCTGGTTCCTTTAGTGAATGGTGTGAGA
GAATTTTCAGAAATTCAGCTTGCTCGGCTAAAAAACTGGGAATAAATAAGACTGATCCGAGCACACTGACAGAA
GAGGAAGTGAGTAAATTTGCCCCGTCTCGACATCGACCCATCTACCATCACGTGGCAGAGAGTATTGGATACAAAT
GACCGATTTCTACGAAAAATAACCATCGGGCAGGGAACACAGAGAAGGGCCATTACCGGCAGGCGCAGTTTGAC
ATCGCAGTGGCCAGCGAGATCATGGCGGTGCTGGCCCTGACGGACAGCCTCGCAGACATGAAGGCACGGCTGGGA
AGGATGGTGGTGGCCAGTGACAAAAGCGGGCAGCCTGTGACAGCAGATGATTTGGGGGTGACAGGTGCTTTGACA
GTTTTGATGAAAGATGCAATAAAACCAAACCTGATGCAGACCCTGGAAGGGACACCTGTGTTCTGTGCATGCGGGC
CCTTTTGCTAACATTGCTCACGGCAACTCTTCAGTGTTGGCTGATAAAATTGCCCTGAACTGGTTGGTGAAGAA
GGATTTGTAGTGACCGAAGCTGGCTTTGGTGTGACATCGGAATGGAGAAATTTCTCAACATCAAGTGCCGAGCT
TCCGGCTTGGTGCCCAACGTGGTTGTGTTAGTGGCAACGGTGCAGCTCTGAAGATGCATGGAGGCGGGCCAAGT
GTAACGGCTGGTGTTCCTCTTAAGAAAGAATATACAGAGGAGAACATCCAGCTGGTGGCAGACGGCTGCTGTAAC
CTCCAGAAGCAAATTCAGATCACTCAGCTCTTTGGGGTTCCCGTTGTGGTGGCTCTGAATGTCTTCAAGACCGAC
ACCCGCGCTGAGATTGACTTGGTGTGTGAGCTTGCAAAGCGGGCTGGTGCCTTTGATGCAGTCCCCTGCTATCAC
TGGTCCGTTGGTGGAAAAGGATCGGTGGACTTGGCTCGGGCTGTGAGAGAGGCTGCGAGTAAAGAAGCCGATTC
CAGTTCCCTGTATGATGTTTCAAGTTCCAATTGTGGACAAGATAAGGACCATTGCTCAGGCTGTCTATGGAGCCAAA
GATATTGAACTCTCTCCTGAGGCACAAGCCAAAATAGATCGTTACACTCAACAGGGTTTTTGGAAATTTGCCCATC
TGCATGGCAAAGACCCACCTTTCTCTATCTCACCAACCTGACAAAAAAGGTGTGCCAAGGGACTTCATCTTACCT
ATCAGTGACGTCCGGGCCAGCATAGGCGCTGGGTTCAATTACCCTTTGGTCCGAACGATGAGCACCATGCCAGGA
CTGCCACCCGGCCCTGCTTTTATGACATAGATCTTGATACCGAAACAGAAAGTTAAAGGCTTGTCTAAGTG
GACAAGGCTCTCACAGGACCCGATGCAGACTCCTGAAACAGACTACTCTTTGCCTTTTTGCTGCAGTTGGAGAAG
AAACTGAATTTGAAAAATGTCTGTTATGCAATGCTGGAGACATGGTGAAATAGGCCAAAGATTTCTTCTTCGTTT
AAGATGAATTTCTGTTTACAGTGGAGTATGGTGTTCGGCAAAGGACCTCCACCAAGACTGAAAGAACTAATTTA
TTTCTGTTTCTGTGGAGTTTCCATTATTTCTACTGCTTACACTTTAGAATGTTTATTTTATGGGGACTAAGGGAT
TAGGAGTGTGAACTAAAAGGTAACATTTTCCACTCTCAAGTTTTTCTACTTTGTCTTTGAACTGAAAAATAACATG

2311/6881
FIGURE 2124B

GATCTAGAAAACC

2312/6881
FIGURE 2125

MVSSGRRWLREQQHRRWRLHCLKLQPLSPVPSDIEISRGQTPKAVDVLAK EIGLLADEIEIYGKSKAKVRLSVLE
RLKDQADGKYVLVAGITPTPLGEGKSTVTIGLVQALTAHLNVNSFACLRQPSQGPTFGVKGGAAGGGYAQVIPME
EFNLHLTGDIHAITAANNLLAAIDTRILHENTQTDKALYNRLVPLVNGVREFSEIQLARLKIIRNWE

2313/6881

FIGURE 2126

ACTCTTGGGAAAAC TGCTGGGCACCGTCGTCGCGCTGAAGGTGGTTCTGTACCTGCTCCGAGTGTGCTTAGCGAT
GGCCTGGAAATCCGGCGGCGCCAGCCACTCGGAGCTAATCCACAATCTCCGCAAAAATGGAATCATCAAGACAGA
TAAAGTATTTGAAGTGATGCTGGCTACAGACCGCTCCCACTATGCAAAATGTAACCCATACATGGATTCTCCACA
ATCAATAGGTTTCCAAGCAACAATCAGTGCTCCACACATGCATGCATATGCGCTAGAACTTCTATTTGATCAGTT
GCATGAAGGAGCTAAAGCTCTTGATGTAGGATCTGGAAGTGGAAATCCTTACTGCATGTTTTGCACGTATGGTTGG
ATGTACTGGAAAAGTCATAGGAATTGATCACATTAAAGAGCTAGTAGATGACTCAGTAAATAATGTCAGGAAGGA
CGATCCAACACTTCTGTCTTCAGGGAGAGTACAGCTTGTGTGGGGGATGGAAGAATGGGATATGCTGAAGAAGC
CCCTTATGATGCCATTTCATGTGGGAGCTGCAGCCCCGTGTGTACCCCAGGCGCTAATAGATCAGTTAAAGCCCGG
AGGAAGATTGATATTGCCTGTTGGTCCTGCAGGCGGAAACCAAATGTTGGAGCAGTATGACAAGCTACAAGATGG
CAGCATCAAAATGAAGCCTCTGATGGGGGTGATATACGTGCCTTTAACAGATAAAGAAAAGCAGTGGTCCAGGTG
GAAGTGAATTTTATCTTCTGCTCTTTCTTCTTCCACACATGCAAGGGATGAATTGTAAAAGCAACATCAGCTTGAC
CAGTATAAAATTACAGTGGATTGCTCATCTCAGTCCTCAAAGCTTTTTGAAAACCAACACCATCACAGCTTGTTT
TGGACTTTGTACACTGTTATTTTTCAGCATGAAAATGTGTGTTTTTTTAGGGTTTCTGATTCTTCAAAGAGGCAC
AGAGCCAAATTGGTAGAGGAAGGATGCAAAGTATAAATTTGTGTAATATTACTTTAACATGCCCATATTTTACTT
GGAAATATTAAAAGAAAGGGTTCTGTAAAATGGAAAACCTTAGTTTGTGAATTGATTTTGAGGAGTGGTTTTTCTT
TTCTTGGACACTTAATTCTGTTCTGATATTAATTTATCAGATTGCTTTTGTGCATTGGATAACACCACCATTAC
AAGTTAAGATTCTTGGTATTTGGATATCTGTTAGATGCTACTAAGAAAATAGAGATGAGCTTTCTTTTTAAAGCT
TTTGATGTGGTGTTCATAGAATAGCATGTTGTAGATACAATCAGCTGCTTTGTTACCTTAAAACTAGGCATTTGTA
AATATTAAACCTTAAGATGGCAGGTGATGTCTGTAAACACTCAGCTGTTTCAGATTGGACATAACTGACTTAGTT
CTTCCCTTCTCTCTCTCTCAAAATTATAGGAGACTTGTAGTTTAGTGTGGTTTTCTGTTTCTAATTTGCTGCTGA
TAATGTATATGAACCTAACATGCTGTGTAAGCTGTGTCCTAGTTCTTGAACAGTTTATGCAGTGCTGCTTTGCCA
AATAAAGTTAAAAGTAAAAGAGGC

2314/6881
FIGURE 2127

MAWKSGGASHSELIHNLKNGIIKTDKVFVMLATDRSHYAKCNPYMDSPQSIGFQATISAPHMHAYALELLFDQ
LHEGAKALDVGSGSGILTACFARMVGCTGKVIKELVDDSVNNVRKDDPTLLSSGRVQLVVGDGRMGYAE
APYDAIHVGAAAPVVPQALIDQLKPGGRLILPVGPAGGNQMLEQYDKLQDGSIKMKPLMGVIYVPLTDKEKQWSR
WK

2315/6881
FIGURE 2128A

ACTCTGGCAAAGTTGCGGGGCGCGGGGAGCTGTGCGGGGACGCGGCCCTCGGGAGGACGTGGCCCCGGCCCCCG
CCCCGAGTGGGCCCCGACCTC**ATG**GGCCCTGAGCAAAGGGCTGCGGCTGCTGGGGCGCCTGGGGGCCGAGGGGGAC
TGTAGCGTGCTGCTGGAGGCGCGGCCGCGACGACTGCCTGCTGTTTCGAGGCCGGCACGGTGGCCACGCTGGCT
CCAGAAGAAAAGGAAGTCATTAAAGGACAGTATGGCAAGCTCACGGACGCGTACGGCTGCCTGGGGGAGCTGAGG
CTGAAATCTGGTGGCACGTCTCTGAGCTTCCTGGTGTGGTGACAGGCTGCACATCTGTGGGCAGAATTCCAGAT
GCTGAAATCTACAAAATCACTGCCACTGACTTTTACCCTCTTCAGGAAGAGGCCAAGGAGGAGGAACGCCCTCATA
GCTTTGAAGAAAATCCTCAGCTCGGGGGTGTTCATTTCTCATGGCCAAACGATGGGTCTCGCTTTGACCTGACT
GTCCGCACGCAGAAGCAGGGGGATGACAGCTCTGAATGGGGGAATCCTTCTTCTGGAACCAGCTGTTGCACGTG
CCCTTGAGGCAGCACCAAGGTGAGCTGCTGTGACTGGCTGCTGAAGATCATCTGCGGGGTGGTCAACCATCCGCACC
GTGTATGCCTCCCAACAAGCAGGCCAAGGCCTGCCTCGTCTCTCGCGTTAGCTGTGAGCGCACAGGCACTCGCTTC
CACACCCGTGGCGTGAACGACGACGGCCATGTGTCCAACCTTCGTGGAGACAGAGCAGATGATTTACATGGACGAT
GGAGTGTATCTTTTGTCCAGATCAGAGGCTCCGTTCCGCTGTTCTGGAACAGCCAGGGCTTCAGGTTGGCTCC
CATCATCTGAGACTCCACAGAGGCTCGAAGCCAATGCCCTGCTTTGACAGGCACATGGTGCTTCTGAAGGAG
CAGTACGGGCAGCAGGTGGTCTGTAACCTTCTGGGAAGCAGAGGCGGAGAGGAGGTGCTCAACAGAGCCTTCAAG
AAGCTGCTCTGGGCTTCTTGCCACGCGGGCGACACGCCTATGATCAATTTTGACTTCCATCAGTTTGCCAAAGGT
GGGAAGCTAGAGAAAATTGGAGACCCTCTTGAGGCCACAGTTAAAGCTGCACTGGGAAGACTTCGATGTGTTTACA
AAGGGGGAGAAGCTCAGTCCACGTTTTTCAGAAAGGCACCTTTCGGATGAACTGTCTTGACTGCCTGGACCGAACC
AACACTGTGCAGAGCTTCATCGCGCTCGAGGTCTGCATCTGCAGCTCAAGACCCTGGGGCTGAGTTCAAAACCC
ATCGTTGACCGCTTTGTGGAGTCTTCAAAGCCATGTGGTCTCTGAATGGCCACAGCCTGAGCAAGGTGTTTACA
GGCAGCAGAGCCCTGGAAGGGAAGGCCAAGGTGGGGAAGCTGAAGGATGGAGCCCGTCCATGTCTCGAACCATC
CAGTCCAACCTTCTTCGACGGGGTGAAGCAGGAGGCCATCAAGCTGCTGCTGGTTGGGGACGTCTACGGCGAGGAG
GTGGCAGACAAAGGGGGCATGTGCTGGACAGCACGGCGCTCCTGGTGAATCCAGGATCCTGAAAGCTATGACT
GAGCGTCAGTCCGAATTCACAAATTTCAAGCGGATCCGGATTGCTATGGGGACCTGGAACGTGAACGGAGGAAAG
CAGTTCCGGAGCAACGTGCTCAGGACGGCGGAGCTGACAGACTGGCTGCTCGACTCGCCCCAGCTCTCGGGAGCT
ACCGACTCCCAGGATGACAGCAGCCCAGCTGACATATTTGCTGTGGGGTTTGAAGAGATGGTGGAATTGAGCGCA
GGGAATATTGTCAATGCCAGTACTACCAACAAGAAGATGTGGGGTGAACAGCTTCAGAAAGCCATCTCACGCTCT
CATAGATACATTCTGTTGACTTCGGCACAGCTGGTGGGCGTCTGTCTTTATATCTTTGTACGTCCATACCATGTC
CCGTTTCATCAGGGACGTAGCCATCGACACAGTGAAGACGGGCATGGGGGGCAAGGCGGGGAACAAGGGCGCCGTC
GGCATCCGCTTCCAGTTCCACAGCACCAGCTTCTGCTTCATATGTAGTCACCTGACGGCCGGGACGTCCCAGGTG
AAGGAGCGGAATGAAGACTACAAGGAGATCAACCCAGAACTCTGCTTCCCAATGGGGAGAAATGTTTTTTCTCAT
GATTATGTATTTTGGTGTGGCGATTTCAACTACCGCATTGATCTTACTTATGAAGAAGTCTTCTATTTTGTAA
CGCCAAGACTGGAAGAACTTCTGGAATTTGATCAACTACAGCTACAGAAATCAAGTGGAATAATTTTAAAGGAC
TTTCACGAAGGAGCCATTAACCTTTGGACCCACCTACAAGTATGACGTTGGCTCAGCCGCTACGATACAAGCGAC
AAATGCCGCACCCCCGCTGGACAGACAGGGTGCTGTGGTGGAGGAAGAAACATCCCTTTGATAAAACAGCTGGA
GAACTCAACCTTCTAGACAGTGATCTAGATGTTGACACCAAAGTCAGACACACCTGGTCTCCTGGTGCCCTGCAG
TATTATGGTTCGTGCGGAGCTACAAGCGTCTGATCACAGACCTGTGCTGGCGATCGTGGAGGTGGAAGTTTCAGGAA
GTCGATGTGGGTGCTCGGGAGAGGGTTTTCCAGGAAGTGTCTCCTTCCAGGGCCCCCTGGATGCCACTGTTGTA
GTAAACCTTCAATCACCGACCTTAGAAGAGAAAAACGAGTTTCCAGAGGACCTGCGTACTGAGCTCATGCAGACC
TTGGGGAGTTATGGGACAATTGTTCTTGTGAGGATCAACCAAGGGCAGATGCTGGTAACTTTTGCAGACAGTCAC
TCGGCTCTCAGTGTCTGACGTGGACGGTATGAAGGTGAAAGGCAGAGCAGTGAAGATTAGACCGAAGACCAAG
GACTGGCTGAAAGGTTTTCGAGAGGAGATCATTCGGAACGAGACAGCATGGCCCCCGTGTCTCCCACTGCCAAC
TCCTGTTTGTGAGGAGAACTTTGACTTCACAAGTTTGGACTATGAGTCAGAAGGGGATATTCTTGAAGACGAT
GAAGACTACTTGGTGGATGAATTCAATCAGCCTGGAGTCTCGGACAGTGAACTCGGGGGAGACGACCTCTCTGAT
GTCCCCGGCCCCACAGCACTGGCTCCTCCCAGCAAGTCACCTGCTCTACCAAAAAGAGCAGCATCCAACGTAC
AAAGATGACGCGACCTGGTGGAGCTCAAGCGGGAGCTGGAAGCCGTGCGGGAGTTCCGCCACCGTTCTCCGAGC
AGGTCTCTGTGCGTCCCCAACCGGCCTCGGCCACCTCAACCCCCGAGAGACCCCCCTCCAACCGGTTTAAATG
GTGAAAAAGTCGGCTTCAGATGCGTCCATCTCCTCCGGCACCCATGGACAGTATTCAATTTTGCAGACGGCAAGA
CTTCTACCAGGAGCACCTCAGCAACCTCCCAAGGCTCGGACTGGAATAAGTAAACCTTATAATGTCAAGCAGATC

2316/6881
FIGURE 2128B

AAAACCACCAATGCCCAGGAGGCAGAAGCAGCAATCCGGTGTCTCCTGGAAGCCAGAGGAGGTGCCTCCGAAGAA
GCCCTAAGTGCCGTGGCCCCAAGGGACCTTGAAGCATCCTCTGAACCAGAGCCCACACCGGGGGCAGCCAAACCA
GAGACCCACAGGCGCCCCACTCCTTCCCCGTCGGCCCCACCCAGAGTTCTTGCCATCAAGAAGCCAACCTTG
AGAAGGACAGGAAAGCCCCCTGTACCGGAAGAAGCAGTTTGAGCAACAGACTGTCCATTTTACAATCGGGCCCCCG
GAGACAAGCGTTGAGGCCCCCTCCTGTGTCGACAGCCCCCTCGAGTCCCTCCTGTTCCCAAACCAAGAACATTTTACG
CCTGGGAAAGCTGCAGAGAGGCCAAGCCACAGGAAGCCAGCATCAGACGAAGCCCCCTCCTGGGGCAGGAGCCTCT
GTGCCACCACCTCTGGAGGCGCCGCTCTTGTGCCAAGGTACCCCCGAGGAGGAAGAAGTCAGCCCCCGCAGCC
TTCCACCTGCAGGTCTGTGAGAGCAACAGCCAGCTTCTCCAGGGCCTCACTTACAATAGCAGTGACAGCCCCCTCT
GGGCACCCACCTGCCGCGGGCACCCTCTTCCCAAGGGGACTTTCTCAGCACTTCATCTGCTACAAGCCCCGAC
AGCGATGGCACCAAAGCGATGAAGCCAGAGGCAGCCCCACTTCTTGGTGATTATCAGGACCCCTTCTGGAACCTT
CTTACACACCTAACTGTTGAATAACACTTGGCTTTCTAAGAGCTCAGACCCCTTTGGACTCAGGAACCAAGGAGC
CCCAAAGAGATCCCATAGACCCAGTGTGAGCTGGCGCTTCAGCTGCCAAGGCAGAGCTGCCACCAGATCATGAA
CACAAAACCTTAGGTCACTGGGTGACAATCAGTGACCAAGAAAAGAGGACAGCACTGCAGGTGTTTTGACCCACTG
GCAAAAACATGAAGTGAAGGCTGCAGTCTATAGAATGCATACCTTCTCCTCCTCTAGACATCCCTC
CACCAGAAGAGACATCTATTTAAAGGCACACTGGCCAAAACGTTTGTGCATCTGTCACTCTCGTGTAGTTTACAA
AAATCGTGTCTCTTATTCAGTAAGATGGTTACTCAGCCACCAAAAATATATTTCACTCAAGGCTTGTACATCTGAA
GTTTGTCTTCAAGGAATGGGAACCTTCTGTAAATTCGGTGTATGGATTTTAAGAAAGGAATCTAGCCAATGA
GGTCCAAGAAGTTCTCACCATTGAATTTTTAAATGGCTGTTTCAAGTTCATGTTGTACGTGATGGAGATTTGTCTT
TTGTTTTATTTGCATTTTACAGATTTGGTATAACATTTTGGGGAGCCACCTGAAGGTTGATGTATAAAGTAAGGA
TTAGAGAAAGAGGTCTGTTGTGACCATTAGTAGCTGTCTGGCCCACTTAAACAAGGTTACAAAAATCAGAGTCG
GAAGCAGCCAAATAGGTCAACCTAATGACTAGACTGTACATTCCCATGAGCCTTCATGTTTAAGTGTGTACATGT
GCGTTAACCTTGATGATGCGTGAATCCCGAGGGAGCCGGTGGCATAACCGTTAGCTTAACCTTAGCTTAAACTA
GCTGAAGGCTCCTGTGCCATGTCTTAGACATTGCATGCCCTATCAATTACTATAATCCTGAGCCATGGTGTGCTA
CTGAAACCAATTTTTATCCACCATCTAGTCTTATTAATGAAACCTCACGGATCCTTTGTTCCGCTTATATTCC
ATGCATACCACATAAAAGCACACAGTGCGAAAACCTTTGCTGATACGCGATATTGATTCTCATTGTTAGAATATG
GAGAGTGTTCAGCCTCGTCTGTCCGGCTGGAGCTTCGGGATGGAAAGTGCTATGTGTCCCTGCATATAAGAATC
ACCAGGCCAGTGTTCCTGGGTTTGCTTGTCTATATGTTTGTCTATATTTTTTGCCTATACATTTTTTCCACGTTT
CCAACAGCACTTCTCACCTATTCAATAACTGAAAAGACATTACCATAGTGCTTTACATTTTTTAAAGTAATGTTA
CAAGGTCTGGAATCCATTTGGAGCAGATACCGTGTTTTTCGCTATTTAATAAGAAGTTCAGTAGTGAAATCTTACT
GTACCGCTGTGTATCTGGGAGCCTCGTACAGAGGCTCGCACAGCAGTGATCAAGTGTATCCCTTACGTGACT
GGGGGATGTCTGTCTAAAGCTGACTGCTAGGATAGTAAGGATCATCTTGCTGGGCTATGCCACTGTCTTGTT
ACCAATTAGACATCTGGAATTTTACATAATTAGTTTTTCAATTGTCACTGTCAAGATATATTGCAGATTACTTAAATAT
GGCCATCAAAACAAAAGTTACAACACGTATCTTTTTCATCTGAAAACATAACCTGGAAAAGGATAAAAAA
AAGGAATCCGTGACCCACAGAGCTAGACAGATAAGATGCATAGTTGACCAGTCATAAAAGGCGGTGTTTAGGTGA
TCAGGATGCCGTTGGTGGCATTTACGTGCTTTATATGATTTTTTACCTCTGTAAACAAACACAAGAAATAAACAGAA
TGGTCTTAACAGAGTTTGGGGGAGAGAGCAAGATGGGTTTCTTGGAGAAGCTGATTGCCAAGATGCACATCGC
TATTAACAGCCAGAGTCATAAATGAAATGAAATTGAAGAATTCATTCAAATGCTCTTTTCCCTATAACCTCTTTT
CTCACCAAAAAGGAGATAAATTTGAAAACAGATAAATGTAACAACCAGTCAAAGAAGCAGGGGAAAAGTAAGCTC
CTCCAAAGTTGCTTGCAAGTGCTGGAAATAGATCTCATTTTTAGGTTTTCTCTTCGTTCCAGATACCAAATAAATG
GGACAGAGAATAAAATTTTTGTTAAAAATATGTGCTCATCTCCTAAGTAGCTCTTCAGAGTCTGACCGTAAGTAAA
AACACACAGAATTGTGTTGACTGGGGGAGGTGAATCACA AAAAAGTTACGAGGAGTTAAGAGTTAAATATTATT
TGATCGTGGCTGTCAAATTTAGTGAACAACATAGATTGGATTTGGAGTTGGTAGTAGGTATGGTTCTCATACCAG
AATTCTCTTAAAAAAGGACAATTGGAATTGCCTTATTTATTTTTTAAATCAATGCTTACTAGTTGGT
AGGATTTCCAGGTGAGCAGCAGGGTTGATTAAATAATCTTGACAATGAGCAGCTGCCATCTGGGGGATTTTCAAT
CTGTGGTTTTTTTAAATGTTTCGTCTTTGATGCTACCATCCAGGGCTTCTTATTGTGACCTTGTAGCCTATTTTGT
TCCTGCTGTTCTTAACATGGTGCAGTTCACGCAGACTGGTTTAGGTACTTCACAACTCACCATTGTCTCTCTGA
CCCCAAGCCTAGTCCCTTTTACATCACCATCTTCTCAGACTTCTTGCCCTATTCTTAAATATGTTTTGGTTAATG
ATTGAATTAGGACATCAGCTTAAGCAATTCCTGTAACGGTTTAAACGTTGTTGAAGTTCAAGGCACATAATAAAT

2317/6881
FIGURE 2128C

TCTCCCTGATGTGTGTGTAAGTATAAACAAAGTAATGTATCAAAGCGTTCACTTTATAATGAAGTCATTTATTG
GGAAGGAAAAGCTGCAAAGATTATTGGGGGACTAGTGATTAATAAAATCCTGTAATATTTTGAAGTGAAAATTG
TACTGAAATTGTACATGATACCTATTAAATGTTTTGTCTTTTTT

2318/6881
FIGURE 2129

MALSKGLRLLGRLGAEGDCSVLLEARGRDDCLLFEAGTVATLAPEEKEVIKGQYGKLTDAYGCLGELRLKSGGTS
LSFLVLVTGCTSVGRIPDAEIIYKITATDFYPLQEEAKEEEERLIALKKILSSGVFYFSWPNDGSRFDLTVRTQKQG
DDSSSEWNSFFWNQLLHVPLRQHQVSCCDWLLKICGVVTIRTIVYASHKQAKACLVSRSVCERTGTRFHTRGVND
DGHVSNFVETEQMIYMDDGVSSFVQIRGSVPLFWEQPGQLQVGSHELLRLHRLGLEANAPAFDRHMLLKEQYQQQV
VNLLGSRGGEEVLNRAFKKLLWASCHAGDTPMINFDFHQFAKGGKLEKLETLLRPQLKLHWEDFDVFTKGENVSP
RFQKGTLRMNCLDCLDRNTNTVQSFIALEVLHLQLKTLGLSSKPIVDRFVESFKAMWSLNGHSLSKVFTGSRALEG
KAKVGKLDGARSMSRTIQSNFFDGVKQEAIKLLLVGDVYGEVADKGGMLLDSTALLVTPRILKAMTERQSEFT
NFKRIRIAMGTWNVNGGKQFRSNVLRTAELTDWLLDSPQLSGATDSQDDSSPADIFAVGFEEVMVELSAGNIVNAS
TTNKKMWGEQLQKAISRSHRYILLTSAQLVGVCLYIFVRPYHVPFIRDVAIDTVKTGMGGKAGNKGAVGIRFQFH
STSFCFICSHLTAGQSQVKERNEDYKEITQKLCFPMGRNVFSDYVFWCGDFNYRIDLTYYEEVFYFVKRQDWKKL
LEFDQLQLQKSSGKIFKDFHEGAINFGPTYKYDVGSAAYDTSKCRTPAWTDRVLWWRKKHPFDKTAGELNLLDS
DLVDVTKVRHTWSPGALQYYGRAELQASDHRPVLAIVEVEVQEVVDVGARERVFQEVSSFQGPLDATVVVNLSPT
LEEKNEFPEDLRTELMQTLGSYGTIVLVRINQGQMLVTFADSHSALSVLDVDGMMKVKGRAVKIRPKTKDWLKGRL
EEIIRKRDSMAPVSPTANSCLLEENFDFTSIDYESEGDILEDDEDYLVDENQPGVSDSELGGDDLSDVPGPTAL
APPSKSPALTKKKQHPTYKDDADLVELKRELEAVGEFRHRSPSRSLSVNRP RPFPQPPQRPPTGLMVKKSASD
ASISSGTHGQYSILQTARLLPGAPQQPPKARTGISKPYNVKQIKTTNAQEAEEAIRCLLEARGGASEEALSAVAP
RDLEASSEPEPTPGAAPKPTQAPPLPRRPPPRVPAIKKPTLRRTGKPLSPREEQFEQQTVHFTIGPPETSVEAP
PVVTAPRVPPVPKPTFPQPGKAAERP SHRPASDEAPPAGASVPPPLEAPPLVPKVPVPRRKSAPAAFLQVLQ
SNSQLLQGLTYNSSDSPSGHPPAAGTVFPQGDFLSTSSATSPDSDGTAMKPEAAPLLGDYQDPFWNLLHHPKLL
NNTWLSKSSDPLDSGTRSPKRDPIDPVSAGASAAKAEPLPDHEHKTGLGHVVTISDQEKRTALQVFDPLAKT

2319/6881
FIGURE 2130

AGGCAGGGCGGGCGGGCGCTCTAAGGGTTCTGCTCTGACTCCAGGTTGGGACAGCGTCTTCGCTGCTGCTGGATA
GTCGTGTTTTTCGGGATCGAGGATACTCACCAGAAACCGAAAATGCCGAAACCAATCAATGTCCGAGTTACCACC
ATGGATGCAGAGCTGGAGTTTGCAATCCAGCCAAATACAACCTGGAAAACAGCTTTTTTGATCAGGTGGTAAAGACT
ATCGGCCTCCGGGAAGTGTGGTACTTTGGCCTCCACTATGTGGATAATAAAGGATTTCTACCTGGCTGAAGCTG
GATAAGAAGGTGTCTGCCCAGGAGGTCAGGAAGGAGAATCCCTCCAGTTCAAGTTCCGGGCCAAGTTCTACCCCT
GAAGATGTGGCTGAGGAGCTCATCCAGGACATCACCAGAAAACCTTTCTTCTCCAAGTGAAGGAAGGAATCCTT
AGCGATGAGATCTACTGCCCCCTGAGACTGCCGTGCTCTTGGGGTCTACGCTGTGCAGGCCAAGTTTGGGGAC
TACAACAAAGAAGTGCACAAGTCTGGGTACCTCAGCTCTGAGCGGCTGATCCCTCAAAGAGTGATGGACCAGCAC
AACTTACCAGGGACCAGTGGGAGGACCGGATCCAGGTGTGGCATGCGGAACACCGTGGGATGCTCAAAGATAAT
GCTATGTTGGAATACCTGAAGATTGCTCAGGACCTGGAAATGTATGGAATCAACTATTTTCGAGATAAAAAACAAG
AAAGGAACAGACCTTTGGCTTGGAGTTGATGCCCTTGGACTGAATATTTATGAGAAAGATGATAAGTTAACCCCA
AAGATTGGCTTTCTTGGAGTGAAATCAGGAACATCTCTTTCAATGACAAAAAGTTTGTCAATTAACCCATCGAC
AAGAAGGCACCTGACTTTGTGTTTTATGCCCCACGTCTGAGAATCAACAAGCGGATCCTGCAGCTCTGCATGGGC
AACCATGAGTTGTATATGCGCCGCAGGAAGCCTGACACCATCGAGGTGCAGCAGATGAAGGCCAGGCCCGGGAG
GAGAAGCATCAGAAGCAGCTGGAGCGGCAACAGCTGGAAACAGAGAAGAAAAGGAGAGAAACCGTGGAGAGAGAG
AAAGAGCAGATGATGCGCGAGAAGGAGGAGTTGATGCTGCGGCTGCAGGACTATGAGGAGAAGACAAAGAAGGCA
GAGAGAGAGCTCTCGGAGCAGATTGAGAGGGCCCTGCAGCTGGAGGAGGAGGAAGCGGGCACAGGAGGAGGCC
GAGCGCCTAGAGGCTGACCGTATGGCTGCACTGCGGGCTAAGGAGGAGCTGGAGAGACAGGCGGTGGATCAGATA
AAGAGCCAGGAGCAGCTGGCTGCGGAGCTTGAGAATACACTGCCAAGATTGCCCTCCTGGAAGAGGCGCGGAGG
CGCAAGGAGGATGAAGTTGAAGAGTGGCAGCACAGGGCCAAAGAAGCCCAGGATGACCTGGTGAAGACCAAGGAG
GAGCTGCACCTGGTGATGACAGCACCCCCGCCGCCACCACCCCCCGTGTACGAGCCGGTGAGCTACCATGTCCAG
GAGAGCTTGCAAGGATGAGGGCGCAGAGCCACGGGCTACAGCGCGGAGCTGTCTAGTGAGGGCATCCGGGATGAC
CGCAATGAGGAGAAGCGCATCACTGAGGCAGAGAAGAACGAGCGTGTGCAGCGGCAGCTGCTGACGCTGAGCAGC
GAGCTGTCCCAGGCCCCGAGATGAGAATAAGAGGACCCACAATGACATCATCCACAACGAGAACATGAGGCAAGGC
CGGGACAAGTACAAGACGCTGCGGCAGATCCGGCAGGGCAACACCAAGCAGCGCATCGACGAGTTGAGGCCCCCTG
TAACAGCCAGGCCAGGACCAAGGGCAGAGGGGTGCTCATAGCGGGCGCTGCCAGCCCCGCCACGCTTGTGTCTTT
AGTGCTCCAAGTCTAGGAACTCCCTCAGATCCCAGTTCTTTAGAAAGCAGTTACCCAACAGAAACATTCTGGGC
TGGAACCAGGGAGGCGCCCTGGTTTGTTCCTCCAGTTGTAATAGTGCCAAGCAGGCCTGATTCTCGCGATTAT
TCTCGAATCACCTCCTGTGTGTGCTGGGAGCAGGACTGATTGAATTACGGAAAAATGCCTGTAAAGTCTGAGTAA
GAACTTCATGCTGGCCTGTGTGATACAAGAGTCAGCATCATTAAAGGAAAACGTGGCAGGACTTCCATCTGTGCC
ATACTTGTCTGTATTTCGAAATGAGCTCAAATTGATTTTTTAATTTCTATGAAGGATCCATCTTTGTATATTTAC
ATGCTTAGAGGGGTGAAAATTATTTTGGAAATTGAGTCTGAAGCACTCTCGCACACACAGTGATTCCCTCCTCCC
GTCACCTCACGCAGCTGGCAGAGAGCACAGTGATCACCAGCGTGAGTGGTGGAGGAGGACACTTGGATTTTTTTT
TTTGTTTTTTTTTTTTTTGTCTTAACAGTTTGTAGAATACATTGTACTTATACACCTTATTAATGATCAGCTATATA
CTATTTATATACAAGTGATAATACAGATTTGTAACATTAGTTTTTAAAAAGGGAAAGTTTGTCTGTATATTTTG
TTACCTTTTACAGAATAAAAGAATTACATATGAAAAACCCCTCTAAACCATGGCACTTGATGTGATGTGGCAGGAG
GGCAGTGGTGGAGCTGGACCTGCCTGCTGCAGTCACGTGTAAACAGGATTATTATTAGTGTATGATGTAAT
GGACTATGCACACTTTTAAATTTTGTGAGATTCACACATGCCACTATGAGCTTTCAGACTCCAGCTGTGAAGAGAC
TCTGTTTGTCTGTGTTTGTGTTTGTGTTTGCAGTCTCTCTGCCATGGCCTTGGCAGGCTGCTGGAAGGCAGCTTGTG
GAGGCCGTTGGTTCCGCCCACTCATTCTCTCTGCTGCACTGCTTCTCTCTTACAGCTAAGATGCCATGTGCAGG
TGGATTCCATGCCGCAGACATGAAATAAAAGCTTTGCAAAGGCA

2320/6881
FIGURE 2131

ATCTTCCGGTAATTCGCCAAAATGACGAACACAAAGGGAAAGAGGAGAGGCACCTGACATATGTTCTCTAGGCCT
TTTAGAAAACATGGAATGGGTACTGTTCAAAAAGGAATGCCCCACAAGTGTCAACCATGGCAAACTGGGAGTCTA
CGATGTTCCCCAGCATGCTGTTGGCATTGTTGTAAACAAACAAGTTAAGGGCAAGATTCTTGCCAAGAGAATTAA
TGTGCGTATTGAGCACATTACGCACTCTAAGAGCCGAGATAGCTTCCTGAAACGCGTGAAGGAAAATGATCAGAA
AAAGAAAGAAGCCAAAGAGAAAGGTACCTGGGTTTCAAGCTAAAGCGCCAGCCTGCTCCACCCAGAGAAACACACTT
TGTGAGAACCAATGGGAAGGAGCCTGAGCTGCTGGAACCTATTCCCTATTAATTCATGGCATAATAGGTGTTAAA
AAGAAAAATAAA

2321/6881
FIGURE 2132

GGCAGCGCAGGGCAGACGGCGGCAGGAGAAGCAAGATGAATGCAGGCTCAGATCCTGTGGTCATCGTCTCGGCGG
CGCGGACCATCATAGGTTTCCTTCAATGGTGCCTTAGCTGCTGTTCCCTGTCCAGGACCTGGGCTCCACTGTCATCA
AAGAAGTCTTGAAGAGGGCCACTGTGGCTCCGGAAGATGTGTCTGAGGTCATCTTTGGACATGTCTTGGCAGCAG
GCTGTGGGCAGAATCCTGTTAGACAAGCCAGTGTGGGTGCAGGAATTCCTACTCTGTTCCAGCATGGAGCTGCC
AGATGATCTGTGGGTGAGGCCTAAAAGCTGTGTGCCTTGCAGTCCAGTCAATAGGGATAGGAGACTCCAGCATTG
TGGTTGCAGGAGGCATGGAAAATATGAGCAAGGCTCCTCACTTGGCTTACTTGAGAACAGGAGTAAAGATAGGTG
AGATGCCACTGACTGACAGTATACTCTGTGATGGTCTTACAGATGCATTTCACTGTGCATATGGGTATTACAG
CTGAAAATGTAGCCAAAAAATGGCAAGTGAGTAGAGAAGATCAGGACAAGGTTGCAGTTCTGTCCCAGAACAGGA
CAGAGAATGCACAGAAAGCTGGCCATTTTGACAAAGAGATTGTACCAGTTTGGTGTCAACTAGAAAAGGTCTTA
TTGAAGTTAAACAGATGAGTTTCCTCGCCATGGGAGCAACATAGAAGCCATGTCCAAGCTAAAGCCTTACTTTC
TTACTGATGGAACGGGAACAGTCACCCAGCCAATGCTTCAGGAATAAATGATGGTGCTGCAGCTGTGCTTCTTA
TGAAGAAGTCAGAAGCTGATAAACGTGGGCTTACACCTTTAGCACGGATAGTTTCCTGGTCCCAAGTGGGTGTGG
AGCCTTCCATTATGGGAATAGGACCAATTCCAGCCATAAAGCAAGCTGTTACAAAAGCAGGTTGGTCACTGGAAG
ATGTTGACATATTTGAAATCAATGAAGCCTTTGCAGCTGTCTCTGCTGCAATAGTTAAAGAAGCTTGGATTAAACC
CAGAGAAGGTCAATATTGAAGGAGGGGCTATAGCCTTGGGCCACCTCTTGGAGCATCTGGCTGTGCAATTCTTG
TGACCCTGTTACACACACTGGAGAGAATGGGCAGAAGTCGTGGTGTGTCAGCCCTGTGCATTGGGGGTGGGATGG
GAATAGCAATGTGTGTTTCAAGAGAGAATGAATTGCTTAACTTTGAACAACCTCAATTTCTTTTAACTAATAAA
GTACTAGGTTGCAATATGTGAAATCAGAGGACCAAAGTACAGATGGAAACCATTTCTTACATCAGAAAAACCCAA
GTTTACAGCTTGTACTTTTACTTTAATGTGTAATACTCAACTCAAGGTACAAGACAATTGCATTTAACATTGTTAT
AAATAAAAGGAACATCAGATCAATCATT

2322/6881
FIGURE 2133

MNAGSDPVVIVSAARTIIGSFNGALAAVPVQDLGSTVIKEVLKRATVAPEDVSEVIFGHVLAAGCGQNPVRQASV
GAGIPYSVPAWSCQMICGSLKAVCLAVQSIGIGDSSIVVAGGMENMSKAPHLAYLRTGVKIGEMPLTDSILCDG
LTDAFHNCHMGITAENVAKKWQVSREDQDKVAVLSQNRTEAQAQAGHFDKEIVPVLVSTRKGLIEVKTDEFPRHG
SNIEAMSKLKPYFLTDGTGTVTPANASGINDGAAAVVLMKKSEADKRGLTPLARIVSWSQVGVEPSIMGIGPIPA
IKQAVTKAGWSLEDVDIFEINEAFAAVSAAIVKELGLNPEKVNIEGGAIALGHPLGASGCRILVTLHHTLERMGR
SRGVAALCIGGGMGIAMCVQRE

2323/6881
FIGURE 2134

ACGTGTATCGCTGCCGTCAAGATGGAGGGCCTTTGTCCGTGTTCCGGTGACCGCAGCACTGGGGAAACGATCCGC
TCCCAAACGTTATGGCTGCAGCTTCGATTGCCAATATTGTAAAAAGTTCTCTTGGTCCAGTTGGCTTGGATAAA
ATGTTGGTGGATGATATTGGTGATGTAACCATTACTAACGATGGTGCAACCATCCTGAAGTTACTGGAGGTAGAA
CATCCTGCAGCTAAAGTTCTTTGTGAGCTGGCTGATCTGCAAGACAAAGAAGTTGGAGATGGAACACTTTCAGTG
GTTATTATTGCAGCAGAACTCCTAAAAAATGCAGATGAATTAGTCAAACAGAAAATTCATCCACATCAGTTATT
AGTGGCTATCGACTTGCTTGCAAGGAAGCAGTGCGTTATATCAATGAAAACCTAATTGTTAACACAGATGAACTG
GGAAGAGATTGCCTGATTAATGCTGCTAAGACATCCATGTCTTCCAAAATCATTGGAATAAATGGTGATTTCCTT
GCTAACATGGTAGTAGATGCTGTACTTGCTATTAAATACACAGACATAAGAGGCCAGCCACGCTATCCAGTCAAC
TCTGTTAATATTTTGAAAGCCCATGGGAGAAGTCAAATGGAGAGTATGCTCATCAGTGGCTATGCACTCAACTGT
GTGGTGGGATCCAGGGCATGCCAAGAGAATCGTAAATGCAAAAATTGCTTGCCTTGACTTCAGCCTGCAAAAA
ACAAAATGAAGCTTGGTGTACAGGTGGTCATTACAGACCTGAAAACTGGACCAAATTAGACAGAGAGAATCA
GATATCACCAAGGAGAGAAATTCAGAAGATCCTGGCAACTGGTGCCAATGTTATTCTAACCACTGGTGGAATTGAT
GATATGTGTCTGAAGTATTTTGTGGAGGCTGGTGCTATGGCAGTTAGAAGAGTTTTTAAAAAGGGACCTTAAACGC
ATTGCCAAAGCTTCTGGAGCAACTATTCTGTCAACCTTGCCAATTTGGAAGGTGAAGAACTTTTGAAGCTGCA
ATGTTGGGACAGGCAGAAGAAGTGGTACAGGAGAGAATTTGTGATGATGAGCTGATCTTAATCAAAAATACTAAG
GCTCGTACGTCTGCATCGATTATCTTACGTGGGGCAAATGATTCATGTGTGATGAGATGGAGCGCTCTTTACAT
GATGCACTTTGTGTAGTGAAGAGAGTTTTTGGAGTCAAAATCTGTGGTTCCCGGTGGGGGTGCTGTAGAAGCAGCC
CTTTCCATATACCTTGAAAATATGCAACCAGCATGGGGTCTCGGGAACAGCTTGCGATTGCAGAGTTTGCAAGA
TCACTTCTTGTTATTCCCAATACACTAGCAGTTAATGCTGCCCAGGACTCCACAGATCTGGTTGCAAAATTAAGA
GCTTTTCATAATGAGGCCCAGGTTAACCCAGAACGTAAAAATCTAAAATGGATTGGTCTTGATTGAGCAATGGT
AAACCTCGAGACAACAAACAAGCAGGGGTGTTTGAACCAACCATAGTTAAAGTTAAGAGTTTGAAATTTGCAACA
GAAGCTGCAATCACCATTCTTCGAATTGATGATCTTATTAAATTACATCCAGAAAGTAAAGATGATAAACATGGA
AGTTATGAAGATGCTGTTCACTCTGGAGCCCTTAATGATTGATCTGATGTTTCCTTTTATTATAACAATGTTAAA
TGCAATTGTCTTGACCTTGAGTTGAGTATTACACATTAAAGTAAAGTACAAGCTGTAACTTGGGTTTTTGTGA
TGTAGGAAATGGTTTCCATCTGTACTTTGGTCCTCTGATTTACATATTGCAACCTAGTACTTTATTAGTTTAAA
AAGAAATTGAGGTTGTTCAAAGTTTAAGCAATTCATTCTCTCTGAACACACATTGCTATTCCCATCCCACCCCA
ATGCACAGGGCTGCAACACCACGACTTCTGCCCATCTCTCCAGTGTGTGTAACAGGGTCACAAGAATTC

2324/6881
FIGURE 2135

TTTGCTTTTGCTTATTTCCGTCCATTTCCTCTCTGCGCGCGGACCTTCCTTTTCCAGATGGTGAGAGCCGCGGG
GACACCCGACGCCGGGGCAGGCTGATCCACGATCCTGGGTGTGCGTAACGCCGCTGGGGCTCCGTGGGCGAGGG
ACGTGTGGGGACAGGTGCACCGGAACTGCCAGACTGGAGAGTTGAGGCATCGGAGGCGGAGAACAGCACTACT
ACTGCGGCGAGACGAGCGCGGCGCATCCCAAAGCCCGGCCAAATGCGCTCGTCCCTGGGAGGGGAGGGAGGCGCG
CCTGGAGCGGGGACAGTCTTGGTCCGCGCCCTCCTCCCGGGTCTGTGCCGGGACCCGGGACCCGGGAGCCGTCGC
AGGTCTCGGTCCAAGGGGCCCTTTTCTCGGAAGGGCGGCGGCCAAGAGCAGGGAAGGTGGATCTCAGGTAGCGA
GTCTGGGCTTCGGGGACGGCGGGGAGGGGAGCCGGACGGGAGGATGAGCTCCCCTGGCACCGAGAGCGCGGGAAA
GAGCCTGCAGTACCGAGTGGACCACCTGCTGAGCGCCGTGGAGAATGAGCTGCAGGCGGGCAGCGAGAAGGGCGA
CCCCACAGAGCGCGAACTGCGCGTGGGCCTGGAGGAGAGCGAGCTGTGGCTGCGCTTCAAGGAGCTCACCAATGA
GATGATCGTGACCAAGAACGGCAGGAGGATGTTTCCGGTGCTGAAGGTGAACGTGTCTGGCCTGGACCCCAACGC
CATGTACTCCTTCCTGCTGGACTTCGTGGCGGCGGACAACCACCGCTGGAAGTACGTGAACGGGGAAATGGGTGCC
GGGGGGCAAGCCGGAGCCGCAGGCGCCCAGCTGCGTCTACATCCACCCGACTCGCCCAACTTCGGGGGCCACTG
GATGAAGGCTCCCGTCTCCTTCAGCAAAGTCAAGCTCACCAACAAGCTCAACGGAGGGGGCCAGATCATGCTGAA
CTCCTTGCATAAGTATGAGCCTCGAATCCACATAGTGAGAGTTGGGGGTCCACAGCGCATGATCACCAGCCACTG
CTTCCCTGAGACCCAGTTCATAGCGGTGACTGCTTATCAGAACGAGGAGATCACAGCTCTTAAATTAAGTACAA
TCCATTTGCAAAAGCTTTCCCTTGATGCAAAAGGAAAGAGTGATCACAAGAGATGATGGAGGAACCCGGAGACAG
CCAGCAACCTGGGTACTCCCAATGGGGGTGGCTTCTTCCCTGGAACCAGCACCCCTGTGTCCACCTGCAAATCCTCA
TCCTCAGTTTGGAGGTGCCCTCTCCCTCCCTCCACGCACAGCTGTGACAGGTACCCAAACCTGAGGAGCCACCG
GTCTCACCCCTACCCAGCCCTATGCTCATCGGAACAATTCTCCAACCTATTCTGACAACTCACCTGCATGTTT
ATCCATGCTGCAATCCCATGACAATTGGTCCAGCCTTGGAATGCCTGCCCATCCCAGCATGCTCCCCGTGAGCCA
CAATGCCAGCCCACCTACCAGCTCCAGTCAGTACCCAGCCTGTGGTCTGTGAGCAACGGCGCCGTACCCCCGGG
CTCCCAGGCAGCAGCCGTGTCCAACGGGCTGGGGGCCAGTTCTTCCGGGGCTCCCCCGCGCACTACACACCCCT
CACCCATCCGGTCTCGGCGCCCTCTTCTCGGGATCCCCACTGTACGAAGGGGCGGCCGCGGCCACAGACATCGT
GGACAGCCAGTACGACGCCGAGCCCAAGSCCGCTCATAGCCTCATGGACACCTGTGTGCCACCTTCCATGTG
AAGCAGCAAGGCCAGGTCCCGAAAGATGCAGTGACTTTTTGTGCTGGCAGCCAGTGGTGACTGGATTGACCTAC
TAGGTACCCAGTGGCAGTCTCAGGTTAAGAAGGAAATGCAGCCTCAGTAACTTCCTTTTCAAAGCAGTGGAGGAG
CACACGGCACCTTTCCCAGAGCCCCAGCATCCCTTGCTCACACCTGCAGTAGCGGTGCTGTCCAGGTGGCTTA
CAGATGAACCCAACTGTGGAGATGATGCAGTTGGCCCAACCTCACTGACGGTGAAAAAATGTTTGCCAGGGTCCA
GAAACTTTTTTTGGTTTATTTCTCATACAGTGTATTGGCAACTTTGGCACACCAGAATTTGTAAACTCCACCAGT
CCTACTTTAGTGAGATAAAAAGCACACTCTTAATCTTCTTCTTGTGCTTTCAAGTAGTTAGAGTTGAGCTGTT
AAGGACAGAATAAAATCATAGTTGAGGACAGCAGGTTTTAGTTGAATTGAAAAATTTGACTGCTCTGCCCCCTAGA
ATGTGTGTATTTTAAAGCATATGTAGCTAATCTCTTGTGTTGTTAAACTATAACTGTTTCATATTTTTCTTTTGAC
AAAGTAGCCAAAGACAATCAGCAGAAAAGCATTTTCTGCAAAATAAACGCAATATGCAAAATGTGATTTCGTCCAGT
TATTAGTGAAGCCCCTCCTTTTGTGAGTATTTACTGTTTATTG

2325/6881
FIGURE 2136

MSSPGTESAGKSLQYRVDHLLSAVENELQAGSEKGDPTERELRVGLEESELWLRFKELTNEMIVTKNGRRMFPVL
KYNVSGLDPNAMYSFLDFVAADNHRWKYVNGEWVPGGKPEPQAPSCVYIHPDSPNFGAHWMKAPVSFSKVCLTN
KLNGGGQIMLNSLHKYEPRIHIVRVGGPQRMITSHCFPETQFIAVTAYQNEEITALKIKYNPFAKAFLDAKERSD
HKEMMEEPGDSQQPGYSQWGWLLPGTSTLCPPANPHPOFGGALS LPSTHSCDRYPTLRSHRSPYPSPYAHNRNS
PTYSDNSPACLSMLQSHDNWSSLGMPAHPSMLPVSHNASPPTSSSQYPSLWSVSNNGAVTPGSQAAAVSNGLGAQF
FRGSPAHYTPLTHPVSAPSSSGSPLYEGAAAATDIVDSQYDAAAQGRLIASWTPVSPPSM

2326/6881
FIGURE 2137

CGCAGCCGTGCGATGTTGTCCTCTACAGCCATGTATTCGGCTCCTGGCAGAGACTTGGGGATGGAACCGCACAGA
GCCGCGGGCCCTTTGCAGCTGCGATTTTCGCCCTACGTTTTCAACGGAGGTACTATACTGGCAATTGCTGGAGAA
GATTTTGCAATTGTTGCTTCTGATACTCGATTGAGTGAAGGGTTTTCAATTCATACGCGGGATAGCCCCAAATGT
TACAAATTAACAGACAAAACAGTCATTGGATGCAGCGGTTTTCATGGAGACTGTCTTACGCTGACAAAGATTATT
GAAGCAAGACTAAAGATGTATAAGCATTCCAATAATAAGGCCATGACTACGGGGGCAATTGCTGCAATGCTGTCT
ACAATCCTGTATTCAAGGCGCTTCTTTCCATACTATGTTTACAACATCATCGGTGGACTTGATGAAGAAGGAAAG
GGGGCTGTATACAGCTTTGATCCAGTAGGGTCTTACCAGAGAGACTCCTTCAAGGCTGGAGGCTCAGCAAGTGCC
ATGCTACAGCCCCCTGCTTGACAACCAGGTTGGTTTTAAGAACATGCAGAATGTGGAGCATGTTCCGCTGTCCTTG
GACAGAGCCATGCGGCTGGTGAAAGATGTCTTCATTTCTGCGGCTGAGAGAGATGTGTACACTGGGGACGCACTC
CGGATCTGCATAGTGACCAAAGAGGGCATCAGGGAGGAAACTGTTTCCTTAAGGAAGGACTGATCTGTGTGCTCT
TATCACCAATCAGTTCAGACCTGGTTGATTTTGTACTTTGGAACGTACCTTGGATGGTTTTGTTTATTAAAA

2327/6881
FIGURE 2138

MLSSTAMYSAPGRDLGMEPHRAAGPLQLRFSPYVFNGGTILAIAGEDFAIVASDTRLSEGFSIHTRDSPKCYKLT
DKTVIGCSGFHGDCLTLTKIIEARLKMYKHSNNKAMTTGAIAAMLSTILYSRRFFPYVYNIIGGLDEEGKGAVY
SFDPVGSYQRDSFKAGGSASAMLQPLLDNQVGFKNMQNVEHVPLSLDRAMRLVKDVFISAAERDVYTGDALRICI
VTKEGIREETVSLRKD

2328/6881

FIGURE 2139

GCTCCCAGCCGGGCCCCCTCAGCGGTGCGCGGGACGGCTCCCGGCTGCAGTCTGCCCGCCCCGCCCGCGCGGGGGC
CGAGTCGCGAAGCGCGCCTGCGACCCGGCGTCCGGGCGCGCTGGAGAGGACGCGAGGAGCCATGAGGCGCCAGCC
TGCGAAGGTGGCGGCGCTGCTGCTCGGGCTGCTCTTGAGTGCACAGAAGCCAAAAAGCATTGCTGGTATTTCGA
AGGACTCTATCCAACCTATTATATATGCCGCTCCTACGAGGACTGCTGTGGCTCCAGGTGCTGTGTGCGGGCCCT
CTCCATACAGTGGCTGTGGTACTTCTGGTTCCTTCTGATGATGGGCGTGCTTTTCTGCTGCGGAGCCGGCTTCTT
CATCCGGAGGCGCATGTACCCCCCGCCGCTGATCGAGGAGCCAGCCTTCAATGTGTCTACACCAGGCAGCCCCC
AAATCCCGGCCCAGGAGCCCAGCAGCCGGGGCCACCCTATTACACCGACCCAGGAGGACCGGGGATGAACCCTGT
CGGGAATTCCATGGCAATGGCTTTCCAGGTCCCACCCACTCACCCAGGGGAGTGTGGCCTGCCCGCCCCCTCC
AGCCTACTGCAACACGCCTCCGCCCCGTACGAACAGGTAGTGAAGGCCAAGTAGTGGGGTGCCACGTGCAAGA
GGAGAGACAGGAGAGGGCCTTTCCCTGGCCTTCTGTCTTCGTTGATGTTCACTTCCAGGAACGGTCTCGTGGGC
TGCTAAGGGCAGTTCCTCTGATATCCTCACAGCAAGCACAGCTCTCTTTCAGGCTTTCCATGGAGTACAATATAT
GAACTCACACTTTGTCTCCTCTGTTGCTTCTGTTTCTGACGCAGTCTGTGCTCTCACATGGTAGTGTGGTGACAG
TCCCCGAGGGCTGACGTCTTACGGTGGCGTGACCAGATCTACAGGAGAGAGACTGAGAGGAAGAAGGCAGTGCT
GGAGGTGCAGGTGGCATGTAGAGGGGCCAGGCCGAGCATCCAGGCAAGCATCCTTCTGCCCGGGTATTAATAGG
AAGCCCCACGCCGGGCGGCTCAGCCGATGAAGCAGCAGCCGACTGAGCTGAGCCCAGCAGGTCTCTGCTCCAGC
CTGTCTCTCGTCAGCCTTCTCTTCCAGAAGCTGTTGGAGAGACATTCAAGGAGAGAGCAAGCCCCCTTGTCTATGT
TTCTGTCTCTGTTTCATATCCTAAAGATAGACTTCTCCTGCACCGCCAGGGAAGGGTAGCACGTGCAGCTCTCACC
GCAGGATGGGGCCTAGAATCAGGCTTGCTTGGAGGCCTGACAGTGATCTGACATCCACTAAGCAAATTTATTTA
AATTCATGGGAAATCACTTCTGCCCCAACTGAGACATTGCATTTTGTGAGCTCTTGGTCTGATTGTGGAGAAAG
GACTGTTACCCATTTTTTGGTGTGTTTATGGAAGTGCATGTAGAGCATCCTGCCCTTTGAAATCAGACTGGGTGT
GTGTCTTCCCTGGACATCACTGCCTCTCCAGGTCATTCTCAGGCCCCGGGGTCTCCTTCCCTCAGGCAGCTCCAG
TGGTGGGTCTGAAGGGTGCTTTCAAACAGGGGGCACATCTGGCTGGGAAGTCACATGGACTCTTCCAGGGAGA
GAGACCAGCTGAGGCGTCTCTCTGAGGTTGTGTTGGGTCTAAGCGGGTGTGTGCTGGGCTCCAAGGAGGAGGA
GCTTGCTGGGAAAAGACAGGAGAAGTACTGACTCAACTGCACTGACCATGTTGTCATAATTAGAATAAAGAAGAA
GTGGTTGGAAATGCACATTCTGGATAGGAATCACAGCTCACCCAGGATCTCACAGGTAGTCTCCTGAGTAGTT
GACGGCTAGCGGGGAGCTAGTTCCGCCGCATAGTTATAGTGTTGATGTGTGAACGCTGACCTGTCTGTGTGCTA
AGAGCTATGCAGCTTAGCTGAGGCGCCTAGATTACTAGATGTGCTGTATCACGGGGAATGAGGTGGGGTGCTTA
TTTTTTAATGAATAATCAGAGACTCTTGAGAAATTGTTACTCATTGAACTGGAGCATCAAGACATCTCATGGAA
ATGGATACGGAGTGATTTGGTGTCCATGCTTTTCACTCTGAGGACATTTAATCGGAGAACCTCTGGGGAATTTT
GTGGGAGACACTTGGGAACAAAACAGACACCCTGGGAATGCAGTTGCAAGCACAGATGCTGCCACCAGTGTCTCT
GACCACCCTGGTGTGACTGCTGACTGCCAGCGTGGTACCTCCCATGCTGCAGGCCTCCATCTAAATGAGACAACA
AAGCACAAATGTTCACTGTTTACAACCAAGACAACCTGCGTGGGTCCAAACACTCCTCTTCCCTCCAGGTCATTTGTT
TTGCATTTTTAATGTCTTTATTTTTTGTAAATGAAAAGCACACTAAGCTGCCCTGGAATCGGGTGCAGCTGAAT
AGGCACCCAAAAGTCCGTGACTAAATTTTCTTTTGTCTTTTTTGATAGCAAATAATGTTAAGAGACAGTGATGGCTA
GGGCTCAACAATTTTGTATTCCCATGTTTGTGTGAGACAGAGTTTGTTTTCCCTTGAACCTGGTTAGAATTGTGC
TACTGTGAACGCTGATCCTGCATATGGAAGTCCCACTTCGGTGACATTTCTGGCCATTCTTGTTTCCATTGTGT
GGATGGTGGGTGTGCCCCTTCTGGAGTGAGACAGCTCCTGGTGTGTAGAATTCCCGGAGCGTCTGTGGTTCA
GAGTAACTTGAAGCAGATCTCTGCATGCTTTTCTCTGCAACAATTGGCTCATTTCTCTTTTTTGTCTCTTTTT
GATAGGATCCTGTTTCTATGTGTGCAAAATAAAAATAAATTTGGGCAA

2329/6881
FIGURE 2140

ATGGCAGGGGAGTCACAAAGGAGAAGCACTCAGCCTGCCGAGAGGTCC¹CAGGACTTTCTGGAGGATCAGTCCCC
AAACTGACTGTGACAGGGAGCTATACCCAGATAACAGCAGAGGCCAGAATAAGAAAGAGTCTGTAGATGGCAAG
TCAATGGGAAATCATTCCAGGAAGGTAGGGAAAGATGGAATTCTGGAGAGCATTGGACCTCAGATTGGGAGTCTG
AACGTCTTTCCATATGCATCAGGAAGCCATGGAAAATTCACAGACTGGAGTGACTTTGGCAAAGGAACAACATAT
AACGCACTCTCCCCTGAACTCTACACAACATATTTTGTACCAAGACCCTACTTCTGACCTCCCTGTTCTTATGC
ATTCGAACAGCATACCCCCGATTCCGCTACGACCAACTCATAACCTCCTATGA

2330/6881
FIGURE 2141

CTAAATACTACCGTATGACCCACCATAATTACCCCCATACTCCTTACACTATTCTCATCACCCAACTAAAAATA
TTAAATACAAATTACCACCTACCTCCCTCACCAAAGCCCATAAAAAATAAAAACTATAACAAACCCTGAGAACCA
AAATGAACGAAAATCTGTTCACTTCATTTCATTGCCCCACAATCCTAGGCCTACCCGCCGAGTACTGATCATTC
TATTTCCCCCTCTATTGATCCCACTCCAAATATCTCATCAACAACCGACTAATTACCACCCAACAATGACTAA
TCCAATAACCTCAAAACAAATGATAGCCATACACAACACTAAGGGACGAACCTGATCTCTTATACTAGTATCCT
TAATCATTTTTTATTGCCACAATAACCTCCTCGGACTCCTGCCTCACTCATTTACACCAACCACCCAACTATCTA
TAAACCTAGCCATGGCCATCCCTTATGAGCGGGCGCAGTGATTATAGGCTTTTCGCTCTAAGATTAAAAATGCC
TAGCCCACTTCTTACCACAAGGCACACCTACACCCCTTATCCCTATACTAGTTATTATCGAAACCATCAGCCTAC
TCATTCAACCAATAGCCCTGGCCGTACGCCTAACCGCTAACATTACTGCAGGCCACCTACTCATGCACCTAATTG
GAAGCGCCACACTAGCAATATCAACTATTAACCTTCCCTCTACACTTATCATCTTCACAATTCTAATTCTACTGA
CTATCCTAGAAATCGCTGTGCGCTTAATCCAAGCCTACGTTTTTACACTTCTAGTAAGCCTCTACCTGCACGACA
ACACATAATGACCCACCAATCACATGCCTATCATATAGTAAAACCCAGCCCATGGCCCCTAACAGGGGGCCCTCTC
AGCCCTCCTAATGACCTCCGGCCTAGCCATGTGATTTCACTTCCACTCCACAACCCTCCTCATACTAGGCCTACT
AACCAACACACTAACCATATACCAATGATGGCGCGATGTAACACGAGAAAGCACATACCAAGGCCACCACACACC
ACCTGTCCAGAAAGGCCTTCGATACGGGATAATCCTATTTATTACCTCAGAAGTTTTTTTTCTTCGCAGGATTTTT
CTGAGCCTTTTACCACTCCAGCCTAGCTCCCACCCCCCACTAGGGGGACACTGGCCCCCAACAGGCATCACCCC
GCTAAATCCCCTAGAAGTCCCACTCCTAAACACATCGGTATTACTCGCATCAGGGGTATCAATCACCTGAGCTCA
CCATAGTCTAATAGTCTATTTTACCCTCCTACAAGCCTCAGAGTACTTCGAG

2331/6881
FIGURE 2142

GTGGGAACATCCAGTTGCGGGAAAACAAGCTTAACACGCCCCTGATTCTACATTATGCTCCTACCTCCCGGCAG
CCTCTCCAGGCCCAGAACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCACAATGGCCTATTTAGGCC
CATAACCTACGTCACGGCAGCCTCCGCAGATGAGCCTACTGCCTCACAACAGCCTCCACAGGCACAGCTCCATCG
TTACAATGGCCTCTTTAGACCCAGCTCCTGCCTCCCAGCCTTCTCTCCAGGCCCTGAACTTTCTCAAGTCGACCT
CACCAGGCCCAGCTCATGCTTCTTTGCAGCCTCTCCAGGCCCAGCTCCTGCATCTTGGTGGCCCCCTCCAGGCCCA
GCCTCTGCCTCCCGTCAGCCTCTACAGTCCCAACGTCTGCCTCACAGCAGATTCTTCAGGCCCAGCATCTGCCTC
ACTTGGACCTCCAGACCCAGATGGTGTCTCACTGTGGCATCCTCAGGCGAAGCTCCTGCCTTTTCGGCAGCCTCT
CCAGGCCCAGCTCCTCCTGCCTCCCAGTGGCCTCTTTCGGCCCAGCCCAGCTCATGCCTCCCGGCGGCCTTCCCA
AGCCCCGCTTTTGACTTTTCGGTGGCCTCTGCAGGCCTCGACAAGGCCAGCCTCCTGCCTCCCGAAGGCCTGCAC
AGGCCAGCCTCTGCCTCACAGCGGACTCTC

2332/6881
FIGURE 2143

MLLPGSLSRPRTFSSQPLQTKLMTHNGLFRPIPYLTAVSADEPTASQQPPQAQLHRYNGLFRPSSCLPAFSPGP
ELSQVDLTRPSSCFFAASPGTPASWWPLQAQPVPPVGLYNPNICLTADSSRPASASQWTLQTQMVSHCGILRRS
SCLSAASPGPAPPASQWPLSAQPSSCLPAAFPSPAEDFWWPLQASTRPSLLPPEGLHRPSLCLTADSPRPASSRL
TAASPVQSSCLSATSAGPATAACQWPL

2333/6881
FIGURE 2144

CTCTCTCACACACACCCCCGCTTGGGCCTCCTCTCTCTCTCCGGCTCCATTTTCTCCGCCGCCGGGGGCCGGGGT
CTCCTGTGGGGGGGCCAGCCGGTATCCCAGGTCTCCCTTCAGTGCCGGGGTGAACCCCCGGGGGAGCCGGGAGCC
GGGGGCAGACGGGCGGGGGTTGGGGCGGAGGGAGCAGCGGCCCCAGCGAGTTTGGGGGGAGAAGTAACCAGGCGG
GGGGAGGGGCGGAGCAGGGAGGGGGCCTCAGGGCCCCCCCCCAGCTATGGACGAACGGCTACTGGGGCCGCCCC
TCCAGGCGGGGGCCGGGGGGCCTGGGATTGGTGAGTGGGGAGCCTGGGGGCCCTGGCGAGCCTCCCGGTGGCGG
AGACCCCGGTGGGGGTAGCGGGGGGTCCCGGGAGGCCGAGGGAAGCAAGACATCGGGGACATTCTGCAGCAGAT
AATGACCATCACCAGCAGAGCCTGGACGAGGCCAGGCCAAGAAACACGCCCTAAACTGCCACCGAATGAAGCC
TGCTCTCTTTAGCGTCTGTGTGAAATCAAGGAGAAAACCTGGCCTCAGCATTCCGAGCTCCCAGGAGGAGGAGCC
GGTGGACCCACAGCTGATGCGCTTGGACAACATGCTTCTGGCAGAGGGTGTGGCTGGGCCCCGAGAAAGGGGGCGG
CTCAGCAGCAGCAGCTGCAGCCGCTGCAGCCTCTGGTGGTGGTGTGTCCCCTGACAACTCCATCGAACACTCGGA
CTATCGCAGCAAACCTTGCCAGATCCGTACATATACCACTCGGAGCTGGAGAAGTATGAGCAGGCATGTAATGA
GTTACGACCCATGTATGAACCTGCTGAGGGAGCAGAGCCGCACCAGGCCCGTGGCCCCCAAAGAGATGGAACG
CATGGTGAGCATCATCCATCGAAAGTTTCAGCGCCATCCAGATGCAGCTGAAGCAGAGCACCTGCGAGGCTGTGAT
GATCCTGCGCTCCCGTTTTCTGGATGCCAGACGAAAGCGCCGTAACCTTCAGCAAACAGGCCACTGAGGTCCTAAA
TGAGTATTTCTACTCCACCTGAGTAACCCATATCCTAGTGAGGAGGCCAAGGAGGAGCTTGCCAAGAAGTGTGG
CATCACCGTGTCTCAGGTCTCCAACCTGGTTTGGCAACAAGAGGATTTCGCTATAAGAAAAACATCGGAAAGTTCCA
AGAGGAGGCAAACATCTATGCTGTCAAGACCGCCGTGTTCAGTCACCCAGGGGGGCCACAGCCGCACCAGCTCCCC
GACACCCCTTCTCTGTCAGGTGGATCCCACTGTCACCCAGCTGACTGTTTTGCACACTTCCTGCTTTTGTTC
CACTTCCTATCTAGGCAGGATCATAGCAGAGAGGGGGCCTTTTGGGGTGAGAGGGACCGAGCTGAGATAGGCTGG
AGATGTCAGGGGACAGAGGCCATTCCAGTGATCTTAGTTCTGCCTTTCTTCCCACGGGTGGCCAAGGAACAGCCT
GCTCTTTCTGTGTGTTGGAATGTTATTTGTGGATAATTGGAGTATAGTAGCATGTCCCCAC

2334/6881

FIGURE 2145

GAGTAGAGTAGGGCAGGAGAAACTGGGCCAGGCTGCACCTAGCTCAAGGGGCCTCGAGGACTCTCTGCGTCTCTG
GAGACAAGGGCACTACACGCACTTCAGAATGAAGAGTTGCGGGAGCATGCTGGGGCTCTGGGGGCAGCGGCTCCC
CGCGGCGTGGGTCTCTGCTTCTGTTGCCTTTCCTGCCGCTGCTGCTGCTTGCAGCCCCCGCGCCCCACCGCGAGTC
CTACAAGCCGGTCATCGTGGTGATGGGCTCTTCGACAGCTCGTACAGCTTCCGCCACCTGCTGGAATACATCAA
TGAGACACACCCCGGGACTGTGGTGACAGTGCTCGATCTCTTCGATGGGAGAGAGAGCTTGCGACCCCTGTGGGA
ACAGGTGCAAGGGTTCCGAGAGGCTGTGGTCCCCATCATGGCAAAGGCCCTCAAGGGGTGCATCTCATCTGCTA
CTCGCAGGGGGGCTTGTGTGCCGGGCTCTGCTTTCGTGCATGGATGATCACAACGTGGATTCTTTCATCTCCCT
CTCCTCTCCACAGATGGGACAGTATGGAGACACGGACTACTTGAAGTGGCTGTTCCCCACCTCCATGCGGTCTAA
CCTCTATCGGATCTGCTATAGCCCCCTGGGGCCAGGAATCTCCATCTGCAACTACTGGCATGATCCCCACCACGA
TGACTTGTACCTCAATGCCAGCAGCTTCCTGGCCCTGATCAATGGGGAAAGAGACCATCCCAATGCCACAGTATG
GCGGAAGAACCTTCTGCGTGTGGGCCACCTGGTGCTGATTGGGGGCCCTGATGATGGTGTTATTACTCCCTGGCA
GTCCAGCTTCTTTGGTTTTCTATGATGCAATGAGACCGTCTCGGAGATGGAGGAGCAACTGGTTTATCTGCGGGA
TTCTTTTGGGTTGAAGACTCTATTGGCCCCGGGGGGCCATAGTGAGGTGTCCAATGGCCGGTATCTCCCACACAGC
CTGGCACTCCAACCGTACCCCTTTATGAGACCTGCATTGAACCTTGGCTCTCCTGAGGATATATTACAGGGGTCCCC
AGGAACTCCTCGGTCCAGAGACCAAGTGGTGGCCTTGGAAGCAGATGTCAGGCTTTGGTGTGCCTGTGACCACC
TCATTGCTCCCATATTATCCCCCATTTTTAGTAGAGACGGGGTTTTAGTAGAGACTTGGCCTCCCAGAACCCCT
TCCTCTGCTCCTCCATGAATGACAATCCAGGCCTCCCTACCTCATGTCTCTCATTGTTGGGGATTGCTCCGTG
CTGTCCCTTTCTCTCAAGGCCGAAGTTGGGAAGTGAGAAACCATGTTTTTAACCTGTGGCTGCTTTTGCTGCTGC
TGCTCCTCCGTATCTGGCTGTATGGGTGGAGAACCCACCCCTGCCACCACAGGGGTCTCCTTCCAGGCCACTC
AGGACATTTTTAGCTTCTCTCCTCCCATGTTCCCTTTTTTCTCTAAAGTCCCTGACATCAGCCCTCCCAACTC
CTAAGAGGGACTACCCATGAGAGTGGGGTTCTGAGGCTCCCTATGGGGACAGTCCGTCTTGAAGTGTGAGT
TTGGGGAATATCTGTGGCCTATGAGGCCATCTCAGGTTTGGGGATCCCCCAGTCCCTATGATCAGTGTGGAGT
ACCCCCCTGGGAGAGCCTAGTTTCTTTGAGGCCCCAGGCCCTCTTTTAACTACCTTTGAATAGGTGTTATCCCTG
TATTTATGGAAATAAAGTTCCATTTCCCTC

2335/6881
FIGURE 2146A

AGAAGGTAGCAGACAGACAGACGGATCTAACCTCTCTTGGATCCTCCAGCCATGAGGCTGCTCTGGGGGCTGATC
TGGGCATCCAGCTTCTTCACCTTATCTCTGCAGAAGCCCAGGTTGCTCTTGTTCTCTCCTTCTGTGGTTTCATCTG
GGGGTCCCCCTATCGGTGGGGGTGCAGCTCCAGGATGTGCCCCGAGGACAGGTAGTGAAAGGATCAGTGTTCCCTG
AGAAACCCATCTCGTAATAATGTCCCCTGCTCCCCAAAGGTGGACTTCACCCTTAGCTCAGAAAGAGACTTCGCA
CTCCTCAGTCTCCAGGTGCCCTTGAAAGATGCGAAGAGCTGTGGCCTCCATCAACTCCTCAGAGGCCCTGAGGTC
CAGCTGGTGGCCCATTCGCCATGGCTAAAGGACTCTCTGTCCAGAACGACAAACATCCAGGGTATCAACCTGCTC
TTCTCCTCTCGCCGGGGGCACCTCTTTTTGTCAGACGGACAGCCCATTTACAACCCTGGCCAGCGGGTTCGGGTAC
CGGGTCTTTGCTCTGGATCAGAAGATGCGCCCCGAGCACTGACACCATCACAGTCATGGTGGAGAACTCTCACGGC
CTCCGCGTGCGGAAGAAGGAGGTGTACATGCCCTCGTCCATCTTCCAGGATGACTTTGTGATCCCAGACATCTCA
GAGCCAGGGACCTGGAAGATCTCAGCCCCGATTCTCAGATGGCCTGGAATCCAACAGCAGCACCCAGTTTGAGGTG
AAGAAATATGTCCTTCCCAACTTTGAGGTGAAGATCACCCCTGGAAAGCCCTACATCCTGACGGTGCCAGGCCAT
CTTGATGAAATGCAGTTAGACATCCAGGCCAGGTACATCTATGGGAAGCCAGTGCAGGGGGTGGCATATGTGCGC
TTTGGGCTCCTAGATGAGGATGGTAAGAAGACTTTCTTTCGGGGGCTGGAGAGTCAGACCAAGCTGGTGAATGGA
CAGAGCCACATTTCCCTCTCAAAGGCAGAGTTCCAGGACGCCCTGGAGAAGCTGAATATGGGCATTACTGACCTC
CAGGGGCTGCGCCTCTACGTTGCTGCAGCCATCATTGAGTCTCCAGGTGGGGAGATGGAGGAGGCAGAGCTCACA
TCCTGGTATTTTGTGTCTATCTCCCTTCTCCTTGGATCTTAGCAAGACCAAGCGACACCTTGTGCTGGGGCCCC
TTCTGCTGCAGGCCTTGGTCCGTGAGATGTCAGGCTCCCAGCTTCTGGCATTCTGTCAAAGTTTCTGCCACG
GTGTCTTCTCCTGGGTCTGTTTCTGAAGTCCAGGACATTAGCAAAACACAGACGGGAGCGGCCAAGTCAGCATT
CCAATAATTATCCCTCAGACCATCTCAGAGCTGCAGCTCTCAGTATCTGCAGGCTCCCCACATCCAGCGATAGCC
AGGCTCACTGTGGCAGCCCCACCTTCCAGGAGCCCCGGGTTTCTGTCTATTGAGCGGCCGGATTCTCGACCTCCT
CGTGTGGGGACACTCTGAACCTGAACTTGCAGAGCCGTGGGCAGTGGGGCCACCTTTTCTCATTACTACTACATG
ATCCTATCCCGAGGGCAGATCGTGTTCATGAATCGAGAGCCCAAGAGGACCCTGACCTCGGTCTCGGTGTTTGTG
GACCATCACCTGGCACCTCTCTTCTACTTTGTGGCCTTCTACTACCATGGAGACCACCCAGTGGCCAACCTCCCTG
CGAGTGGATGTCCAGGCTGGGGCCTGCGAGGGCAAGCTGGAGCTCAGCGTGGACGGTGCCAAGCAGTACCGGAAC
GGGGAGTCCGTGAAGCTCCACTTAGAAACCGACTCCCTAGCCCTGGTGGCGCTGGGAGCCTTGGACACAGCTCTG
TATGCTGCAGGCAGCAAGTCCCACAAGCCCCCTCAACATGGGCAAGGTCTTTGAAGCTATGAACAGCTATGACCTC
GGCTGTGGTCTTGGGGGTGGGGACAGTGCCCTTCCAGGTGTTCCAGGCAGCGGGCCTGGCCTTTTCTGATGGAGAC
CAGTGGACCTTATCCAGAAAGAGACTAAGCTGTCCCAAGGAGAAGACAACCCGAAAAAGAGAAACGTGAACCTC
CAAAAGGCGATTAAATGAGAAATTGGGTGAGTATGCTTCCCCGACAGCCAAGCGCTGCTGCCAGGATGGGGTGACA
CGTCTGCCCATGATGCGTTTCTGCGAGCAGCGGGCAGCCGCGTGCAGCAGCCGACTGCCGGGAGCCCTTCTCTG
TCCTGCTGCCAATTTGCTGAGAGTCTGCGCAAGAAGAGCAGGGACAAGGGCCAGGCGGGCCTCCAACGAGCCCTG
GAGATCCTGCAGGAGGAGGACCTGATTGATGAGGATGACATTCCCGTGCAGCTTCTTCCCAGAGAAGTGGCTC
TGGAGAGTGGAAACAGTGGACCGCTTTCAAATATTGACACTGTGGCTCCCCGACTCTCTGACCACGTGGGAGATC
CATGGCCTGAGCCTGTCCAAAACCAAAGGCCTATGTGTGGCCACCCAGTCCAGCTCCGGGTGTTCCGCGAGTTC
CACCTGCACCTCCGCTGCCCATGTCTGTCCGCCGCTTTGAGCAGCTGGAGCTGCGGCCTGTCTCTATAACTAC
CTGGATAAAAACCTGACTGTGAGCGTCCACGTGTCCCAGTGGAGGGGCTGTGCTGGCTGGGGGCGGAGGGCTG
GCCCAGCAGGTGCTGGTGCCTGCGGGCTCTGCCCGGCTGTTGCTTCTCTGTGGTGCCACGGCAGCCACCGCT
GTGTCTCTGAAGGTGGTGGCTCGAGGGTCTTTCGAATTCCCTGTGGGAGATGCGGTGTCCAAGGTTCTGCAGATT
GAGAAGGAAGGGGCGATCCATAGAGAGGAGCTGGTCTATGAACTCAACCCCTTGGACCACCGAGGCCGGACCTTG
GAAATACCTGGCAACTCTGATCCCAATATGATCCCTGATGGGGACTTTAACAGCTACGTCAGGGTTACAGCCTCA
GATCCATTGGACACTTTAGGCTCTGAGGGGGCCTTGTACCAGGAGCGTGGCCTCCCTCTTGAGGCTTCTCTGA
GGCTGTGGGGAGCAAACCATGATCTACTTGGCTCCGACACTGGCTGCTTCCCGCTACCTGGACAAGACAGAGCAG
TGGAGCACACTGCCTCCCGAGACCAAGGACCACGCCGTGGATCTGATCCAGAAAGGCTACATGCGGATCCAGCAG
TTTCGGAAGGCGGATGGTTTCTATGCGGCTTGGTTGTACGGGGCAGCAGCACCTGGCTCACAGCCTTTGTGTTG
AAGGTCTGAGTTTGGCCAGGAGCAGGTAGGAGGCTCGCTGAGAACTGCAGGAGACATCTAACTGGCTTCTG
TCCAGCAGCAGGCTGACGGCTCGTTCCAGGACCTCTCTCCAGTGATACATAGGAGCATGCAGGGGGGTTTGGTG
GGCAATGATGAGACTGTGGCACTCACAGCCTTTGTGACCATCGCCCTTCATCATGGGCTGGCCGTCTTCCAGGAT
GAGGGTGCAGAGCCATTGAAGCAGAGAGTGGAAGCCTCCATCTCAAAGGCAAGCTCATTTTTGGGGGAGAAAGCA

2336/6881
FIGURE 2146B

AGTGCTGGGCTCCTGGGTGCCACGCAGCTGCCATCACGGCCTATGCCCTGACACTGACCAAGGCCCTGCGGAC
CTGCGGGGTGTTGCCACAACAACCTCATGGCAATGGCCCAGGAGACTGGAGATAACCTGTACTGGGGCTCAGTC
ACTGGTTCTCAGAGCAATGCCGTGTCGCCCACCCGGCTCCTCGCAACCCATCCGACCCCATGCCCCAGGCCCA
GCCCTGTGGATTGAAACCACAGCCTACGCCCTGCTGCACCTCCTGCTTCACGAGGGCAAAGCAGAGATGGCAGAC
CAGGCTGCGGCCTGGCTCACCCTGTCAGGGCAGCTTCCAAGGGGGATTCCGCAGTACCCAAGACACGGTGATTGCC
CTGGATGCCCTGTCTGCCTACTGGATTGCCTCCCACACCACTGAGGAGAGGGGTCTCAATGTGACTCTCAGCTCC
ACAGGCCGGAATGGGTTCAAGTCCCACGCGCTGCAGCTGAACAACCGCCAGATTTCGCGGCCTGGAGGAGGAGCTG
CAGTTTTCTTGGGCAGCAAGATCAATGTGAAGGTGGGAGGAAACAGCAAAGGAACCTGAAGGTCTTCGTACC
TACAATGTCCTGGACATGAAGAACACGACCTGCCAGGACCTACAGATAGAAGTGACAGTCAAAGGCCACGTCGAG
TACACGATGGAAGCAAACGAGGACTATGAGGACTATGAGTACGATGAGCTTCCAGCCAAGGATGACCCAGATGCC
CCTCTGCAGCCCGTGACACCCCTGCAGCTGTTTGAGGGTCGGAGGAACCGCCGAGGAGGGAGGCGCCCAAGGTG
GTGGAGGAGCAGGAGTCCAGGGTGCCTACACCGTGTGCATCTGGCGGAACGCAAGGTGGGGCTGTCTGGCATG
GCCATCGCGGACGTCACCCCTCTGAGTGGATTCCACGCCCTGCGTGCTGACCTGGAGAAGCTGACCTCCCTCTCT
GACCGTTACGTGAGTCACTTTGAGACCGAGGGGCCCCACGTCTCTGTATTTTGAAGTGGTCCCCACCTCCCGG
GAGTGCGTGGGCTTTGAGGCTGTGCAGGAAGTGCCGGTGGGGCTGGTGCAGCCGGCCAGCGCAACCCCTGTACGAC
TACTACAACCCCGAGCGCAGATGTTCTGTGTTTTACGGGGCACCAAGTAAGAGCAGACTCTTGGCCACCTTGTGT
TCTGCTGAAGTCTGCCAGTGTGCTGAGGGGAAGTGCCCTCGCCAGCGTCGCGCCCTGGAGCGGGGTCTGCAGGAC
GAGGATGGCTACAGGATGAAGTTTGCCTGCTACTACCCCGTGTGGAGTACGGCTTCCAGGTAAAGGTTCTCCGA
GAAGACAGCAGAGCTGCTTTCCGCCTCTTTGAGACCAAGATCACCCAAGTCCTGCACTTCACCAAGGATGTCAAG
GCCGCTGCTAATCAGATGCGCAACTTCTTGTTTCGAGCCTCCTGCCGCCTTCGCTTGGAACCTGGGAAAGAATAT
TTGATCATGGGTCTGGATGGGGCCACCTATGACCTCGAGGGACACCCCAAGTACCTGCTGGACTCGAATAGCTGG
ATCGAGGAGATGCCCTCTGAACGCCTGTGCCGGAGCACCCGCCAGCGGCAGCCTGTGCCAGCTCAACGACTTC
CTCCAGGAGTATGGCACTCAGGGGTGCCAGGTGTGAGGGCTGCCCTCCCACCTCCGCTGGGAGGAACCTGAACCT
GGGAACCATGAAGCTGGAAGCACTGCTGTGTCCGCTTTCATGAACACAGCCTGGGACCAGGGCATATTAAAGGCT
TTTGGCAGCAAAGTGTCAGTGTTGGC

2337/6881
FIGURE 2147

TGTGGCCACCCAGTTTCAGCTCCGGGTGTTCCGCGAGTTCCACCTGCACCTCCGCCTGCCCATGTCTGTCCGCCG
CTTTGAGCAGCTGGAGCTGCGGCCTGTCTCTATAACTACCTGGATAAAAACCTGACTGTGAGCGTCCACGTGTC
CCAGTGAGGGGCTGTGCCTGGCTGGGGGCGGAGGGCTGGCCAGCAGGTGCTGGTGCTGCGGGCTCTGCCCG
GCCTGTTGCCTTCTCTGTGGTGCCACGGCAGCCACCGCTGTGTCTCTGAAGGTGGTGGCTCGAGGGTCTTCGA
ATTCCCTGTGGGAGATGCGGTGTCCAAGTTCTGCAGATTGAGAAGGAAGGGGCCATCCATAGAGAGGAGCTGGT
CTATGAACCAACCCCTTGGACCACCGAGGCCGACCTTGGAAATACCTGGCAACTCTGATCCCAATATGATCCC
TGATGGGGACTTTAACAGCTACGTCAGGGTTACAGCCTCAGATCCATTGGACACTTTAGGCTCTGAGGGGGCCTT
GTCACCAGGAGGCGTGGCCTCCCTCTTGAGGCTTCCTCGAGGCTGTGGGGAGCAAACCATGATCTACTTGGCTCC
GACACTGGCTGCTTCCCGCTACCTGGACAAGACAGAGCAGTGGAGCACACTGCCTCCCGAGACCAAGGACCACGC
CGTGATCTGATCCAGAAAGGCTACATGCGGATCCAGCAGTTTCGGAAGGCGGATGGTTTCTATGCGGCTTGGTT
GTCACGGGGCAGCAGCACCTGGCTCACAGCCTTTGTGTTGAAGGTCTGAGTTTGGCCCAGGAGCAGGTAGGAGG
CTCGCTGAGAACTGCAGGAGACATCTAACTGGCTTCTGTCCAGCAGCAGGCTGACGGCTCGTTCCAGGACCT
CTCTCCAGTGATACATAGGAGCATGCAAGGGGGTTTGGTGGGCAATGATGAGACTGTGGCACTCACAGCCTTTGT
GACCATCGCCCTTCATCATGGGCTGGCCGTCTTCCAGGATGAGGGTGCAAGCCATTGAAGCAGAGAGTGGAAGC
CTCCATCTCAAAGGCAAGCTCATTTTTGGGGGAGAAAGCAAGTGCTGGGCTCCTGGGTGCCACGCAGCTGCCAT
CACGGCCTATGCCCTGACACTGACCAAGGCCCTGCGGACCTGCGGGGTGTTGCCACAACAACCTCATGGCAAT
GGCCAGGAGACTGGAGATAACCTGTACTGGGGCTCAGTCACTGGTTCTCAGAGCAATGCCGTGTGCCCCACCC
GGCTCCTCGCAACCCATCCGACCCCATGCCCCAGGCCCCAGCCCTGTGGATTGAAACCACAGCCTACGCCCTGCT
GCACCTCCTGCTTACGAGGGCAAAGCAGAGATGGCAGACCAGGCTGCGGCCTGGCTACCCCGTCAGGGCAGCTT
CCAAGGGGGATTCCGCAGTACCAAGACACGGTGATTGCCCTGGATGCCCTGTCTGCCTACTGGATTGCCTCCCA
CACCCTGAGGAGAGGGGTCTCAATGTGACTCTCAGCTCCACAGGCCGGAATGGGTTCAAGTCCACGCGCTGCA
GCTGAACAACCGCCAGATTGCGGCCTGGAGGAGGAGCTGCAGTTTCTTGGGCAGCAAGATCAATGTGAAGGT
GGGAGGAAACAGCAAAGGAACCTGAAGGTCTTTCGTACCTACAATGTCTGGACATGAAGAACACGACCTGCCA
GGACCTACAGATAGAAGTGACAGTCAAAGGCCACGTGAGTACACGATGGAAGCAAACGAGGACTATGAGGACTA
TGAGTACGATGAGCTTCCAGCCAAGGATGACCCAGATGCCCTCTGCAGCCCGTGACACCCCTGCAGCTGTTTGA
GGGTGCGAGGAACCGCCGAGGAGGGAGGCGCCCAAGGTGGTGGAGGAGCAGGAGTCCAGGGTGCCTACACCGT
GTGCATCTGGCGGAACGGCAAGGTGGGGCTGTCTGGCATGGCCATCGCGGACGTCACCCCTCTGAGTGGATTCCA
CGCCCTGCGTGCTGACCTGGAGAAGCTGACCTCCCTCTCTGACCGTTACGTGAGTCACTTTGAGACCGAGGGGCC
CCACGTCTGTGTATTTTGAAGTCTGGTCCCCACCTCCCGGAGTGCGTGGGCTTTGAGGCTGTGCAGGAAGTGCC
GGTGGGGCTGGTGCAGCCGGCCAGCGCAACCCCTGTACGACTACTACAACCCCGAGCGCAGATGTTCTGTGTTTTA
CGGGGCACCAAGTAAGAGCAGACTCTTGGCCACCTTGTGTTCTGCTGAAGTCTGCCAGTGTGCTGAGGGGAAGTG
CCCTCGCCAGCGTTCGCGCCCTGGAGCGGGGTCTGCAGGACGAGGATGGCTACAGGATGAAGTTTGCCTGCTACTA
CCCCGTGTGGAGTACGGCTTCCAGGTTAAGGTTCTCCGAGAAGACAGCAGAGCTGCTTTCCGCCTCTTTGAGAC
CAAGATCACCCAAGTCTGCACTTCACCAAGGATGTCAAGGCCGCTGCTAATCAGATGCGCAACTTCTGTTGCG
AGCCTCCTGCGCCTTCGCTTGGAACTTGGGAAAGAATATTTGATCATGGGTCTGGATGGGGCCACCTATGACCT
CGAGGGACACCCCAAGTACCTGCTGGACTCGAATAGCTGGATCGAGGAGATGCCCTCTGAACGCCTGTGCCGGAG
CACCCGCCAGCGGGCAGCCTGTGCCCAGCTCAACGACTTCTCCAGGAGTATGGCACTCAGGGGTGCCAGGTGTG
AGGGCTGCCCTCCCACCTCCGCTGGGAGGAACCTGAACCTGGGAACCATGAAGCTGGAAGCACTGCTGTGTCCGC
TTTCATGAACACAGCCTGGGACCAGGGCATATTAAAGGCTTTTGGCAGCA

2338/6881
FIGURE 2148

ATTCTTGTCTGTTCTGCCTCACTCCCGAGCTCTACTGACTCCCAACAGAGCGCCCAAGAAGAAA**ATG**GCCATAAG
TGGAGTCCCTGTGCTAGGATTTTTTCATCATAGCTGTGCTGATGAGCGCTCAGGAATCATGGGCTATCAAAGAAGA
ACATGTGATCATCCAGGCCGAGTTCTATCTGAATCCTGACCAATCAGGCGAGTTTATGTTTGAAGTTTGGACGATTGCGCAGCTT
TGAGATTTTCCATGTGGATATGGCAAAGAAGGAGACGGTCTGGCGGCTTGAAGAATTTGGACGATTGCGCAGCTT
TGAGGCTCAAGGTGCATTGGCCAACATAGCTGTGGACAAAGCCAACCTGGAAATCATGACAAAGCGCTCCAACTA
TACTCCGATCACCAATGTACCTCCAGAGGTAAGTGTGCTCACGAACAGCCCTGTGGAAGTGAAGAGAGCCCAACGT
CCTCATCTGTTTCATAGACAAGTTCACCCACCAAGTGGTCAATGTCACGTGGCTTCGAAATGGAAAACCTGTCAC
CACAGGAGTGTGAGAGACAGTCTTCCTGCCCAGGGAAGACCACCTTTTCCGCAAGTTCCACTATCTCCCTTCCT
GCCCTCAACTGAGGACGTTTACGACTGCAGGGTGGAGCACTGGGGCTTGGATGAGCCTCTTCTCAAGCACTGGGA
GTTTGTATGCTCCAAGCCCTCTCCAGAGACTACAGAGAACGTGGTGTGTGCCCTGGGCCTGACTGTGGGTCTGGT
GGGCATCATTATTGGGACCATCTTCATCATCAAGGGATTGCGCAAAAGCAATGCAGCAGAACGCAGGGGGCCTCT
GTAAGGCACATGGAGGTGATGGTGTTCCTTAGAGAGAAGATCACTGAAGAACTTCTGCTTTAATGGCTTTACAA
AGCTGGCAATATTACAATCCTTGACCTCAGTGAAAGCAGTCATCTTCAGCATTTTCCAGCCCTATAGCCACCCCA
AGAGTGGTTATGCCTCCTCGATTGCTCCATACTCTAACATCTAGCTGGCTTCCTGTCTATTGCCTTTTCCTGTA
TCTATTTTCCCTCTATTTCCCTATCATTTTATTATCACCATGCAATGCCTCTGGAATAAAACATACAGGAGTCTGTC
TCTGCTATGGAATGCCCCATGGGGCATCTCTTGTGTACTTATTGTTTAAGGTTTCCTCAAAGTGTGATTTTTCTG
AACACAATAAACTATTTTGAAGATCTTGGGTGGAA

2339/6881
FIGURE 2149

MAISGVPVLGFFIIAVLMSAQESWAIKEEHVIIQAEFYLNPDQSGEFMFDFDGD EIFHVDMAKKETVWRLEEFGR
FASF EAQ GALANI AVDKANLEIMTKRSNYTPITNVPPEVTVL TNSPVELREPNVLICFIDKFTPPVVNVTWLRNG
KPVTTGVSETVFLPREDHLFRKFHYLPFLPSTEDVYDCRVEHWGLDEPLLKHWEFDAPSPLPETTENVVCALGLT
VGLVGIIIGTIFI IKGLRKSNA AERRGPL

2340/6881
FIGURE 2150

ATGAAGGCCAACTACAGCGCAGAGGAGCGCTTTCTCCTGCTGGGTTTCTCCGACTGGCCTTCCCTGCAGCCGGTC
CTCTTCGCCCTTGTCCTCCTGTGCTACCTCCTGACCTTGACGGGCAACTCGGCGCTGGTGCTGCTGGCGGTGCGC
GACCCGCGCCTGCACACGCCCATGTACTACTTCCTCTGCCACCTGGCCTTGGTAGACGCGGGCTTCACTACTAGC
GTGGTGCCGCCGCTGCTGGCCAACTGCGCGGACCAGCGCTCTGGCTGCCGCGCAGCCACTGCACGGCCCAGCTG
TGCGCATCGCTGGCTCTGGGTTCGCGCGAATGCGTCCTCCTGGCGGTGATGGCTCTGGACCGCGCGGCCGAGTG
TGCCGCCCCGCTGCGCTATGCGGGGCTCGTCTCCCCGCGCCTATGTGCGACGCTGGCCAGCGCCTCCTGGCTAAGC
GGCCTCACCAACTCGGTTGCGCAAACCGCGCTCCTGGCTGAGCGGCCGCTGTGCGCGCCCCGCCTGCTGGACCAC
TTCATCTGTGAGCTGCCGGCGTTGCTCAAGCTGGCCTGCGGAGGCGACGGAGACACTACCGAGAACCAGATGTTT
GCCGCCCCGCTGGTCATCCTGCTGCTGCCGTTTGCCGTCATCCTGGCCTCCTACGGTGCCGTGGCCCCGAGCTGTC
TGTTGCATGCGGTTTACGCGGAGGCCGGAGGAGGGCGGTGGGCACGTGTGGGTCCCACCTGACAGCCGTCTGCCTG
TTCTACGGCTCGGCCATCTACACCTACCTGCAGCCGCGCAGCGCTACAACCAGGCACGGGGCAAGTTCGTATCG
CTCTTCTACACCGTGGTCACACCTGCTCTCAACCCGCTCATCTACACCCTCAGGAATAAGAAAGTGAAGGGGGCA
GCGAGGAGGCTGCTGCGGAGTCTGGGGAGAGGCCAGGCTGGGCAGTGA

2341/6881
FIGURE 2151

MEGTQEYDSSMQTVRFQGERRKSPSNATFSPFFWMPHSAKSLVADAGIHSRNQHSYATIASFIKYSQLHFKSRESR
AGARDQPIIWKLKANYSAEERFLLLGFSDWPSLQPVLFALVLLCYLLTLTGNSALVLLAVRDPRLHTPMYYFLCH
LALVDAGFTTTSVVPPLLNLRGPALWLPRSHCTAQLCASLALGSAECVLLAVMALDRAAAVCRPLRYAGLVSPRL
CRTLASASWLSGLTNSVAQTALLAERPLCAPRLLDHFICELPALLKLACGGDGDTTENQMFARVVILLLPFAVI
LASYGAVARAVCCMRFSGGRRRAVGTCGSHLTAVCLFYGSAIYTYLQPAQRYNQARGKFVSLFYTVVTPALNPLI
YTLRNKKVKGAARRLLRSLGRGQAGQ

2342/6881
FIGURE 2152

GAGAGCACGACGTGCGCGCACCCCTCTCCCCTTGTCCACTGCTGCCGCCTCCTTCTTCTGCCGCTCCTGGTGCTGC
TTGTGTGCTCGTTTGGAGCGGACCTGGTACCTCTTTTGTGAAGCGGCAGCTGAGGAGACTCCGGCGCTCGCCATG
GCCGAAGAAAAGCCCAAGGAAGGAGTCAAGACTGAGAACAACGATCATATTAATTTGAAGGTGGCGGGGCAGGAT
GGTTCTGTGGTGCAGTTTAAAGATTAAGAGGCATACACCACTTAGTAACTAATGAAAGCCTATTGTGAACGACAG
GGATTGTCAATGAGGCAGATCAGATTCCGATTGACGGGCAACCAATGAAACAGACACACCTGCACAGTTGGAAA
TGGAGGATGAAGATACAATTGATGTGTTCCAACAGCAGACGGGAGGTGTCTACTGAAAAGGGAACCTGCTTCTTT
ACTCCAGAACTCTGTTCTTTAAAGACCAAGATTACATTCTCAATTAGAAAAGTCAATTTGCTTCCACCACATCC
TGACTACTACCGTATAGTTTTCTCTATTCTTTCAATTTCCCCCTTCCCCATTCTTTACTGTACATAAAGTAACTG
GTATATGTGCACAAGCATATTACTTTTTTTTTTTTAAACTAAACAGCCAATGGTATGTTTTGATTGACATCAAGT
GGAGACGGGGCGGAAAAATACTGATTCTGTGAAAATACCCCCCTTCTCCATTAGTGGCATGCTCATTGAGCTCTT
ATCTTTATATTCCAGTAAGTTATTTTGCTCTCACTGTTTTAACAACAACAACAAAAACAACAACATAAAAAATC
CTTGCAACCTTGTTCATTGGAGAATTTAATGTTTTTCATTTATCATTGTAAAACCAAGGACAATTTTATAAC
TTTTTTGTACTTAGCTGTTACATGCAGAGCAATCTGTCTTTAAGTAGGGATAAATTACTCTAAAAACAAAAAGAA
TCCTAGATAGTTTTCCCTTCAAGTCAAGCGTCTTGTTGTTTAAATAAACTTCTTGTTTAAAA

2343/6881
FIGURE 2153

MAEEKPKEGVKTENNDHINLKVAGQDGSVVQFKIKRHTPLSKLMKAYCERQGLSMRQIRFRFDGQPMKQTHLHSW
KWRMKIQLMCSNSRREVSTEGTCFFTPELCSLTKITFSIRKLQFASTTS

2344/6881
FIGURE 2154

GCGCACCCCTCTCCCCTTGTCCACTGCTGCCGCCTCCTTCTTCTGCCGCTCCTGGTGCTGCTTGTGTGCTCGTTTG
GAGCGGACCTGGTACCTCTTTTGTGAAGCGGCAGCTGAGGAGACTCCGGCGCTCGCCATGGCCGAAGAAAAGCCC
AAGGAAGGAGTCAAGACTGAGAACAACGATCATATTAATTTGAAGGTGGCGGGGCAGGATGGTTCTGTGGTGCAG
TTTAAGATTAAGAGGCATACACCACTTAGTAACTAATGAAAGCCTATTGTGAACGACAGTGGAAATGGAGGATG
AAGATACAATTGATGTGTTCCAACAGCAGACGGGAGGTGTCTACTGAAAAGGGAACCTGCTTCTTTACTCCAGAA
CTCTGTTCTTTAAAGACCAAGATTACATTCTCAATTAGAAAAGTCAATTTGCTTCCACCACATCCTGACTACTA
CCGTATAGTTTTCTCTATTCTTTCATTTCCCCCTTCCCCATTCTTTACTGTACATA

2345/6881
FIGURE 2155

AGACGCCGAGATGCTGGTCATGGCGCCCCGAACCGTCCTCCTGCTGCTCTCGGCGGCCCTGGCCCTGACCGAGAC
CTGGGCGCGCTCCCACTCCATGAGGTATTTCTACACCTCCGTGTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCAT
CTCAGTGGGCTACGTGGACGACACCCAGTTCGTGAGGTTGACAGCGACGCCGCGAGTCCGAGAGAGGAGCCGCG
GGCGCCGTGGATAGAGCAGGAGGGGCCGGAGTATTGGGACCGGAACACACAGATCTACAAGGCCCAGGCACAGAC
TGACCGAGAGAGCCTGCGGAACCTGCGCGGCTACTACAACCAGAGCGAGGCCGGGTCTCACACCCTCCAGAGCAT
GTACGGCTGCGACGTGGGGCCGGACGGGCGCCTCCTCCGCGGGCATGACCAGTACGCCTACGACGGCAAGGATTA
CATCGCCCTGAACGAGGACCTGCGCTCCTGGACCGCCGCGGACACGGCGGCTCAGATCACCCAGCGCAAGTGGA
GGCGGCCCGTGAGGCGGAGCAGCGGAGAGCCTACCTGGAGGGCGAGTGCGTGAGTGCTCCGCAGATACCTGGA
GAACGGGAAGGACAAGCTGGAGCGCGCTGACCCCCAAAGACACACGTGACCCACCACCCCATCTCTGACCATGA
GGCCACCCTGAGGTGCTGGGCCCCTGGGTTTCTACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGCGAGGA
CCAAACTCAGGACACTGAGCTTGTGGAGACCAGACCAGCAGGAGATAGAACCTTCCAGAAGTGGGCAGCTGTGGT
GGTGCCTTCTGGAGAAGAGCAGAGATACACATGCCATGTACAGCATGAGGGGCTGCCGAAGCCCCTCACCTGAG
ATGGGAGCCGTCTTCCCAGTCCACCGTCCCCATCGTGGGCATTGTTGCTGGCCTGGCTGTCCTAGCAGTTGTGGT
CATCGGAGCTGTGGTCGCTGCTGTGATGIGTAGGAGGAAGAGTTTCAAGGTGGAAAAGGAGGGAGCTACTCTCAGGC
TGCCTGCAGCGACAGTGGCCAGGGCTCTGATGTGTCTCTCACAGCTTGAAAAAGCCTGAGACAGCTGTCTTGTGAG
GGACTGAGATGCAGGATTTCTTCACGCCITCCCCTTTGTGACTTCAAGAGCCTCTGGCATCTCTTTCTGCAAAGGC
ACCTGAATGTGTCTGCGTCCCTGTTAGCATAATGTGAGGAGGTGGAGAGACAGCCCACCCTTGTGTCCACTGTGA
CCCCTGTTTCGCATGCTGACCTGTGTTTCCTCCCA .

2346/6881
FIGURE 2156

MLVMAPRTVLLLLSAALALTETWAGSHSMRYFYTSVSRPGRGEPRFISVG YVDDTQFVRFDS DAASPREEPRAPW
IEQEGPEYWDRNTQIYKAQAQTDRESLRNLRGYYNQSEAGSHTLQSMY GCDVGP DGRLLRGHDQYAYDGKDYIAL
NEDLRSWTAADTAAQITQRKWEAAREAEQRRAYLEGECEVEWLRRYLENGKDKLERADPPKTHVTHHPISDHEATL
RCWALGFYPAEITLTWQRDGEDQTQDTIELVETRPAGDRTFQKWA AVVVP SGEEQRYTCHVQHEGLPKPLTLRWE P
SSQSTVPIVGIVAGLAVLAVVVIGAVVAAVMCRRKSSGGKGGSYSQAACSDSAQGS DVSLTA

2347/6881
FIGURE 2157

GGCGCCCCGAACCGTCCTCCTGCTGCTCTCGGCGGCCCTGGCCCTGACCGAGACCTGGGCGCCCCAGGCTCCCA
CTCCATGAGGTATTTGACACCGCCATGTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCTCAGTGGGCTACGT
GGACGACACGCAGTTCGTGAGGTTGACAGCGACGCCGCGAGTCCGAGAGAGGAGCCGCGGGCGCCGTGGATAGA
GCAGGAGGGGCGGAGTATTGGGACCGGAACACACAGATCTTCAAGACCAACACACAGACTGACCGAGAGAGCCT
GCGGAACCTGCGCGGCTACTACAACCAGAGCGAGGCCGGGTCTCACACCCTCCAGAGCATGTACGGCTGCGACGT
GGGGCCGGACGGGCGCCTCCTCCGCGGGCATAACCACTACGCTACGACGGCAAGGATTACATCGCCCTGAACGA
GGACCTGCGCTCCTGGACCGCGGCGGACACCGCGGCTCAGATCACCCAGCGCAAGTGGGAGGCGGCCCGTGTGGC
GGAGCAGGACAGAGCCTACCTGGAGGGCACGTGCGTGGAGTGGCTCCGCAGATACCTGGAGAACGGGAAGGACAC
GCTGGAGCGCGCGGACCCCCCAAAGACACACGTGACCCACCACCCCATCTCTGACCATGAGGCCACCCTGAGGTG
CTGGGCCCTGGGCTTCTACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGCGAGGACCAAACCTCAGGACAC
TGAGCTTGTGGAGACCAGACCAGCAGGAGATAGAACCTTCCAGAAGTGGGCAGCTGTGGTGGTGCCTTCTGGAGA
AGAGCAGAGATACACATGCCATGTACAGCATGAGGGGCTGCCGAAGCCCCCTCACCCCTGAGATGGGAGCCGTCTTC
CCAGTCCACCGTCCCCATCGTGGGCATTGTTGCTGGCCTGGCTGTCTTAGCAGTTGTGGTCATCGGAGCTGTGGT
CGCTGCTGTGATGTGTAGGAGGAAGAGCTCAGGTGGAAAAGGAGGGAGCTACTCTCAGGCTGCGTGCAGCGACAG
TGCCAGGGCTCTGATGTGTCTCTCACAGCTTGAAAAGCCTGAGACAGCTGTCTTGTGAGGGACTGAGATGCAGG
ATTTCTTCACGCCTCCCCTTTGTGACTTCAAGAGCCTCTGGCATCTCTTTCTGCAAAGGCACCTGAATGTGTCTG
CGTCCCTGTTAGCATAATGTGAGGAGGTGGAGAGACAGCCCACCCCTTGTGTCCACTGTGACCCCTGTTCCCATGC
TGACCTGTGTTTCTCCCCAGTCATCTTTCTTGTTCAGAGAGGTGGGGCTGGATGTCTCCATCTCTGTCTCAAC
TTTACGTGCACTGAGCTGCAACTTCTTACTTCCCTACTGAAAATAAGAATCTGAATATAAATTTGTTTTCTCAAA
TATTTGCTATGAGAGGTTGATGGATTAATTAAATAAGTCAATTCTGGAATTTGAGAGAGCAAATAAAGACCTGA
GA

2348/6881
FIGURE 2158

MLVMAPRTVLLLLSAAALALTETWAGSHSMRYFDTAMSRPGRGEPRFISVGYVDDTQFVRFDSDAASEFREEPRAPW
IEQEGPEYWDNRNTQIFKTNTQTDRESLRNLRGYYNQSEAGSHTLQSMYGC DVGPDGRLLRGHNQYAYDGKDYIAL
NEDLRSWTAADTAAQITQRKWEAARVAEQDRAYLEGTCVEWLRRYLENGKDTLERADPPKTHVTHHFISDHEATL
RCWALGFYPAEITLTWQRDGEDQTQDTEL VETRPAGDRTFQKWA AVVVP SGEEQRYTCHVQHEGLPKPLTLR WEP
SSQSTVPIVGIVAGLAVLAVVIGAVVAAVMCRRKSSGGKGGSYSQAACSDSAQGS DVSLTA

2350/6881
FIGURE 2160

TCTAATACCTATTGATCTGTTACTTTCTCCCATCACGCTCAGGTGGGAACATCCAGTTGCAGGAAAACAAGCTTA
ACACGCCCCACTGATTCTACATTATGGTGAGTTCTATAATTATTTTATTATATATTACAGTGTAATAATGGAAATA
AAGTGCCTAATAAAATGCAAATGTGCTTACATCTTTTGGCCCAGCTCCTACCTCCCGGCAGCCTCTCCAGGCCCAG
AACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCTCAATGGCCTATTTAGGCCCATAACCCTACGTCAC
GGCAGCCTCCGCAGATGAGGCTACTGCCTCACAACAGCCTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTT
TAGACCCAGCTCCTGCCTCCAGCCTTCTCTCCAGGCCCTGAACTTTCTCAAGTTGACCTCACCAGGCCAGCTC
ATGCTTCTTTGCAGCCTCTCCAGGCCAGCTCCTGCATCTTGGTGGCCCCTCCAGGCCAGCCTCTGCCTCCCGT
CAGCCTCTACAGTCCCAACGTCTGCCTCACAGCAGATTCTTCACGCCCAGCTTCTACCTCACTTGGACCCCTCCAG
ACCCAGATGGTGTCTCACTGTGGCATCCTCAGGTGAAGCTCCTGCCTTTCGGCAGCCTCTCCAGGCCAGCTCCT
CCTGCCTCCCAGTGGCCTCTTTTCGGCCCAGCCCAGCTCATGCCTCCCGGCGGCCTTCCCAAGCCCCGCTTTTGAC
TTTCGGTGGCCTCTGCAGGCCTCGACAAGGCCAGCCTCCTGCCTCCCGAAGGCCTGCACAGGCCAGCCTCTGC
CTCACAGCGGACTCTC

2351/6881
FIGURE 2161

TGAGGGAGTGAGGGAAGCTTCCTCTGTATTTACAGCCACTCCCCTTTGCTCACATTCCCGCCTGAGCTCCACCTT
CTCAGATGAGCAGCAGCATTAGATGCTCATAGGAGAACGCACCCTGTTGTGAACCATGCATGTGAGGGATCTAGG
TTGCGCTGTCCTTATGAGAGTCTAATACCTATTGATCTGTCACTTTCTCCCATCACGCTCAGGTGGGAACATCCA
GTTGCAGGAAAACAAGCTTAACACGCCCCTGATTCTACATTATGCTCCTACCTCCCGGCAGCCTCTCCAGGCCC
AGAACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCAAAATGGCCTATTTAGGCCCATAACCCTACGTC
ACGGCAGCCTCCGCAGATGAGGCTACTGCCTCACAACAGCCTCCACAGGCACAGCTCCATCGTTACAATGGCCTC
TTTAGACCCAGCTCCTGCCTCCCAGCCTTCTCTCCAGGCCCTGAACATTCTCAGGTCTCCCTCTGTTGTCCAAGG
CTGGAGTGTAGTAGTGCTATCGCAGCTGACTGCAGCCTCAACCTTCCAGGCTGAAGCGATCCTCCACGTCAACC
TCCACGTGGCTGAGACTACAGGTGCTTGCCACTATGCCCAACTAATATTTGGAATTTTCATATACGTGGATTCC
AGAGGGGTGACAGCGAAACGTGGGAACATCCAGTTGCAGGAAAACAAGCTTAACACGCCCCTGATTCTACATTA
TGCTCCTACCTCCCGGCAGCCTCTCCAGGCCCAGAACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTC
TCAATGGCCTATTTAGGCCCATAACCCTACGTCACGGCAGCCTCCGCAGATGAGGCTACTGCCTCACAACAGCCTC
CACAGGCACAGCTCCATCGTTACAATGGCCTCTTTAGACCCAGCTCCTGCCTCCCAGCCTTCTC

2352/6881
FIGURE 2162

MAYLGPYPTSRQPPQMRLPHNSLHRHSSIIVTMASLDPAPASQPSLQALNFLKLTSPGPAHASLQPLQAQLLHLG
GPSRPSLCLP SASTVPTSASQQILHAQLLPHLDPPDPDGVSLWHPQVKLLPFGSLSRPSSSLPVASFGPAQLMP
FGGLPKPRF

2353/6881
FIGURE 2163

GGCACGAGGGCCGGAAGGCGGCGTCCGCGACGCAGCTGTTACGCTTAGGTGGGCGACGTGGGCGCAGGTGGGCG
CAGG**ATG**GCAAAACAGAAGAGAAAAGTTCTGAAGTGACAGAGAAAAAGAACAAAAAGCTGAAGAAGGCGTCAGC
AGAGGGGGCCACTGCTGGGGCCCTGAGGCTGCACCAAGTGGCGAAGGAGCCGGCTCCAAGGGCGAAGCTGTGCTCAG
GCCCCGGGCTGGACGCAGAGCCAGAGCTGTCCCCAGAGGAGCAGAGGGTCCTGGAAAGGAAGCTGAAAAAGGAACG
GAAGAAAGAGGAGAGGCAGCGTCTGCGGGAGGCAGGCCTTGTGGCCCAGCACCCGCTGCCAGGCGCTCGGGGGC
CGAACTGGCCCTGGACTACCTCTGCAGATGGGCCCCAAAAGCACAGAAGTGGAGGTTTCAGAAGACGAGGCAGAC
GTGGCTCCTGCTGCACATGTATGACAGTGACAAGGTTCCCGATGAGCACTTCTCCACCCTGCTGGCCTACCTGGA
GGGGCTGCAGGGCCGGGCCGAGAGCTGACGGTGCAGAAGGCGGAAGCCCTGATGCGGGAGCTGGATGAGGAGGG
CTCTGATCCCCCCTGCCGGGGAGGGCCCAGCGCATCCGACAGGTGCTGCAGCTGCTCTCC**TAG**TGGGTTTCAGCG
CGGGGCGGGGCCGCTGCCAGTGCAGGGCTGCCTCAGACCACACAGGGTGCAGCTCCTCCGGCGGTGGGGGCCGG
GTTACACCAGCAGGGCAGCGGCTGAGCAAGGGCTTTCAGCTCCTCCGGTGGTGGGGGCCGGGATCACCAGCACCAG
AGCCTCGCAAGGGCCCCCTTCCCTCCTCCAGACCCTCCTTGGCCGGTGACGGCTGTGACAGTGATGGCAGGTTTCAG
TGCTTTCAGCGCAGAGCGTGGATGCTCTGGAATCACCCGGACCCCTGGCCTTGGAGGGACCCTCCAGCCCCAGGA
ATCTGCTTTGGAGGGAAATGTCTATTTTTCTACCGGGAATATTTTAGAGATTGGGGCATGCTGGCTCCTCCCGCC
AGCTGCAAACCTGCACCTTCCGCCTGATTCCCCGATCCCCCTGCGTGGGCCGCGATTCTGGTCCCCCTGCCTGCGTC
CATCGAGGGGCGCTGGCTGTGGCCTGTTTTCTTTGACCCACACAGCGTCATTGCGGGTCATGGGGAGCCCCCTGG
TGGGAGCTTGTGGAGTCGGATCACGTACCTGTGCAGAAACCGCCTCTGTGGCTGCATTTGAAATAAAACCCGACC
CAGCAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

2354/6881
FIGURE 2164

MAKQKRKVPEVTEKKNKKLKKASAEGLLGPEAAPSGEGAGSKGEAVLRPGLDAEPELSPEEQRVLERKLLKKERK
KEERQRLREAGLVAQHPPARRSGAELALDYLCRWAQKHKNWRFQKTRQTWLLHMYDSKVPDEHFSLLAYLEG
LQGRARELTVQKAEALMRELDEEGSDPPLPGRAQRIRQVLQLLS

2355/6881
FIGURE 2165

GCGGCGCGCTGCAGGCGCGGGGAACACCAATGGCGGGGTACTTGAAGCTGGTGTGTGTTTCCTTTCAGCGTCAAG
GGTTCCACACTGTTGGGAGTCGCTGCAAGAATCGGACAGGCGCTGAGCACCTGTGGCTGACCCGACATCTCAGGG
ACCCATTTGTGAAGGCTGCGAAGGTGGAGAGTTACCGGTGTGCGAAGCGCCTTCAAGCTCCTGGAGGTGAACGAGA
GGCACCAGATTCTGCGGCCCGGCCTTCGGGTGTTAGACTGTGGGGCAGCTCCTGGGGCCTGGAGTCAGGTGGCGG
TGCAGAAGGTCAACGCCGCAGGCACAGATCCCAGCTCTCCTGTTGGCTTCGTGCTTGGGGTAGATCTTCTTCACA
TATTCCTCCCTGGAAGGAGCAACTTTTCTGTGCCCTGCTGACGTGACTGACCCGAGAACCTCACAGAGAATCCTCG
AGGTGCTTCCTGGCAGGAGAGCAGATGTGATTCTGAGCGACATGGCGCCCAATGCCACAGGGTTCCGGGACCTCG
ATCATGACAGGCTCATCAGCCTGTGCCTGACCCTTCTCAGCGTGACCCCAGACATCCTGCAACCTGGGGGGACAT
TCCTTTGTAAAACCTGGGCTGGAAGTCAAAGCCGTCGGTTACAGAGGAGACTGACAGAGGAATTCAGAATGTAA
GGATCATCAAACCTGAAGCCAGCAGGAAAAGAGTCATCAGAAGTGTACTTCTTGGCCACACAGTACCACGGAAGGA
AGGGCACTGTGAAGCAGTGAAGGATTTCTTGTGCCATTTTCATAATGGTCATTAGCTCCTTTTAAGCTAGAAACGT
AGCCTGAGCTCCTGAAGAGTTTCTGGGAGATTTGAGCTGATTTTGGAGATGGAGCAGGACAAGTGGGGAGTCTCT
CTCTCTCTTTCTCTCTCTCTCTTTTTTAACCAAAAAGAGATGACAAAATAAGTTCAGGGGCCATGGAATAATGAAA
AAGTCCGCTATATTGTGATTTGGGAAGAGAAAAGTTATCAAGAGAAAAGAGGTGAGGATGGAAGGATGGAGAAAAAC
AGACTGTGGGAAGGATCAGAAGGAATCCGCCGAGGCAGGGATGGGTGTGCCCATGTGTGCCTTGACGGGACTTCA
TCTTATAGACTGTTAACTGTACACACAAACAGGCTTTCCACCCCTGCTCTGAGAGCACCACGCACAGATTTCC
AGTTCTTAGTGTGGCTGTTTAAAGTAGAAAATCTGGGGGCTGGGTGAGGCCACTCATGCCTGTAAACCCAGGGCT
TTAGAAGGCTGAGGCTGGGGGATTGCTTGAAGTCAGGAGTTCAAGACCAACCTGGGCAACATAGCAACACCCCCC
ATGTCTACAAAAATGAAAAACCAAAAAGCAAACCAAAAGAAAAATCTGAAATTTCCATCTGGGGATTAACTTCTG
TCTTTCTGGTGAACAATATAGCAATTCACGCATTCTTCAAGCAGCAAAAGTTCCCGGAACAATTAGGGAAGACGT
ATGGTCTGAATTTATCCAGGCAGTGGGTCTGCTTTGGTTTTTGCTGGAAATTTATATCAGTGTCTGGGCTCCCAA
GAACATAAATGTAATTGCCAAAGCAAAAAA

2356/6881
FIGURE 2166

MAGYLKLVCSFQRQGFHTVGSRCNRTGAEHLWLTRHLRDPFVKAAKVESYRCRSFAFKLLEVNERHQILRPGLR
VLDCGAAPGAWSQVAVQKVNAAGTDPSSPVGFVLGVDLLHIFPLEGATFLCPADVTDPRTSQRILEVLPGRRADV
ILSDMAPNATGFRDLDDHRLISLCLTLLSVTPDILQPGGTFLCKTWAGSQSRRLQRRLTEEFQNVRIIKPEASRK
ESSEVYFLATQYHGRKGTVKQ

2357/6881
FIGURE 2167

CGGCGGCCGCGGAGCCCTGCGAGTAGGCAGCGTTGGGCCCCATGCAGGACGCGGAGAACGTGGCGGTGCCCCGAGGC
GGCCGAGGAGCGCGCCGAGCCCGGCCAGCAGCAGCCGGCCGCGCCAGCCGCCAGCCGAGGGGCTGCTGCGGCC
CGCGGGGCCCCGCGCTCCGAGAGCGCGGGGACCGAGGCCTCCAGTGAGGAGGTGGGGATCGCGGAGGCCGGGCC
GGAGTCCGAGGTGAGGACCGAGCCGGCGGCCGAGGCAGAGGCGGCCTCCGGCCCGTCCGAGTCGCCCTCGCCGCC
GGCCGCGGAGGAGCTGCCCGGGTCGCATGCTGAGCCCCCTGTCCCGGCACAGGGCGAGGCCCCAGGAGAGCAGGC
TCGGGACGAGCGCTCCGACAGCCGGGCCAGGCGGTGTCCGAGGACGCGGGAGGAAACGAGGGCAGAGCGGCCGA
GGCCGAACCCCGGGCGCTGGAGAACGGCGACGCGGACGAGCCCTCCTTCAGCGACCCCGAGGACTTCGTGGACGA
CGTGAGCGAGGAAGAATTACTGGGAGATGTACTCAAAGATCGGCCCCAGGAAGCAGATGGAATCGATTTCGGTGAT
TGTAAGTGGACAATGTCCCTCAGGTGGGACCCGACCGACTTGAGAACTCAAAAATGTCATCCACAAGATCTTTTC
CAAGTTTGGGAAAATCACAAATGATTTTTATCCTGAAGAGGATGGGAAGACAAAAGGGTATATTTTCTGAGGTA
CGCGTCCCCTGCCCACGCTGTGGATGCTGTGAAGAAGCCGACGGCTACAAGCTTGACAAGCAGCACACATTCCG
GGTCAACCTCTTTACGGATTTTGACAAGTATATGACGATCAGTGACGAGTGGGATATTCCAGAGAAACAGCCTTT
CAAAGACCTGGGGAACCTTACGTTACTGGCTTGAAGAGGCAGAATGCAGAGATCAGTACAGTGTGATTTTTGAGAG
TGGAGACCGCACTTCCATATTCTGGAATGACGTAAAGACCCCTGTCTCAATTGAAGAAAGAGCGAGATGGACAGA
GACGTATGTGCGTTGGTCTCCTAAGGGCACCTACCTGGCTACCTTTTCATCAAAGAGGCATTGCTCTATGGGGGGG
AGAGAAATTCAAGCAAATTCAGAGATTCAGCCACCAAGGGGTTAGCTTATTGACTTCTCACCTTGTGAAAGGTA
CCTGGTGACCTTTAGCCCCCTGATGGACACGCAGGATGACCCCTCAGGCCATAATCATCTGGGACATCCTTACGGG
GCACAAGAAGAGGGGTTTTCACTGTGAGAGCTCAGCCATTGGCCTATTTTTAAGTGGAGCCATGATGGCAAATT
CTTTGCCAGAATGACCCTGGATACGCTTAGCATCTATGAACTCCTTCTATGGGTCTTTTGGACAAGAAGAGTTT
GAAGATCTCTGGGATAAAAGACTTTTCTTGGTCTCCTGGTGGTAACATAATCGCCTTCTGGGTGCCTGAAGACAA
AGATATTCCAGCCAGGGTAACCCCTGATGCAGCTCCCTACCAGGCAAGAGATCCGAGTGAGGAACCTGTTCAATGT
GGTGGACTGCAAGCTCCATTGGCAGAAGAACGGAGACTACTTGTGTGTGAAAGTAGATAGGACTCCGAAAGGCAC
CCAGGTGTTGTCAAAATTTTGAATTTTCCGAATGAGGGAGAAACAGGTACCTGTGGATGTGGTCGAGATGAA
AGAAACCATCATAGCCTTTGCCTGGGAACCAAATGGAAGTAAGTTTGCTGTGCTGCACGGAGAGGCTCCGCGGAT
ATCTGTGTCTTTCTACCACGTCAAAAACAACGGGAAGATTGAACTCATCAAGATGTTTCGACAAGCAGCAGGCGAA
CACCATCTTCTGGAGCCCCCAAGGACAGTTCGTGGTGTGGCGGGCCTGAGGAGTATGAACGGTGCCTTAGCGTT
TGTGGACACTTCGGACTGCACGGTCATGAACATCGCAGAGCACTACATGGCTTCCGACGTCGAATGGGATCCTAC
TGGGCGCTACGTCGTCACCTCTGTGTCTGGTGGAGCCATAAGGTGGACAACGCGTACTGGCTGTGGACTTTCCA
GGGACGCCTCCTGCAGAAGAACAACAAGGACCGCTTCTGCCAGCTGCTGTGGCGGGCCCCGGCCTCCACACTCCT
GAGCCAGGAACAGATCAAGCAAATTAAGGATCTGAAGAAATACTCTAAGATCTTTGAACAGAAGGATCGTTT
GAGTCAGTCCAAAGCCTCAAAGGAATTGGTGGAGAGAAGGCGCACCATGATGGAAGATTTCCGGAAGTACCGGAA
AATGGCCCAGGAGCTCTATATGGAGCAGAAAAACGAGCGCCTGGAGTTGCGAGGAGGGGTGGACACTGACGAGCT
GGACAGCAACGTGGAGCACTGGGAAGAGGAGACCATTGAGTTCTTCGTCACTGAAGAAATCATTCCCCTCGGGAA
TCAGGAGTGACCTGGAGCACTGTGCGCAGCCGTGTGTGCTGTGGAGCCGAGGCCGTCTGCAGGAAGCCGCGTGA
CTCCCGCCTCCTCCCTGTGCTCTCTGGCTCTGGACTGTGACTGCGCCTGGATTCTGCCATTGCGACACATTTTTG
TGCCTTTTCAGCCCCCTGGTGTCTGCAGTGGGGGATTTAAGGCACCCGCTTCCACTTCTTTCTTGTGTTGGAGTTTT
TGTTGGAACCGCCGGCGTTGGCTCCGAAGACTTAGCGACGCCACTGGCGGCACCTTCTCCTGCGCCCAGTGATGT
TTCCACGGTGCCTGTACACAGCCGAGCAGCATTTCGTTGAAGGACTTGCATCCCCATTGCGGGCAGTGCTGGAC
GTGTCCCGGAGACCCACCGGGAGGGCGCCGCCATGCCTTGTACCCCCACCGTGCAGGTTGTGGCCGGTTTTCTCC
GCAGGTTGAACATGGAAATAAAAGCAAACCTTGATG

2358/6881
FIGURE 2168

GTCCGAGCGACCGGCTTGGCGCCTGCCTGTCCCCAGCCCCTCTCAGCTTGAACCTCCTTCCTTCAAGTCTGGGCCC
TCGAGGCTTCCAGAGCGGCCTCCAGGGGTGCAGTCTCAGTTCCCCACGCCAGCCGTCTCCGTCTCCGCCCTCCTC
CGGGCCTGGCAGGTGGCACTGTCCGGAGGCGGAGCCTTGGGCGAGGGGTGGTTGCGGCGGAGGACGCAACCGAGC
GGGCCTGCGGCCTCACCATGGACCCAGAATGCGCCCAGCTGCTCCCGGCTCTCTGTGCTGTTCTGGTAGATCCCA
GGCAGCCGGTGGCAGATGACACCTGTTTGGAGAAGCTCCTGGACTGGTTTAAAACGGTCACTGAAGGAGAGTCCA
GTGTCGTGCTGCTGCAGGAGCACCCCTGCCTGGTGGAGCTGCTGTCCC**ATG**TGCTGAAAGTCCAGGACCTGAGTT
CTGGGGTCTCTCCTTCTCACTGCGCCTGGCAGGAACCTTCGCAGCCCAGGAAAAGTCTTCCAGTATCTTCAGG
TGCGGTCGACACCATCTTCTCCCTGCAGGGAGACTCCAGCCTGTTTGTGGCCTCGGCGGCCAGTCAGCTCCTGGT
GCAGTCTCTGGCTTTGTCCATGCGAGGTGGAGCCGAGGGGCGAGCCCTGCCTGCCGGGGGGTGAAGTGGCCCCGCGT
TGCCCAAGATCATGGATCACGTTGAAGAGTCCTTGTGCTCCGCGGCCACCCCCAAGGTCACTCAGGCCCTGAA
CGTCTTGACACGACCTTCGGGCGCTGCCAGAGCCCCTGGACGGAAGCCCTGTGGGTGCGGCTGAGTCCCCGCGT
GGCCTGTCTGCTGGAGAGAGACCCCATCCCCGCCGCACACTCGTTCGTGGACCTGCTTCTCTGTGTGGCTCGTTC
TCCCGTGTTCAAGTTCTTCCGACGGCAGCCTGTGGGAGACAGTGGCGCGGGCTCTGAGCTGCCTGGGTCCCACCCA
CATGGGACCCCTGGCTTTGGGGATCCTGAAGCTCGAGCACTGTCCACAGGCACTGAGGACCCAGGCCTTCCAGGT
CCTTCTCCAGCCCCTGGCCTGTGTCTGAAGGCCACGGTTTCAAGCCCCCGACCCCCAGGCTTGTGGACGGGAC
GGCAGACGATGCCACGACGGTGGACACACTCCTGGCCTCCAAGTCGTCCTGCGCCGGCCTCCTGTGCCGCACCT
GGCTCACCTGGAGGAGCTGCAGCCGCTGCCCCAGCGCCCTTCAACCGTGGCCCCAGGCGTCTCTACTGGGGGCTAC
AGTGAAGTGTCTGCGGCTCTGTGACGGCTCGGCTGCCCCCTGCCTCCAGTGTGGGGGGCCACCTCTGTGGGACCT
GGCGGGCTGCGTCCGGGTCCAGCGAGCAGCCCTCGACTTCCTGGGGACGCTGTACAGGGGACAGGCCCCCAGGA
GCTGGTGACGCAGGCGCTTGTGTCTCCTGGAGTGCCTCGAGAGCCCCGGCTCCAGCCCCACGGTTCTGAAGAA
GGCCTTCCAGGCCACGCTCAGGTGGCTCCTGAGCTCACCAAGACCCCCGGCTGCTCTGATCTCGGCCCCCTCAT
CCCGCAGTTTCTCAGAGAGCTGTTCCCTGTGCTGCAGAAACGCTGTGCCACCCCTGCTGGGAGGTGAGGGACTC
CGCCCTCGAGTTCTTGACCCAGCTGAGCAGGCACTGGGGAGGACAGGCTGACTTCAGATGCGCACTCTTGGCTTC
AGAGGTGCCTCAGCTGGCCCTGCAGCTCCTCCAGGACCTGAGAGTTATGTCCGAGCGAGTGCAGTGACCGCCAT
GGGGCAGCTGTCCAGCCAGGGCCTGCACGCCCCACCAGCCCTGAGCATGCAGAGGCCCCGGCAGAGCCTGTTCT
GGAGCTCCTGCACATCCTCTCCGTAGACTCGGAGGGCTTCCACGGCGGGCGGTTCATGCAAGTCTTCACTGAGTG
GCTGCGGGACGGCCACGCCGACGCGGCCAGGACACGGAGCAGTTTCGTGGCCACTGTGCTGCAGGCGGCGAGCCG
AGACCTGGACTGGGAGGTCCGCGCCCAGGGCCTGGAGCTGGCCCTCGTGTTCCTGGGCCAGACTTTGGGGCCGCC
GCGTACCCACTGCCCCATATGCCGTGGCCCTACCCGAGGTGGCCCCAGCCAGCCACTCACCGAGGCACTGAGGGC
TCTCTGCCACGTGGGGCTCTTTGACTTCGCCCTTTTGTGCTTGTGTTGACTGCGACCGCCCTGTGGCGCAGAAGTC
TTGTGACCTCCTTCTTCTTCTGAGGGACAAGATTGCTTCTACAGCAGCCTGCGGGAGGCCAGGGGCGAGCCCCAA
CACTGCCTCCGCAGAGGCCACCCCTGCCGAGGTGGCGGGCGGGTGAAGCAGGCCAGCCCCAGGGGACCAGGAGCC
TGAGGCTGTGCTGGCCATGCTCAGGTCCCTAGACCTGGAGGGCCTGCGGAGCACGCTGGCCGAGAGCAGCGACCA
CGTGGAAAAGAGTCCCCAGTCCCTCCTGCAGGACATGCTGGCCACGGGAGGCTTCTGTCAGGGGGACGAGGCCGA
CTGCTACTGAGCAGAACCAGAGTCTGCCACTGGGGCTCAGGACCAAGGGAGGCAGCACCATGTCTTCTGTGGGA
CACTGCCAGCCCCAGGGCTCCAGCCCAGCCCGGTGGATCCTCTGGGGAAGCCAGGACCAGGAGAGAAGCAAGGTC
AAGAAATCCCACAGTTTGATGTATTAAAGAAATGACTTATTTCTACTCAAATAAATGGCATTGAAGTCTTTCTT
T

2359/6881
FIGURE 2169

MRGGAEGQPCLPGGDWPACAQKIMDHVEESLCSAATPKVTQALNVLTTFGRQCSPWTEALWVRLSPRVACLLER
DPIPAAHSFVDLLLCVARSPVFSSSDGSLWETVARALSCLGPTHMGPLALGILKLEHCPQALRTQAFQVLLQPLA
CVLKATVQAPGPPGLLDGTADDATTVDITLLASKSSCAGLLCRTLAHLEELQPLPQRPSWPWQASLLGATVTVLRL
CDGSAAPASSVGGHLCGTLAGCVRVQRAALDFLGTLISQGTGPQELVTQALAVLLECLESPGSSPTVLKKAQATL
RWLLSSPKTPGCSDLGFLIPQFLRELFPVLQKRLCHPCWEVRDSALEFLTQLSRHWGGQADFRCALLASEVPQLA
LQLLQDPESYVRASAVTAMGQLSSQGLHAPTSPEHAEARQSLFLELLHILSVDSEGFPRRAVMQVFTEWLRDGH
DAAQDTEQFVATVLQAASRDLDWEVRAQGLELALVFLGQTLGPPRTHCPYAVALPEVAPAQPLTEALRALCHVGL
FDFAFCALFDCDRPVAQKSCDLLLFLRDKIASYSSLREARGSPNTASAEATLPRWRAGEQAQPPGDQEPEAVLAM
LRSLDLEGLRSTLAESSDHVEKSPQSLLQDMLATGGFLQGDEADCY

2360/6881
FIGURE 2170A

GGCGGCCGAGCGGAGCCGAGCGCAGCCGAGCCGGGCGGAGCCGGGCGGCGGCCAGGAGCGCGCGGATGAT
GCGGGCGGCCAGGCGGGGGTTCGACGGGTCCCTGAAGCCCGCGCCCCGGGCCAGCAAGGGAGCCCCGCGCAGGCCG
CGCGCATCCGAGGCGGGCGGGCCCCGCCATGCGCGGGGTTCAGCTACGCGGCGCCCTGGTGGGTGAGCCTCCTGC
ACCGGCTGCCCCACTTCGACCTGAGCTGGGAGGCCACTAGCAGCCAGTTCCGGCCCCGAGGACACCGACTACCAGC
AGGCCCTGCTGCTCCTGGGGGCGCGCCCTGGCCTGCCTCGCCCTGGACCTCCTCTTCTGCTCTTCTACTCCT
TCTGGCTGTGCTGCCGGCGGCGCAAGAGCGAGGAGCACCTGGACGCCGACTGCTGCTGCACGGCCTGGTGTGTCA
TCATCGCCACGCTGGTGTGTCAGCGCCGGCATCGCAGTGGGATTCTACGGCAACGGGGAGACCAGTGATGGCATCC
ATAGGGCCACCTACTCGCTCCGCCACGCCAACCGCACGGTGGCCGGGTCCAGGACCGCGTGTGGGACACGGCGG
TGGGGCTGAACCACACGGCGGAGCCAGCCTGCAGACCCTGGAGCGGCAGCTGGCCGGGCGGCCCCGAGCCCCCTGC
GAGCCGTACAGAGGCTGCAGGGCCTGCTGGAGACGCTGCTGGGCTACACGGCCGCCATCCCCCTTTTGGAGGAACA
CGGCGGTGTGCTGGAGGTGCTGGCGGAGCAGGTGGATCTCTACGACTGGTACAGGGTCTGCCTGCTGGGAGTCC
TGGCCCTGGTCATCAGCTGGGGCGCGCTGGGCTTGGAGCTGGCTGTGTCCGTGGGCTCCAGCGACTTCTGTGTGG
ACCCTGACGCCTACGTGACCAAAATGGTGGAGGAGTACTCGGTGCTGAGTGGGGACATCCTGCAGTACTACCTGG
CCTGCTCGCCCCGCGCCGCCAACCCCTTCCAGCAGAAGCTGTGCGGCAGCCACAAGGCACTGGTGGAGATGCAGG
ATGTCGTGGCTGAGCTTCTGAGGACCGTCCCCTGGGAGCAGCCGGCCACTAAGGACCCCTCCTCCGCGTCCAGG
AGGTGCTGAATGGCACGGAGGTGAACCTGCAGCACCTCACCGCCCTGGTGGACTGCCGCAGCCTGCATCTGGACT
ACGTGCAAGCGCTGACCGGCTTCTGCTATGACGGCGTGGAGGGCTCATCTACCTGGCCCTCTTCTCCTTCGTCA
CAGCCCTCATGTTTCTGCTCCATCGTCTGCAGCGTCCCGCACACCTGGCAGCAAAAGAGAGGGCCCTGATGAGGACG
GGGAGGAGGAGGCCGCTCCAGGGCGCGGCAGGCGCACGACAGCCTCTACCGCGTCCACATGCCAGCCTGTACA
GCTGTGGCAGCAGCTACGGCAGTGGAGACGATCCCGGCCGCGGCCACACCGTCAGCAACGCCCCGGTCACTG
AGTACATGAGCCAGAACGCTAATTTCCAGAACCCCCGCTGTGAGAACACCCCACTCATTGGGCGCGAGTCCCCGC
CGCCCTCATACACCTCCAGCATGAGAGCCAAATACCTCGCCACGAGCCAGCCTCGCCCTGACTCCAGCGGCAGCC
ACTAGACCGCGCCCCGCGACGCCACCCACCCACGTGCCAACTTCCCCTCCCCGTGCCAGCACTGCCGCTTCCACCT
GGGCCACCCACCGGACCTTCGCACGCCGTGCCAGGCCTGCCCCAGACGCGTCTGCAGGCCGCTTGCCTCCTGTC
CCCTCCCCGCGAGGGGCACAGTGGAGACGCGAGGGCTCTGGGCCGTACCGCCAACTCGGGTCACACCTGAACGCT
GCTGCCAGCCGATGCCCCAGCCCTGCACGCCACCCACTATCCCGGCACGCTCCCTCTGCAGATGGTCCGCCACCC
TACAAGCCCTGGCCGACCCAACTGTGTTGTTGCCGCCCGGCCCTTCCCTCCACAGCTCTCCTTCCCTCCCGCCC
GGCACTTCTGTGGACCCCTTCTTAGTTACAGGCACGGCTGGGGCCGCTCTGTGCTGGCGCCTGCTGGCCACTGA
GGGACAGGGACAGTGCCACCTGCTCATCTCTGCCCTGAGGTACCCCGTGGTCCCTCCACGTGCCCATCTCTCT
GCAGTGGCCTCCTCGCCTGTGCAGCCCGCCACCCACAGGCTCACCCCTCCTGCCGGCTGCCAGAGGCCCCCTCC
AGCAGGGCCTCTCTCCGTTGCCCCAGCTTCACTCTCTCCCTCAGCACCTGCCCTGCTGGAGGGCCCCAGCCCTCCG
TGGACAGCAGGGGCCACGTGGAGCCCGGGCCGCTACCCGCCACCCAGTGTGGCCGCTTCTTGGTGCCAAACC
CCCTTCCCCCACCCAGAGACTGGGCAGCTGTGTCTGGTTCTTTGCTACTAACCACATTTGTCTCTCTAGGG
CAGGCTGGGGCTGCGGGCTGAGGGGGACCGCTGGCACCCCTTCCCTCCCTTCTTGGTTCCATTTCCATCCATG
ACAGGTACAGCATCCCAGGAGCCCGGCTGAGGGGCTGGACCCGAGCCGGCTGTGAACATCCCTCAGCCCCCTGCT
GTCCCCCTTGGGACTAACCACTAACCTCACCCCAAACCTCCACGGGTGCCCTAGCTGGCCAGAGCCGGCAGT
GTGAGCCCAAGTCCGGGCTGGAGCCGAGGCCGAGCAGCTGTCTGGGAGTCAAGGCTGCAGTAGCGTTTCTTCAT
GGGGTGCTCCAGGGGGTGCCACAGACCGACAGGCAGCCCAAGGGCCTGGACACCCCTCCCCAGGCAGGTGCTGCC
CCAGGAGGACTGTCTTCGGAATGAACCTCCCGCGGGCTTTGGACTGAGGTCCCTGTGGCCTCGGTCTCCTCCCC
ATGAAGTGGGAGCGAGGCTCCCCAATGGTGCTTTTGGCTTTAGTGTACGATGTTTGCTGTGCTTCCCGCCGTGGA
GGGCAGAGCCACCCACATCAGGATCGGACGTGTACCCCTCCCGGTCCCGGCCCTGGCCCAGCCAGCCAGCCCC
TCGAGGCTCGATGCCTGTGCCAAGGCCAGGGGCGAGCCAGAGGCGAGCTGGATGGCCACGTGCAGGGGTCAAGGCT
GGGCCCTGCAGTGGGGCGGGCCGCCAGCCCCAGCAGTTTACAGACGCATGGCTCTTCTCCAGAGCAGCCGGCA
GCTACCTGGACCGGAAATGTCTCATCCCCCTCCCTGGGGCCAGGCTCTGCCCTGGCCTTCTCTGTGAACCCCTC
CTTTCTTTGTGCTGGTGTCTGGGACCAAAAAGGGGAATATGGGAGGGCAGAGTGGGGAGGGGAGTCCATGGGCC
TGGGGCCCCAAGCCGGGCGTCTGAGCTCCCCAGGCATGACCAACCTCAGTGGAGGGGCTCTGCTTCAGGCCC
CGCCTGGCTGACATTCTGAGCCCCCTCGGAGGCCCGCCACAGCCAACCTGCCCAGTCTTTCTCTGGGCTTGA
CCCGCCAGGGGAGTTCTCCAGGCCTAGGGCCAGGAGAGAGGCCCTGGCACCTGGCGTGGGTGCCCGCCAAACGC

2361/6881
FIGURE 2170B

CCTGCGACCGCTCAGAAGCACAAATGCTGTCCATGGCCGTGAGGCTGCCTGCCAGGTGAATGGACATAGCGTGAG
AGGCGGTGAGGCCAGGGCTTCCAGCCTCGTGCTGTCTCGGGACTCCTGACCGTGGTGTGCGTGTGTGCCCCTCTG
TGACTTTCTACTACCAAGGTTGAAGAAAGGAAACGGGGAAAATCAAAGGGGTTCAAACCCACCTCAGTAGGT
GGAGGGGAGCGCCTGCCATTGGTTGTATTTTGTTCGTGAGTTTTCGGTGCCGTGTTCCCTAACTACTCCATCCCAT
GACCTCGCCACACCTACTGGGGCATCTGGCTGGTGCCCTGCTGCCATGGCCAGCCCCACTCTCACCTGCACAGG
GGGTCTTGACAGCCCCCAGGCCCACAGCCTCGTTGGGAGGACAGGGTGGCCCTGGGGACAAGAGGGAGGAGCCCAG
GGGCTTACCTCACTGAGAGTGCTCCCCAGCAGGCATCCACTACCCAGGGCCCCCACAATGTCATGGCAAGGTTG
GTAGTGAATGGGCCTGGTTGGGAGCAGCCCCTGGCCCATTGCCCACCCACCCATCTCACTATGCAATTCGAGTTC
CAAGCAACATTTGCTCCTGCCCTGGGGCCAGCTCTGCCCCAGCCCTGAGAGGGGTGGTGAGGCAGCCCCCTGGAC
CCCAGAACCCAGACAAGGGGGCAGGCGGGGGACCAGGGCCTCTCCTGTGGGATCTTTGTTTTGTGTTTAACCAT
AATGGTTGTGTACTGAACCACTTCATATTTGTTATATATAATATATATATATAATCTCCTTAAGACTCAGCCT
CCTGGTTTACCCCCCGGCCTGGGCATCTGACCTCCCCACCCAGTGTGATTTAACATCCAGGAACTGAGGCCT
GAACCATTTTGCATTTCCCCCTCCTCCAGCCTCTGTAGGGCCATGGCTGTATGTACTGTGCTGTGTTTTTTTGT
TTTTTTAGAACTGGGTTTGGGGGCTGATTTTTATTTCTTTGGGGGCTTTTTTTCTTGGCAAATACTAAAAATCTC
GTCAATGTAATTTCTGTGGTTTCTATTTCAGCTTGGGTTTCATGTTTTAAATAAATTTTAAAAAGC

2362/6881
FIGURE 2171

MAGVSYAAPWWVSLHRLPHFDLSWEATSSQFRPEDTDYQQALLLLGAAALACLALDLLFLLFYSEFWLCCRRRKS
EEHLDADCCCTAWCVIIATLVCSAGIAGFYGNGETSDGIHRATYSLRHRANRTVAGVQDRVWDTAVGLNHTAEPS
LQTLERQLAGRPEPLRAVQRLQGLETLLGYTAAIPFWRNTAVSLEVLAEQVDLYDWYRVCLLGVLALVISWGAL
GLELAVSVGSSDFCVDPDAYVTKMVEEYSVLSGDILQYYLACSPRAANPFQQKLSGSHKALVEMQDVVAELLRTV
PWEQPATKDPLL RVQEV L NGTEVN LQH L TALVD CRSLHLDYVQALTGFCYDGVEGLIYLA L FSEVTALMFSSIVC
SVPHTWQQKRGPD EDG EEEA A PGPRQA HD SLYRVHMP SLYSCGSSYGSETSIPAAAHTVSNAPVTEYMSQANFQ
NPRCENTPLIGRESPPPSYTSSMRAKYLATSQFRPDSSGSH

2363/6881
FIGURE 2172

ACAGAACAGAGAGAAAGGAACCTTTGTCTTTTCGTGTGAATGCTCGTGAGGGGCCATCCTTAGAGTGGAAATGCTC
CTGAGGCTCCAGCGAATCAAGACCCTCAGACCCCGGGCTGTCCCCACCCCATGACCACATGTTCCGCAGGCACC
CTCAGCGCTGTGCCCTGCGTGTGCGCCAGGCAGGTGTTTGTGTTTTTGAGCGCAGATTCTGCCTGTGGCATAGCCAT
GTGGAGATGTTACGCGATGTACTTCCCTTTGTGATTTAGCCGATACGGAAGATGTGTGCATTGTAGAGAGATTG
TTCTCCAGCAGCCTAGTGGCCATCGTGAGCCTTAAAGCACCAAGGAAGCTAAAGGTTTGCCACTTTAAGAAGGGA
ACTGAGATCTGCAACTACAGCTACTCCAACACGATTCTGGCTGTGAAGCTCAACAGGCAGAGGCTGATAGTATGC
CTGGAGGAGTCCCTGTACATCCACAACATTTCGGGACATGAAGGTGCTGCATACGATCAGGGAGACGCCTCCAAAC
CCTGCAGGCCTGTGTGCGCTGTCAATCAACAACGACAACCTGCTACTTGGCGTACCCAGGGAGCGCGACCATCGGA
GAGGTGCAGGTCTTCGATACCATTAATTTGAGAGCTGCAACATGATTCCGGCTCACGACAGTCCTTTAGCGGCA
CTGGCCTTTGACGCAAGTGGAATAAAGTTGCCACGGCTTCGGAGAAGGGGACCGTGATTAGGGTATTTTCCATT
CCAGAAGGACAAAACTCTTTGAGTTTCGGAGAGGAGTAAAGAGGTGCGTGAGCATCTGCTCCCTGGCCTTCAGC
ATGGACGGCATGTTCTCTCCGCCTCCAGCAACACTGAGACCGTGACATCTTCAAACCTCGAGACTGTGAAAGAA
AAACCCCGAGAGGAGCCACCACCTGGACCGGGTACTTCGGGAAAGTGCTCATGGCCTCCACCAGCTACCTGCCT
TCCCAAGTGACAGAAATGTTCAACCAGGGCAGAGCTTTTCGCCACGGTCCGCCTGCCATTCTGCGGCCACAAAAAC
ATCTGCTCGCTAGCCACAATTCAGAAGATCCCGCGGTTGTTGGTGGGTGCCGCCGACGGGTACCTGTACATGTAC
AACCTGGACCCCCAGGAGGGCGGGCAGTGTGCCCTGATGAAGCAGCACCGGCTGGACGGCAGTCTGAAAACGACC
AATGAGATCTTGGACTCTGCCTCTCAGACTGCCCCCTTAGTCACTCAGACATACGGCGCAGCTGCAGGAAAAGCC
TACACAGACGACCTGGGTGCTGTGGGTGGCGCCTGCCTGGAGGACGAGGCCAGCGCCCTGCGCCTGGATGAGGAC
AGCGAGCACCCGCCCATGATTCTTCGACTGACTGAACCTTGACCTGTGACCTCTGACCCGGGGAGCAGAGAACAC
TGGCTTCACAGAGGACTTTGTGCATTGCTGCTATGAACCTTGACCTGAGTCGGGGGAGAGGATGGCAGAGACTTT
ATT

2364/6881
FIGURE 2173

MLLRLQRIKTLRPPGCPHPMTTCSAGTLSAVPCVSPRQVFVFERRFCLWHSVEMFTHVLPFVISADTEDVCIVE
RLFSSSLVAIVSLKAPRKLVCHFKKGTEICNYSYSNTILAVKLNQRRLIVCLEESLYIHNIRD MKVLHTIRETP
PNPAGLCALSINNDNCYLAYPGSATIGEVQVFD TINLRAANMIPAHDSPLAALAFDASGTKLATASEKGT VIRVF
SIPEGQKLFEFRRGVKRCVSICSLAFSMDGMFLSASSNTETVHIFKLETVKEKPPEEPTTWTGYFGKVLMASTSY
LPSQVTEMFNQGRAFATVRLPFCGHKNICSLATI QKIPRLLVGAADGYLYMYNLDPQEGGECALMKQHRLDGS LK
TTNEILDSASHDCPLVTQTYGAAAGKAYTDDLGA VGGACLEDEASALRLDEDSEHPPMILRTD

2365/6881
FIGURE 2174

CGCGTCCGCCCCGCGAGCACAGAGCCTCGCCTTTGCCGATCCGCCGCCCGTCCACACCCGCCGCCAGCTCACCAT
GGATGATGATATCGCCGCGCTCGTCGTCGACAACGGCTCCGGCATGTGCAAGGCCGGCTTCGCGGGCGACGATGC
CCCCCGGGCCGTCTTCCCTCCATCGTGGGGCGCCCCAGGCACCAGGGCGTGATGGTGGGCATGGGTGAGAAGGA
TTCCTATGTGGGCGACGAGGCCCAGAGCAAGAGAGGCATCCTCACCCCTGAAGTACCCCATCGAGCACGGCATCGT
CACCAACTGGGACGACATGGAGAAAATCTGGCACCACACCTTCTACAATGAGCTGCGTGTGGCTCCCGAGGAGCA
CCCCGTGCTGCTGACCGAGGCCCCCTGAACCCCAAGGCCAACCGCGAGAAGATGACCCAGATCATGTTTGAGAC
CTTCAACACCCCGAGCCATGTACGTTGCTATCCAGGCTGTGCTATCCCTGTACGCCTCTGGCCGTACCACTGGCAT
CGTGATGGACTCCGGTGACGGGGTCACCCACACTGTGCCCATCTACGAGGGGTATGCCCTCCCCCATGCCATCCT
GCGTCTGGACCTGGCTGGCCGGGACCTGACTGACTACCTCATGAAGATCCTCACCGAGCGCGGCTACAGCTTCAC
CACCACGGCCGAGCGGGAAATCGTGCGTGACATTAAGGAGAAGCTGTGCTACGTGCCCCTGGACTTCGAGCAAGA
GATGGCCACGGCTGCTTCCAGCTCCTCCCTGGAGAAGAGCTACGAGCTGCCTGACGGCCAGGTCATCACCATTGG
CAATGAGCGGTTCCGCTGCCCTGAGGCACTCTTCCAGCCTTCCTTCCTGGGCATGGAGTCCTGTGGCATCCACGA
AACTACCTTCAACTCCATCATGAAGTGTGACGTGGACATCCGCAAAGACCTGTACGCCAACACAGTGCTGTCTGG
CGGCACCACCATGTACCCTGGCATTGCCGACAGGATGCAGAAGGAGATCACTGCCCTGGCACCCAGCACAAATGAA
GATCAAGATCATTGCTCCTCCTGAGCGCAAGTACTCCGTGTGGATCGGCGGCTCCATCCTGGCCTCGCTGTCCAC
CTTCCAGCAGATGTGGATCAGCAAGCAGGAGTATGACGAGTCCGGCCCCCTCCATCGTCCACCGCAAATGCTTCTA
GGCGGACTATGACTTAGTTGCGTTACACCCTTTCTTGACAAAACCTAACTTGCGCAGAAAACAAGATGAGATTGG
CATGGCTTTATTTGTTTTTTTTTGTTTTGTTTTGGTTTTTTTTTTTTTTTTTTGGCTTGACTCAGGATTTAAAAACTG
GAACGGTGAAGGTGACAGCAGTCGTTGGAGCGAGCATCCCCAAAGTTCACAATGTGGCCGAGGACTTTGATTG
CACATTGTTGTTTTTTTTTAATAGTCATTCCAAATATGAGATGCATTGTTACAGGAAGTCCCTTGCCATCCTAAAAG
CCACCCCACTTCTCTCTAAGGAGAAATGGCCCAGTCCTCTCCCAAGTCCACACAGGGGAGGTGATAGCATTGCTTT
CGTGTAATATGTAATGCAAAATTTTTTTAATCTTCGCCCTTAATACTTTTTTATTTTGTGTTTTATTTTGAATGAT
GAGCCTTCGTGCCCCCCTTCCCCCTTTTTGTCCCCAACTTGAGATGTATGAAGGCTTTTGGTCTCCCTGGGAG
TGGGTGGAGGCAGCCAGGGCTTACCTGTACACTGACTTGAGACCAGTTGAATAAAAGTGCACACCTTA

2366/6881
FIGURE 2175

MDDDIAALVVDNGSGMCKAGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQKDSYVGDEAQS KRGILTLKYPIEHGI
VTNWDDMEKIWHHTFYNELRVAPEEHPVLLTEAPLNPKANREKMTQIMFETFNTPAMYVAIQAVLSLYASGRITG
IVMDSGDGVTHTVPIYEGYALPHAILLRLDLAGRDLDYLMKILTERGYSFTTTAEREIVRDIKEKLCYVALDFEQ
EMATAASSSSLEKSYELPDGQVITIGNERFRCPEALFQPSFLGMESCGIHETTFNSIMKCDVDIRKDLYANTVLS
GGTTMYPGIADRMQKEITALAPSTMKIKIIAPPERKYSVWIGGSILASLSTFQQMWISKQEYDESGPSIVHRKCF

2367/6881
FIGURE 2176

GCGGAGGGTGCCTGCGGGCCGCGGCAGCCGAACAAAGGAGCAGGGGCGCCGCGCAGGGACCCGCCACCCACCTC
CCGGGGCCGCGCAGCGGCCTCTCGTCTACTGCCACCATGACCGCCAACGGCACAGCCGAGGCGGTGCAGATCCAG
TTGGGCTCATCAACTGCGGCAACAAGTACCTGACGGCCGAGGCGTTTCGGGTTCAAGGTGAACGCGTCCGCCAGC
AGCCTGAAGAAGAAGCAGATCTGGACGCTGGAGCAGCCCCCTGACGAGGCGGGCAGCGCGGCCGCTGTGCCCTGCGC
AGCCACCTGGGCCGCTACCTGGCGGGCGGACAAGGACGGCAACGTGACCTGCGAGCGCGAGGTGCCCGGTCCCGAC
TGCCGTTTCCTCATCTGCGGCACGACGCGTCTGGTCTGCTGCGAGGCGCACCGGCGCTACTTCGGC
GGCACCGAGGACCGCCTGTCTGCTTCGCGCAGACGGTGTCCCCCGCCGAGAAGTGGAGCGTGACATCGCCATG
CACCTCAGGTCAACATCTACAGTGTACCCGTAAGCGCTACGCGCACCTGAGCGCGCGGCCGCGGCCGACGAGATC
GCCGTGGACCGGACGTGCCCTGGGGCGTGCAGTCTGCTCATCACCTTCGCTTCCAGGACCAGCGCTACAGCGTG
CAGACCGCCGACCACCGCTTCTGCGCCACGACGGGCGCTGGTGGCGCGCCCCGAGCCGGCCACTGGCTACACG
CTGGAGTTCCGCTCCGGCAAGGTGGCCTTCCGCGACTGCGAGGGCCGTTACCTGGCGCCGTCGGGGCCCCAGCGGC
ACGCTCAAGGCGGGCAAGGCCACCAAGGTGGGCAAGGACGAGCTCTTTGCTCTGGAGCAGAGCTGCGCCACAGTCT
GTGCTGCAGGCGGCCAACGAGAGGAACGTGTCCACGCGCCAGGGTATGGACCTGTCTGCCAATCAGGACGAGGAG
ACCGACCAGGAGACCTTCCAGCTGGAGATCGACCGCGACACCAAAAAGTGTGCCTTCCGTACCCACACGGGCAAG
TACTGGACGCTGACGGCCACCGGGGCGTGCAGTCCACCGCCTCCAGCAAGAATGCCAGCTGCTACTTTGACATC
GAGTGGCGTGACCGGCGCATCACACTGAGGGCGTCCAAATGGCAAGTTTGTGACCTCCAAGAAGAATGGGCAGCTG
GCCGCTCGGTGGAGACAGCAGGGGACTCAGAGCTCTTCTCATGAAGCTCATCAACCGCCCCATCATCGTGTTC
CGCGGGGAGCATGGCTTCATCGGCTGCCGCAAGGTACGCGGCACCTGGACGCCAACCGCTCCAGCTATGACGTC
TTCCAGCTGGAGTTCAACGATGGCGCCTACAACATCAAAGACTCCACAGGCAAATACTGGACGGTGGGCAGTGAC
TCCGCGGTACACAGCAGCGGCGACACTCCTGTGGACTTCTTCTTCGAGTTCTGCGACTATAACAAGGTGGCCATC
AAGGTGGGCGGGCGCTACCTGAAGGGCGACCACGAGGCGTCTGAAGGCCTCGGGCGAAACCGTGGACCCCGCC
TCGCTCTGGGAGTACTAGGGGCCGGCCCGTCTTCCCCGCCCTGCCACATGGCGGCTCCTGCCAACCTCCCTG
CTAACCCCTTCTCCGCCAGGTGGGCTCCAGGGCGGGAGGCAAGCCCCCTTGCTTTCAAACCTGGAAACCCAGAG
AAAACGGTGCCCCACCTGTGCCCCCTATGGACTCCCCACTCTCCCTCCGCCCCGGGTTCCCTACTCCCTCGGG
TCAGCGGCTGCGGCCTGGCCCTGGGAGGGATTTCAGATGCCCTGCCCTCTTGCTGCCACGGGGCGAGTCTGGC
ACCTCTTTCTTCTGACCTCAGACGGCTCTGAGCCTTATTTCTCTGGAAGCGGCTAAGGGACGGTTGGGGGCTGGG
AGCCCTGGGCGTGTAGTGTAACTGGAATCTTTGCTCTCCCAGCCACCTCCTCCCAGCCCCCAGGAGAGCTGG
GCACATGTCCAAGCCTGTAGTGGCCCTCCCTGGTGCAGTGTCCCCGAAACCCCTGCTTGGGAAGGGAAGCTGT
CGGGAGGGCTAGGACTGACCCTTGTGGTGTTTTTTGGGTGGTGGCTGGAAACAGCCCCCTCTCCACGTGGGAGA
GGCTCAGCCTGGCTCCCTTCCCTGGAGCGGCAGGGCGTGACGGCCACAGGTCTGCCCGCTGCACGTTCTGCCAA
GGTGGTGGTGGCGGGCGGGTAGGGGTGTGGGGGCGTCTTCTCCTGTCTCTTTCTTTACCCCTAGCCTGACTG
GAAGCAGAAAATGACCAAATCAGTATTTTTTTAATGAAATATTATTGCTGGAGGCGTCCAGGCAAGCCTGGCT
GTAGTAGCGAGTGATCTGGCGGGGGCGTCTCAGCACCTCCCCAGGGGTGCATCTCAGCCCCCTCTTTCCGTC
CTTCCCGTCCAGCCCCAGCCCTGGGCCTGGGCTGCCGACACCTGGGCCAGAGCCCCTGCTGTGATTGGTGTCTCC
TGGGCTCCCGGGTGGATGAAGCCAGGCGTCCCCCTCCGGGAGCCCTGGGGTGAAGCGCCGGGGCCCCCTGCG
TGCCAGCCTCCCCGTCCCCAACATGCATCTCACTCTGGGTGTCTTGGTCTTTTATTTTTTTGTAAGTGTCAATTG
TATAACTCTAAACGCCCATGATAGTAGCTTCAAACCTGGAAATAGCGAAATAAAATAACTCAGTCTGC

2368/6881
FIGURE 2177

MTANGTAEAVQIQFGLINCGNKYLTAEAFGFKVNASASSLKKKQIWTLEQPPDEAGSAAVCLRSHLGRYLAADKD
GNVTCEREVPGPDCRFLIVAHDDGRWSLQSEAHRRYFGGTEDRLSCFAQTVSPA EKWSVHIAMHPQVNIYSVTRK
RYAHL SARPAD EIAVDRDVPWGVD SLITLAFQDQRYSVQTADHRFLRHDGRLVARPEPATGYTLEFRSGKVAFRD
CEGRYLAPSGPSGTLKAGKATKV GKDELFALEQSCAQVVLQAANERNVSTRQGMDLSANQDEETDQETFQLEIDR
DTKKCAFRTHTGKYWTLTATGGVQSTASSKNASCYFDIEWRDRRITLRASNGKFVTSKKNQQLAASVETAGDSEL
FLMKLINRPIIVFRGEHGFIGCRKVTGTLDANRSSYDVFQLEFNDGAYNIKDSTGKYWTVGSDSAVTSSGDT PVD
FFFEFC DYNKVAIKVGGRYLKGDHAGVLKASAETVDPASLWEY

2369/6881
FIGURE 2178

CCGAACGCCCCGCAGCAGGGTCAGAAGGGAGGTGGCCGGTCTCCGTCGTGACCTCTGACGGTTTCTGAGCGTTGGC
CTTTGGCACGCGCTACACCCTTTTGCTTTGGTTCTGCCATGCCGATGTACCAGGTAAAGCCCTATCACGGGGGCG
GCGCGCCTCTCCGTGTGGAGCTTCCCACCTGCATGTACCGGCTCCCCAACGTGCACGGCAGGAGCTACGGCCCAG
CGCCGGGCGCTGGCCACGTGCAGGAAGAGTCTAACCTGTCTCTGCAAGCTCTTGAGTCCCGCCAAGATGATATTT
TAAAACGTCTGTATGAGTTGAAAGCTGCAGTTGATGGCCTCTCCAAGATGATTCAAACACCAGATGCAGACTTGG
ATGTAACCAACATAATCCAAGCGGATGAGCCACGACTTTAACCACCAATGCGCTGGACTTGAATTCAGTGCTTG
GGAAGGATTACGGGGCGCTGAAAGACATCGTGATCAACGCAAACCCGGCCTCCCCCTCCCCTCTCCCTGCTTGTGC
TGCACAGGCTGCTCTGTGAGCACTTCAGGGTCCTGTCCACGGTGCACACGCACTCCTCGGTCAAGAGCGTGCTG
AAAACCTTCTCAAGTGCTTTGGAGAACAGAAATAAAAAACAGCCCCGCCAAGACTATCAGCTGGGATTCACTTTAA
TTTGGAAGAATGTGCCGAAGACGCAGATGAAATTCAGCATCCAGACGATGTGCCCCATCGAAGGCGAAGGGAACA
TTGCACGTTTCTTGTTCTCTGTTTGGCCAGAAGCATAATGCTGTCAACGCAACCCTTATAGATAGCTGGGTAG
ATATTGCGATTTTTTTCAGTTAAAAGAGGGAAGCAGTAAAGAAAAAGCCGCTGTTTTCCGCTCCATGAACTCTGCTC
TTGGGAAGAGCCCTTGGCTCGCTGGGAATGAACTCACCGTAGCAGACGTGGTGCTGTGGTCTGTACTCCAGCAGA
TCGGAGGCTGCAGTGTGACAGTGCCAGCCAATGTGCAGAGGTGGATGAGGTCTTGTGAAAACCTGGCTCCTTTTA
ACACGGCCCTCAAGCTCCTTAAGTGAATTGCCGTAAGTGAATTTTAAAGGGTTTAGATTTTAAAGAATGGTGCTCTT
TCATGCCTATTATCAGTAAGGGGACTTGTATTAGAGTCAGAGTCTTTTTATTTAGGCCAGTTGTCAAGTGTCAAT
AAAAGCGCATCATGTAATTTA

2370/6881
FIGURE 2179

MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEE SNLSLQALESRQDDILKRLYELKAAVDG
LSKMIQTPDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALKDIVINANPASPLSLLVLHRLLCHEHFRVLS
TVHTHSSVKSVFENLLKCFGEQNKKQPRQDYQLGFTLIWKNVPKTQMKFSIQTMCPIEGEGNIARFLFSLFGQKH
NAVNATLIDSWVDIAIFQLKEGSSKEKA AVFRSMNSALGKSPWLAGNELTVADVVLWSVLQQIGGCSVTVPANVQ
RWMRSCENLAPFNTALKLLK

2371/6881
FIGURE 2180

ATCGGAGTGTGGCAGTGCTGGGCTGGCCGGCGGGCTGGGCTGCGGCCCGCGCGCGGCCCGGCGATGCAGGGGGGCA
ACTCCGGGGTCCGCAAGCGCGAAGAGGAGGGCGACGGGGCTGGGGCTGTGGCTGCGCCCGGCCATCGACTTTC
CCGCCGAGGGCCCGGACCCCGAATATGACGAATCTGATGTTCCAGCAGAAATCCAGGTGTTAAAAGAACCCTAC
AACAGCCAACCTTCCCTTTTGCAGTTGCAAACCAACTCTTGCTGGTTTCTTTGCTGGAGCACTTGAGCCACGTGC
ATGAACCAAACCCACTTCGTTCAAGACAGGTGTTTAAGCTACTTTGCCAGACGTTTATCAAAATGGGGCTGCTGT
CTTCTTTCACTTGTAGTGACGAGTTTAGCTCATTGAGACTACATCACAACAGAGCTATTACTCACTTAATGAGGT
CTGCTAAAGAGAGAGTTCGTCAGGATCCTTGTGAGGATATTTCTCGTATCCAGAAAATCAGATCAAGGGAAGTAG
CCTTGGAAGCACAACTTCACGTTACTTAAATGAATTTGAAGAACTTGCCATCTTAGGAAAAGGTGGATACGGAA
GAGTATACAAGGTCAGGAATAAATTAGATGGTCAGTATTATGCAATAAAAAAATCCTGATTAAGGGTGCAACTA
AAACAGTTTGCATGAAGGTCCTACGGGAAGTGAAGGTGCTGGCAGGTCTTCAGCACCCCAATATTGTTGGCTATC
ACACCGCGTGATAGAACATGTTTCATGTGATTACGCCACGAGCAGACAGAGCTGCCATTGAGTTGCCATCTCTGG
AAGTGCTCTCCGACCAGGAAGAGGACAGAGAGCAATGTGGTGTTAAAAATGATGAAAGTAGCAGCTCATCCATTA
TCTTTGCTGAGCCCCACCCAGAAAAAGAAAAACGCTTTGGAGAATCTGACACTGAAAATCAGAATAACAAGTCGG
TGAAGTACACCACCAATTTAGTCATAAGAGAATCTGGTGAACCTTGAGTCGACCCTGGAGCTCCAGGAAAAATGGCT
TGGCTGGTTTGTCTGCCAGTTCAATTGTGGAACAGCAGCTGCCACTCAGGCGTAATTCCCACCTAGAGGAGAGTT
TCACATCCACCGAAGAATCTTCCGAAGAAAATGTCAACTTTTTGGGTGAGACAGAGGCACAGTACCACCTGATGC
TGCACATCCAGATGCAGCTGTGTGAGCTCTCGCTGTGGGATTGGATAGTCGAGAGAAACAAGCGGGGCCGGGAGT
ATGTGGACGAGTCTGCCTGTCTTATGTTATGGCCAATGTTGCAACAAAAATTTTTCAAGAATTGGTAGAAGGTG
TGTTTTACATACATAACATGGGAATTGTGCACCGAGATCTGAAGCCAAGAAATATTTTTCTTCATGGCCCTGATC
AGCAAGTAAAAATAGGAGACTTTGGTCTGGCCTGCACAGACATCCTACAGAAGAACACAGACTGGACCAACAGAA
ACGGGAAGAGAACACCAACACATACGTCCAGAGTGGGTACTTGTCTGTACGCTTCACCCGAACAGTTGGAAGGAT
CTGAGTATGATGCCAAGTCAGATATGTACAGCTTGGGTGTGGTCTCTGCTAGAGCTCTTTCAGCCGTTTGAACAG
AAATGGAGCGAGCAGAAAGTTCTAACAGGTTTAAGAAGTGGTCAGTTGCCGGAATCCCTCCGTAAAAGGTGTCCAG
TGCAAGCCAAGTATATCCAGCACTTAACGAGAAGGAACCTCATCGCAGAGACCATCTGCCATTGAGCTGCTGCAGA
GTGAACTTTTCCAAAATCTTGGAATGTTAACCTCACCTACAGATGAAGATAATAGAGCAAGAAAAAGAAATTG
CAGAACTAAAGAAGCAGCTAAACCTCCTTTCTCAAGACAAAGGGGTGAGGGATGACGGAAAGGATGGGGGCGTGG
GATGAAAGTGGACTTAACTTTTAAGGTAGTTAACTGGAATGTAAATTTTTAATCTTTATTAGGGTATAGTTGGTA
CAATGCTTCGTTGTATTTAGTAAGCCTTTACAAGACTTGTTAAAGATGTCAGAGTGCCCCAAGCTGCCGTTCTCT
CCCTTCCTGCCCCACAAGCTCCTTTTCTGAATTTCTACCTAAATATTAACCATATGCCTAGTCTCTGAAACTA
AAAACCTGGACCTCATCTCAATTATTTTCTCCTTTCAACTCTGTTGACCTCTGTCTGGTCTTCTCTAGAAGG
TTCTACCGCAGAAATTGATGTGTGCTCCCTGCCCTCGTCACTGCCCAAGCCCGGGCCTGCACATACTCACTGGAC
TGTTCCAGTTTTGACAGCTGCCAGTCTTCTGCCCTTTACACTGCAGCTGAAGTTCATTACCTGAAGGACGCC
TCATCATTTCACTTCTGGCTCCAAACCTTCTGCTGCCTCTAAGATAAAAGCTCAACTTCTTAACAGTGTACAGT
GTGCAACTTCCAACCTTTTTATCTGTTCTCTCCACCTTCAAGTTAGCGTCATTCCAAAACCACACCCTTGCAAAG
CTTTGTACTCCGCACCCAGATGATCTCCAGGCAGCTCAGATCTCTTCTGCTTTGCCCTTGGCCCTGCACTGTTCCCCG
GTACTTCTCTCTTTATTGTAGCACTCAGCTCCCCAGCCAATCTGTACATCCCTCAGAGGCAGCGATCTGATGAAT
TGGTTTTTGAATCCAGAAAGGGTCTGCCATGGAGTTGGCAGTCATCACGGTAGATGGCGTATGATTTTGCTGAA
TTTTAAATAAAATGAAAACCATAAAAA

2372/6881
FIGURE 2181

MQGGNSGVRKREEEGDGAGAVAAPPAIDFPAEGPDPEYDESDVPAEIQVLKEPLQQPTFFFAVANQLLLVSLEH
LSHVHEPNPLRSRQVFKLLCQTFIKMGLLSSFTCSDEFSSLRLHHNRAITHLMRSAKERVQRDPCEDISRIQKIR
SREVALEAQTSTRYLNEFEELAILGKGGYGRVYKVRNKLDGQYYAIKKILIKGATKTVCMKVLREVKVLAGLQHPN
IVGYHTAWIEHVHVIQPRADRAAIELPSLEVLSDQEEDREQCGVKNDESSSSSIIFAEPTPEKEKRFGESDTENQ
NNKSVKYTTNLVIRESGELESTLELQENGLAGLSASSIVEQQPLRRNSHLEESFTSTEESESEENVNVLGQTEAQ
YHMLLHIQMQLCESLWDWIVERNKRGREYVDESACPYVMANVATKIFQELVEGVFYIHNMGIVHRDLKPRNIFL
HGPDQQVKIGDFGLACTDILQKNTDWTNRNGKRTPTHTSRVGTCLYASPEQLEGSEYDAKSDMYSLGVVLELFLQ
PFGTEMERAEVLTGLRTGQLPESLRKRCPVQAKYIQHLTRRNSSQRPSAIQLLQSELFQNSGNVNLTLQMKIIEQ
EKEIAELKKQLNLLSQDKGVRDDGKDGGVG

2373/6881
FIGURE 2182

ATGCAGGCCATCAAGTGTGTGGTGGTGGGAGACGGAGCTGTAGGTAAAACCTGCCTACTGATCAGTTACACAACC
AATGCATTTCCCTGGAGAATATATCCCTACTGTCTTTGACAATTATTCTGCCAATGTTATGGTAGATGGAAAACCG
GTGAATCTGGGCTTATGGGATACAGCTGGACAAGAAGATTATGACAGATTACGCCCCCTATCCTATCCGCAAACA
GATGTGTTCTTAATTTGCTTTTCCCTTGTGAGTCCTGCATCATTTGAAAATGTCCGTGCAAAGTGGTATCCTGAG
GTGCGGCACCACTGTCCCAACACTCCCATCATCCTAGTGGGAATAAATTGATCTTAGGGATGATAAAGACACG
ATCGAGAACTGAAGGAGAAGAAGCTGACTCCCATCACCTATCCGCAGGGTCTAGCCATGGCTAAGGAGATTGGT
GCTGTAAAATACCTGGAGTGCTCGGCGCTCACACAGCGAGGCCTCAAGACAGTGTTTGACGAAGCGATCCGAGCA
GTCTCTGCCCCGCTCCCGTGAAGAAGAGGAAGAGAAAAATGCCTGCTGTTGTAA

2374/6881
FIGURE 2183

MQAIKCVVVG DGAVGKTCLLISYTTNAFPGEYIPTVFDNYSANVMVDGKPVNLGLWDTAGQEDYDRLRPLSYPQT
DVFLICFSLVSPASFENVRAKWYPEVRHHCPNTP IILVGTKLDLRDDKDTIEKLKEKKLTPIITYPQGLAMAKEIG
AVKYLECSALTQRGLKTVFDEAIRAVLCPPPVKKRKRKCLLL

2375/6881
FIGURE 2184

GCCGCCGCCGCCATGAACATTTTCCGGCTGACTGGGGACCTGTCCCACCTGGCGGCCATCGTCATCCTGCTGCTG
AAGATCTGGAAGACGCGCTCCTGCGCCGGTATTTCTGGGAAAAGCCAGCTTCTGTTTGCACTGGTCTTCACAACT
CGTTACCTGGATCTTTTTACTTCATTTATTTTATTGTATAACACATCTATGAAGGTTATCTACCTTGCCTGCTCC
TATGCCACAGTGTACCTGATCTACCTGAAATTTAAGGCAACCTACGATGGAAATCATGATACCTTCCGAGTGGAG
TTTCTGGTGGTCCCTGTGGGAGGCCTCTCATTTTTAGTTAATCACGATTTCTCTCCTCTTGAGATCCTCTGGACC
TTCTCCATCTACCTGGAGTCCGTGGCTATCCTTCCGCAGCTGTTTATGATCAGCAAGACTGGGGAGGCCGAGACC
ATCACCACCCACTACCTGTTCTTCCTGGGCCTCTATCGTGCTTTGTATCTTGTCAACTGGATCTGGCGCTTCTAC
TTTGAGGGCTTCTTTGACCTCATTGCTGTGGTGGCCGGCGTAGTCCAGACCATCCTATACTGTGACTTCTTCTAC
TTGTACATTACAAAAGTACTCAAGGGAAAGAAGCTCAGTTTGCCAGCATAAGTGCCAAAGACCATCACCAGCATC
TGTCTTCAGGGTGCTCGGACAGAATTCTTACCACAGCAAAGGCATAAGATGCTTGATACGGAATAATCAGAACT
TAACTCTTTTGTTCAGATAGTCATCAGTGGCTCTGTAAAAACGCAGAGGAAAAGAGCCAGAAGGTTTCTGTTTA
ATGCATCTTGCCTTATCTTTTTTTATTACTGTGTACAAAGATTTTTTTTACACAAAGAACTTAATGCTGTATTAA
TAAATTCAGTGTGTAGCTTCAATTGGGATAGTTCCAAAAGTGAAGATTTTGTGAGGAATAAGTGCAAATTTTTTT
TTTATTTTAAAAAATCTTTGAACTCTTAAGTCTTGTGTCTGCAATGAAATTGTACTCCTTGACAGTTGATAG
ATTATGTATTCTTCCATCCCTCAAACCTGCATTCCACTATATTTATTTTTTTGGCAAAGATGAGCTGTATTTGTT
TGAAATCTGAGACACTATGTTCAATTGG

2376/6881
FIGURE 2185

MNIFRLTGDLSHLAAIVILLLLKIWKTRSCAGISGKSQLLFALVFTRYLDLFTSFISLYNTSMKVIYLACSYATV
YLIYLFKFKATYDGNHDTFRVEFLVVPVGGLSFLVNHDFSPLEILWTFISIYLESVAILPQLFMISKGTGEAETITTH
YLFGLGLYRALYLVNWIWRFYFEGFFDLIAVVAGVVQTILYCDFFYLYITKVLKGKKLSLPA

2377/6881
FIGURE 2186

ATGAGCGACATCCGCCACTCGCTGCTGCGCCGCGATGCGCTGAGCGCCGCCAAGGAGGTGTTGTACCACTGGAC
ATCTACTTCAGCAGCCAGCTGCAGAGCGCGCCGCTGCCCATCGTGGACAAGGGCCCCGTGGAGCTGCTGGAGGAG
TTCGTGTTCCAGGTGCCCAAGGAGCGCAGCGCGCAGCCCCAAGAGACTGAATTCCTTCAGGAGCTTCAACTTCTT
GAAATCATGTGCAATTATTTCCAGGAGCAAACCAAGGACTCTGTTTCGGCAGATTATTTTTTTCATCCCTTTTCAGC
CCTCAAGGGAACAAAGCCGATGACAGCCGGATGAGCTTGTGTTGGGAAAACCTGGTCTCCATGGCGGTGGCTGTGTGT
CGAATCCCGGTGTTGGAGTGTGCTGCCTCCTGGCTTCAGCGGACGCCCGTGGTTTACTGTGTGAGGTTAGCCAAG
GCCCTTGTAGATGACTACTGCTGTTTGGTGCCGGGATCCATTGACACGCTGAAGCAGATATTCAGTGCCAGCCCCG
AGATTCTGCTGCCAGTTCATCACCTCCGTTACCGCGCTCTATGACCTGTCATCAGATGACCTCATTCCACCTATG
GACTTGCTTGAAATGATTGTACCTGGATTTTTGAGGACCCAAGGTTGATTCTCATCACTTTTTTAAATACTCCG
ATTGCGGCCAATCTGCCAATAGGATTCTTAGAGCTCACCCCGCTCGTTGGATTGATCCGCTGGTGCCTGAAGGCA
CCCCCTGGCTTATAAAAGGAAAAAGAAGCCCCCTTATCCAATGGCCATGTCAGCAACAAGGTCACAAAGGACCCG
GGCGTGGGGATGGACAGAGACTCCCACCTCTTGTACTCAAACTCCACCTCAGCGTCCTGCAAGTGCTCATGACG
CTGCAGCTGCACCTGACCGAGAAGAATCTGTATGGGCGCCTGGGGCTGATCCTCTTCGACCACATGGTCCCGCTG
GTAGAGGAGATCAACAGGTTGGCGGATGAACTGAACCCCTCAACGCCTCCCAGGAGATTGAGCTCTCGCTGGAC
CGGCTGGCGCAGGCTCTGCAGGTGGCCATGGCCTCAGGAGCTCTGCTGTGCACGAGAGATGACCTGAGAACCTTG
TGCTCCAGGCTGCCCCATAATAACCTCCTCCAGCTGGTGATCTCGGGTCCCGTGCAGCAGTCGCCTCACGCCGCG
CTCCCCCGGGGTCTACCCCCACATCCACACGCCCCCGCTGGGCTACGGGGCTGTCCCGGCCACCCCGCCGCC
CACCCCGCCCTGCCACGCACCCCGGCCACACCTTCATCTCCGGCGTGACCTTTCCTTCAGGCCCATCCGCTTAG

GCTGGCCCGTGTGTGCCTTCTGCGCTCTCGCTGGACGAAGCCTTTTCGAGATGGAAGGGGTGGCCGGACTCCCAGA
AGAGAACCTCGGGGAAGGGGTTCGGGCAGCCCCCTCCCGCCGGCAGAACCGTCTTGGTGTACGGAGTCCAGGTGC
TTCCACCCGGTTCGCAATTCTTTGACATGCAGATTGGATGGTGGAGGGAAGAGTCCAGCCTCTGCCGAGAGCCTGC
TGCGTGCATTTTTAAAAAGATGCCGATCCIGGGAGCCTCTGTTCTCTGCGCATTTTCAGACACAGCCTGTGTGGCGA
GGAGTGTGACGGCAGGAGCCACGGGTGCAAGCCCGTGTGTCTGGCCTCTTTCCTCGTGAAGACGATGTGTCCCCG
CCAGAAAAAGTGGGCACCTTCTGCAGCCCCGTGAGCTGAGCCCAGGCTGCGTAGTGACCACAAGCTTATGTGCAG
CACTGCTCAGGGAGGCTGTCAGGAATTCCTTCACCTCGGAAAGGAACTTCTCAGTTTTATTGGGGGTGTCTAAA
TTTCCTTTCATATGTTCAAATAAATTTTTCTAAACAGT

2378/6881
FIGURE 2187

MSDIRHSLRRDALSAAKEVLYHLDIYFSSQLQSAPLP IVDKGPVELLEEFVFQVPKERSAQPKRLNSIQELQLL
EIMCNYFQEQT KD SVRQII FSSLFSPQGNKADDSRMSLLGKLVSM AVAVCRIPVLECAASWLQRTPVVYCVRLAK
ALVDDYCCLVPGSIQTLKQIFSASPRFCCQFITSVTALYDLSSDDLIPPMDLLEMIVTWIFEDPRLILITFLNTP
IAANLP IGFLELTPLVGLIRWCVKAPLAYKRKKKPPLSNGHVS NKVTKDPGVGMDRDSHLLYSKLHLSVLQVLMT
LQLHLTEKNLYGRLGLILFDHMPVPLVEEINRLADELNPLNASQEIELSLDRLAQALQVAMASGALLCTRDDLRTL
CSRLPHNNLLQLVISGPVQQSPHAALPPGFYPHIHTPPLGYGAVPAHPAAHPALPTHPGHTFISGVTFFPRPIR

2379/6881
FIGURE 2188

GGCACGAGGAAGCTACTCAGATAAGAGGCTCCAAGAGGACATTTTTGGATGTGAAAAACAATGAGAAGGAGGACA
ACACACATTTACAATCGTCTTAATTTTGTACTCAGAAAAAGGATGTGAAGACAATGCACAGGGAATACAATAGTT
TCAGATCTGTGTACAGTTTCCTTTTGCTTCATCTCCTGCAACAATGTAATGAAGACACCATGATATCATTAAACAT
TTCACACAAAAAGGAAAATGAGGCTGAAATGGTGTGGGCAAGGCCAGGAATCTGGAGCATCCCTAACCAAGCAGC
AGAGCACCTGGGATAGAGAAAGTGCTCAAGAATGTTCACTTACTGATTACTACAATCAAAAAAGATACGACACT
AATTTACCACATTCTTCTTACTTATTTTATGAGATACTATTCTTCCAAGGTGGAGAAAGTGAGAAAAGTAGAGTG
ACGCAGCTAAGGGAGTAAATCGACCCTCAGCCAACAAGTGGCAAAAGCCTGAAGAAAGTGATCAAGATCACTGAT
GACCCCGCGGCCCATCTCCAAGGGGGCGGGTATCACAACCCCGACGCCACACCACGTATCATTCCGCAAAACTCC
CGCGCCTCCACGCAGAACTGGCAAGAGGGAAGGCGAGACAGCAGTGAACAGCTGGTACGCAGCACCCACAGCAC
CGCGGCAGCAGCTAGTGCCGACTCCCGCCTAGCTCTTTTGACTCTGTTTCGCGGGAAGAATGGGGAAACAGTAAGG
TTGCGGCGCCTCCCGCGAGACGAGGTACCTGAGGCTGGCCCCGAGTCCCCCGCCGACCAGCACCGGAGCTTCA
CACCCCACTTCGGGGTCAAGTCACCGCCGGGAATCCTGTGATCGCAGAAAGGTAGTCTCAGGTTCCGCCCCAT
CCAAGTCCCGCCTCCACTGCCTCTCGCCCTGTATCTGTCAACTTCCGGGACGCGCGCGCTCACTAAGCAGCCAAT
CTCCACTTCCGGACTCATCCAGCCCCTTCTCCACCCCTTTCAGAGACAGCGCGATTGCGATTTAGGTTTCCGCGC
ATTTAATTGGCGAAGCTGGAGCGCTAGTCTTCGCTGATTGGTGGCGAGAAATCTGCCCCATAGACACCCGCGGGG
CGCACAGTTTCAGTCGTCCGTGGGTTTCCCGCCAGCCGAGTCTTGGACCATAATCATGGTGGACATGATGGACT
TGCCAGGTGCGCATCAACGCCGGCATGCTAGCTCAATTCATCGACAAGCCTGTCTGCTTCGTAGGGAGGCTGG
AAAAGATTATCCACCGGAAAAATGTTTATTTCTTTCAGATGGAGAAGGAAAAAATGGAACCATCGAGTTGATGG
AACCCTTGATGAAGAAATCTCTGGAATTGTGGAAGTGGTTGGAAGAGTAACCGCCAAGGCCACCATCTTGTGTA
CATCTTATGTCCAGTTTAAAGAAGATAGCCATCCTTTTGATCTTGGACTTTACAATGAAGCTGTGAAAATTATCC
ATGACTTCCCTCAGTTTTATCCTTTAGGGATTGTGCAACATGATTGATCTTGATGGATTTTCATACGATTGTAAA
TGAGCTATATTAAAGTCTATTAAAGGAAAAAAAAAAAAAAAAAAAAA

2380/6881
FIGURE 2189

MVDMMDLPRSRINAGMLAQFIDKPVCFVGRLEKIHPTGKMFILSDGEGKNGTIELMEPLDEEISGIVEVVGRVTA
KATILCTSYVQFKEDSHPFDLGLYNEAVKIIHDFPQFYPLGIVQHD

2381/6881
FIGURE 2190

CAACCGAATGGTCAACCATTTTATTGCTGAGCTCAAGCGCAAGCATAAGAAGGACATCAGTGAGAGCAAGAGAGC
TGTAAGATGCCTCCGTACTGCTTGTGAACATGCTAAGCGTACTCTCTCTTCCAGCACCCAAGTCAGTATTGAGAT
CGATTCTCTCTATGTAGGAATTGACTTCTATACCTCCATTACCTGTGCCCAGTTTGAAGAATTGAATGCCTGGGG
GATTCCCTGTTGGTGGAGCTCCTCCTTCTGGTGGTGCTTCCTTAGGGCCCACCATCGAAGAGGTTGATTAAAGCCA
ACCCAAGTATAGATGTAGCATTGTTCCACACATTTAAAACATTTGAAGGACCTAAATTTGTAGCAAATTCGTGG
CAGTTTTAAAAAGTTAAGCTGCTATAGTAAGTTACTGGGCATTCTCAATACTTGAATATGGAACATATGCACAGG
GGAAGGAAATAACATTGCACTTTATAAACACTGTATTGTAAGTGGAATGCAATGTCTTAAATAAACTATTTA
AAATTGGCACCAT

2382/6881
FIGURE 2191

CAGCCATCCTGTCTGGAGACAAGTCTGAAAATGTTCAAGATTTGCTGCTCTTGGACGTCACCTCCTTTCCCTTG
GTATTGAAACTGCTAGTGGAGTCAATGACCATCCTCATCAACTGTAATACCACCATTCTACCAAGCAGACACAGA
CCTTCATTACCTATTCTGACAACCAGCCTGGTGTGCTTATTCAGGTTTATGAAGGTGAGCGTGCCATGTCCAAGG
ATAACAACCTGCTTGGCAAGTTTGAATTCACGGGCATACCTCCTGAACCCCAAGGTGTTCTCAGATTGAAGTCA
CTTTTGACATTGATGCCAATGGTATCCTCAGTGTCTCTGCTGTGGACAAAAGTACAGGAAAAGAGAATAAAATTA
CTATCACTAATAATAAGGGCCATTTGAGCAAGGAAGACATTGAACGTATGGTCCAGGAAGCTGAGAATTAAAAAG
CTGAAGATGAGAAGCAGAGGGACAAGGCGTCATCCAAGAATTCACTTGAGTCCTATGCATTCAACATGAAAGCAA
CTGTCGAAGATGAGAACTTCAAGACAAGATTAATGATGAGGACAAACAGAAGATTCTGGACAGGTGTAATGAAA
TTATCAACTGGCACAATAAGAATCGGACTGCCAAGAAGGAAGAATTTGAACATCAGCAGAAAGAGCTGGAGGAAC
TTTGCAACCCAATCATCACCAAGCTGTACCAGAGTGCAGAAGGCATGCCAGGAAGAATGCCTGGGGGATTCCCTG
TTGGTGGAGCTCCTCCTTCTGGTGGTGTCTTCCTTAGGGCCCACCATCGAAGAGGTTGATTAAGCCAACCCAAGTA
TAGATGTAGCATTGTTCCACACATTTAAACATTTGAAGGACCTAAATTTGTAGCAAATTCCTGTGGCAGTTTTAA
AAAGTTAAGCTGCTATAGTAAGTTACTGGGCATTCTCAATACTTGAATATGGAACATATGCACAGGGGAAGGAAA
TAACATTGCACTTTATAAACACTGTATTGTAAGTGAAAATGCAATGTCTTAAATAAACTATTTAAAATTGGCA
CCAT

2383/6881
FIGURE 2192

MTILINCNTTIPTKQTQTFITYSDNQPGVLIQVYEGERAMSKDNNLLGKFEFTGIPPEPQGVFQIEVTFDIDANG
ILSVSAVDKSTGKENKITITNNKGHLKEDIERMVQEAEN

2384/6881

FIGURE 2193

CCGTAGTGTCTCATTGCAGATAATTTTGTAGCTTAGGGCCTGGTGGCTAGGTCGGTTCTCTCCTTCCAGTCGGAG
ACCTCTGCCGCAAACATGCTCCGCCAGATCATCGGTCAGGCCAAGAAGCATCCAAGCTTGATCCCCCTCTTTGTA
TTTATTGGAAGTGGAGCTACTGGAGCAACACTGTATCTCTTGCCTCTGGCATTGTTCAATCCAGATGTTTGTGG
GACAGAAATAACCCAGAGCCCTGGAACAACTGGGTCCCAATGATCAATACAAGTTCTACTCAGTGAATGTGGAT
TACAGCAAGCTGAAGAAGGAACGTCCAGATTTCTTAAATGAAATGTTTCACTATAACGCTGCTTTAGAATGAAGGT
CTTCCAGAAGCCACATCCGCACAATTTTCCACTTAACCAGGAAATATTTCTCCTCTAAATGCATGAAATCATGTT
GGAGATCTCTATTGTAATCTCTATTGGAGATTACAATGATTAAATCAATAAATAACTGAAAAAAAAA

2385/6881
FIGURE 2194

MLRQIIIGQAKKHPSLIPLFVFIGTGATGATLYLLRLALFNPVCWDRNNPEPWNKLGPNQYKFYSVNVDSKLN
KERPDF

2386/6881
FIGURE 2195

GCCATCTTCCAGTAATTCGCCAAAATGACGAACACAAAGGGAAAGAGGAGAGGCACCCGATATATGTTCTCTAGG
CCTTTTAGAAAACATGGAGTTGTTCCCTTTGGCCACATATAIGCGAATCTATAAGAAAGGTGATATTGTAGACATC
AAGGGAATGGGTACTGTTCAAAAAGGAATGCCCCACAAGTGTTACCATGGCAAAACTGGAAGAGTCTACAATGTT
ACCCAGCATGCTGTTGGCATTGTTGTAAACAAACAAGTTAAGGGCAAGATTCTTGCCAAGAGAATTAATGTGCGT
ATTGAGCACATTAAGCACTCTAAGAGCCGAGATAGCTTCCTGAAACGTGTGAAGGAAAATGATCAGAAAAAGAAA
GAAGCCAAAGAGAAAGGTACCTGGGTTCAACTAAAGCGCCAGCCTGAGCTGCTGGAACCTATTCCCTATGAATTC
ATGGCATAATAGGTGTT

2387/6881
FIGURE 2196

MTNTKGKRRGTRYMFSRPFRKHGVVPLATYMRIYKKGDIVDIKGMGTVQKGMPHKCYHGKTGRVYNVTQHAVGIV
VNKQVKGKILAKRINVRIEHIKHSKSRDSFLKRVKENDQKKKEAKEKGTWVQLKRQPELLEPIPYEFMA

2388/6881

FIGURE 2197

GCTCGGGCGCGGGGCGTTCTTGGTGCGCCGGGCCGTGGTGAGTCCGGGCTCCCGTGGCCGCGTGCTGGGAGGAGA
CTGGAGCCCCGTTAGGAAGAATGGAGTTGGCGACTCGCTACCAGATCCCTAAAGAAGTGGCTGACATCTTTAACG
CCCCAGTGATGATGAAGAGTTTGTGGCTTCCGAGATGATGTTCCCATGGAAACCCTCTCGTCAGAGGAGAGCT
GCGATAGTTTTGACTCACTAGAGTCAGGGAAACAGCAGGATGTGCGCTTTCATTCCAAATACTTCACAGAAGAGC
TAAGAAGAATTTTTATAGAGGACACTGACTCAGAGACTGAGGATTTTGCAGGATTTACGCAGAGTGATCTGAATG
GAAAGACTAACCCAGAAGTAATGGTCGTGGAGTCAGATTTGAGTGATGATGGCAAAGCATCTTTGGTGAGCGAGG
AAGAGGAAGATGAAGAAGAAGATAAGGCTACCCCTAGAAGAAGCAGGTCTAGAAGAAGTAGTATTGGTCTTCGAG
TAGCCTTTCAGTTCCCCACCAAGAAGCTGGCCAACAAACCAGATAAAAACAGTTCTTCCGAGCAGTTGTTTTCTA
GCGCACGCTTACAGAATGAGAAAAAACAATTCTTGAAAGAAAGAAAGACTGTAGACAGGTGATACAAAGGGAAG
ATTCTACCTCTGAGTCTGAGGATGACTCTCGGGATGAGAGCCAGGAGAGTTTCTAGATGCTTTTGCTGAAAAGGACCA
TGAACATCAAGGAGAACAAGCCATGCTTGCCAGTTATTGGCGGAATTGAACTCGATGCCAGATTTCTTCCAG
TACGAACCCCAACCTCAGCTTCTAGGAAGAAGACAGTGAGGCGGGCCTTCTCGGAGGGACAGATCACGCGGCGTA
TGAACCCCAACCCGAGTGCGCGGCCTCCTGAGAAGTTTGCTCTAGAGAACTTCACTGTCTCAGCCGCTAAATTTG
CGGAAGAGTTTTACAGCTTCCGAAGAAGGAAGACAATTGGGGGGAAATGCCGGGAGTACAGACGACGTCACCGTA
TATCTTCTTTTCGGCCAGTGGAGGATATCACCGAAGAGGACTTAGAAAATGTTGCCATAACTGTTTCGAGATAAAA
TCTATGATAAAGTTCTGGGTAACACGTGCCATCAGTGTGACAAAAGACCATCGACACCAAGACAGTGTGTGCGGA
ACCAGGGTTGCTGTGGTGTGCGAGGACAGTTCTGTGGACCATGCCTGCGGAACCGCTATGGGGAGGATGTCAGAT
CGGCATTGCTGGACCCGATTGGGTGTGTCCCCCTGTCTGGGATCTGCAATTGCAGCTACTGTGCGGAAGCGTG
ACGGCCGCTGTGCCACAGGAATCCTCATTCTGCGCAAGTTTTATGGTTATGACAATGTTAAGGAATATCTGG
AGAGCTTACAAAAGGAGCTGGTAGAAGACAATTAAGAGGAAAACAAACAGAACCAGCCACCTCACCATAGAGTAC
TCCAACAAGACATGCATACCATTGGTGCCTAAGATTTATTAAACTTGACTGAACAAAAGGGGACCATCAACATT
GTAGACACTGGACACTGGAGGCCTTACAGAGTGCTAGCCTCTTCCTTCAGGACTCACCTGGGGCCTGCTGCTTTT
ATATTTTGAAAGAGTTTAAGGGCTAATAATTTAATTTGTTGTTTGTAAATAATTAATCTCCGTTCTTTCCGGC
TGCATTGCTTTTGCATGTTACATATGATGTACTTTTATGATGTACTTTTTTTTTTTTGGAGATGGAGTCTTGTTT
TGTTGCCCAGGAGGGAGTGAGTGCTGCAACCTCGGCTCACTGCAACCTTTGCCTCCTAGGTTCAAGTGATTCTC
CTACCTCCTGAGTAACTGGGATTACAGTCGTGTGCCACCACGCTCAGCCCTGAGTTAGTTTCTAGTATTTTTTTC
TGACTTTCCTCTAAGGATAGCGTTGAAAAAGAATGCACGTGTGAGTTACTAAAAAGTTAGAATAATGTGCATG
GGAACAGTGCAGCAACATGCTAGAAAATCCTCACTGCACTCCAGCAGAGGCTAGAGGAATGCCAGTGTTACCTTA
CGCTTCTAGAAGCAGAGCCACTCCAGCCAGAACCCATTTTGCAGTCTTCTCTTCGCTCTTCAGCCTGAAGGTCCA
GATGTAGCTGGGGCCTCTCAGTTTGGTTCTATACACAGGGCACTCGTAGGTCTGTTTGGTTTCTTGCTGTGCCAC
GGGGGTGGCTTTTGCAAAGATGACCGGCATAGGGCATGCCAGCTCCTTGAGACGGGCTTCAACAATGGTTCCTGC
TTGGGTGTCCCAGCGGGCGCCTATGGCAAAAAACACAGCGTTGCAATGTGTGGCAGCTTGCTACTAATGATAAT
GATCAAGTAAGTTGTTTGATGCAATAAACATTCAACATTCTGGTTTTGTCAT

2389/6881
FIGURE 2198

CTTTTTTCGCAACGGGTTTGGCCGCCAGAACACAGGTGTCGTGAAAACCTACCCCTAAAAGCCAAAATGGGAAAGGAA
AAGACTCATATCAACATTGTCGTCATTGGACACGTAGATTGAGGCAAGTCCACCACTACTGGCCATCTGATCTAT
AAATGCGGTGGCATCGACAAAAGAACCATTGAAAAATTTGAGAAGGAGGCTGCTGAGATGGGAAAGGGCTCCTTC
AAGTATGCCTGGGTCTTGGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTGTGGAAA
TTTGAGACCAGCAAGTACTATGTGACTATCATTGATGCCCCAGGACACAGGGACTTCATCAAAAACATGATTACA
GGGACATCTCAGGCTGACTGTGCTGTCTGATTGTTGCTGCTGGTGTGGTGAATTTGAAGCTGGTATCTCCAAG
AATGGGCAGACCCGAGAGCATGCCCTTCTGGCTTACACACTGGGTGTGAAACAACATAATTGTCGGTGTAAACAAA
ATGGATTCCACTGAGCCACCCTACAGCCAGAAGAGATATGAGGAAATTGTAAAGGAATCAGCACTTACATTAAGA
AAATTGGCTACAACCCCGACACAGTAGCATTGTGTCCAATTTCTGGTTGGAATGGTGACAACATGCTGGAGCCAA
GTGCTAACATGCCTTGGTTCAAGGGATGGAAAGTCACCCGTAAGGATGGCAATGCCAGTGGAACACGCTGCTTG
AGGCTCTGGACTGCATCCTACCACCAACTCATCCAAGTGAACAAGCCCTTGCGCCTGCCTCTCCAGGATGTCTACA
AAATTGGTGGTATTGGTACTGTTCTGTTGGCCGAGTGGAGACTGGTGTCTCAAACCCGGTATGGTGGTCACCT
TTGCTCCAGTCAACGTTACAACGGAAGTAAAAATCTGTGCAAAATGCACCATGAAGCTTTGAGTGAAGCTCTTCCTG
GGGACAATGTGGGCTTCAATGTCAAGAATGTGTCTGTCAAGGATGTTTCGTGCTGGCAACGTCGCTGGTGACAGCA
AAAATGACCCACCAATGGAAGCAGCGGGCTTCACTGCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGCA
CCGGCTATGCCCCGTGATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTG
ATCGCCGTTCGTGTAAGCTGGAAGATGGCCCTAAATTTCTTGAAGTCTGGTGATGCTGCCATTGTTGATATGG
TTCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTGCTGTTCTGTGATATGA
GACAGACAGTTGCGGTGGGTGTATCAAAGCAGTGGACAAGAAGGCTGCTGGAGCTGGCAAGGTCACCAAGTCTG
CCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGAAGAA
TGGTCTCAGAACTGTTTGTGTTCAATTGGCCATTTAAGTTTAGTAGTAAAAGACTGGTTAATGATAACAATGCATC
GTAAAACCTTCAGAAGGAAAGGAGAATGTTTTGTGGACCACTTTGGTTTTCTTTTTTGGGTGTGGCAGTTTTAAG
TTATTAGTTTTTAAAATCAGTACTTTTAAATGGAACAACCTGGACCAAAATTTGTCACAGAATTTTGAGACCCA
TT

2390/6881
FIGURE 2199

MLEPSANMPWFKGWKPTRKDGNASGTTLLEALDCILPPTHPTDKPLRLPLQDVYKIGGIGTVPVGRVETGVLKPG
MVVTFAPVNVTEVKSVEMHHEALSEALPGDNVGFNVKNVSVKDVRRGNVAGDSKNDPPMEAAGFTAQVIILNHP
GQISTGYAPVLDCHTAHIACKFAELKEKIDRRSGKKLEDGPKFLKSGDAAIVDMVPGKPMCVESFSDYPPLGRFA
VRDMRQTVAVGVKAVDKKAAGAGKVTKSAQKAQKAK

2391/6881
FIGURE 2200

GAAATTTGAGACCAGCAAGTACTATGTGACTATCATTGATGCCCCAGGACACAGGGACTTCATCAAAAACATGAT
TACAGGGACATCTCCAAGAATGGGCAGACCCGAGAGCATGCCCTTCTGGCTTACACACTGGGTGTGAAACAATA
ATTGTCGGTGTTAACAAAATGGATTCCACTGAGCCACCCTACAGCCAGAAGAGATATGAGGAAATTGTTAAGGAA
TCAGCACTTACATTAAGAAAATTGGCTACAACCCCGACACAGTAGCATTGTGCAATTTCTGGTTGGAATGGTG
ACAACATGCTGGAGCCAAGTGCTAACATGCCTTGGTTCAAGGGATGGAAAGTCACCCGTAAGGATGGCAATGCCA
GTGGAACCACGCTGCTTGAGGCTCTGGACTGCATCCTACCACCAACTCATCCAAGTACAAGCCCTTGCGCCTGC
CTCTCCAGGATGTCTACAAAATTGGTGCTATTGGTACTGTTCCCTGTTGGCCGAGTGGAGACTGGTGTTCTCAAC
CCGGTATGGTGGTCACCTTTGCTCCAGTCAACGTTACAACGGAAGTAAAATCTGTCGAAATGCACCATGAAGCTT
TGAGTGAAGCTCTTCCCTGGGGACAATGTGGGCTTCAATGTCAAGAATGTGTCTGTCAAGGATGTTTCGTCTGGCA
ACGTCGCTGGTGACAGCAAAAATGACCCACCAATGGAAGCAGCGGGCTTCACTGCTCAGGTGATTATCCTGAACC
ATCCAGGCCAAATAAGCACCGGCTATGCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGCTG
AGCTGAAGGAAAAGATTGATCGCCGTTCTGGTAATATGGTTCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAG
ACTATCCACCTTTGGGTCGCTTTGCTGTTCTGTGATATGAGACAGACAGTTGCGGTGGGTGTCATCAAAGCAGTGG
ACAAGAAGGCTGCTGGAGCTGGCAAGGTCACCAAGTCTGCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCC
TAATACCTGCCACCCCACTCTTAATCAGTGGTGGAAGAA

2392/6881
FIGURE 2201

MVTTCSQVLTCLGTMLLEALDCILPPTRPTDKPLHLPLQDVYKIGGIGSVPVGRVETGVLKPGMVVTFAPVNV
TEVKSVEMHHEALSEALPGDNVGFNVKNVSVDVRHGNVAGDSKNDPPMEAAGFTAQVIIILNHPGQISTGYAPVL
DCHTAHIACKFAELKEKIDHRSGNMVPGKPMCVESFSDYPSLGCFAVRDMRQIVTVGVKAVDKKTAGAGKVTKS
AQKAQKAK

2393/6881
FIGURE 2202

TATAAATGCGGTGGCATCGACAAAAGAACCATTGAAAAATTTGAGAAGGAGGCTGCTGAGATGGGAAAGGGCTCC
TTCAAGTATGCCTGGGTCTTGGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTGTGG
AAATTTGAGACCAGCAAGTACTATGTGACTATCATTGATGCCCCAGGACACAGGGACTTCATCAAAAACATGATT
ACAGGGACATCTCAGGCTGACTGTGCTGTCCTGATTGTTGCTGCTGGTGTGGTGAATTTGAAGCTGGTATCTCC
AAGAATGGGCAGACCCGAGAGCATGCCCTTCTGGCTTACACACTGGGTGTGAAACAATAATTGTCGGTGTTAAC
AAAATGGATTCCACTGAGCCACCCTACAGCCAGAAGAGATATGAGGAAATTGTTAAGGAATCAGCACTTACATTA
AGAAAATTGGCTACAACCCCGACACAGTAGCATTTGTGCCAATTTCTGGTTGGAATGGTGACAACATGCTGGAGC
CAAGTGCTAACATGCCTTGGTTCAAGGGATGGAAAGTCACCCGTAAGGATGGCAATGCCAGTGGAACCACGCTGC
TTGAGGGCTCCAGTCAACGTTACAACGGAAGTAAAATCTGTGCGAAATGCACCATGAAGCTTTGAGTGAAGCTCTT
CCTGGGGACAATGTGGGCTTCAATGTCAAGAATGTGCTGTCAAGGATGTTTCGTTCGTGGCAACGTCGCTGGTGAC
AGCAAAAATGACCCACCAATGGAAGCAGCGGGCTTCACTGCTCAGG

2394/6881

FIGURE 2203

GTGAAACTACCCCTAAAAGCCAAAATGGGAAAGGAAAAGACTCATATCAACATTGTCGTCATTGGACACGTAGA
TTCAGGCAAGTCCACCACTACTGGCCATCTGATCTATAAATGCGGTGGCATCGACAAAAGAACCATTGAAAAATT
TGAGAAGGAGGCTGCTGAGATGGGAAAGGGCTCCTTCAAGTATGCCTGGGTCTTGGATAAACTGAAAGCTGAGCG
TGAACGTGGTATCACCATTGATATCTCCTTGTGGGGCAGACCCGAGAGCATGCCCTTCTGGCTTACACACTGGGT
GTGAA

2395/6881
FIGURE 2204

GAAAACTACCCCTAAAAGCCAAAATGGGAAAGGAAAAGACTCATATCAACATTGTCGTCATTGGACACGTAGATT
CAGGCAAGTCCACCACTACTGGCCATCTGATCTATAAATGCGGTGGCATCGACAAAAGAACCATTGAAAAATTTG
AGAAGGAGGCTGCTGAGATGGGAAAGGGCTCCTTCAAGTATGCCTGGGTCTTGGATAAACTGAAAGCTGAGCGTG
AACGTGGTATCACCATTGATATCTCCTTGTGGAAATTTGAGACCAGCAAGTACTATGTGACTATCATTGATGCCC
GGGACATCTCAGGCTGACTGTGCTGTCCTGATTGTTGCTGCTGGTGTGGTGAATTTGAAGCTGGTATCTCCAAG
AATGGGCAGACCCGAGAGCATGCCCTTCTGG

2396/6881
FIGURE 2205

CTCTCTCCGGTCCATGCCTCCAAGATGACAAAGAAAAGAAGGAACAACGTTTCGTGCCAAAAGGGCCGCGGCCAC
GTGCAGCCTATTCGCTGCACTAACTGTGCCCAGATGCGTGCCCAAGGACAACGCCATTAAGAAATTCGTCATTCTGA
AACATAGTGGAGGCTGCAGCAGTCAGGGACATTTCTGAAGCGAGCGTCTTCGATGCCTATGTGCTTCCCAAGCTG
TGTGTGAAGCTACATTACTGTGTGAGTTGTGTAATTCACAGCAAAGTAGTCAGGAATCGATCTCGTGAAGCCCGC
AAGGACCGAACACCCCCACCCCGATTTAGACCTGCGGGTGCTGCCGCACGTCCCCACCAAAGCCCATGTAAGGA
GCTGAGTTCTTAAAGACTGAAGACAGACTATTCTCTGGAGAAAAATAAAATGGACATTGTACTTAAAAAAAACA
AAAAAAAAAAAAAAAAAAAA

2397/6881
FIGURE 2206

CCGTGATGTGGCGCCTGCACAXTCCTTTCCCTTTTCGGATTCCCGACGCTGTGGTTGCTGTAAGGGGTCCTCCCTG
CGCCACACGGCCGTCGCCATGGTGAAGCTGAGCAAAGAGGCCAAGCAGAGACTACAGCAGCTCTTCAAGGGGAGC
CAGTTTGCCATTCGCTGGGGCTTTATCCCTCTTGATTTACCTGGGATTTAAGAGGGGTGCAGATCCCGGAATG
CCTGAACCAACTGTTTTGAGCCTACTTTGGGGATTAAAGGATTATTTGGTCTTCTGGATTTGGAGGCAATCAGCGG
ACAGCATGGAAGATGTGTGCTCTGGCTCGGATAAGAGATGGGACATCATTCAGTCACTAGTTGGATGGCACAAGG
CTCTTCACAGACGCATCTGTAGCAGAGTGGAAGTTGTACTAACTTATGATAGAATGTATCAGAATAAATGTTTTT
AACAGTGTA

2398/6881
FIGURE 2207

MVKLSKEAKQRLQQLFKGSQFAIRWGFIPLVIIYLGFKRGADPGMPEPTVLSLLWG

2399/6881
FIGURE 2208A

GGACGTCCGGCTTCGGAGCGGGAGTGTTCGTTGTGCCAGCGACTAAAAAGAGAATTAAATATGCGGTGATGTTGAG
AAAGGCAAGAAGATTTTTATTATGAAGTGTTCACAGTGCCACACCGTTGAAAAGGGAGGCAAGCACAAGACTGGG
CCAAATCTCCATGGTCTCTTTGGGCGGAAGACAGGTGAGGCCCTGGATACTCTTACACAGCCGCCAATAAGAAC
AAAGGCATCATCTGGGGAGAGGATACACTGATGGAGTATTTGGAGAATCCCAAGAAGTACATCCCTGGAACAAAA
ATGATCTTTGTCGGCATTAAAGAAGAAGGAAGAAAGGGCAGACTTAATAGCTTATCTCAAAAAAGCTACTAATGAG
TAAATAATTGGCCACTGCCTTATTTATTACAAAACAGAAATGTCTCATGACTTTTTTATGTGTACCATCCTTTAAT
AGATCTCATACACCAGAATTCAGATCATGAATGACTGACAGAATATTTTGTGGGCAGTCCTGATTTAAACTAA
GACTGGCTTGTGGTTAAATGAATATGTTTCAGTTTTTGAATTTTAATAGTAACTCCAATTCAGTAAATGGTATCAC
TGTTTACCCCTTTTAAAGATATGATTAGACTTCGTTAGTAATGTTCAACTTTTCACAAAGATGGTGAGTGCCATC
TTAAACTTACTGGAGATTGGTTTTATATTTAGATTTATATAACTGGTTATGTGAATATATTTAAATACTGGGGA
AATTGCTTCACTGTCTTAGAACCAAGCAAGATTACCTGTGTTTTGTGTTTCATGTTTCAATTTGCCTCTTAAAGGCA
AGGGTTGAAGATAAATAAGGTTGCAATGTCTATAGTTTTGGCCTTAACTATGCCAATCTAATTATAATTCCTGT
ATTTAAATGTTTTCTTTTACTTATTGAAAGGCATTTTAGTGTGGTTTATGTGTAATATTAAAGATTATTCACAA
CCTCTCACATCTTACAGATCTATAAGGTCACATGCTTTTAAATAGTAGCAAGTTAACTTCACTCTTGAATTC
TTACAATCTAAGTCAAATAAGTTATAATTTAGGATTGTCTTTAAACAGCCATTTCAGAAACAAAACTGTAGAACT
GTGATTTGATTGGGAATGGTGCTTTTGCCAACTTAAAGGATTAAAGTAACGGAGATATACACAAATTTTAAAA
TTATGTGTGATCACAAGACTAAAGATAATTAAGAAAGAAACCACAGATCATGACTTTTTGACTGTGCTTGATTC
ATGACTGATGCACAAATTTTAATGATTAAAAAGTGCAGGAGCCCTAAATGTCAGTGCAGCAGCCCTAAATGTCAG
TGCAGCAGTGTTAACAGTCATGGTGCTAGATTGTTTACTTGGTTTTCTAGGACTGCCTCAACTAGAATAACACT
TCACTAATTGACTCTTAGTTTTCTTTGCTCAGATTGAGAAGTGCAGCATTTATGCCAGACATGGACAGAGGAATGC
CTGTGGTCATAGTTTTGTGATGTGTAACAGTGATAATTACATACTGAATTATTTTCATGCATAGTCTGTGCCATA
CACATTTAGAGTAGTCCTTGAGATTTTATGGAGATGGTGAGCACAAGGTAAGTCATAAAGAATAATGAGAAAT
AAATCTATGCTGGTGACAGCTGAGAAGTGTATCTTTGTGGGACAGTGAGAAGACTGAGAAGATGTGAATCCATGGT
CTCAAAGGTGATAGGGACGATTAGATAGGTGTTTTAAGGCCTGAAAGCAATTTATAACATATGAGTCTTATTTTT
ATTTATAGAAATGTGGAAAGCTTGCTGTAATTCATATTTGAAGTCCTAGTCTGAGTCTGGTGGGGAATTTAAAA
ATGCATCCTGGAAATCCTTTAAAGATTTTCAGACTTTGAAAGGCCTTGTAGCAGAGGACTTGGTGACTGTATAAG
TTAGTGGTATTCAGGGACAGTGTAAGTAGCTTACAAGGGGACAATTCTGGACTAATGAGAAAGACCTGAAGT
GAAGGCTAGAGAGTTGATTTTTTTTTTTTTTTTGGCATCCTGGAAATGATACAGGAAACATATTAAGATAGATACAG
AAATGTGTTCAACCTTCCATCTTGGCTAGTTGTGGCGTTAGTTTGTTTTTTGGAGACATGGTCACGCTGTGTGCG
CAAGGCTGGAGTGCAGTGGTGCGATCTCGGCTGGCTGCAGCCTCTATTTCCAGGCTCAAGCGATTCTCTCACTT
CAGCTTCCCAAGTAGCTGGGACTGCGGGTGTTCGCCACCATGCCAGCTAATTTTTTTGTAGAGATGGAGTTTTG
CCATGTGGTCCCAGGCTGGTCTCAAACCTCTGAGCTCAAGCAATCCGTCCACTTGCTTGGCTCCCCAAAGTGCT
GGGATTGCAGGCGTGAGCCACCAGGCCCTGCTGGTTTTCAAATTCAGAAATCTTATTATTTAACCAGAAAGTAA
TCAGCCCAGTAGTAACCTAGGTTTAAATTTTTTTTTCAGGTTTAAATTTTTCTCATTTATTTTTCTGAGACGGAG
TTTCGCCCTTTTCGCCAGGCTGAGTACAGTGGTGCAATCTCACTGCAACCTCCGCCCTCCAGTTGCAAGTGATT
CTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTGCAGGCACCCGCCACCACGCCTGGCTAATTTTTGTATTTTTAG
TGGAGATGGTGTTCACCATGTTGGCCAGACTGGTCTTGGACTCCTGACCTCGTGATCCACCCACCTTGGCCTCC
CAAAGTTCTAGGATTACAGGTGTGAGCCACCACGTCCGGCCAATTTTTCTCATTTCTATGCCTCCTATATTAAGG
TCTGTGTTGGCACAGATGAGTAACTGCCATGTTCTAGGTGAGTTATACCCAAGCACTTCTGGTGGTTTTAAATGT
GATTCTGTAACTTTTTTATTTTTATTTTTTGGAGATAATTTCACTCTTGTGTTGCCAGGCTGGAGTGCAATGGCGT
GATCGCTGCTCACCGCAACCTCCGCCCTCCAGGTTCAAGCGATTCTCCTGACTCAGCCTCTCAAGTAGCTGGGAT
TACAAGCATGCGCCACCATGCCAGCTTATTTTGTGTTTTTAGTAGAGACAGGGTTTCTCCATGCTGGACAGGCT
GGTCTTGAACCTCCGACGTGGGTGATCTGCCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCAC
CACGCCTGGCCAATTATGTAATTTTTTAAAAAGGACATTTCTATCAGGGATATATACCTTCAGAAATAAGGAAAT
AGGGGAAAAAAGAGCACTATAAACACATGTTTTCAATTTCTAGTGCTTCGCTGTAAGTGGCTAGGTTGGTAGAA
TCAAAAACAAGGGCCAGATGTATTTAAGGGGTATTAGATGCCACCTACATGCTTATTTTGTCTAGAACAGTGCT
GTCTAATAGAATTTCTGTGACGATGGATATTTTGTAGACTTTTGTGTCCAGTGTGGTAGCCACTAACACATG
TGGCTGTAAAGCCCTTGAAATATAGCTAGTGTGACTAGAAAGTATTTTATTTTAAATTTACATAGGCACAAGTGG

2400/6881

FIGURE 2208B

CTAGTGGCTACTGTATTGACATTCTGGGTCTAGGACTAGAACCAGTGGTCTGTAACAAAAGTACTTTCTCTTTAC
TCTATTAAATCTAGAATTAGCCGGGCATGGTCGCTCATGCCTGTGGTCCCAGCACTTTGGGAGGCCAAGGCAGGC
AGATCACTTGAGGTCGGGCGTTTGAGACCAGCCTGGTCAACATGGCGAAACCCTGTCTCTACAAAAACATAAAA
GTTAGCCAGGTGTGGTGGTGGGCACCTGTAGTCTCAGCTACTTGGGAGGCTGAGGCACAAGAATCACTTGAAGTT
GGGAGGTGGAGGTTGCAGTGAGCCAGGATTGTGCCACTGCACTCAAGCCTGGGTGACGAGTGAAACTGTCTCCAA
AAAAAAAAAAAAAAAA

2401/6881
FIGURE 2209

MGDVEKGKKIFIMKCSQCHTVEKGGKHKTGPNLHGLFGRKTGQAPGYSYTAANKNKGIIWGEDTLMEYLENPKKY
IPGTMIFVGIKKKEERADLIAYLKATNE

2402/6881
FIGURE 2210

AGTAGCAGCAGCGCCGGGTCCCGTGCGGAGGTGCTCCTCGCAGAGTTGTTTCTCGAGCAGCGGCAGTTCTCACTA
CAGCGCCAGGACGAGTCCGGTTCGTGTTTCGTCCGCGGAGATCTCTCTCATCTCGCTCGGCTGCGGGAAATCGGGC
TGAAGCGACTGAGTCCGCGATCGGAGAGAGAGAAAAGGAACAGTTCCGTAAGCTCTTTATTGGTGGCTTAAGCTTTGA
AACCACAGAAGAAAGTTTGAGGAACTACTACGAACAATGGGGAAAGCTTACAGACTGTGTGGTAATGAGGGATCC
TGCAAGCAAAAGATCAAGAGGATTGGTTTTGTAACTTTTTCATCCATGGCTGAGGTTGATGCTGCCATGGCTGC
AAGACCTCATTCAATTGATGGGAGAGTAGTTGAGCCAAAACGTGCTGTAGCAAGAGAGGAATCTGGAAAACAGG
GGCTCATGTAACTGTGAAGAAGCTGTTTGTGGCGGAATTAAAGAAGATACTGAGGAACATCACCTTAGAGATTA
CTTTGAGGAATATGGAAAAATTGATACCATTGAGATAATTACTGATAGGCAGTCTGGAAAGAAAAGAGGCTTTGG
CTTTGTTACTTTTGATGACCATGATCCTGTGGATAAAATCGTATTGCAGAAATACCATACCATCAATGGTCATAA
TGCAGAAGTAAGAAAGGCTTTGTCTAGACAAGAAATGCAGGAAGTTTCAGAGTTCTAGGAGTGGAAGAGGAGGCAA
CTTTGGCTTTGGGGATTTCAGTGGTGGCGGTGGAAATTCGGACCAGGACCAGGAAGTAACTTTAGAGGAGGATC
TGATGGATATGGCAGTGGACGTGGATTTGGGGATGGCTATAATGGGTATGGAGGAGGACCTGGAGGTGGCAATTT
TGGAGGTAGCCCCGGTTATGGAGGAGGAAGAGGAGGATATGGTGGTGGAGGACCTGGATATGGCAACCAGGGTGG
GGGCTACGGAGGTGGTTATGACAACTATGGAGGAGGAAATTATGGAAGTGGAATTACAATGATTTTGAAAATTA
TAACCAGCAACCTTCTAACTACGGTCCAATGAAGAGTGGAACCTTTGGTGTTAGCAGGAACATGGGGGGACCATA
TGGTGGAGGAAACTATGGTCCAGGAGGCAGTGGAGGAAGTGGGGGTTATGGTGGGAGGAGCCGATACTGAGCTTC
TTCCTATTTGCCATGGGCTTCACTGTATAAATAGGAGAGGATGAGAGCCCAGAGGTAACAGAACAGCTTCAGGTT
ATCGAAATAACAATGTTAAGGAACTCTTATCTCAGTCATGCATAAATATGCAGTGATATGGCAGAAGACACCAG
AGCAGATGCAGAGAGCCATTTTGTGAATGGATTGGATTATTTAATAACATTACCTTACTGTGGAGGAAGGATTGT
AAAAAAAAATGCCTTTGAGACAGTTTCTTAGCTTTTTAATTGTTGTTTCTTCTAGTGCTTTTGTAAGAGTGTA
GAAGCATTCTTTCTTTGATAATGTTAAATTTGTAAGTTTCAGGTGACATGTGAAACCTTTTTTAAGATTTTCTC
AAAGTTTTGAAAAGCTATTAGCCAGGATCATGGTGTAAATAAGACATAACGTTTTCTTTAAAAAAATTTAAGTG
CGTGTGTAGAGTTAAGAAGCTGTTGTACATTTATGATTTAATAAAATAATTCTAAAGGAAAAAA

2403/6881

FIGURE 2211

MEREKEQFRKLFIGGLSFETTEESLRNYEQWGKLTDCVVMRDPASKRSRGFGFVTFSSMAEVDAAAMAARPHSID
GRVVEPKRAVAREESGKPGAHVTVKKLFVGGIKEDTEHHLRDYFEEYGKIDTIEIITDRQSGKKRGFGFVTFDD
HDPVDKIVLQKYHTINGHNAEVRKALSRQEMQEVQSSRSRGGNFGFGDSRGGGGNFGPGPGSNFRGGSDGYGSG
RGFGDGYNGYGGGPGGGNFGGSPGYGGGRGGYGGGGPGYGNQGGGYGGGYDNYGGGNYGSGNYNDFGNYNQQPSN
YGPMKSGNFGGSRNMGGPYGGGNYGPGGSGGSGGYGGRSRY

2404/6881
FIGURE 2212

AGTAGCAGCAGCGCCGGGTCCCGTGCGGAGGTGCTCCTCGCAGAGTTGTTTCTCGAGCAGCGGCAGTTCTCACTA
CAGCGCCAGGACGAGTCCGGTTTCGTGTTTCGTCCGCGGAGATCTCTCTCATCTCGCTCGGCTGCGGGAAATCGGGC
TGAAGCGACTGAGTCCGCGATGGAGAGAACTTTAGAACTGTTCCTTTGGAGAGGAAAAAGAGAGAAAAAGGAACA
GTTCCGTAAGCTCTTTATTGGTGGCTTAAGCTTTGAAACACAGAGAAAGTTTGAGGAAGTACTACGAACAATG
GGGAAAGCTTACAGACTGTGTGGTAATGAGGGATCCTGCAAGCAAAAGATCAAGAGGATTTGGTTTTGTAACTTT
TTCATCCATGGCTGAGGTTGATGCTGCCATGGCTGCAAGACCTCATTCAATTGATGGGAGAGTAGTTGAGCCAAA
ACGTGCTGTAGCAAGAGAGGAATCTGGAACCAGGGGCTCATGTAAGTGTGAAGAAGCTGTTTGTGGCGGAAT
TAAAGAAGATACTGAGGAACATCACCTTAGAGATTACTTTGAGGAATATGGAAAAATTGATACCATTGAGATAAT
TACTGATAGGCAGTCTGGAAAGAAAAGAGGCTTTGGCTTTGTTACTTTTGATGACCATGATCCTGTGGATAAAAT
CGTATTGCAGAAATACCATAACCATCAATGGTCATAATGCAGAAAGTAAAGAAAGGCTTTGTCTAGACAAGAAATGCA
GGAAGTTCAGAGTTCTAGGAGTGAAGAGGAGGCAACTTTGGCTTTGGGGATTACGTTGGTGGCGGTGGAAATTT
CGGACCAGGACCAGGAAGTAACTTTAGAGGAGGATCTGATGGATATGGCAGTGGACGTGGATTTGGGGATGGCTA
TAATGGGTATGGAGGAGGACCTGGAGGTGGCAATTTTGGAGGTAGCCCCGTTATGGAGGAGGAAGAGGAGGATA
TGGTGGTGGAGGACCTGGATATGGCAACCAGGGTGGGGGCTACGGAGGTGGTTATGACAACCTATGGAGGAGGAAA
TTATGGAAGTGGAAATTACAATGATTTTGGAAATTATAACCAGCAACCTTCTAACTACGGTCCAATGAAGAGTGG
AACTTTTGGTGGTAGCAGGAACATGGGGGGACCATATGGTGGAGGAACTATGGTCCAGGAGGCAGTGGAGGAAG
TGGGGGTTATGGTGGGAGGAGCCGATATCGAGCTTCTTCCTATTTGCCATGGGCTTCACTGTATAAATAGGAGAG
GATGAGAGCCCAGAGGTAACAGAACAGCTTCAGGTTATCGAAATAACAATGTTAAGGAACTCTTATCTCAGTCA
TGCATAAATATGCAGTGATATGGCAGAAGACACCAGAGCAGATGCAGAGAGCCATTTTGTGAATGGATTGGATTA
TTTAATAACATTACCTTACTGTGGAGGAAGGATTGTAAAAAAAATGCCTTTGAGACAGTTTCTTAGCTTTTTAA
TTGTTGTTTCTTTCTAGTGGTCTTTGTAAAGAGTGTAGAAGCATTCTTCTTTGATAATGTTAAATTTGTAAGTTT
CAGGTGACATGTGAAACCTTTTTTAAGATTTTCTCAAAGTTTTGAAAAGCTATTAGCCAGGATCATGGTGTAAAT
AAGACATAACGTTTTTCTTTAAAAAAATTTAAGTGCCTGTGTAGAGTTAAGAAGCTGTTGTACATTTATGATTT
AATAAAATAATTCTAAAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

2405/6881
FIGURE 2213

MEKTLETVPLEKREKEQFRKLFIGGLSFETTEESLRNYEQWGKLTDCVVMRDPASKRSRGFGFVTFSSMAEV
DAAMAARPHSIDGRVVEPKRAVAREESGKPGAHVTVKKLFVGGIKEDTEEHHLRDYFEEYGKIDTIEIITDRQSG
KKRGFGFVTFDDHDPVDKIVLQKYHTINGHNAEVRKALSRQEMQEVQSSRSRGGNFGFGDSRGGGNGFGPGPGS
NFRGGS DGYGSGRGFGDGYNGYGGGPGGGNFGGSPGYGGGRGGYGGGGPGYGNQGGGYGGGYDNYGGGNYGSGNY
NDFGNYNQQPSNYGPMKSGNFGGSRNMGGPYGGGNYGPGGSGGSGGYGGRSRY

2406/6881
FIGURE 2214

CGCTGAGGAGACTCCGGTCACTGTCCTCGCCCCGCCTCCCCCTTCCCTCCCCTTGGGGACCACCGGGCGCCACGC
CGCGAACGTAATAGCTCTTCAAGTCTGCAATAAAAAATGCGCCTCCAACAAAACCTACATTGCAAAAAATGGGAAAA
AAACAGAAATGGAAAGAGTAAAAAGTTGAAGAGGCAGAGCCTGAAGAATTTGTCGTGGAAAAAGTACTAGATCGA
CGTGTAGTGAATGGGAAAGTGGAATATTTCTGGAAGTGGGAAGGGATTTACAGATGCTGACAATACTTGGGAACCT
GAAGAAAAATTTAGATTGTCCAGAATTGATTGAAGCGTTTCTTAACTCTCAGAAAGCTGGCAAAGAAAAAGATGGT
ACAAAAAGAAAATCTTTATCTGACAGTGAATCTGATGACAGCAAATCAAAGAAGAAAAGAGATGCTGCTGACAAA
CCAAGAGGATTTGCCAGAGGTCTTGATCCTGAAAAGAATAATTGGTGCCACAGACAGCAGTGGAGAATTGATGTTT
CTCATGAAATGGAAAGATTGAGATGAGGCAGACTTGGTGCTGGCGAAAGAGGCAAATATGAAGTGTCCTCAAATT
GTAATTGCTTTTTATGAAGAGAGACTAACTTGGCATTCTTGTCAGAAAGATGAAGCTCAAATAATTGTTTCACATTG
TTCTTTTATATATATTTATATATATATAAAAAATTGGGTCTTAGATTTTGATTTACTAGTGTGACAAAATAACT
ACATCCTAATGAAAATCAAGTTTGATATGTTTGTTTTGAAAGTAGCGTTGGAAGAGTTGTTGGGGGTTTTTTTGCA
TCCATAGCACTGGTTACTTTGAACAAATAAAATAAAAGCTTTCTGTAGTTGCTTCCCTTTATCAGAAAAGAACATTT
GATACCATGGTATATCATTTCCTCTTCATTAAAGAACAGCTTTTCTAAATGTTGGGGGAAAATGTCCATAGTCATT
ACTCAGTCAAACTTGTGTTCTCATGAGCCTAAGGACCATTCTAGATTTTATTACGTGTTTTTTGTGTGTGTGTGT
GTGTGTGTGTGTGTGTGTATCCATAAAATGCATATGTAAATTTTTTTTTTGTTTTTTAAGCATTACCCAAACAAAA
AAATCACAGGTAAACCCATGTTTCTGAGATGCCATTATTCCAAGCAAATAAGAGATAATCCCTTCAAGTTAAAT
TGAAAATTTTCTGAAACCATAACATTTCAAGTGAATAAGTAATTCTAGATAGGACAATTTAAATTGGATAATTT
TAAAGTGTCTATAATTGCAGTGGTTTATTTGCAAAATTCCTAAAGGAAAAATTTTATCACTGCCATCACAGCAG
GTTTCCTCATCCAGATGAGGAACTAGACAAATGCTAGTGTGTTTTAACTAGCTAAACAAAACCTAAGTTAAATGA
ACATTTAAAAGTTTCCCTAGCGGGCCATTCCCTTAGCAAAATGTTGGAATCCCTGTTGCTACATTGACTAAAAGGT
CATGATGAATGGAATATGTAAGACTTGGCTCATAGAAACCTAATCAGATGGTTAGAGGTGTTGGCAGTTTAGGAC
CTGCTGTCATAAATGTGTGAACAACCTTTTGTAACCTAACCTATTGACCTGCATGTTTTTTCTTTACCCCAATTC
ATTACATGGAGGCTCAATCTTGAGTTTGCTTTACTGGTTCAGCAAAAGCCAGGAAGAACAACCTTTGTAGTAATCA
AAATGTTATCCAACGTATATTGTTTACTTTATTGTAAATACTGGTGAACAGTGGTTAATAAATAGTTTTATATT
CCTTTATGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

2407/6881
FIGURE 2215

MASNKTTLQKMGGKQNGKSKKVVEEAPEEFVVEKVLDRRVVNGKVEYFLKWKGFTDADNTWEPEENLDCPELIEA
FLNSQKAGKEKDGTKRKSLSDSESDDSKSKKKRDAADKPRGFARGLDPERIIGATDSSGELMFLMKWKDSDEADL
VLAKEANMKCPQIVIAFYEERLTWHSCPEDEAQ

2408/6881
FIGURE 2216

TCCCCCGGCGGCCCCGCGCGCAGCTCCCGGCTCCCTCCCCCTTCGGATGTGGCTTGAGCTGTAGGCGCGGAGGG
CCGGAGACGCTGCAGACCCGCGACCCGGAGCAGCTCGGAGGCGGTGAATAATAGCTCTTCAAGTCTGCAATAAAA
AATGGCCTCCAACAAAACCTACATTGCAAAAAATGGGAAAAAACAGAATGGAAAGAGTAAAAAGTTGAAGAGGC
AGAGCCTGAAGAATTTGTCGTGGAAAAAGTACTAGATCGACGTGTAGTGAATGGGAAAGTGGAATATTTCCCTGAA
GTGGAAGGGATTTACAGATGCTGACAATACTTGGGAACCTGAAGAAAAATTTAGATTGTCCAGAATTGATTGAAGC
GTTTCTTAACTCTCAGAAAGCTGGCAAAGAAAAAGATGGTACAAAAAGAAAATCTTTATCTGACAGTGAATCTGA
TGACAGCAAATCAAAGAAGAAAAGAGATGCTGCTGACAAACCAAGAGGATTTGCCAGAGGTCTTGATCCTGAAA
AATAATTGGTGCCACAGACAGCAGTGGAGAATTGATGTTTCTCATGAAATGGAAAGATTGAGATGAGGCAGACTT
GGTGCTGGCGAAAGAGGCAAATATGAAGTGTCTCAAATTGTAATTGCTTTTTATGAAGAGAGACTAAGTTGGCA
TTCTTGTCAGAAAGATGAAGCTCAAT**TA**ATTGTTACATTGTTCTTTTATATATATTTATATATATATAAAAAAT
TGGGTCTTAGATTTTGATTTACTAGTGTGACAAAATAACTACATCCTAATGAAAATCAAGTTTGATATGTTTGT
TTGAAAGTAGCGTTGGAAGAGTTGTTGGGGGTTTTTTTGCATCCATAGCACTGGTTACTTTGAACAAATAAATAAA
AGCTTTCTGTAGTTGCTTCCCTTTATCAGAAAAGAACATTTGATACCATGGTATATCATTTCCCTCTTCATTAAAGA
ACAGCTTTTCTAAATGTTGGGGGAAATGTCCATAGTCATTACTCAGTCAAACTTGTGTTCTCATGAGCCTAAGG
ACCATTCTAGATTTATTACGTGTTTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTATCCATAAAATGCATAT
GTAAATTTTTTTTTTGTTTTTAAGCATTCACCCAAACAAAAAATCACAGGTAAACCCATGTTTCTGAGATGCCAT
TATTCCAAGCAAAATAAGAGATAATCCCTTCAAGTTAAATTGAAAATTTTCTGAAACCATACATTTCAAGTGAA
ATAAGTAATTTCTAGATAGGACAATTTAAATTGGATAATTTTAAAGTGTCTATAATTGCAGTGTTTTATTTGCAA
ATTCCTAAAAGGAAAAATTTTATCACTGCCATCACAGCAGGTTTCCCTCATCCAGATGAGGAACTAGACAAATGC
TAGTGTGTTTTAACTAGCTAAACAAAACCTAAGTTAAATGAACATTTAAAAGTTTCCCTAGCGGGCCATTCTTAG
CAAAATGTTGGAATCCCTGTTGCTACATTGACTAAAAGGTCATGATGAATGGAATATGTAAGACTTGGCTCATAG
AAACCTAATCAGATGGTTAGAGGTGTTGGCAGTTTAGGACCTGCTGTCATAAATGTGTGAACAACCTTTTGTAAC
CTAACCTATTGACCTGCATGTTTTTTCTTTACCCCAATTCATTACATGGAGGCTCAATCTTGAGTTTGCTTTACT
GGTTCAGCAAAAGCCAGGAAGAACAACCTTGTAGTAATCAAATGTTATCCAACGTATATTGTTTACTTTATTG
TAAATACTGGTGAACAGTGGTTAATAAATAGTTTTATATTCCTTTATGCAA

2409/6881

FIGURE 2217

MASNKTTLQKMGKKQNGKSKKVVEAEPEEFVVEKVLDRRVVNGKVEYFLKWKGF
TDADNTWEPEENLDCPELIEA
FLNSQKAGKEKDGTKRKSLSDESDDSKSKKKRDAADKPRGFARGLDPERIIGATDSSGELMFLMKWKDSDEADL
VLAKEANMKCPQIVIAFYEERLTWHSCPEDIAQ

2410/6881
FIGURE 2218

GACGGCAAATGGCGGACTTCGACACCTACGACGATCAGGCCTACAGCAGCTTCGGCAGCGGCAGAGGGTCCCGCG
GCAGTGCTGGTGGCCATGGTTCCCGTAGCCAGAAGGAGTTGCCACAGAGCCCCCTACACAGCATACGTAGGAA
ATCTACCTTTCAATACGGTTCGGGGCGACATAGATGCTATCTTTAAGGATCTCAGCATAAGGAGTGACGGCTAG
TCAGAGACAAAGACACAGATAAATTTAAAGGATTCTGCTATGTAGAATTCGATGAAGTGGATTCCCTTAAGGAAG
CCTTGACATACGATGGTGCCTGTTGGGCGATCGGTCCTTCGTGTGGACATTGCAGAAGGCAGAAAACAAGATA
AAGGTGGCTTTGGATTAGAAAAGGTGGACCAGATGACAGAGGCTTCAGGGATGACTTCTTAGGGGGCAGGGGAG
GTAGTCGCCCAGGCGACCGGGCGAACAGGCCCCCATGGGCGAGCCGCTTCGGAGATGGCCCTCCCTCGGTGGAT
CCAACATGGATTTAGAGAACCCACAGAAGAGGAAAAGCGCACAGAGACCACGACTCCAGCTTAAACCTCGAACAG
TCGCGACGCCCCCTCAATCAAGTAGCCAATCCCAACTCTGCTATCTTCGGGGGTGCCAGGCCTAGAGAGGAAGTTG
TTCAAAAGGAGCAAAAATGAGCCTGCGGTTGGGAGGGAATGGGGCGTGGGGGGTTAGAGCAGGACCACAGCCTGG
TGAGTCCCCGGGCAGCCGTCCTGCAGCCGCCACTCCTGCGCCTGCCATTGGCCTCCTCACAGCGGAAACACAGCT
TGTGAGTGATGTCAGCTGTTAACAAGTGGTTTTTGTAGTACATTCTGGGCTTTGCTGTATCTATCTAGTGCCTGTT
TGTGCGTTTTTTTTCTTTCTTCCGCTGCTTCCCCATTTTCTTCTGTCTTTTTCTCCTGCTCCTTGTTCCTCCAG
CAGCACACGGGGTTCCTCGGAGGAGCAGAGGTGGCCGCCGTGGGGGGCGTTTGGGCTGCGGTGCTGCGTCATTT
TTCCTTTGCTTTCTCTTTACTTTAGACACTGGCCCACTCCAGGAGTTTCTTTTATTCCCTCAGTGCTTCTCTT
CTGACCTGCATGTTGAGTTCTGTATTGCTGGGGCTTCCAACAAAACCAGAGTCACTGACAGAGGGAAGTGCAGA
GACCTTGTGTTGGTATTAGCTGTGATGGATATAGAGAATCGGAGGCACCTTGTTTTCACTAGGATAAAAATAT
CTGCAGGGTCTTTTCCATTCTATTTAGAGGGAGTCTGGCTCCATGACCCCTCCCGAGTGGACTGTCCAAGCA
GATAGGCTCACACGAGAAACAGTGAGGCTGAAAGGGGGGGCCATGGAAGAGCGGTAGGGAGTCCACGGAGAAGAT
GCAGTGAATGCTTGATGCATTACACGTGTGTGTGTCCCAGCTAGTTCACTCCTTTGCGCGTGCCTGGTGGAGG
CTCGCCTCTCTGGCCGGGTGCAGTGAACGGCCAGCGGGTTTTCTTTCTGCTGGGCAAGGCGCTTTGGGGGTGGA
GGGGGTGGTGTGCTGGCGCTGCACTGGGCTGACTGCGGCGCTGACACAGCGTTTCCCCCATCCCTGTTGCCTGTGT
GTTGTGTGGATCTGTTCTAGTATAGGCAACATAATGAGATACTGTGCTTCCCACCTCCCTTCAGTTCAGAGCC
AAAATGGGTCTAGAATCTGGCACTTTACTCATTTCTTTTGATAAATTGTACTGTGCAGAGCTGTCAGGAACCTTC
AGATAGCAGTAGAGGACTGCAGCTGCCTAGGTCTGCGGCCACATCTTGGGGACACACTGGATTGTTCCCATGTGC
AGGGTTTACGCACTTACGTGGGAGTGCTAGGGGTTAGGCTTTTGTAGCTTGAACGCTGCGTGTGAACAGATGAAA
ATCCTTCAGTACCCAAGTCCCAGTCTGTCTATGGGGAGCAGTTTGGGGGCGGCCGCGCAGCAGGAGCCTGGGAAA
GAGGCCCTCGCCAGGTGATGGCAGGGCCAGGGTGGCTGGGGCACCCAGCGGAATGTGCTTAGTATTTGGTCACC
AGCCGTCATCCTGGGCTTTTCTACTGTGTCTTGTACAAAGGCCTCAGCAATCCACAGAACTCTCTCTCTCTCT
TCCACCTGTCAGCTTCTCTGCTTCTGAGATAAGAACCATTTGTGTAACACCAACACTTAACTTCAGAAAGACATG
CATTATGTGGTGTAAATCAAACCCGAGGCTTTTTCAGATGACCTACTTACATCTTCAATGTGGATAAGATAAAGAACA
AAACACATGCATCTAACTGCTGGGCAATCCAGTTGACTTTTAAATGTAAGAATGGAATTCCAAACACTTAACAC
ATTCAGCTATATGACAGAAAGTAAATCTATGGATATGGTATTTTGTGAATGATCTTTTAAATAAAAGAAAACCTT
ACGTAATATTT

2411/6881
FIGURE 2219

GGAGCGGAGACGGCAAATGGCGGACTTCGACACCTACGACGATCAGGCCTACAGCAGCTTCGGCAGCGGCAGAGG
GTCCCGCGGCAGTGCTGGTGGCCATGGTTCCCGTAGCCAGAAGGAGTTGCCACAGAGCCCCCTACACAGCATA
CGTAGGAAATCTACCTTTCAATACGGTTCGGGGCGACATAGATGCTATCTTTAAGGATCTCAGCATAAGGAGTGT
ACGGCTAGTCAGAGACAAAGACACAGATAAAATTTAAAGGATTCTGCTATGTAGAATTTCGATGAAGTGGATTCCCT
TAAGGAAGCCTTGACATACGATGGTGCCTGTTGGGCGATCGGTCACTTCGTGTGGACATTGCAGAAGGCAGAAA
ACAAGATAAAGGTGGCTTTGGATTTCAGAAAAGGTGGACCAGATGACAGAGGCTTCAGGGATGGCCCTCCCCTCGG
TGGATCCAACATGGATTTTCAGAGAACCCACAGAAGAGGAAAGCGCACAGAGACCACGACTCCAGCTTAAACCTCG
AACAGTCGCGACGCCCCCTCAATCAAGTAGCCAATCCCAACTCTGCTATCTTCGGGGGTGCCAGGCCTAGAGAGGA
AGTTGTTCAAAGGAGCAAAAATGAGCCTGCGGTTGGGAGGGAATGGGGCGTGGGGGGTTAGAGCAGGACCACAG
CCTGGTGAGTCCCCGGGCAGCCGTCCTGCAGCCGCCACTCCTGCGCCTGCCATTGGCCTCCTCACAGCGGAAACA
CAGCTTGTGAGTGCATGTCAGCTGTTAACAAGTGGTTTTTAGTACATTCTGGGCTTTGCTGTATCTATCTAGTGC
CTGTTTGTGCGTTTTTTTTCTTTCTTCCGCTGCTTCCCCATTTTCCTTCCACCTGTCAGCTTCTCT

2412/6881
FIGURE 2220

GGAGCGGAGACGGCAAATGGCGGAC.TTCGACACCTACGACGATCAGGCCTACAGCAGCTTCGGCAGCGGCAGAGG
GTCCCGCGGCAGTGCTGGTGGCCATGGTTCCCGTAGCCAGAAGGAGTTGCCACAGAGCCCCCTACACAGCATA
CGTAGGAAATCTACCTTTCAATACGGTTCGGGGCGACATAGATGCTATCTTTAAGGATCTCAGCATAAGGAGTGT
ACGGCTAGTCAGAGACAAAGACACAGATAAATTTAAAGGATTCTGCTATGTAGAATTCGATGAAGTGGATTCCCT
TAAGGAAGCCTTGACATACGATGGTGCCTGTTGGGCGATCGGTCACCTTCGTGTGGACATTGCAGAAAGGCAGAAA
ACAAGATAAAGGTGGCTTTGGATTTCAGAAAAGGTGGACCAGATGACAGAGGCTTCAGGGATGACTTCTTAGGGGG
CAGGGGAGGTAGTCGCCCAGGCGACCGGCGAACAGGCCCCCCCCATGGGCAGCCGCTTCGGAGATGGCCCTCCCT
CGGTGGATCCAACATGGATTTCAGAGAACCCACAGAAGAGGAAAGCGCACAGAGACCACGACTCCAGCTTAAACC
TCGAACAGTCGCGACGCCCCTCAATCAAGTAGCCAATCCCAACTCTGCTATCTTCGGGGGTGCCAGGCCTAGAGA
GGAAGTTGTTCAAAAAGGAGCAAAAATGAAGCCTGCCATTGGCCTCCTCACAGCGGAAACACAGCTTGTGAGTGCAT
GTCAGCTGTAAACAAGTGGTTTTTAGTACATTCTGGGCTTTGCTGTATCTATCTAGTGCCTGTTTGTGCGTTTTT
TTCTTTCTTCCGCTGCTTCCCCATTTTCCTTC

2413/6881
FIGURE 2221

MADFDTYDDQAYSSFSGSGRSRGSAGGHGSRSQKELPTEPPYTAYVGNLPPFNTVVRGDIDAIFKDLSIRSVRLVRD
KDTDKFKGFCYVEFDEVDSLKEALTYDGALLGDRSLRVDIAEGRKQDKGGFGFRKGGPDDRGFRDDFLGGRGGSR
PGDRRTGPPMGSRFGDGPPLGGSNMDFREPTEESAQRPRQLKPRTVATPLNQVANPNSAIFGGARPREEVVQK
EQK

2414/6881
FIGURE 2222

CGCGTCAGGCCGCTCCTCTCGGCTCCGCGCTCCTTCCCTCGCGCGTGGGCACCCGCCCCCGAGCGGTGAGAGCGC
GTGCGCGCGCGCCCTTCTCCGTGGGCGAGCCAGCCAGTCCCGCTGCACACGCTCGCAGTCTGTGGGCCCTCCGGG
AGGCGGCGGAGGTACCGCGGGGAGAGGGGCGGGCGCAGCATGGCAGCCTCCTTACGGCTCCTCGGAGCTGCCTC
CGGTCTCCGGTACTGGAGCCGGCGGCTGCGGCCGGCAGCCGGCAGCTTTGCAGCGGTGTGTTCTAGGTCAGTGGC
TTCAAAGACTCCAGTTGGATTCAATTGGAAGTGGGCAACATGGGGAATCCAATGGCAAAAAATCTCATGAAACATGG
CTATCCACTTATTATTTATGATGTGTTCCCTGATGCCTGCAAAGAGTTTCAAGATGCAGGTGAACAGGTAGTATC
TTCCCCAGCAGATGTTGCTGAAAAAGCTGACAGAATTATTACAATGCTGCCACCAGTATCAATGCAATAGAAGC
TTATTCCGGAGCAAATGGGATTCTAAAAAAGTGAAGAAGGGCTCATTATTAATAGATTCCAGCACTATTGATCC
TGCAGTTTCAAAGAATTGGCCAAAGAAGTTGAGAAAATGGGAGCAGTTTTTCATGGATGCCCTGTCTTCTGGTG
TGTAGGAGCTGCACGATCTGGGAACCTCACGTTTATGGTGGGAGGAGTTGAAGATGAATTTGCTGCTGCCAAGA
GTTGCTGGGGTGATGGGCTCCAACGTGGTGTACTGTGGAGCTGTTGGGACTGGGCAGGCGGCAAAGATCTGCAA
CAACATGCTGTTAGCTATTAGTATGATTGGAAGTCTGAAGCTATGAATCTTGGAATCAGGTTAGGGCTTGACCC
AAACTACTGGCTAAAATCCTAAATATGAGCTCAGGACGGTGTGGTCAAGTGACACTTATAATCCTGTACCTGG
AGTGATGGATGGCGTTCCCTCGGCTAATAACTATCAGGGTGGATTTGGAACAACACTCATGGCTAAGGATCTGGG
ATTGGCACAAGACTCTGCTACCAGCACAAAGAGCCCAATCCTTCTTGGCAGTCTGGCCCATCAGATCTACAGGAT
GATGTGTGCAAAGGGCTACTCAAAGAAAGACTTCTCATCCGTGTTCCAGTTCCTACGAGAGGAGGAGACCTTCTTC
AGTGTGCCCTTTGGCCACGGACACTGTTGGGAACCAAACCTCTGTCTTGGAGCCTCCTTTTAGCTCACTCCACAAG
TAAATGGATTTAATCAAAGGTCACCTATCTGCTTTTGATTGTCTAGGTCACAGTAATCCCTAGGATTTTTTACCG
CTTATTCCTTTTGTCTTTTAAACAAACATATTATCCGAATTTTTTTTCTGCAAGCCACTGATAGTCTCTGCTAAC
TAGCTTAATTGACCTTTTTTACAAAGTTTGATCCCCAAGCATCCTCAACTAAATCATTGAATACTTCAATCAGGAT
ATTATCTGCTTTACTTTACAAATAAAACCAAATCTTTTGTCAACAGGATGAAACCCATCTTAAAGGAAAGAAAAG
GAATTGGTGTGAAGAGAGAAGTTAGAGAAGGGAAATGCAGTGAATTACTATCTGTGTCCATCAGGAAGTTGTCC
TGTTAACCAAATGGTTACTGCACTACCAGGGTTACTGGTTTATTTTCCAGGGAGCTGATAAAGCAGGAGAACTGT
TGCTGCATGTTTTCTATTTGGACTCCGTCACAATATGGTAGGATATCCCTCACCAACTCCCGACACTCAGCAGAC
TTGTTTTTATATTTTTTTCTTTCTTGTTCATTCTTACTACGTATTTTTTTGACTTAAGAATGACATCTTTAGATGC
ATTTAGAGCCAATGATGATATTTGCTTTAGATAATTATTATATTATTATAAATATAGCCATATTATTTTGAATT
CAAATAAATTTCTATACTGGT

2415/6881
FIGURE 2223

MAASLRLLGAASGLRYWSRRLRPAAGSFAAVCSRSVASKTPVGFIGLGNMGNPMAKNLMKHGYPLIIYDVFPDAC
KEFQDAGEQVSSPADVAEKADRIITMLPTSINAIEAYSGANGILKKVKKGSLLIDSSTIDPAVSKELAKEVEKM
GAVFMDAPVSGGVGAARSGNLTFMVGGVEDEFAAAQELLGCMGSNVVYCGAVGTGQAAKICNNMLLAISMIGTAE
AMNLGIRLGLDPKLLAKILNMSSGRCWSSDTYNPVPGVMDGVPSANNYQGGFGTILMAKDLGLAQDSATSTKSPI
LLGSLAHQIYRMMCAKGYSKKDFSSVFQFLREEETF

GACGCAAGGCCTACTGTCTGGCTGGGAGGGAGGTGTAGCCGGTCTTTGGGGGTAGGCGGCTAGTGGCGGAAGAGGAT
TCGGCGGCTGATGGCGGATCAGGATCGGAAGCCTGCGTAACTTTCTCCCTTGATCCGGGAGTCTTTCCACTGGAT
TCACAATGACATCCTTTCAAGAAGTCCCATTGCAGACTTCCAACCTTTGCCCATGTCATCTTTCAAAATGTGGCCA
AGAGTTACCTTTCTAATGCACACCTGGAATGTCATTACACCTTAACTCCATATATTTCATCCACATCCAAAAGATT
GGGTTGGTATATTCAAGGTTGGATGGAGTACTGCTCGTGATTATTACACGTTTTTATGGTCCCTATGCCTGAAC
ATTATGTGGAAGGATCAACAGTCAATTGTGTACTAGCATTCCAAGGATATTACCTTCCAAATGATGATGGAGAAT
TTTATCAGTTCTGTTACGTTACCCATAAGGGTGAAATTCGTGGAGCAAGTACACCTTTCCAGTTTCGAGCTTCTT
CTCCAGTTGAAGAGCTGCTTACTATGGAAGATGAAGGAAATTCGTGACATGTTAGTGGTGACCACAAAAGCAGGCC
TTCTTGAGTTGAAAATTGAGAAAACCATGAAAGAAAAAGAAACTGTTAAAGTTAATTGCCGTTCTGGAAAAAG
AAACAGCACAACTTCGAGAACAAGTTGGGAGAATGGAAAGAGAACTTAACCATGAGAAAGAAAGATGTGACCAAC
TGCAAGCAGAAACAAAAGGGTCTTACTGAAGTAACACAAAGCTTAAAAATGGAAAATGAAGAGTTAAGAAGAGGT
TCAGTGATGCTACATCCAAAGCCCATCAGCTTGAGGAAGATATTGTGTGAGTAACACATAAAGCAATTGAAAAAG
AAACCGAATTAGACAGTTTAAAGGACAACTCAAGAAGGCACAACATGAAAGAGAACTTGAATGTGAGTTGA
AGACAGAGAAGGATGAAAAGGAACCTTTATAAGGTACATTTGAAGAATACAGAAATAGAAAATACCAAGCTTATGT
CAGAGGTCCAGACTTTAAAAAATTTAGATGGGAACAAAGAAAGCGTGATTACTCATTTCAAAGAAGAGATTGGCA
GGCTGCAGTTATGTTTGGCTGAAAAGGAAAATCTGCAAAGAACTTTCTGCTTACAACCTCAAGTAAAGAAGATA
CTTGTTTTTTTAAAGGAGCAACTTCGTAAAGCAGAGGAACAGGTTTCAGGCAACTCGGCAAGAAGTTGTCTTTCTGG
CTAAAGAACTCAGTGATGCTGTCAACGTACGAGACAGAACGATGGCAGACCTGCATACTGCACGCTTGGAAAACG
AGAAAGTGAAAAAGCAGTTAGCTGATGCAGTGGCAGAACTTAACTAAATGCTATGAAAAAGATCAGGACAAGA
CTGATACACTGGAACACGAACTAAGAAGAGAAGTTGAAGATCTGAAACTCCGTCTTCAGATGGCTGCAGACCATT
ATAAAGAAAAATTTAAGGAATGCCAAAGGCTCCAAAAACAAATAAACAACTTTTCAGATCAATCAGCTAATAATA
ATAATGTCTTCACAAAAGAAAAACGGGGAATCAGCAGAAAGTGAATGATGCTTCAGTAAACACAGACCCAGCCACTT
CTGCCTCTACTGTAGATGTAAAGCCATCACCTTCTGCAGCAGAGGCAGATTTTGACATAGTAACAAAGGGGCAAG
TCTGTGAAATGACCAAAGAAAATTGCTGACAAAACAGAAAAGTATAATAAATGTAAACAACCTCTTGCAGGATGAGA
AAGCAAAATGCAATAAATATGCTGATGAACTTGCAAAAATGGAGCTGAAATGGAAGAACAAGTGAAAATTGCTG
AAAATGTAAACTTGAAGTACAGTGAAGTACAGGACAAATTATAAAGAACTTAAAGGAGTCTAGAAAATCCAGCAG
AAAGGAAAATGGAAGGTGAGAATTCCCAGAGTCTCAATGTTTCAAACATGCTCAGAGCAAAATGGTTATGTTG
TCACATTGTCAAATGCACAACCAGTTCTGCAATATGGTAATCCTTATGCATCTCAGGAAACAAGAGATGGAGCAG
ATGGTGCTTTTTTACCCAGATGAAATACAAAGGCCACCTGTCAGAGTCCCTCTTGGGGACTGGAAGACAATGTTG
TCTGCAGCCAGCCTGCTCGAAACTTTAGTCGGCCTGATGGCTTAGAGGACTCTGAGGATAGCAAAGAAGATGAGA
ATGTGCCTACTGCTCCTGATCCTCCAAGTCAACATTTACGTGGGCATGGGACAGGCTTTTGCTTTGATTCCAGCT
TTGATGTTTACAAGAAGTGTCCTCTGTGAGTTAATGTTTCCCTCCTAACTATGATCAGAGCAAATTTGAAGAAC
ATGTTGAAAGTCACTGGAAGGTGTGCCCCGATGTGCAGCGAGCAGTTCCCTCCTGACTATGACCAGCAGGTGTTTG
AAAGGCATGTGCAGACCCATTTTGATCAGAATGTTCTAAATTTTGACTAGTTACTTTTTATTATGAGTTAATATA
GTTTAGCAGTAAAAAAAAAAAAAAAAAACACACCTAAAAATAGACCACTGAGGAGACCATAGAGCGGATGCTTTTCA
TGCACCCTTTACTGCACTTTCTGACCAGGAGCTACTTTGAGTTTGGTGTACTAGGATCAGGGTCAGTCTTTGGC
TTATCAATAAATTTTAACTCTCTGTTAATCTTACCTGCTTTAAAAAAAAGTTCTTGTGTGTTTCGTATCTTTATTTA
TTCCCTAGTTTGCAGAACTGTCTGAATAAAGGATACAAGGATTATTTCAATGTTACTGCACTGAAAAACGTGTAT
GTATTAGTGTGCTAGATTATTTAGCAGAATATTCAACAAGTTTCTGTTGACCTTGTTGATTGAGCATGACTACTAA
ATATTATGTAATAAAAAGCATTGTGTCATAAC

2417/6881
FIGURE 2225

ATGGAGAAGCAGAGAGGGAAGTGCAGAGACAGGTCACCCAGGCGCCTGGAACTGCCTCTATGGCCTTCACGGGA
AACGGCCTCTTTCTACTCCGGATCCCAGACTGTGTTTCTTTGAACTGACCGTCAGAGGAGAGCGGCTGGAGGCG
GACAGACGTCTGCAGTGGGAGGCGCTCCAGGCGTTCCAGGCAGTGTCCTGCCGGCGAGTCACCCGCGACCGCGAG
TCACCTACCAAGCCCTGAATTGGGACAGGAGACGAGACGTGTCGACGAGCTGCGGAGTTCTCGCTTCTCTGGG
CCCTGCCAGCTCACAGCCAAGGTGCACCAGAGCCTCCGTCACCGCCCCCTACAGAGCACGTACTTTTATCACACGA
ACTATGACTCAGACACCACAAACCCAGACCAGGCTCCAGGTCAGAAGTTGACTCCCCTGAGGCCTGTGGTAGGA
GAATGTGGTCTGGAAAATGAGGTGTCACTGGTGATCAGACATCATCACTTTTCTAGTGACTGTCAGCTTAGTTTT
GTCCTACAGTTGTCTTGA

2418/6881
FIGURE 2226A

CCCCGACTAGCCCCGACAGTCCCCGACTAGCCCCGACAGCCCCAGCAGGATCTGCATCGTCATCGAGCCGGCCCCAGC
TTCTGAAGGGAGATGTCATGGTGAAATGCTACCACAAGAAATACCGCTCGGCCACCCGTGACGTCAATTTTCCGCC
TGCAGTTTCACACTGGGGCTGTGCAGGGCTACGGGCTGGTGTGTTGGGAAGGAGGATCTGGACAATGCCAGCAAAG
ATGACCGTTTTTCTGACTATGGGAAGGTTGAATTAGTCTTCTCTGCCACGCCTGAGAAGATTCAAGGGTCCGAAC
ACTTGTACAACGACCACGGTGTGATTGTGGACTACAACACAACAGACCCACTGATACGCTGGGACTCGTACGAGA
ACCTCAGTGCAGATGGAGAAGTGCTACACACGCAGGGCCCTGTGCGATGGCAGCCTTTACGCGAAGGTGAGGAAGA
AAAGCTCCTCGGATCCTGGCATCCCAGGTGGCCCCCAGGCAATCCCGGCCACCAACAGCCCAGACCACAGTGACC
ACACCTTGTCTGTGACGAGTACTCCGGCCACTCTACAGCCTCTGCCAGGACGGATAAGACGGAAGAGCGCCTGG
CCCCAGGAACCAGGAGGGGCCCTGAGTGCCAGGAGAAGGCAGAGTTGGACCAGCTGCTCAGTGGCTTTGGCCTGG
AAGATCCTGGAAGCTCCCTCAAGGAAATGACTGATGCTCGAAGCAAGTACAGTGGGACCCGCCACGTGGTGCCAG
CCCAGGTTACAGTGAATGGAGACGCTGCTCTGAAGGATCGGGAGACAGACATTCTGGATGACGAGATGCCCCACC
ACGACCTGCACAGTGTGGACAGCCTTGGGACCCCTGTCTCTCGGAAGGGCCTCAGTCGGCCACCTGGGTCCCT
TCACCTGCCACAAGAGCAGCCAGAACTCACTCCTATCTGACGGTTTTTGGCAGCAACGTTGGTGAAGATCCGCAGG
GCACCTCGTTCCGGACCTGGGCCTTGGCATGGACGGCCCTATGAGCGGGAGCGGACTTTTGGGAGTCGAGAGC
CCAAGCAGCCCCAGCCCCCTGCTGAGAAAGCCCTCAGTGTCCGCCCAGATGCAGGCCTATGGGCAGAGCAGCTACT
CCACACAGACCTGGGTGCGCCAGCAGCAGATGGTTGTAGCTCACCAGTATAGCTTCGCCCCAGATGGGGAGGCC
GGCTGGTGAGCCGCTGCCCTGCAGACAATCTGGCCTCGTCCAGGCCCAGCCCAGAGTGCCACTCACCCCCACCC
GAGGGACCAGCAGTAGGGTGGCTGTCCAGAGGGGTGTAGGCAGTGGGCCACATCCCCCTGACACACAGCAGCCCT
CTCCCAGCAAAGCGTTCAAACCCAGGTTTCCAGGAGACCAGGTTGTGAATGGAGCCGGCCCAGAGCTGAGCACAG
GCCCCCTCCCCAGGCTCGCCCCACCCTGGACATCGACCAGTCCATCGAGCAGCTCAACAGGCTGATCCTGGAGCTGG
ATCCCACCTTCGAGCCCATCCCTACCCACATGAACGCCCTCGGTAGCCAGGCCAATGGCTCTGTGTCTCCAGACA
GCGTGGGAGGTGGGCTCCGGGCAAGCAGCAGGCTGCCTGACACAGGAGAGGGCCCCAGCAGGGCCACCGGGCGGC
AAGGCTCCTCTGCTGAACAGCCCCCTGGGCGGGAGACTCAGGAAGCTGAGCCTGGGGCAGTACGACAACGATGCTG
GGGGGCAGCTGCCCTTCTCAAATGTGCATGGGGAAAGGCTGGTGTGGACTATGCCCCAAACCTGCCGCCATTCC
CCTCACCAGCGGACGTCAAAGAGACGATGACCCCTGGCTATCCCCAGGACCTCGATATTATCGATGGCAGAATTT
TAAGTAGCAAGGAGTCCATGTGTTCAACTCCAGCATTTCCTGTGTCTCCAGAGACACCGTATGTGAAAACAGCGC
TGCGCCATCCTCCGTTAGCCCCACCTGAGCCCCCGCTGAGCAGCCCAGCCAGTCAGCACAAAGGAGGACGTGAAC
CACGAAGCTGCCCTGAGACGCTCACTCACGCTGTGGGGATGTGAGAGAGCCCCATCGGACCCAAATCCACGATGC
TCCGGGCTGATGCGTCTCTGACGCCCTCCTTTACAGCAGGCTTTTGCTTCTTCTGACCATTTCCAGCAACGGCC
CTGGGCAGAGGAGAGAGAGCTCCTCTTCTGACAGAACGCCAGTGGGTGGAGAGCAGCCCCAAGCCCATGTTTTCC
TGCTGGGGAGCGGCCCGGCCACCGGAAGTCCCTCAGCGCTGAGTTCTCCGGTACCAGGAAGGACTCCCCAGTGC
TGCTCTGCTTCCCGCCGTGAGAGCTCCAGGCTCCTTTCCACAGCCATGAGCTGTCCCTAGCAGAGCCACCGGACT
CCCTGGCGCCTCCCAGCAGCCAGGCTTCTTGGGCTTCGGCACCGCCCCAGTGGGAAGTGGCCTTCCGCCCCGAGG
AGGACCTGGGGGCCCTTGTGAGCCAATTCTCATGGAGCGTCACCGACCCCCAGCATCCCGCTGACAGCGACAGGGG
CTGCCGACAATGGCTTCTGTGTCACAACTTCTCACGGTGGCGCCTGGACACAGCAGCCACCACAGTCCAGGCC
TGCAGGGCCAGGGTGTGACCCTGCCCCGGCAGCCACCCCTCCCTGAGAAGAAGCGGGCCTCGGAGGGGGATCGTT
CTTTGGGCTCAGTCTCTCCCTCCTCCAGTGGCTTCTCCAGCCCGCACAGCGGGAGCACCATCAGTATCCCCTTCC
CAAATGTCTCTCCGACTTTTCCAAGGCTTCAGAAGCGGCCTCACCTCTGCCAGATAGTCCAGGTGATAAACTTG
TGATCGTGAAATTTGTTCAAGACACTTCCAAGTTCTGGTACAAGGCGGATATTTCAAGAGAACAAGCCATCGCCA
TGTTGAAGGACAAGGAGCCGGGCTCATTCAATTGTTTCGAGACAGCCATTCTTCCGAGGGGCCTATGGCCTGGCCA
TGAAGGTGGCCACGCCCCACCTTCAGTCTGACGCTGAACAAGAAAGCTGGAGATTTGGCCAATGAACTCGTCC
GGCACTTTTTGATCGAGTGTACCCCGAAGGGAGTGGCGTTGAAAGGGTGTCTGAATGAACCATATTTCCGGGAGCC
TGACGGCCTTGGTGTGCCAGCATTCCATCACGCCCTTGGCCTTGCCGTGCAAGCTGCTTATCCAGAGAGAGATC
CATTGGAGGAAATAGCAGAAAGTTCTCCCCAGACGGCAGCCAATTTCAGCAGCTGAGCTGTTGAAGCAGGGGGCAG
CCTGCAACGTGTGGTACTTGAACCTCTGTGGAGATGGAGTCCCTCACCGGCCACCAGGCGATCCAGAAGGCCCTGA
GCATCACCTGGTCCAGGAGCCTCCACCTGTGTCCACAGTTGTGCACTTCAAGGTGTGAGCCCAGGGGCATCACCC
TGACAGACAATCAGAGGAAGCTCTTCTTCCGGAGGCATTACCCCGTGAACAGTGTGATTTTCTGTGCCTTGGACC
CACAAGACAGGAAGTGGATCAAAGATGGCCCTTCTCAAAGTCTTTGGATTTGTGGCCCGGAAGCAGGGCAGTG

[illegible]

2420/6881
FIGURE 2227

MVKCYHKKYRSATRDVIFRLQFHTGAVQGYGLVFGKEDLDNASKDDRFDPDYGKVELVFSATPEKIQGSEHLYNDH
GVIVDYNTTDPLIRWDSYENLSADGEVLHTQGPVDGSLYAKVRKKSSSDPGIPGGPQAIPATNSPDHSDHTLSVS
SDSGHSTASARTDKTEERLAPGTRRGLSAQEKAELDQLLSGFGLEDPGSSLKEMTDARSKYSGTRHVVPAQVHVN
GDAALKDRETDILDDEMPHHDLHSVDSLGLTSSSEGPQSAHLGPF TCHKSSQNSLLSDGFGSNVGEDPQGTILVPD
LGLGMDGPYERERTFGSREPKQPQLLRKPSVSAQMQAYGQSSYSTQTWVRQQQMVVAHQYSFAPDGEARLVSRC
PADNPGLVQAQPRVPLTPTRGTSSRVAVQRGVSGSPHPPDTQQPSPSKAFKPRFPDQVVNGAGPELSTGSPSGS
PTLDIDQSIEQLNRLILELDP TFEPIPTHMNALGSQANGSVSPDSVGGGLRASSRLPDTGEGPSRATGRQGSSAE
QPLGGRLRKL SLGQYDNDAGGQLPFSKCAWGKAGVDYAPNLPPFPSPADV KETMTPGYPQDLDIIDGRILSSKES
MCSTPAFPVSPETPYVKTALRHPPFSPPEPPLSSPASQHKGGREPRSCPETLTHAVGMSESPIGPKSTMLRADAS
STPSFQQAFASSCTISSNGPGQRRESSSSAERQWVESSPKPMVSLLGSGRPTGSPLSAEFSGTRKDSPVLSCFPP
SELQAPFHSHEL SLAEPPDSLAPPSSQAFLGFGTAPVGSGLPPEEDLGALLANSHGASPTPSIPLTATGAADNGF
LSHNFLT VAPGHSSHHSPGLQGQGVTLPGQPPLPEKKRASEGDRSLGSVSPSSSGFSSPHSGSTISIPFPNVLPD
FSKASEAASPLPDSPGDKLVIVKFVQDTSKFYKADISREQAIAMLKDKEPGSFIVRDSHSFRGAYGLAMKVATP
PPSVLQLNKKAGDLANELVRHFLIECTPKGVRLKGCSNEPYFGSLTALVCQHSITPLALPCKLLIPERDPLEEIA
ESSPQTAANSAAELLKQGAACNVWYLN SVEMESLTGHQAIQKALSITLVQEPPPVS TVVHFKVSAQGITLTDNQR
KLFFRRHYPVNSVIFCALDPQDRKWIKDGPSSKVF GFVARKQGSATDNVCHLFAEHDPEQPASAI VNFVSKVMIG
SPKKV

2421/6881
FIGURE 2228

GGCACGAGGCACAGCTTCGCGCCGTGTACTGTGCGCCCATCCCTGCGCGCCAGCCTGCCAAGCAGCGTGCCCCG
GTTGCAGGCGTCAATGCAGCGGGCGCGACCCACGCTCTGGGCCGCTGCGCTGACTCTGCTGGTGCTGCCGCGG
CCGCCGGTGGCGCGGGCTGGCGCGAGCTCGGGGGGCTTGGGTCCCGTGGTGCGCTGCGAGCCGTGCGACGCGCGT
GCACTGGCCCACTGCGCGCCTCCGCCCGCCGTGTGCGCGGAGCTGGTGCGCGAGCCGGGCTGCGGCTGCTGCCTG
ACGTGCGCACTGAGCGAGGGCCAGCCGTGCGGCATCTACACCGAGCGCTGTGGCTCCGGCCTTCGCTGCCAGCCG
TCGCCCCGACGAGGCGCGACCGCTGCAGGCGCTGCTGGACGGCCGCGGGCTCTGCGTCAACGCTAGTGCCGTCAGC
CGCCTGCGCGCTACCTGCTGCCAGCGCGCCAGCTCCAGGAAATGCTAGTGAGTCGGAGGAAGACCGCAGCGCC
GGCAGTGTGGAGAGCCCGTCCGTCTCCAGCACGCACCGGGTGTCTGATCCCAAGTTCCACCCCTCCATTCAAAG
ATAATCATCATCAAGAAAGGGCATGCTAAAGACAGCCAGCGCTACAAAGTTGACTACGAGTCTCAGAGCACAGAT
ACCCAGAACTTCTCCTCCGAGTCCAAGCGGGAGACAGAATATGGTCCCTGCCGTAGAGAAATGGAAGACACACTG
AATCACCTGAAGTTCTCAATGTGCTGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAGGGATTTTAT
AAGAAAAAGCAGTGTGCGCCCTTCAAAGGCAGGAAGCGGGGCTTCTGCTGGTGTGTGGATAAGTATGGGCAGCCT
CTCCCAGGCTACACCACCAAGGGGAAGGAGGACGTGCACTGCTACAGCATGCAGAGCAAGTAGACGCGCTGCCGCA
AGGTTAATGTGGAGCTCAAATATGCCTTATTTTGCACAAAAGACTGCCAAGGACATGACCAGCAGCTGGCTACAG
CCTCGATTTTATATTTCTGTTTGTGGTGAAGTATTTTTTTTAAACCAAAGTTTAGAAAGAGGTTTTTGAAATGCC
TATGGTTTTCTTTGAATGGTAACTTGAGCATCTTTTCACTTTCCAGTAGTCAGCAAAGAGCAGTTTTGAATTTTCT
TGTCGCTTCTATCAAAAATATCAGAGACTCGAGCACAGCACCCAGACTTCATGCGCCCGTGGAATGCTCACCAC
ATGTTGGTTCGAAGCGGCCGACCACTGACTTTGTGACTTAGGCGGCTGTGTTGCCTATGTAGAGAACACGCTTCAC
CCCCACTCCCCGTACAGTGCACAGGCTTTATCGAGAATAGGAAAACCTTTAAACCCCGGTATCCGGACATCC
CAACGCATGCTCCTGGAGCTCACAGCCTTCTGTGGTGTCAATTTCTGAAACAAGGGCGTGGATCCCTCAACCAAGA
AGAATGTTTATGTCTTCAAGTGACCTGTACTGCTTGGGGACTATTGGAGAAAATAAGGTGGAGTCCTACTTGTTT
AAAAAATATGTATCTAAGAATGTTCTAGGGCACTCTGGGAACCTATAAAGGCAGGTATTTGCGGGCCCTCCTCTTC
AGGAATCTTCTGAAGACATGGCCCAGTCGAAGGCCAGGATGGCTTTTGCTGCGGGCCCGTGGGGTAGGAGGGA
CAGAGAGACAGGGAGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAATGTCACAATTCTTCGGATGACTGCAG
AAAATAGTGTTTTGTAGTTCAACAACCTCAAGACGAAGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAGGCTTT
ATTTTCATCTCTCATCTTTTGTCTCTTAGCACAATGTAAAAAGAATAGTAATATCAGAACAGGAAGGAGGAA
TGGCTTGCTGGGGAGCCCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTTGTGAACTTAGAGTCAT
TCTCATGCTTTTCTTTATAATTCACACATATATGCAGAGAAGATATGTTCTTGTTAACATTGTATACAACATAGC
CCCAAATATAGTAAGATCTATACTAGATAATCCTAGATGAAATGTTAGAGATGCTATTTGATACAACCTGTGGCCA
TGACTGAGGAAAGGAGCTCACGCCCAGAGACTGGGCTGCTCTCCCGGAGGCCAAACCAAGAAGGTCTGGCAAAG
TCAGGCTCAGGGAGACTCTGCCCTGCTGCAGACCTCGGTGTGGACACACGCTGCATAGAGCTCTCCTTGAAAACA
GAGGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTCTTTATTTTTTTTAACTTTTGGGGGAAAGTATTTT
TGAGAAGTTTGTCTTGCAATGTATTTATAAATAGTAAATAAAGTTTTTACCATTAAAAAATAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

2422/6881
FIGURE 2229

MQRARPTLWAAALTLVLRLRGPPVARAGASSGGLGPFVVRCEPCDARALAQCAPPPAVCAELVREPGCGCCLTCAL
SEGQPCGIYTERCGSGLRCQSPDEARPLQALLDGRGLCVNASAVSRLRAYLLPAPPAPGNASESEEDRSAGSVE
SPSVSSTHRVSDPKFHLHSKIIIIKKGHAKDSQRYKVDYESQSTDTONFSSESKRETEYGPCRREMEDTLNHLK
FLNVLSFRGVHIPNCDKKGFYKKKQCRPSKGRKRGFCWCVDKYGQPLPGYTTKGKEDVHCYSMQSK

2423/6881
FIGURE 2230A

GCGGGTGTTCGCCTACGTCACTGGGGCGCTACAGTACCTGGAGCTGGGCAGTCTTCTCATCAGAGTGGGGACTAA
TAACAGTGACCTCCCCGCCAGGTCCTGTGTGTTGCCGGCTGAAGAAGGATGATGATTATTTCCACCTTCTGAGA
GACAAAGACCAACGAGCCACCACAGCCACCAGTCCCAGAACCCGCCAATGCTGGGGAACGGAAAAATGAGGGAGTT
CAACTCTGGCCCTCACAATCCAGTGGAGGAGACGAACTCATCTGCCTCTGTCCCTCTGGGCACGCTTCATGCCA
GGTGCATCTGTGGACAGGGGCCATGCTCCTGGGCTTCCAAAGTTGGAGAAAGCTGCCAGGCTCAGAGCCACCTAA
GCTGAAGATTCCCTTGAGAACAAGTACTGTCTGTGGTTTCATGGCCTTTCTTCCATTTGTGGTTCTTGTGAAGT
GGAATTTAAATGACATCTTATCAAGATGGATAAACCCCTAGTTTCCAGTGCTGGAATATAGAAAATGGATGGACA
AGTAAATCCCCTCATCACCATAGTCCAGGCATGGGGACCTCAACACACCTGAGCCCCAGACATCACCTTTCAT
TCTGGACCTACCATGAAAGACTTCTGAATCCAGGAAGAGAGACTGACTGGGCAACATGTTGTTTCAGAAACAGGAC
CTTGCCCTGTCAATTTAGGATGGAGTTCAGTGGTCCAATCATGGCTCATTGTAGCCTCAAACCTCCAGGCTCAAGC
AATCCTACCATGTGAGCCTTCCAGTAGCTGGGACTACAGCTGGATCTACCATGAAAGACTTCTGAATCCAGGAA
GAGAGACTGACTGGGCAACATGTTATTCAGGGTCTCCCTCTCTTGTCCAAGGCTGGAGTGTAGTAGTGCTATCAC
AGCTGACTGCAGCCTCAACCTTCCAGGCTGAAGCGATCCTCCCATCTCAACCTCCCACGTGGCTGAGACTATAGG
TGCTTGCCACTATGCCCACTAATATTTGGAATTTTCTTATACGTGGATTCCAGAGGGGTGACAGCGAAACGTGA
GACCATCCAGTTGCAGAAAAACAAGCTTAACACGCCCACTGATTCTACATTATGCCCCTACCTCCCGGCAGCCTC
TCCAGGCCCAGAACTTTCTCCAGTCAGCCTCCACAGACCAAGCTCATGACTCACAATGGCCTATTTAGGCCATA
CCCTACCTCACGGCAGTCTCTGCAGATGAGGCTACTGCCTCACAACAGCCTCCACAGGCACAGCTCCACCGTTAC
AATGGCCTCTTTAGACCCAGCTCCTGCCTCCCAGCCTTCTCTCCAGGCCCTGAGCTTTCTCAAGTCGACCTCACC
AGGCCAGCTCATGCTTCTTGGCAGCCTCTCCAGGCCAGCTCCTGCATCTTGGCAGCCTCTCCAGGCCAGCCT
CTGCCTCCTGTGAGCCTCTACAGTCCCAACATCTGCCTCACAGCAGATTCTTCCAGGCCAGTATCTGCCTCACTG
TGGACCACCCAAGCCAAGCTCCCAACCTTTCAGCAGCTTCTACACACCCAGCTCCTGCCACCCAGTGGCCTCTTT
AGGCCAAGCTCATGCCTCACAAGGGCCTTTCAGGCCCAACTTTTGTCTCATGGCAACCTTCCCTGGCCACATTC
CTGCCTGTCTCCAGCAGCCTAGACAGGCCAGGTCTTGCTCAGCTGGCCTGTCTACATCCAGCTCTTGCCTC
ACGGTGGCCTCTCCAGGCCAGCTCCTGTCCCAGGACGTATCTCCAGGCCCAAACTTCTCAAGTCAGCCTCT
CTAGTCCCAACTGCTGCCTCCTGGTGGCCTATGAAGGCCCAAAATCTCTCAAGTTGACCTCTCCAGGCCAGCT
CCTGCCTCCTGTGAGCCTCTACAGGCCCAACCTCTGCCTCATGGGGGCTTCTCCAGGCCAGCTCTTCTCTGGG
CTGAGTCTACAGGCACAACCTGCTGCCTCACAACAGCCTTTTTTGGCCAGTTCTGTCCAGCTCACAGCGACCA
TGTAGGCCCAAACTTCTCAAGTCAAACCTCTCCAGGCCTGCCTTCTTCTGGTGGCATGAACAGGCCAGCTTT
GACTTGAGAACAGCCTCTGCAGGCCCTGCTCTTGCCTCCAGGGGCTTCTCCAGGCCAGCTCTTGCCTCATGGC
GGCTGCCCCAGGCCAAGTTTCTGCCTGCCTGCCAGCAGCCTCAACAGGCACAGCTCTTCCCTCACAGTGGCCAT
TTAGGCCCAACTCATGACTGTGCGGCCATTTCCAGGCCTAGTGCCTGCCTCCTGGCTGACTCTTGAAGCCAAAA
CTTCTCAAATCAGCCTTTTGGCCAACTTCTGTCTACTGTGCGACTCTACAGGCCAGCCTCTGCCTCACAGTGA
CCCTCCAGACCCAGATGGTGTCTCACTGTGGCATCCTCAGGCGAAGCTCCTGCCTTTCAGCAGCCTCTACGGCC
CAGCTCCTGCCTTGCAATGGCCTCTTTAGGCCAAGCTCATGCCCCACGGCGACTTTTCCAGGCACAGCTTTTGGC
TTTTGCAGCCTGTCCAGGCCCAGAATGTCCTTAACTCGGCGTCTCCAGGACGAGCTCATCCTCCAGTGCCTCTA
CAGGCCCGTCTCCTGCCTCACAACAACCTCCTTTGGTCCAACCTCCTGCTGAGCTGCTTGGCAGCCTCTGTAGGCC
ACAGAGTTCTTAAAGTAAAGCTTTCAGGCCACCTTCGGCCTCCCGGCAGCCTCAGCAATCAAACCTATTCCCTC
ACTGCGGCCACCGAAAGCCAAGTTTCTCCCTGCCTCACAGCATCCTCCGAAAACCTGAGCATTTCCTCACGGTGG
CCTCCCCAGGCCACGAATCTGCCTGCCTCCCAGGCAGCTGCTGCCTCACAATGGTCTCTTTAGGCCAGCTCTTG
CTAAAAGACAGACTCTCCAGGCACAGCTCTTGCCTCCTGGCAGGCTCTGCAGGCCCAAACTTCCAAAAGTTGGC
CTCTCCTAACTCAGCTCCTGCCTCATGTGGCCTACACAGGCCAGACTCTTACCACACAGTAGACCTCCAGGC
CCACCACTTGCTGAGCATAGCCTCCTAAGGCCAAGCTCCTGCCTTTCGGCAGCCTCTACAGGCCAGCTCCTGC
CTCGCAATTGCCTTTGTAGGCCAAGATCATGCCGCGAAGTGGCCTTTCCTAGCCTAACTTTTGCTTTTTGACGCA
TACTCCGGTCCCAAACTTCTCCAGTCAGCCAGTCCAGGCCAAGCTCTTCTCCCAAAGGCTTCTGCAGGCCAA
AATCGTCTGAAGTCACCTCTGCAGGCCAGCTCCTGCCTCCAAGTGTGTAGGCCAAGCTAATGCCTCACA
GCACACTTTCCAGGCTGAGCATTTCCTTTTGTGCATCCTCTCCAAGCCCTGAACTTACTCCAGTTGGCCTCTCCA
GACCAAGCTCTCCCTCCCAGTGGCCTCTACAGGCCAAAATTGTCTCAAGTCAGCCTCTCCAGGGCCAACTCCTA
GCTACCGGTGGCTTCTGCAGGCCAAAATCGACCTCAAGTCAGCCTCTTTCACACCCAGCTCTTGTCTGTAAGTGGC

2424/6881
FIGURE 2230B

CTCTGCAGGAGCAAACTGCCTCAAGTCGGCCTCTCCAGGCCAGCCTCCTGCTTCCCGAGGGCATGTACAGGCC
CAGCCTCTGCCTCACAGCAGACTCTCCATGCCCAGCTCTTCCCTGTCTGCTGCCTCTCCAGTCCAAAGCTGCGCC
TGCCTTTCGGCAACTTGTACGGGCCCAGCTCCTCCCTCACGGTGGCCTCTTTTCGCCAACTCATGCCTCTTGCA
ACCTGCCCCAAGTGTCAGCTCCTGCCTCACACTGGCCTCTTGAGGCTCAGCTCATGCCTCTCGTGGCCTCAACGGG
CCCAGCCCCCTGCCTGTCGGCGGCCTCTACAGGCCAGCCTCTACCTCACAGTGGGCTCTCCAGGCCACCTCTTT
CTCACCGTGGCCTCCTGGGGCAATGCTCCCCGCTCTCGGGAGCCTCTGCGGGCCCAGCTCCTGCCTCCAGTGGC
CTCTGTAGGCCAAGCCCGTGCCTCAGGGCAGCCTTTCAGGCCTAGCGTTTGCTGCTTTGCATCCTCTCCAGGCT
CTGGACTTCCTCCAGTCGGCCTCTCCAGGCCAGCTCTTCTCCCGGCGGCCTCTGCAGGCCAGACTGTTGTCA
AGTCGGCCTGTCCAGGGCCAGCTCCTGCCTCCCGGTGCCCTCTGCAGGCCAAGTCGTCCTCAAGTCGGCCTCCC
CAGGCCAGCTCCGGCCTCTCGGCGGCCGCTCCAGGTGCAAAAGTTCCTCGAGTCAGCCTCTCCAGGCCAGCTC
CTCCTGCCTCCCAGCGGCCTCTTTTCGGCCCAGCCCAGCTCATGCCTCCCGGCTGCGTCTCTAGGCCCGACTCCGG
CCTCCCAACAACCTCTTTGGACTCAGCTCCTGCCTCTCGAAGGCCTGCACGGGGCCCAGCCTCAGCCTCACAGCGG
ACTCTCCACGCCCAGCTAGCTCTCGCCTCACTGCGGCCTCCCCAGTCGAAAGCTCCTGCCTTTCGGCCGCTTTGG
CAGGCCAGCTCCTGCCTGCCAGTGGCCTCTTTAGGCCAGCTCATTCTCACAACGGCCTTTCAGGCCCGCTT
TTTCCCTTCCGGCAGCCTTTTGGCCTCTAATTTGTTTATCTTTTGTGTATAAATCCCAAAATATGGAATTTTGA
ATATTGCTACCATT

2425/6881
FIGURE 2231

MLLPGLSLSRPRTFSSQPLQTKLMTHNGLFRPIPYLTAVSADEFTASQQPPQAQLHRYNGLFRPSSCLPAFSPGP
ELSQVDLTRPSSCFFAASPGPAPASWWPLQAQPLPPVGLYSPNICLTADSSGPASASLWTPQAKLPTFQQLLHTQ
LLPPSGLSRPSSCFTRAFAGPTFVSWQPSLARFLLVSQQPRQAQVLPHTGLSTSSSCLTLASPGPTPVPGRHLRA
QNLLKSDSLVPTAAFWWPMKAQNLLKLTSPGPAPASCOHLQAQPLPHGVFSRPTSSSWLGLQAQLLPHNSLFWPS
SCPAHGGQCRPKTSSSQTQAHL LLPGGMNRPSFDLRTASAGPALASQGLFPGPALASWQLPEAKFLLACQQPQQ
AQLLPHSGPFSPNS

2426/6881
FIGURE 2232A

GGGAAGCGCGCCGCGCACCTCATGGTTCCGGGGACAGTTAGGGCGGCGGATGGAGGTCAGCGGTGGTGCTCGCTG
CGGTTTGAATCACTTGCTAGGAGTCTTGTCTCTCTGCCACCCAGGACATC**ATG**GCGAGCTCACCTGGTAAAGCGA
TGCACGTGCCTCCTGAGAGAAGCTGCTCGTCAGGCCCCCTGCCATGGCTCCAGTTGGCCGACTGAGACTTGCCTGG
GTAGCCCATAAGACTCTGACTTCCTCAGCCACCTCACCCATTTCACCTCCCAGGTTCTTGATGGAGCCGGTG
GAGAAGGAACGAGCATCTACTCCCTACATAGAGAAGCAGGTGGACCACCTCATCAAGAAGGCCACAAGGCCAGAG
GAGCTCCTGGAGCTACTTGGTGGCAGTCACGACTTGGACAGCAATCAAGCAGCAATGGTACTTATCCGGCTCTCT
CACTTGCTGTCTGAGAAGCCAGAAGATAAAGGCTTGCTCATACAGGATGCCCACTTTCATCAACTTCTCTGTCTG
CTCAACAGTCAGATTGCCTCGGTCTGGCATGGTACCCTCTCGAAGCTGCTGGGAAGCCTGTATGCTCTGGGCATC
CCCAAGGCCCTCCAAGGAGCTGCAGTCGGTGGAGCAGGAGGTCCGCTGGCGCATGCGGAAGCTCAAGTACAAGCAC
CTGGCCTTCCCTGGCAGAGTCCTGTGCCACCCCTCTCACAGGAGCAGCACTCGCAGGAGCTGCTGGCTGAGCTGCTC
ACACACCTGGAAGGCGTTGGACAGAAATTGAAGATTCCCACACATTAGTGACCGTCATGATGAAGGTGGGACAC
CTCTCGGAGCCACTAATGAACCGCCTGGAAGACAAGCACGTCTCTGAACAGAGCGCAGGACATCACCCCTGCCCCAC
CTGTGCAGCGTACTTCTGGCTTTTTCGCGCTCTGAACCTCCATCCAGACCAAGAGGATCAGTTCTTCAGCCTGGTA
CATGAGAAGCTGGGGTCAGAGCTGCCAGGCCTGGAGCCAGCCCTGCAGGTGGACCTGGTGTGGGCCCTGTGTGTG
CTGCAGCAGGCACGGGAAGCAGAGCTGCAAGCCGTCCTCCACCCTGAATTTACATCCAATTTCTAGGGGGCAAG
TCTCAGAAGGATCAGAACACCTTCCAGAAGCTGCTCCACATCAACGCCACTGCCCTGCTGGAGTACCCCGAGTAC
TCGGGTCCCCTTCTGCCTGCCTCGGCTGTGGCCCCCTGGGCCCTCAGCCCTTGACAGGAAGGTGACCCCCCTGCAA
AAGGAGCTGCAGGAGACGCTGAAGGGGCTGCTGGGGAGCGCCGACAAGGGCAGCCTCGAGGTGGCCACGCAGTAT
GGCTGGGTGCTGGATGCTGAGGTGCTGCTGGACAGTGACGGCGAGTTTCTGCCCCGTAAGGGACTTTGTGGCACCT
CACCTTGCCCAGCCAACCTGGGAGCCAGTCACCACCTCCAGGGTCTAAGAGGCTAGCGTTCTTGCGGTGGGAGTTC
CCCAACTTCAACAGCCGAAGCAAGGACTTGCTGGGTGCTTTGTTCTGGCCCGGCGACACATAGTGCTGCAGGC
TTCTTGATAGTGAGCGTCCCATTCTATGAGTGCTGGAACCTCAAGTCTGAATGGCAGAAAGGCGCTACCTCAAG
GACAAGATGCGCAAAGCGGTGGCTGAGGAGCTGGCCAAG**TG**ACTTGTGCCAGCAGCATGGACTGCGTGCCTCTCC
GCCGGAGGTCTAGCTGTGGGCGGCCAAGAAGGGTCAACCCTTGAGGACAAACCTCTGTGCAGGACCTTGGCCAGAG
TGGGGAGGGTGGCCAGCCACTCTGAGGGACAGAACGTCCTCTTGTGTATAATAAACCTTTAATTTTGGTGTGGGA
CCCCTGGGGCCTTCCCAGGCTTGGTCACCCTCTGCACTGTGACCACTTGTCTGTCTGCTTTGTTGAGCAGGGCGT
GGTTCTCCAGTCTGCCCTGTGCACTCCCCCGCCACGCCAGCCCAAGAGGGCTGCTTTAGGGACAGACCTGGGTT
GTTACCTGCCTGTCTCTCCAGCTTCTTCCCTCCATGAGTGCTTATTACATATGCCGGCTCTTGCGTAGGGGT
CTGTATCAGCCCCAGCAGGCAGGTGGAGTCCTAGAATTCTGAACCTCCAGAGCAGAGGAGCTTCCCAGGGAAGCT
GATTGGAGATTGAGTGCATGGCTGGGGGTTCTGATGGAGCTGTGGCTACTGAACCACAGCCATCCTGGGAGGCTT
TCTCCCATCAGTTGTCTCACACTTAGCTGAGTGAAAGGCACCCTGACAGCATGTGGTGACAGGTGATGTGAGGGC
TGGGTGAGCACTTGGGAGGCGCTGGCTCTGGGAGAGGAGAAGATCCCCTTGGCTGACACCACGGCACCAAGAGC
CAAACCTCCATCGTTGTCTTACCACCCCTGACCAGAGCCTTGTGCTGTCTATAGGAACTGGCTGCCCAAACAGGA
CCCTGGCAGCCTCCCTGCTGCTGCGGGGATTACCAGGTGCTGGGAGGCAACAAGCTTTCTACCTTCCAGCCTCTC
CTTAGAGACACCTATTGGCAGAACCTGACTAAATAGCAGTCAGGGAACCTGGGTTGCCCTCCAGCCATACAGAACAG
AGAGTAGGACAGTGGGGTGGAGCTGAGATGGAGAGGCCACAGCCCTCAGCACTGTAGGCTCCCAACCCTAGGCT
GTTTCCCCAAAAAGAAAAAGTCTAGTCACTGCTCTGATGCTTGGCCACTCACCCAAGCATTGGGGTAGTTTGTGC
TGGCTTCACTGGGCACCATCAGGCACACCCAGCCTGTAGTTTTTGTGTTTATATTACCTAAGTCGGCCAGGTGTGG
TGGGATCACGCTGTAATCCAGCACTTAGGGAGGCTGGGGCGGGCGAATCGCCTGAGGCCAGGAATTCAAGACC
AACCTGGCCAACATTGTGAAACCCTGTCTCTACTAAAAATATAAAAAATTAGTCGGGCATGATGACAGGCACCTGT
AATCCAGCTACTCAGGAGGCTGAGGCAGGTGAATCACTTGAACCCGGGAGGTGGAGGCTGCAGTGAGTTAAGAT
TGTGCCACTGCACTCCAGCCTGGGTAACAGAGCAAGACTCTGTCTCAAAAAATATATATGTGTGTGTGTGTGTGT
GTATATATATGTACATGTGTATATAAGTATATATGTGTGTATATATGTATATATACACGTATATACACACACACC
CCTAAGTCATGATTTTGGAGCAATTGTAAGTGGTGTAGTGCTTAATTTTGGCATTACACATTGATTGTTAGCAT
ATAGAAAATGGGATTGATTTTTATGTGATCTTGCTAAACTTTATGCATTTTTTAAATTCCTTTGGATTTCCTATGT
AGATATTTATGTCTGAAAACAGGAATGTATTTATCCTTTCAAATCAATATGCTTTTTTATTTTGTATTTATGAC
CACTTCATTAAAAATATAATTACATGCCATACACTTCACCCATTTAAATGTATAATTAGGCCAGGTGTGGTGGC
TCACGTCTGTAATCCCAGCAGTTTTGGGAGGCCAAGGCCCTCAGATCTTGAGCCAGGAGTCAAGACCACCCCTGG

2427/6881

FIGURE 2232B

GCAACAGGCAAAACCCTGTCTCTATTTTTTAAAATACAAGAATTAGCCGCAGTGGCACGCACCTGTCGTCCCAGC
AACCCAGGAGGCTGAGGTAGGAGGATCACTTAAGCCTGGGAAGTCAAGCCTGCAGTGAACCATGATAGCACCCT
GCAGTCCAGCCTGGGCGACAGAGTGAGACCCCATCTCGAAAACAAAAATGTATAATTCAGTGGTTTTTTAGTCTCT
TTGCAGATACATGCAACCATCACCACAATTTGCACATTTTCTAAGCCTCATATACTGATGTGATATTTTGGTGTT
TTGTGACTGGCTTCATTTACTTAGCATATTGTTTTTCATGTTTCATTCATGTCGCATGTATGAGTATTCATTCCTT
TATTTGGCTGAATAATATTCATTATAGTTTGTGCCACATTTTGTTTATCCATTCATCCATTGATGGACATGTGG
ATTGTTTCCACCTTCTGGATAATATGAACTGATACAGTTTGGATATTTTGTCCCCTCCAAATCTCATGAAATAGG
ATCACCAGTGTGGAGAATGGGGCCTGTTAGGAAGTGTGGATCATAGGAACATCTGTCATAAATGGCTTGGTG
CCATCCTTGTAATGAGTGAGTTCTTGCTCTATATTAGTTCACTTGAAAGCTGGTTGTTGGGAACTCCTGCCCTAT
CTGTTCTGCCCTCTCTCGTCATGTGACATGCCTGCTCCTTGTTACCTTCTGTCATGAGTAAAAGCTTCCTAAGG
CCTTCCCAGGAGCCAAGCAGATGTCAGTACCATGCTTGTACAGCCTGCAGAACTGTGAGCCAAATAAACTTCTTT
ATAAATT

2428/6881

FIGURE 2233

MAAHLVKRCTCLLREARQAPAMAPVGRLRLAWVAHKTTLTSSATSPISHLPGSLMEPVEKERASTPYIEKQVDHL
IKKATRPEELLELLGGSHDLDNQAAMVLIRLSHLLSEKPEDKGLLIQDAHFHQLLCLLNSQIASVWHGTL SKLL
GSLYALGIPKASKELQSVEQEVWRMRKLKYKHLAFLAESCATLSQEQHSQELLAELLTHLERRWTEIEDSHTLV
TVMMKVGHLSPEPLMNRLEDKHVLNRAQDITLPHLCSVLLAFARLNFHPDQEDQFFSLVHEKLGSELPGLEPALQV
DLVWALCVLQQAREAELOAVLHPEFHIQFLGGKSQKDQNTFQKLLHINATALLEYPEYSGP LLPASAVAPGPSAL
DRKVTPLQKELQETLKGLLGSADKGSLEVATQYGWVLDAEVLLDSGFEFLPVRDFVAPHLAQPTGSQSPPPGSKR
LAFLRWEEFPNFNSRSKDLLGRFVLARRHIVAAGFLIVDVPFYEWLELKSEWQKGAYLKDKMRKAVAEELAK

2429/6881
FIGURE 2234

GGCACGAGGCCCGGGTCGAGCATGTAGCGGCTGCTGGCGGCGGGGCTCCCGGGGCGGGCCGGGCGGGCCGCGGGA
GCCGCACGCGGCGATATGGGAAGAGGAGGGCAAGAAGGGCAAGAAGCCTGGAATTGTCTCGCCATTTAAACGAGTA
TTCCTAAAAGGTGAAAAGAGTAGAGATAAGAAAGCCCATGAGAAAGGTGACAGAGAGGCGCCCTCTGCACACTGTG
GTGTTGTTCATTGCCTGAGCGCGTCGAGCCAGACAGACTGCTGAGCGACTATATTGAGAAGGAGGTAAAGTATTTA
GGTCAGTTAACGTCCATACCAGGATACCTGAATCCCTCCAGTAGGACTGAAATCCTGCATTTTCATAGACAATGCA
AAGAGAGCCCCACCAGCTTCCGGGACACTTGACTCAGGAGCACGATGCTGTGCTCAGCCTGTCTGCGTACAACGTC
AAGCTGGCCTGGAGGGACGGGGAGGATATCATCCTCAGGGTGCCCATCCATGACATCGCCGCCGTCTCCTATGTT
CGGGATGACGCTGCACACCTGGTGGTCCTGAAGACAGCCCAGGACCCAGGGATCTCCCCAGCCAGAGTCTGTGT
GCGGAAAGTTCCAGAGGCCTCAGTGCAGGCTCCCTGTGCGGAGAGTGAGTTGGGCCCCGTGGAGGCATGCTGCCTG
GTCATCCTGGCTGCAGAGAGCAAGGTGCGTGCAGGAGGAGCTTTGCTGTCTGCTAGGCCAGGTCTTCCAGGTTGTT
TACACGGAGTCCACCATCGACTTTCTGGACAGAGCGATATTTGATGGGGCCTCTACCCCGACCCACCACCTGTCC
CTGCACAGCGATGACTCTTCTACAAAAGTGGACATTAAGGAGACCTACGAGGTGGAAGCCAGCACTTTCTGCTTC
CCTGAATCTGTGGATGTGGGTGGTGCATCACCCACAGCAAGACCATCAGTGAGAGCGAGCTGAGCGCCAGCGCC
ACTGAGCTGCTGCAGGACTACATGCTGACGCTGCGCACCAAGCTGTCATCACAGGAGATCCAGCAGTTTGCAGCA
CTGCTGCACGAGTACCGCAATGGGGCCTCTATCCACGAGTTCTGCATCAACCTGCGGCAGCTCTACGGGGACAGC
CGCAAGTTCCCTGCTGCTTGGTCTGAGGCCCTTCATCCCTGAGAAGGACAGCCAGCACTTCGAGAACTTCTGGAG
ACCATTGGCGTGAAGGATGGCCGCGGCATCATCACTGACAGCTTTGGCAGGCACCGCGGGCCCTGAGCACCACA
TCCAGTTCCACCACCAATGGGAACAGGGCCACGGGCAGCTCTGATGACCGGTCGGCACCCCTCAGAGGGGGATGAG
TGGGACCGCATGATCTCGGACATCAGCAGCGACATTGAGGCGCTGGGCTGCAGCATGGACCAGGACTCAGCATGA

TGGACAGTGGATGGGGGGGCACCCACACCTTCCGCGCAGTCGTCATAGGCCTTCCCAGAAGGAGCTGCCCAGACC
TGCCTGTCAGCCCTTGGTGGTGGCCAGGGAGAGGCGCCCGGTGCAGATGGCCCCGGGCGGGCCAGGTCTCTACT
GTGAAGGAGCAGGGAGCTGCCGAGGGACACGAGCCTCAGTGCGGGGTGGAAGGCTCTTTGCCTTGTCCACCAGGG
CTCAGCCAAGCCCTGCAGTGTGTCCCCGCTCGGGGAGGGCCCCGGCCGAGCGGGCAGGGAGAGCCAGTCCTGTCCG
CTGGGCCCTTGGACGGCTGTCAGTTTTTGACATGATGTTCCATTGTAACCTCTCAGAGACCTTAAAAAGAAGTTT
ACTGCAATGTGAATAATTTAAAAAAAAAAAAAAAAAAAA

2430/6881
FIGURE 2235

MEEEGKKGKKPGIVSPFKRVFLKGEKSRDKKAHEKVTERRPLHTVVLSLPERVEPDRLSDYIEKEVKYLGQLTS
IPGYLNPSSRTEILHFIDNAKRAHQLPGHLTQEHDVLSLSAYNVKLAWRDGEDIIILRVPIHDIAAVSYVRDDAA
HLVVLKTAQDPGISPSQSLCAESSRGLSAGSLSES AVGPVEACCLVILAAESKVAAEELCCLLGQVFQVVYTEST
IDFLDRAIFDGASTPTHHLSLHSDDSS TKVDIKETYEVEASTFCFPESVDVGGASPHSKTISESELSASATELLQ
DYMLTLR TKLSSQEIQQFAALLHEYRNGASIHEFCINLRQLYGDSRKFLLLGLRPFIPEKDSQHFENFLETIGVK
DGRGIITDSFGRHRRALSTTSSTTNGNRATGSSDDRSAPSEGDEWDRMISDISSDIEALGCSMDQDSA

2431/6881
FIGURE 2236

TGGGGTTCGAACCAGCAAGACAAGCGGGCATTGGCCACAGCAGCGCGAGGCGGGCACGGGGTATTGTCCGGCTCC
GGCGGCGGGCGGTTCGGTGCTGCGAGAGCGGCGGGCGGGCGGGTTCGGCAGCGGGAGGGCGCGCGGGCCGAGCGGA
GGCGGAGTCGGCGCCGAGAAC**ATGG**CTGGAGGCAAAGCTGGAAAGGACAGTGGGAAGGCCAAGGCTAAGGCAGTA
TCTCGCTCACAGAGAGCTGGGCTACAGTTTCCTGTGGGCCGCATCCACAGACACTTGAAGACTCGCACCACAAGC
CATGGAAGGGTGGGTGCCACTGCTGCCGTGTACAGTGCTGCGATTCTGGAGTACCTCACTGCAGAGGTGCTGGAG
CTGGCAGGTAATGCTTCTAAGGATCTCAAAGTAAAGCGTATCACTCCGCGTCACTTGCAGCTTGCAATCCGTGGT
GATGAAGAGTTGGATTCTCTTATCAAGGCTACCATAGCTGGGGGTGGTGTGATCCCTCACATCCACAAATCTCTG
ATTGGAAAGAAGGGACAGCAGAAAAGTCT**TAG**AGGGATGCTTTAACCAACCCTCTTCCTCCCCGTCATTGTACT
GTAAGTGGGACAGAAGAAATAATGGGGATATGTGGAATTTTAAACAACAGTTAAATGGAAAAGCATAGACAATTA
CTGTAGACATGATAAAAGAAACATTTGTATGTTCTTAGACTCGAAGTTTGATAAAAGTACCTTTTCATGTGGTGA
CAGTTGTGTGTTGATTGGCTAGGTTTCTCCCGTGTGTTTTATACAAAATGGAATTGATAAACCATTTTTTACAA
AATTAAAAAAAAAAAAAAAAAAAA

2432/6881
FIGURE 2237

MAGGKAGKDSGKAKAKAVSRSQRAGLQFPVGRIHRHLKTRTTSHGRVGATAAVYSAAILEYLTAEVLELAGNASK
DLKVKRITPRHLQLAIRGDEELDSLKATIAGGGVIPHIHKSLIGKKGQQKTA

2433/6881
FIGURE 2238

GTTTTGCAGACGCCACCGCCGAGGAAAACCGTGTACTATTAGCCATGGTCAACCCACCGTGTTCTTCGACATTG
CCGTGACGGCGAGCCCTTGGGCCGCGTCTCCTTTGAGCTGTTTGCAGACAAGGTCCCAAAGACAGCAGAAAATT
TTCGTGCTCTGAGCACTGGAGAGAAAGGATTTGGTTATAAGGGTTCCTGCTTTCACAGAATTATTCAGGGTTTA
TGTTGTCAGGGTGGTGACTTCACACGCCATAATGGCACTGGTGGCAAGTCCATCTATGGGGAGAAAATTGAAGATG
AGAACTTCATCCTAAAGCATACGGGTCTTGGCATCTTGTCCATGGCAAATGCTGGACCCAACACAAATGGTTCCC
AGTTTTTTCATCTGCACTGCCAAGACTGAGTGGTTGGATGGCAAGCATGTGGTGTTTGGCAAAGTGAAAGAAGGCA
TGAATATTGTGGAGGCCATGGAGCGCTTTGGGTCCAGGAATGGCAAGACCAGCAAGAAGATCACCATTGCTGACT
GTGGACAACTCGAATAAGTTTGACTTGTGTTTTATCTTAACCACCAGATCATTCCTTCTGTAGCTCAGGAGAGCA
CCCCTCCACCCCATTTGCTCGCAGTATCCTAGAATCTTTGTGCTCTCGCTGCAGTTCCCTTTGGGTTCATGTTT
TCCTTGTTCCCTCCCATGCCTAGCTGGATTGCAGAGTTAAGTTTATGATTATGAAATAAAAACTAAATAACAATT
GTC

2434/6881
FIGURE 2239

MVNPTVFFDIAVDGEPLGRVSFELFADKVPKTAENFRALSTGEKGFYKGSCHFRIIPGFMCQGGDFTRHNGTGG
KSIYGEKFEDENFILKHTGPGILSMANAGPNTNGSQFFICTAKTEWLDGKHVVFGKVKEGMNIVEAMERFGSRNG
KTSKKITIADCGQLE

2435/6881

FIGURE 2240A

GCAGTTGTGAAAACTTCAGGACAAAAATGTTTCATTTAAGGACTTGTGCTGCTAAGTTGAGGCCATTGACGGCT
TCCCAGACTGTTAAGACATTTTCACAAAACAGACCAGCAGCAGCTAGGACATTTCAACAGATTCCGGTGCTATTCT
GCACCTGTTGCTGCTGAGCCCTTTCTCAGTGGGACTAGTTTGAACATATGTGGAGGAGATGTACTGTGCTTGGCTG
GAAAACCCCCAAAAGTGTTACATAAGTCATGGGACATTTTTTTTCGCAACACGAATGCCGGAGCCCCACCGGGCACT
GCCTACCAGAGTCCCCTTCCCTGAGCCGAGGCTCCCTGGCTGCTGTGGCCCATGCACAGTCCCTGGTAGAAGCA
CAGCCCAACGTGGACAAGCTCGTGGAGGACCACCTGGCAGTGCAGTCGCTCATCAGGGCATATCAGATACGAGGG
CACCATGTAGCACAGCTGGACCCCTGGGGATTTTGGATGCTGATCTGGACTCCTCCGTGCCCGCTGACATTATC
TCATCCACAGACAACTTGGGTTCTATGGCCTGGATGAGTCTGACCTCGACAAGGTCTTCCACTTGCCCACCACC
ACTTTTCATCGGGGGACAGGAATCAGCACTTCCCTCTGCGGGAGATCATCCGTGCGCTGGAGATGGCCTACTGCCAG
CATATTGGGGTGGAGTTCAITGTTTCATCAATGACCTGGAGCAGTGCCAGTGGATCCGGCAGAAGTTTGAGACCCCT
GGGATCATGCAGTTTACAAATGAGGAGAAACGGACCCTGCTGGCCAGGCTTGTGCGGTCCACCAGGTTTGAGGAG
TTCCTACAGCGGAAGTGGTCCTCTGAGAAGCGCTTTGGTCTAGAAGGCTGCGAGGTACTGATCCCTGCCCTCAAG
ACCATCATTGACAAGTCTAGTGAGAATGGCGTGGACTACGTGATCATGGGCATGCCACACAGAGGGCGGGCTGAAC
GTGCTTGCAAATGTCATCAGGAAGGAGCTGGAACAGATCTTCTGTCAATTTCGATTCAAAGCTGGAGGCAGCTGAT
GAGGGCTCCGGAGATGTGAAGTACCACCTGGGCATGTATCACCGCAGGATCAATCGTGTACCCGACAGGAACATT
ACCTTGTCCTTGGTGGCCAACCTTCCCACCTTGAGGCCGCTGACCCCGTGGTGTATGGGCAAGACCAAAGCCGAA
CAGTTTTACTGTGGCGACACTGAAGGGAAAAAGGTCATGTCCATCCTGTTGCATGGGGATGCTGCATTTGCTGGC
CAGGGCATTGTGTACGAGACCTTCCACCTCAGCGACCTGCCATCCTACACAACCTCATGGCACCGTGCACGTGGTC
GTCAACAACAGATCGGCTTACCACCGACCCTCGGATGGCCCGCTCCTCCCCCTACCCCACTGACGTGGCCCGA
GTGGTGAATGCCCCCATTTTCCACGTGAACCTCAGATGACCCCGAGGCTGTCATGTACGTGTGCAAAGTGGCGGCC
GAGTGGAGGAGCACCTTCCACAAGGACGTGGTTGTGCAATTTGGTGTGTTACCGGCGCAACGGCCACAACGAGATG
GATGAGCCCATGTTACGCAGCCGCTCATGTACAAGCAGATCCGCAAGCAGAAGCCTGTGTTACAGAAGTACGCT
GAGCTGCTGGTGTGCGAGGGTGTGGTCAACCAGCCTGAGTATGAGGAGGAAATTTCCAAGTATGATAAGATCTGT
GAGGAAGCTTTTGCCAGATCTAAAGATGAGAAGATCTTGACATTAAGCACTGGCTGGACTCTCCCTGGCCTGGC
TTCTTACCCTGGACGGGCAGCCAGGAGCATGTCTGCCCTCCACGGGTCTGACGGAGGATATTCTGACACAC
ATCGGGAATGTGGCTAGTTCTGTGCTGTGGAAAACCTTACTATTTCATGGAGGGCTGAGCCGGATCTTGAAGACT
CGTGGGGAAATGGTGAAGAACCGGACTGTGGACTGGGCTCTAGCGGAGTACATGGCGTTTGGCTCGCTCCTGAAG
GAGGGCATCCACATTGGCTGAGCGGCCAGGACGTGGAGCGGGGCACATTCAGCCACCGCCACCATGTGCTCCAT
GACCAGAATGTGGACAAGAGAACCTGCATCCCCATGAACCATCTCTGGCCCAATCAGGCCCCCTATACTGTGTGC
AACAGCTCACTGTCTGAGTACGGCGTGTCTGGGCTTTGAGCTGGGCTTCGCCATGGCCAGTCTTAATGCCCTGGTC
CTCTGGGAAGCCCCAATTTGGTGAATTCACACAACACGGCCCCAGTGTATCATCGACCAGTTTCATCTGCCCGGGACAA
GCCAAGTGGGTGCGGCAGAATGGCATCGTGTGCTGCTGCCCATGGCATGGAGGGCATGGGTCCAGAACATTCC
TCCGCCCCCCCAGAGCGGTTCTTGAGATGTGCAACGATGACCCAGATGTCTTGCCAGACCTTAAAGAAGCCAAC
TTCGACATCAATCAGCTATATGACTGCAATTGGGTTGTTGTCAACTGCTCCACTCCTGGCAACTTCTTCCACGTG
CTACGACGCCAGATCCTGCTGCCATTCCGGAAGCCGTTAATTATCTTACCCCCAAATCCCTGTTGCGCCACCCC
GAGGCCAGATCCAGCTTTGATGAGATGCTTCCAGGAACCCACTTCCAGCGGGTGATCCCAGAAGATGGCCCTGCA
GCTCAGAACCCAGAAAATGTCAAAGGCTTCTCTCTGCACCGGCAAAGTGTATTATGACCTCACCCGGGAGCGC
AAAGCACGCGACATGGTGGGGCAGGTGGCCATCACAAGGATTGAGCAGCTGTGCGCATTTCCCTTTGACCTCCTG
CTGAAGGAGGTGCAGAAGTACCCCAATGCTGAGCTGGCCTGGTGCCAGGAGGAGCACAAGAACCAAGGCTACTAT
GACTACGTGAAGCCAAGACTTCGGACCACCATCAGCCGCGCCAAGCCCGTCTGGTATGCCGGCCGGGACCCAGCG
GCTGCTCCAGCCACCGGCAACAAGAAGACCCACCTGACGGAGCTGCAGCGCCTCCTGGACACGGCCTTCGACCTG
GACGTCTTCAAGAACTTCTCGTAGATGCTGCCTAGGGTTGCTTGGGCCACTGCCCTCTCCACACCCATGACTGCC
CCTTGCTTCTCAACTAAAGAATAGTGCCTCAGCGCTGCCACACCACCGCCCTCCTCGCTGTGCCACCACCCCTC
CCTCTGCTCTCATAGGAGTTAGGCTGTGCTCCCTCCAGTGCTTGGCTGCCCCACAGGCCACACGCTGCCCAGG
CTCTGCTGACTTCTGAGCAGTTTTTCCAGGAGGCCGGGGGAGCAGGAGGAGGAAAGGTAGCCCCCGAGGGATGTC
CTTGGGGAGGGGTCAGCTCTGGCCACAATCCTCCCCACCACTCTACCCACTAGGATAGGAAGTGGGCCCTTGTGT
GCTGGCTTCCGCTGTACCCAGCAAGGCACAGGCTCCTGTATTTGAGACTAGGATAGCTTCATCTTGAGCCTGAG
CCTTAGAATCTGTAGAGGAGCCTGGAGTCGGATCTAGCCATGGCTGGCAGAGGTTTCTAGGGTGGGCCCCAGCCG

2436/6881

FIGURE 2240B

TGGCGTGAAGTGAAGGATGACCCGGGGCAGCTGGCAGGAGAGAGCCTTGGCCTGACCTGGCACAGAAAGGGCAGCT
TCAGTCTCTGCAGTGTCCATTATCTGCTGTTCCCTTCGAGGGTTCCAGGCTGTGTGTGGGGCCCAAGCATGCCCCA
CCCACCCCTCCTGGGGCCAGGCAGCACCTGGAGCCCACAGAGTCTGTGTGTAGCCAGGAAGCCCCGCTCAGGTAG
CCACCACCGGGGCACTGGCTGCTCTGTCTTGGTCCTGTTAACCCTCCACCTCCTCTCTTGGACTCCCTCCCCACC
CCAACCACTCTTTCTTTCTCCTTTAACCCAATGGAGACTTTCTGATGCATCGTTTTCTTTGCTGTGCCAAAGCAG
GTCAGAAGAGGGAGAGGAGGGGCTGGGGGTGAGGGGCCAGGCCATGGCCAAGGGGCCAGCTGCCCCTCATTTATC
ACTCTGACCTTCACAGGGACAGATCTGATTTATTTATTTTGGTT

2437/6881
FIGURE 2241

MFHLRTCAAKLRPLTASQTVKTF SQNRPAARTFQQIRCYSAPVAAEPFLSGTSSNYVEEMYCAWLENPKSVHKS
WDIFFRNTNAGAPPGTAYQSPLPLSRGSLAAVAHAQSLVEAQPNVDKLVEDHLAVQSLIRAYQIRGHHVAQLDPL
GILDADLDSSVPADIISSTDKLGFYGLDESDLDKVFHLPTTTFFIGGQESALPLREIIRRLMAYCQHIGVEFMFI
NDLEQCQWIRQKFETPGIMQFTNEEKRTLLARLVRSTRFEFLQRKWSSEKRFGLGCEVLIPALKTIIDKSSSEN
GVDYVIMGMPHRGRLNVLANVIRKELEQIFCQFDSKLEAADEGSGDVKYHLGMYHRRINRVTDNRNITLSLVANPS
HLEAADPVVMGKTKAEQFYCGDTEGKKVMSILLHGDAAFAGQGIVYETFHLSDLPSYTTHTGTVHVNVNQGFTT
DPRMARSSPYPTDVARVVNAPIFHVNSDDPEAVMYVCKVAAEWRSTFHKDVVVDLVCYRRNGHNEMDEPMFTQPL
MYKQIRKQKPV LQKYAELLVSQGVVNQPEYEEEEISKYDKICEEAFARSKDEKILHIKHWDSPWPGFFTLDGQPR
SMSCPSTGLTEDILTHIGNVASSVPVENFTIHGGLSRILKTRGEMVKNRTVDWALAEYMAFGSLLKEGIHIRLSG
QDVERGTFSHRHHVLHDQNVDKRTCIPMNLWPNQAPYTVCNSSLSEYGVLGFEFGFAMASPINALVLWEAQFGDF
HNTAQCIIDQFICPGQAKWVRQNGIVLLLPHGMEGMGPEHSSARPERFLQMCNDDPDVLPDLKEANFDINQLYDC
NWVVNCSTPGNFFHVLRRQILLPFRKPLIIFTPKSLLRHPEARSSFDEMLPGTHFORVIPEDGPAAQNPNENVKR
LLFCTGKVYYDLTREKARDMVGQVAITRIEQLSPFPFDLLLKEVQKYPNAELAWCQEEHKNQGYDYVKPRLRT
TISRAPVWYAGRDPAAAPATGNKKTHLTELRLLDTAFDLDVFKNF S

2438/6881
FIGURE 2242

GCTGCTCCCGCTCGCGTCGGTGGCGTTTTTTCCTGCAGCGCGTGCGTGCTGCGCTACTGAGCAGCGCC**ATCG**GAGGA
CTCTGAAGCACTGGGCTTCGAACACATGGGCCTCGATCCCCGGCTCCTTCAGGCTGTCACCGATCTGGGCTGGTC
GCGACCTACGCTGATCCAGGAGAAGGCCATCCCACTGGCCCTAGAAGGGAAGGACCTCCTGGCTCGGGCCCGCAC
GGGCTCCGGGAAGACGGCCGCTTATGCTATTCCGATGCTGCAGCTGTTGCTCCATAGGAAGGCGACAGGTCCGGT
GGTAGAACAGGCAGTGAGAGGCCTTGTTCTTGTTTCCTACCAAGGAGCTGGCACGGCAAGCACAGTCCATGATTCA
GCAGCTGGCTACCTACTGTGCTCGGGATGTCCGAGTGGCCAATGTCTCAGCTGCTGAAGACTCAGTCTCTCAGAG
AGCTGTGCTGATGGAGAAGCCAGATGTGGTAGTAGGGACCCCATCTCGCATATTAAGCCACTTGACAGCAAGACAG
CCTGAAACTTCGTGACTCCCTGGAGCTTTTGGTGGTGGATGAAGCTGACCTTCTTTTTTTCCTTTGGCTTTGAAGA
AGAGCTCAAGAGTCTCCTCTGTCACTTGCCCCGGATTTACCAGGCTTTTCTCATGTCTAGCTACTTTTAACGAGGA
CGTACAAGCACTCAAGGAGCTGATATTACATAACCCGGTTACCCTTAAGTTACAGGAGTCCCAGCTGCCTGGGCC
AGACCAGTTACAGCAGTTTCAGGTGGTCTGTGAGACTGAGGAAGACAAATTCTCCTGCTGTATGCCCTGCTCAA
GCTGTCAATTGATTTCGGGGCAAGTCTCTGCTCTTTGTCAACACTCTAGAACGGAGTTACCGGCTACGCCTGTTCTT
GGAACAGTTACAGCATCCCCACCTGTGTGCTCAATGGAGAGCTTCCACTGCGCTCCAGGTGCCACATCATCTCACA
GTTCAACCAAGGCTTCTACGACTGTGTCTATAGCAACTGATGCTGAAGTCCTGGGGGCCCCAGTCAAGGGCAAGCG
TCGGGGCCGAGGGCCCAAAGGGGACAAGGCCTCTGATCCGGAAGCAGGTGTGGCCCGGGGCATAGACTTCCACCA
TGTGTCTGCTGTGCTCAACTTTGATCTTCCCCAACCCCTGAGGCCTACATCCATCGAGCTGGCAGGACAGCACG
CGCTAACAACCCAGGCATAGTCTTAACCTTTGTGCTTCCACAGGAGCAGTTCCACTTAGGCAAGATTGAGGAGCT
TCTCAGTGGAGAGAACAGGGGCCCCATTCTGCTCCCCTACCAGTTCCGGATGGAGGAGATCGAGGGCTTCCGCTA
TCGCTGCAGGGATGCCATGCGCTCAGTGACTAAGCAGGCCATTTCGGGAGGCAAGATTGAAGGAGATCAAGGAAGA
GCTTCTGCATTCTGAGAAGCTTAAGACATACTTTGAAGACAACCCTAGGGACCTCCAGCTGCTGCGGCATGACCT
ACCTTTGCACCCCGCAGTGGTGAAGCCCCACCTGGGCCATGTTCTGACTACCTGGTTCCTCCTGCTCTCCGTGG
CCTGGTACGCCCTCACAAAGAAGCGGAAGAAGCTGTCTTCTCTTGTAGGAAGGCCAAGAGAGCAAAGTCCCAGAA
CCCCTGCGCAGCTTCAAGCACAAAGGAAAGAAATTACAGACCCACAGCCAAGCCCTCCT**TGAG**GTGTTGGGCCTC
TCTGGAGCTGAGCACATTGTGGAGCACAGGCTTACACCCTTCGTGGACAGGCGAGGCTCTGGTGCTTACTGCACA
GCCTGAACAGACAGTTCTGGGGCCGGCAGTGCTGGGCCCTTTAGCTCCTTGGCATTCCAAGCTGGCATCTTGCC
CCTTGACAACAGAATAAAAAATTTTAGCTGCCCCAAAAAAAAAAAAAAAAAAAAA

2439/6881

FIGURE 2243

MEDSEALGFHEMGLDPRLQAVTDLGWSRPTLIQEKAIPLALEGKDLLARARTGSGKTAAYAIPMLQLLLHRKAT
GPVVEQAVRGLVLVPTKELARQAQSMIQQLATYCARDVRVANVSAAEDSVSQRAVLMEKPDVVVGTPSRILSHLQ
QDSLKL RDSLELLVDEADLLFSFGFEEELKSLLCHLPRIYQAF LMSATFNEDVQALKELILHNPVTLKLQESQL
PGPDQLQQFQVVCETEEDKFLLLYALLKLSLIRGKSLLFVNTLERSYRLRLFLEQFSIPTCVLNGELPLRSRCHI
ISQFNQGFYDCVIATDAEVLGAPVKGKRRGRGPKGDKASDPEAGVARGIDFHHVSAVLNFDLPPTPEAYIHRAGR
TARANNPGIVLTFVLPTEQFHLGKIEELLSGENRGPILLPYQFRMEEIEGFRYRCRDAMRSVTKQAIREARLKEI
KEELLHSEKLKTYFEDNPRDLQLLRHDLPLHPAVVKPHLGHVPDYLVPPALRGLVRPHKKRKKLSSSSCRKAKRAK
SQNPLRSFKHKGKKFRPTAKPS

2440/6881
FIGURE 2244

TCTTCCTCGGCGCTGCCTACGGAGGTGGCAGCCATCTCCTCCTCGGCATCATGGCCGCCCTCAGACCCCTTGTGA
AGCCCAAGATCGTCAAAAAGAGAACCAAGAAGTTCATCCAGCACCAGTCAGACCAATATGTCAAAAATTAAGCGTA
ACTGGCGGAAACCCAGAGGCACTGACAACAGGGTTTCGTAGAAGATTCAAGGGCCAGATCTTGATGCCCCAACATTG
GTTATGGGAGCAACAAAAAACAAGCACATGCTGCCCAGTGGCTTCCGGAAGTTCCTGGTCCACAACATCAAGG
AGCTGGAAGTGCTGCTGATGTGCAACAAATCTTACTGTGCCGAGATCGCTCACAATGTTTCCTCCAAGAACCGCA
AAGCCATCGTGGAACAGCTGCCCACTGGCCATCAGAGTCACCAACCCCAATGCCAGGCTGCGCAGCGAAGAAA
ATGAGTAGACAGCTCGTGTGCACGTTTTCTGTTTAAATAAATGTAAAACTGC

2441/6881
FIGURE 2245

GCTGCTCCCTGAGAACGGGTCCCGCAGCTGGGCAGGCGGGCGGCCTGAGGGCGCGGAGCCATGAAGCTGTACAGC
CTCAGCGTCCTCTACAAAGGCGAGGCCAAGGTGGTGTCTGCTCAAAGCCGCATACGATGTGTCTTCCTTCAGCTTT
TTCCAGAGATCCAGCGTTCAGGAATTCATGACCTTCACGAGTCAACTGATTGTGGAGCGCTCATCGAAAGGCACT
AGAGCTTCTGTCAAAGAACAAGACTATCTGTGCCACGTCTACGTCCGGAATGATAGTCTTGCAGGTGTGGTCATT
GCTGACAATGAATACCCATCCCGGGTGGCCTTTACCTTGCTGGAGAAGGTACTAGATGAATTCTCCAAGCAAGTC
GACAGGATAGACTGGCCAGTAGGATCCCCTGCTACAATCCATTACCCAGCCCTGGATGGTCACCTCAGTAGATAC
CAGAACCCACGAGAAGCTGATCCCATGACTAAAGTGCAGGCCGAAGTACTAGATGAGACCAAAATCATTCTGCACAAC
ACCATGGAGTCTCTGTTAGAGCGAGGTGAGAAGCTAGATGACTTGGTGTCCAAATCCGAGGTGCTGGGAACACAG
TCTAAAGCCTTCTATAAACTGCCCCGAAACAAAACCTCATGCTGTGCCATCATGTGATGCAGCCTGCCAGAGGCC
CAATGCTGGAATGGCACCATCATTACATCAGAACTGCAGCCCCTGGAAAAGAAGAGACA

2442/6881
FIGURE 2246

CGGGATGCGGGCGCGCCGCGCGTTGAACCTCCTTGGCCTGGGCGAAGCTGTGTGGACCAAGCAAGTCAGGAGTGTG
GCC**ATG**TTTTTCTGAGCAGGCTGCCCAGAGGGCCCACACTCTACTGTCCCCACCATCAGCCAACAATGCCACCTTT
GCCCCGGGTGCCAGTGGCAACCTACACCAACTCCTCACAACCTTCCGGCTAGGAGAGCGCAGCTTTAGCCGGCAG
TATGCCACACATTTATGCCACCCGCCTCATCCAAATGAGACCCTTCCTGGAGAACCGGGCCCAGCAGCACTGGGGC
AGTGGAGTGGGAGTGAAGAAGCTGTGTGAACTGCAGCCTGAGGAGAAGTGCTGTGTGGTGGGCACTCTGTTCAAG
GCCATGCCGCTGCAGCCCTCCATCCTGCGGGAGGTGAGCGAGGAGCACAACCTGCTCCCCCAGCCTCCTCGGAGT
AAATACATACACCCAGATGACGAGCTGGTCTTGGAAGATGAACTGCAGCGTATCAAATAAAAGGCACCATTTGAC
GTGTCAAAGCTGGTTACGGGGACTGTCTGGCTGTGTTTGGCTCCGTGAGAGACGACGGGAAGTTTCTGGTGGAG
GACTATTGCTTTGCTGACCTTGCTCCCCAGAAGCCCGCACCCCCCACTTGACACAGATAGGTTTGTGCTACTGGTG
TCCGGCCTGGGCCTGGGTGGCGGTGGAGGCGAGAGCCTGCTGGGCACCCAGCTGCTGGTGGATGTGGTGACGGGG
CAGCTTGGGGACGAAGGGGAGCAGTGCAGCGCCGCCCACGTCTCCCGGGTTATCCTCGCTGGCAACCTCCTCAGC
CACAGCACCCAGAGCAGGGATTCTATCAATAAGGCCAAATACCTCACCAAGAAAACCCAGGCAGCCAGCGTGGAG
GCTGTTAAGATGCTGGATGAGATCCTCCTGCAGCTGAGCGCCTCAGTGCCCGTGGACGTGATGCCAGGCGAGTTT
GATCCCACCAATTACACGCTCCCCCAGCAGCCCCCTCACCCCTGCATGTTCCCGCTGGCCACTGCCTACTCCACG
CTCCAGCTGGTCACCAACCCCTACCAGGCCACCATTGATGGAGTCAGATTTTTTGGGGACATCAGGACAGAACGTG
AGTGACATTTTCCGATACAGCAGCATGGAGGATCACTTGGAGATCCTGGAGTGGACCCTGCGGGTCCGTCACATC
AGCCCCACAGCCCCGGACACTCTAGGTTGTTACCCCTTCTACAAAACCTGACCCGTTTCATCTTCCCAGAGTGCCCG
CATGTCTACTTTTGTGGCAACACCCCCAGCTTTGGCTCCAAAATCATCCGAGGTCCTGAGGACCAGACAGTGCTG
TTGGTGA CTGTCCCTGACTTCAGTGCCACGCAGACCGCCTGCCTTGTGAACCTGCGCAGCCTGGCCTGCCAGCCC
ATCAGCTTCTCGGGCTTCGGGGCAGAGGACGATGACCTGGGAGGCCTGGGGCTGGGCCCC**TGAC**TCAAAAAAGTG
GTTTTGACCAGAGAGGCCCCAGATGGAGGCTGTTTCATTCCCTGCAGTGTGCGCATTGTAAATAAAGCCTGGCACTT
GCTGATGCG

2443/6881
FIGURE 2247

MFSEQAAQRAHTLLSPPSANNATFARVPVATYTNSSQPFRLGERSFSRQYAHYATR LIQMRPFLENRAQQHWGS
GVGVKKLCELQPEEKCCVVGTLFKAMPLQPSILREVSEEHNLLPQPPRSKYIHPDDELVLEDELQRIKLKGTIDV
SKLVTGTVLAVFGSVRDDGKFLVEDYCFADLAPQKPAPPLDTRFVLLVSGGLGGLGGGGESLLGTQLLV DVVTGQ
LGDEGEQCSAAHVSRVILAGNLLSHSTQSRDSINKAKYLT KKTQAASVEAVKMLDEILLQLSASVPVDVMPGEFD
PTNYTLPQQPLHPCMFPLATAYSTLQLVTNPYQATIDGVRFLGTSGQNVSDIFRYSSMEDHLEILEWTLRVRHIS
PTAPDTLGCYPFYKTDPFIFPEC PHVYFCGNTPSFGSKIIRGPEDQTVLLVTVPDFSATQTACLVNLRSLACQPI
SFSGFGAEDDDLGGGLGLGP

2444/6881
FIGURE 2248A

TCCCTCGCTCACCCCATCCTCTCTCCCGCCCCCTTCTGGATTCCCTCACCCGTCTCGATCCCCTCTCCGCCCTTT
CCCAGAGACCCAGAGCCCCCTGACCCCCCGCGCCCTCCCCGGAGCCCCCGCGCGTGCCCGGGCCATGGCGGCCGT
GCGCGGGGCGCCCCCTGCTCAGCTGCCTCCTGGCGTTGCTGGCCCTGTGCCCTGGAGGGCGCCCGCAGACGGTGCT
GACCGACGACGAGATCGAGGAGTTCCTCGAGGGCTTCTGTGAGAGCTAGAACCTGAGCCCCGGGAGGACGACGT
GGAGGCCCCCGCCCTCCCGAGCCCACCCCGCGGGTCCGAAAAGCCCAGGCGGGGGGCAAGCCAGGGAAGCGGCC
AGGGACGGCCGACAGAAAGTGCCTCCGGAAAAGACCAAGACAAAAGGGAAGAAAGGCAAGAAAGACAAAGGCCCCAA
GGTGCCCAAGGAGTCCCTTGGAGGGGTCCCCAGGCCGCCCAAGAAGGGGAAGGAGAAGCCACCCAAGGCCACCAA
GAAGCCCAAGGAGAAGCCACCTAAGGCCACCAAGAAGCCCCGTGAGGGAAGAGGCCCCCATTCTGGCTCCCTCAGAAACCT
GGAGTGGCCACTGCCCCACCCCCCAGCCCTGGCCCCGAGGAGCTACCCAGGAGGGAGGGGCGCCCTCTCAA
TAACTGGCAGAATCCAGGAGAGGAGACCCATGTGGAGGCACGGGAGCACCAGCCTGAGCCGGAGGAGGAGACCGA
GCAACCCACACTGGACTACAATGACCAGATCGAGAGGGAGGACTATGAGGACTTTGAGTACATTGCGCGCCAGAA
GCAACCCAGGCCACCCCCAAGCAGAAGGAGGAGGCCCGAGCGGGTCTGGCCAGAGCCCCCTGAGGAGAAGGCCCC
GGCCCCAGCCCCGGAGGAGAGGATTGAGCCTCCTGTGAAGCCTCTGTGCCCCCGCTGCCCCCTGACTATGGTGA
TGTTTACGTGATCCCCAACTACGATGACATGGACTATTACTTTGGGCCTCCTCCGCCCCAGAAGCCCGATGCTGA
GCGCCAGACAGACGAAGAGAAGGAGGAGCTGAAGAAACCCAAAAAGGAGGACAGCAGCCCCAAGGAGGAGACCGA
CAAGTGGGCAGTGGAGAAGGGCAAGGACCACAAAGAGCCCCGAAAGGGCGAGGAGTTGGAGGAGGAGTGGACGCC
TACGGAGAAAGTCAAGTGTCCCCCATTTGGGATGGAGTCACACCGTATTGAGGACAACCAGATCCGAGCCTCCTC
CATGCTGCGCCACGGCCTGGGGGCACAGCGCGGCCGGCTCAACATGCAGACCGGTGCCACTGAGGACGACTACTA
TGATGGTGCCTGGTGTGCCGAGGACGATGCCAGGACCCAGTGGATAGAGGTGGACACCAGGAGGACTACCCGGTT
CACAGGCGTCATACCCAGGGCAGAGACTCCAGCATCCATGACGATTTTGTGACCACCTTCTTCGTGGGCTTCAG
CAATGACAGCCAGACATGGGTGATGTACACCAACGGCTATGAGGAAATGACCTTTTCATGGGAACGTGGACAAGGA
CACACCCGTGCTGAGTGAGCTCCCAGAGCCGGTGGTGGCTCGTTTTTCATCCGCATCTACCCACTCACCTGGAATGG
CAGCCTGTGCATGCGCCTGGAGGTGCTGGGGTGTCTGTGGCCCCCTGTCTACAGCTACTACGCACAGAATGAGGT
GGTGGCCACCGATGACCTGGATTTCCGGCACCACAGCTACAAGGACATGCGCCAGCTCATGAAGGTGGTGAACGA
GGAGTGGCCACCATACCCGCACTTACAGCCTGGGCAAGAGCTCACGAGGCCCTCAAGATCTATGCCATGGAGAT
CTCAGACAACCCTGGGGAGCATGAACTGGGGGAGCCCCGAGTTCCGCTACACTGCTGGGATCCATGGCAACGAGGT
GCTGGGCCGAGAGCTGTTGCTGCTGCTCATGCAGTACCTGTGCCGAGAGTACCGCGATGGGAACCCACGTGTGCG
CAGCCTGGTGCAGGACACACGCATCCACCTGGTGCCCTCACTGAACCCTGATGGCTACGAGGTGGCAGCGCAGAT
GGGCTCAGAGTTTGGGAACCTGGGCGCTGGGACTGTGGACTGAGGAGGGCTTTGACATCTTTGAAGATTTCCCGGA
TCTCAACTCTGTGCTCTGGGGAGCTGAGGAGAGGAAATGGGTCCCCTACCGGGTCCCCAACATAACTTGCCCAT
CCCTGAACGCTACCTTTTCGCCAGATGCCACGGTATCCACGGAGGTCCGGGCCATCATTGCCTGGATGGAGAAGAA
CCCCCTTCGTGCTGGGAGCAAATCTGAACGGCGGCGAGCGGCTAGTATCCTACCCCTACGATATGGCCCGCACGCC
TACCCAGGAGCAGCTGCTGGCCGCAGCCATGGCAGCAGCCCGGGGGGAGGATGAGGACGAGGTCTCCGAGGCCCA
GGAGACTCCAGACCACGCCATCTTCCGGTGGCTTGCCATCTCCTTCGCCTCCGCACACCTCACCTTGACCGAGCC
CTACCGCGGAGGCTGCCAAGCCCAGGACTACACCGGCGGCATGGGCATCGTCAACGGGGCCAAGTGGAAACCCCG
GACCGGGACTATCAATGACTTCAGTTACCTGCATACCAACTGCCTGGAGCTCTCCTTCTACCTGGGCTGTGACAA
GTTCCCTCATGAGAGTGAGCTGCCCCGCGAGTGGGAGAACAAAGGAGGCGCTGCTCACCTTCATGGAGCAGGT
GCACCGCGGCATTAAGGGGGTGGTGACGGACGAGCAAGGCATCCCCATTGCCAACGCCACCATCTCTGTGAGTGG
CATTAAATCACGGCGTGAAGACAGCCAGTGGTGGTGATTACTGGCGAATCTTGAACCCGGGTGAGTACCGCGTGAC
AGCCACGCGGAGGGCTACACCCCGAGCGCCAAGACCTGCAATGTTGACTATGACATCGGGGCCACTCAGTGCAA
CTTCATCCTGGCTCGCTCCAACCTGGAAGCGCATCCGGGAGATCATGGCCATGAACGGGAACCGGCCTATCCCACA
CATAGACCCATCGCGCCCTATGACCCCCCAACAGCGACGCCTGCAGCAGCGACGCCTACAACACCGCCTGCGGCT
TCGGGCACAGATGCGGCTGCGGCGCCTCAACGCCACCACCACCTAGGCCCCACACTGTGCTCCACGCTGCC
CCCTGCCCCTGCCACCACCTGAGCACTACCATAGAGCCCTGGGGCCTCATACCGCCAACACCGCTGGCTGGGA
GGAGTCGGAGACTGAGACCTACACAGAGGTGGTGACAGAGTTTGGGACCGAGGTGGAGCCCCGAGTTTGGGACCAA
GGTGGAGCCCGAGTTTGGAGCCAGTTGGAGCCTGAGTTTGGAGCCAGCTGGAACCCGAGTTTGGGAAGAGGA
GGAGGAGGAGAAAGAGGAGGAGATAGCCACTGGCCAGGCATTCCCCTTACAACAGTAGAGACCTACACAGTGAA

2445/6881

FIGURE 2248B

CTTTGGGGACTTCTGAGATCAGCGTCCTACCAAGACCCCAGCCCAACTCAAGCTACAGCAGCAGCACTTCCCAAG
CCTGCTGACCACAGTCACATCACCCATCAGCACATGGAAGGCCCCCTGGTATGGACACTGAAAGGAAGGGCTGGTC
CTGCCCCCTTTGAGGGGGTGCAAACATGACTGGGACCTAAGAGCCAGAGGCTGTGTAGAGGCTCCTGCTCCACCTG
CCAGTCTCGTAAGAGATGGGGTTGCTGCAGTGTGGAGTAGGGGCAGAGGGAGGGAGCCAAGGTCACCTCCAATAA
AACAAGCTCATGGC

2446/6881
FIGURE 2249

GTTTCCCTCTGCGTTCGCTCCGCGCTGCTGGAGGCTGTCGTCCCAATGCTCCCCAAACGGCGGGCGAGCGCGGGTC
GGGTCCCCCTAGCGGCATGCCGCTTCTCCACGCCGCCCTCGACGCGCTTCCCGGGAGTCGCCATCTACCTGGTC
GAGCCTCGCATGGGTTCGACGCCCGGGCCCTTCTCACAGGCCCTGGCGCGCTCCAAAGGCTTCCGCGTCTTGAC
GCCTGCAGCTCCGAAGCGACACATGTTGTGATGGAAGAGACCTCAGCAGAGGAGGCCGTGAGCTGGCAGGAGCGC
AGGATGGCAGCTGCTCCCCCGGGTTGCACCCCCCAGCTCTGCTGGACATAAGCTGGTTAACAGAGAGCCTGGGA
GCTGGGCAGCCTGTACCTGTGGAGTGCCGGCACCGCCTGGAGGTGGCTGGGCCAAGGAAGGGGCTCTGAGCCCA
GCATGGATGCCCTGCCTATGCCTGCCAGCGCCCTACGCCCTCACACACCACAACACTGGCCTCTCCGAGGCTCTG
GAGATACTGGCCGAGGCAGCAGGCTTTGAAGGCAGTGAGGGCGCCCTCCTCACCTTCTGCAGAGCAGCCTCGGTG
CTCAAGGCCCTTCCAGCCCTGTCAACCCCTGAGCCAGCTGCAGGGGCTTCCCCACTTTGGAGAACACTCCTCT
AGGGTTGTCCAGGAGCTGCTGGAGCATGGAGTGTGTGAGGAGGTGGAGAGAGTTCCGCGCTCAGAGAGGTACCAG
ACCATGAAGCTCTTACCCAGATCTTCGGGGTCGGTGTGAAGACTGCTGACCGGTGGTACCGGGAAGGACTGCGA
ACCTTAGATGACCTCCGAGAGCAGCCCCAGAACTAACCACAGCAGAAAGCGGGGCTCCAGCACCACCAGGAC
CTGAGCACCCAGTCTGCGGTCCGATGTAGATGCCCTGCAGCAGGTGGTGGAGGAAGCTGTGGGGCAGGCCCTG
CCTGGGGCCACCGTCACGCTGACGGCGGCTTCCGCAGGGGGAAGTTGCAGGGCCATGACGTGGACTTCTCATC
ACCCACCCCAAGGAGGGTCAAGAGGCGGGGCTGCTGCCTAGAGTGTGTGCCGCTGCAGGACCAGGGCCTCATC
CTGTACCACCAGCACCAGCACAGCTGCTGTGAGTCCCCTACCGCCTGGCCCAACAGAGCCACATGGACGCTTTT
GAGAGAAGTTTCTGCATTTTCCGCCTACCACAACCTCCAGGGGCTGCTGTGGGGGATCCACGAGGCCCTGCCCA
TCCTGGAAGGCCGTGAGAGTGGACTTGGTAGTTGCACCCGTGAGCCAGTTCCCTTTCCGCCCTGCTCGGTTGGACT
GGCTCCAAGCTTTTCCAGCGGGAGCTGCGCCGCTTCAGCCGGAAGGAGAAGGGCCTGTGGCTGAACAGCCATGGG
CTGTTTGACCCGGAGCAGAAGACATTTTCCAAGCGGCTTCAGAGGAAGACATCTTCAGACACCTGGGCCTTGAG
TACCTTCCTCCAGAGCAGAGAAACGCCTGAGCCTGCCTGTGTCCCCACTTCCACTCAGGAAATTGGGCTGCCCC
CAACCTGGCCACTGAATGTCTCCAGGCAGATATGCTGCCCCCTGACCCCCACCTTCACCCCTCCCCGCCAAGGCC
TGGCTCTTCCGGAGGTCAATTGTGCCTGCAGGATCAGTTGAGCCCCTGCTGGTGTGCTGCAGGGTGTGATGAGGT
GGGAGCCCTCAGTGCCAGCCTCATCACTGTGTGACCTGGGTCTGCTCTTAGCCTCCCCATGGCTCACGTTCTCTG
CCCTGGATGGGATGTGAGTGGGGCCACATCGTGGAGCTGTGGTGGGGCCTGCAGTCATGAATGGCAAGTGGTCC
CTGATGTGCAGTGTCTCATTAGTTGCACTGCAGTTAACTGTGGCTCCTGCAGGGCACCCTGCCCAGAATGCCAG
AAGAGAACCAIGCATACCTGCACTGCATTTGAGAGCCATGAGCTGGAGGCTGTGGTTCGTGCCAGCAAGGAGCCT
ACTGTCTGGTGTGCTGTAGGCATCTGGAGAGGGAGAGGGCCTGGGTAGGAGCTGGGAGGAAGATAATTTTCAACT
ATGGGGCTTCACTACTGCAGCGCCCCGAGCCAGGCTCTGTGCTTCTGCCTTTAAGGCCTGTTCTCAGCACAAATGT
CTCAAAAATAGGTCATATCCTGCCACTCCCGTCGCAGAGCCCTTTAATGGTTCCAAACCCTAAGTCCACACATAG
CCCCTGGCTCTGGCATCTCTCCAGCCCCACTGGCCCCGAGCTGCTTGACTCACCGGCTTCTTATTTGATGCACCC
AGGCCCCCTTGTGGCCAACTCCCTCCCCCTCTCACTGAGGCAGAAGCACTGAGGTGGGCTGGACATGGGTGCCCT
CCACGTCCCTCATATCCCCAGGCACACTCTGGCCTCAGGTTTTGCCCTGGCCATGTCATCTACCTGGAGTGGGCC
CTCCCCTTCTTCAGGCCTTGAATCAAAAGCCACTTTGTAGGCGAGGATTTCCAGACCACTCATCACATTAAAA
AATATTTTGAAAACATGCAGT

2447/6881

FIGURE 2250

MLPKRRRARVGSPPSGDAASSTPPSTRFPGVAIYLVEPRMGRSRRRAFLTGLARSKGFRVLDACSSEATHVVMETS
AEEAVSWQERRMAAAPPGCTPPALLDISWLTESLGAGQVPVVECRHRLEVAGPRKGPLSPAWMPAYACQRPTPLT
HHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKALPSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCCEV
ERVRRSERYQTMKLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGLQHHQDLSTPVLRSVDALQQ
VVEEAVGQALPGATVTLTGGFRRGKLQGHVDVFLITHPKEGQEAGLLPRVMCRLQDQGLILYHQHQHSCCESPTR
LAQQSHMDAFERSFCIFRLPQPPGAAVGGSTRPCPSWKAVRVDLVVAPVSQFPFALLGWTGSKLFQRELRRFSRK
EKGLWLNSHGLFDPEQKTFQAASEEDIFRHLGLELYLPPEQRNA

2448/6881
FIGURE 2251

GGCACGAGGGCGGAGACTGCGGGGCGGGCC**ATG**GCGGCGAACCTGAGCCGGAACGGGGCCAGCGCTGCAAGAGGCC
TACGTGCGGGTGGTCACCGAGAAGTCCCCGACCGACTGGGCTCTCTTTACCTATGAAGGCAACAGCAATGACATC
CGCGTGGCTGGCACAGGGGAGGGTGGCCTGGAGGAGATGGTGGAGGAGCTCAACAGCGGGAAGGTGATGTACGCC
TTCTGCAGAGTGAAGGACCCCACTCTGGACTGCCCAAATTTGTCCTCATCAACTGGACAGGCGAGGGCGTGAAC
GATGTGCGGAAGGGAGCCTGTGCCAGCCACGTGAGCACCATGGCCAGCTTCCTGAAGGGGGCCCATGTGACCATC
AACGCACGGGCGGAGGAGGATGTGGAGCCTGAGTGCATCATGGAGAAGGTGGCCAAGGCTTCAGGTGCCAACTAC
AGCTTTCACAAGGAGAGTGGCCGCTTCCAGGACGTGGGACCCAGGCCCCAGTGGGCTCTGTGTACCAGAAGACC
AATGCCGTGCTGAGATTAAAGGGTTGGTAAAGACAGCTTCTGGGCCAAAGCAGAGAAGGAGGAGGAGAACCCT
CGGCTGGAGGAAAAGCGGCGGGCCGAGGAGGCACAGCGGCAGCTGGAGCAGGAGCGCCGGGAGCGTGAGCTGCGT
GAGGCTGCACGCCGGGAGCAGCGCTATCAGGAGCAGGGTGGCGAGGCCAGCCCCAGAGCAGGACGTGGGAGCAG
CAGCAAGAAGTGGTTTTCAAGGAACCGAAATGAGCAGGAGTCTGCCGTGCACCCGAGGGAGATTTTCAAGCAGAAG
GAGAGGGCCATGTCCACCACCTCCATCTCCAGTCCCTCAGCCTGGCAAGCTGAGGAGCCCCCTTCCTGCAGAAGCAG
CTACCCCAACCAGAGACCCACTTTGGCAGAGAGCCAGCTGCTGCCATCTCAAGGCCAGGGCAGATCTCCCTGCT
GAGGAGCCGGCGCCAGCACTCCTCCATGTCTGGTGCAGGCAGAAGAGGAGGCTGTGTATGAGGAACCTCCAGAG
CAGGAGACCTTCTACGAGCAGCCCCACTGGTGCAGCAGCAAGGTGCTGGCTCTGAGCACATTGACCACCACATT
CAGGGCCAGGGGCTCAGTGGGCAAGGGCTCTGTGCCGTGCCCTGTACGACTACCAGGCAGCCGACGACACAGAG
ATCTCCTTTGACCCCGAGAACCTCATCACGGGCATCGAGGTGATCGACGAAGGCTGGTGGCGTGGCTATGGGCCG
GATGGCCATTTTGGCATGTTCCCTGCCAACTACGTGGAGCTCATTGAG**TG**AGGCTGAGGGGCACATCTTGCCCTTC
CCCTCTCAGACATGGCTTCCTTATTGCTGGAAGAGGAGGCCTGGGAGTTGACATTGAGCACTCTTCCAGGAATAG
GACCCCGAGTGAGGATGAGGCCTCAGGGCTCCCTCCGGCTTGGCAGACTCAGCCTGTCACCCCAAATGCAGCAAT
GGCCTGGTGATTCCACACATCCTTCCTGCATCCCCGACCCTCCAGACAGCTTGGCTCTTGCCCTGACAGGA
TACTGAGCCAAGCCCTGCCTGTGGCCAAGCCCTGAGTGGCCACTGCCAAGCTGCGGGGAAGGGTCTTGAGCAGGG
GCATCTGGGAGGCTCTGGCTGCCTTCTGCATTTATTTGCCTTTTTTCTTTTCTTCTTCTTAAGGGGTGGTGG
CCACCACTGTTTAGAATGACCCTTGGGAACAGTGAACGTAGAGAATTGTTTTTAGCAGAGTTTGTGACCAAAGTC
AGAGTGGATCATGGTGGTTTGGCAGCAGGGAATTTGTCTTGTGGAGCCTGCTCTGTGCTCCCCACTCCATTTCT
CTGTCCCTCTGCCTGGGCTATGGGAAGTGGGGATGCAGATGGCCAAGCTCCCACCCTGGGTATTCAAAAACGGCA
GACACAACATGTTCCCTCCACGCGGCTCACTCGATGCCTGCAGGCCCCAGTGTGTGCCTCAACTGATTCTGACTTC
AGGAAAAGTAACACAGAGTGGCCTTGGCCTGTTGTCTTCCCCTATTTTCTGTCCCAGCTCATCCGTGTCTCTGAA
GAACAAATATGCTTTTGGACCACGAAA

2449/6881
FIGURE 2252

MAANLSRNGPALQEAYVRVTEKSPTDWALFTYEGNSNDIRVAGTGEGGLEEMVEELNSGKVMYAFCRVKDPNSG
LPKFVLINWTGEGVNDVRKGACASHVSTMASFLKGAHVTINARAEEDVEPECIMEKVAKASGANYSFHKESGRFQ
DVGPQAPVGSVYQKTNAVSEIKRVGKDSFWAKAEKEEENRRLEEKRRAEAAQRQLEQERRERELREAAARREQRYQ
EQGGEASPSRTWEQQQEVVSRNRNEQESAVHPREIFKQKERAMSTTSISSPQPGKLRSFFLOKQLTQPETHFGR
EPAAAI SRPRADLP AE EPAPSTPPCLVQAE EEA VYEE PPEQET FYEQPPLVQQQAGSEHIDHHIQGQGLSGQGL
CARALYDYQAADDTEISFDPENLITGIEVIDEGWWRGYGPDGHFGMFPANYVELIE

2450/6881
FIGURE 2253

GGGGAGAGCGGGTGTGTTGAAGGCTCCGCGGACCGGCACTAGGAGCCGGGGGCGGGTCCGTGACCCCTCCGGCTGCT
CGGAGTGAACAGGCGGCCAGGAAAGAAGCGGGCCTGAACACCATGATCCCTTTGGAGAAGCCAGGCAGCGGCGGC
TCCTCCCCAGGCGCCACCTCAGGCTCGGGCCGGGCAGGCCGGGGTCTGAGCGGGCCGTGCCGGCCGCCGCCGCCG
CCCCAGGCCCGCGGGCTGCTGACAGAGATACGCGCCGTGGTGCGCACCGAGCCCTTCCAGGACGGCTACAGCCTG
TGCCCCGGGCCGGGAGCTGGGCAGGGGGAAATTTGCAGTGGTGAGAAAATGTATAAAGAAAGATTCTGGGAAAGAA
TTTGCTGCAAAGTTCATGAGAAAAAGAAGAAAAGGCCAAGATTGTCGGATGGAAATAATTCATGAGATTGCTGTA
CTTGAAC TAGCACAAAGACAATCCTTGGGTCAATTAATTTACATGAAGTTTATGAGACTGCATCAGAAATGATCTTA
GTTCTGGAATATGCTGCTGGGGGTGAAATCTTTGACCAGTGTGTTGCAGACAGAGAAGAAGCCTTTAAAGAAAAA
GATGTTCAAAGACTTATGCGACAGATTTTAGAAGGTGTTCACTTTTTACACACTCGTGATGTAGTTTCATCTTGAT
TTGAAGCCTCAGAATATTCTGTTGACAAGTGAATCTCCATTGGGTGACATTAAGATTGTTGATTTTGGCCTTTCA
AGAATATTGAAGAACAGTGAAGAGCTCCGAGAAATTATGGGTACCCCTGAATATGTGGCTCCTGAAATTCTTAGT
TATGATCCTATAAGCATGGCAACAGATATGTGGAGCATTGGAGTGTTAACATATGTCATGCTTACAGGAATATCA
CCTTTCTTAGGCAATGATAAACAAGAAACATTTCTTAAACATCTCACAGATGAATTTAAGTTATTCTGAGGAAGAA
TTTGATGTTTTGTCTGAGTCGGCTGTTGATTTTCATCAGGACACTTTTAGTTAAGAAACCTGAAGATCGAGCCACT
GCTGAAGAATGTCTAAAGCACCCCTGGTTGACACAGAGCAGTATTCAAGAGCCTTCTTTTCAGGATGGAAAAGGCA
CTAGAAGAAGCAAATGCCCTCCAAGAAGGTCATTCTGTGCCTGAAATTAATTCGGATACCGACAAATCAGAAACC
AAGGAATCCATTGTAACCGAAGAGTTAATTGTAGTTACTTCATATACTCTAGGACAATGCAGACAGTCTGAAAAA
GAGAAAATGGAGCAAAGGCCATTTCCAACGATTTAAATTTGAGGAACCTTTGCTACAAGAAATTCAGGAGAA
TTTATCTACTGAGCAATATTTCCCTTTAGAACTTCAAGATTTCTACATTGAAAATGTTAATATTATTTATGGACC
TCTGGCCAAATGGTACATGTACTGGAAGTGGATAACCAGTATCACTTACACAAACAAAAATAACTTTGTCAAATT
TGTGGAGTTAGGTGGAAGCCAGATTTTAAAAGTTGCCAACAGGAGATTTAACAGGTACAGTTACCCGTTTCAAT
GTTATTTTTAAGAAGGGAGATGTTGGCACCTTTGAATTCTACATCCTGTTTCTCCAGAATGAGAATTTGTGTACA
AAGATATTTGTATTCACTTTCTTTAAAAAATCCAAGTAAAAGTGCCAAAACACTACACTTCTGTAAATCTCTTGCAT
TATTCATATGTGTATCTATATCTGCATAATGTTTGTTAATGTCTACTAAAATTGCTACTTTTTTCACTTTGGATTT
GTTTTTGGCAAATTTTAGTCTAAACAGACATCTAAATTTTCGAGACTTAGAATAACATTCATAAAGTTTGATA
ATGTCTTTTTTAAATATTTTCTTACTGCTTTATAGTGACTTGATTTGGTTTCTGTTGTGTTTTTGCCTAAATACT
AGTAACATATCAGTGAAAAACCCCTAATTTTTTTTCTCTTCAATGTCACTAGTAAGAGAGGTGGTAATTTTTTACC
TCTGAAATTATTCTGGGTTTAGGTGTCAGCTCTTGAGCTGCTTCCCTCATCACACCACACTCACATGCATCTGTT
CTCTCTCACACTCTATAACCCCTGCCACTTCCCTGGCACCTCCCCCATGCTTGTCATTTAATTTTGGCCACTTGTA
GGTATCAGTGTGATCTGATCAACACTCTGGTTACCTTGGTCAGTGAAAAGATGCTACTATATTGCTTTTGTCCCA
AAGTGAGTAAAATCCCCTAGAGCAGAGAGAGAGAGAGAGAGAGAGAGTGTCTTCATGCCAACCACAGCCTGTTTC
TGCTGAGTTTCTTATCAGCCCTCAAGCTATGCTAGGAAAAGTTATAAAATGCCAAAATATTTATAAACATTTACT
TTGTCCATAAAAAATTTACATTGGATACTCTGTAAGTAGGAGGTACTTTGTCCCAAAAAGATGTATAAGAATGTA
CTAATAGTTTTTATTTGATTAGGATTGAACAGTTCAGTTGTATCTATGCCCCACAGTGACCAGTAAAGTCCAATTA
AAATATGGAAATGTAAAAGTGATGCCGAATACCTTAAAGTAACTAATTATCCTTACACACAAAAGGCTCAGTGC
ATTAAATATTTGCCTATC

2451/6881
FIGURE 2254

ATGGCGGAGCGCGGGTACAGCTTTTCGCTGACTACATTCAGCCCGTCTGGTAAACTTGTCCAGATTGAATATGCT
TTGGCTGCTGTAGCTGGAGGAGCCCCGTCCGTGGGAATTAAAGCTGCAAATGGTGTGGTATTAGCAACTGAGAAA
AAACAGAAATCCATTCTGTATGATGAGCGAAGTGTACACAAAGTAGAACCAATTACCAAGCATATAGGTTTGGTG
TACAGTGGCATGGGCCCCGATTACAGAGTGCTTGTGCACAGAGCTCGAAAAGTAGCTCAACAATACTATCTTGTG
TACCAAGAACCCATTCTACAGCTCAGCTGGTACAGAGAGTAGCTTCTGTGATGCAAGAATATACTCAGTCAGGT
GGTGTTTCGTCCATTGAGTTTCTTTACTTATTTGTGGTTGGAATGAGGGACGACCATATTTATTTTCAGTCAGAT
CCATCTGGAGCTTACTTTGCCTGGAAAGCTACAGCAATGGGAAAGAACTATGTGAATGGGAAGACTTTCCTTGAG
AAAAGATATAATGAAGATCTGGAACCTGAAGATGCCATTCATACAGCCATCTTAACCTAAAGGAAAGCTTTGAA
GGGCAAAATGACAGAGGATAACATAGAAAGTTGGAATCTGCAATGAAGCTGGATTTAGGAGGCTTACTCCAAGTAA
GTTAAGGATTACTTGGCTGCCATAGCATAACAATGAAGTACTGAAAAATCCAGAAATTCAGATAATCTATCTAC
TTAAACATGTTTAAAGTATGTTTTGTTTTGCAGACTTTTGCATACTTATTTCTACATGGTTTAAATCGACTGTT
TTTAAATGACACTTATAAATCCTAATAAACTGTAAACCC

2452/6881
FIGURE 2255

MAERGYSFSLTTFSPSGKLVQIEYALAAVAGGAPSVGIKAANGVVLATEKKQKSILYDERSVHKVEPITKHIGLV
YSGMGPDYRVLVHRARKLAQQYYLVYQEPIPTAQLVQRVASVMQEYTQSGGVRPFGVSLICGWNEGRPYLFQSD
PSGAYFAWKATAMGKNYVNGKTFLEKRYNEDLELEDAIHTAILTLKESFEGQMTEDNIEVGICNEAGFRRLTPTE
VKDYLAAlA

2453/6881
FIGURE 2256

GCTCGGCGCCCTCTTCCCTGCAAACCATGTTTGCCAAAGGCAGAGGCTCGGCGGTGCCCTCGGATGGGCAGGCTT
GGGAAAAGTTAGCTTCATACGTCTACGAATATTTACTGCACGTAAGAGTACAGAAATCTGCAGAGACCTTCTTGT
CGGAGATTTCGATGGGAAAAAACATCACGTTGGGAGAACCGCTGGGTTTTTGCACCTCGTGGTGGTGTGTTATTTG
GGGACCTTTACTGTGCAGCTCCTCAAAGGAGAGACACTTGTGAACATTCAAGTGAAGCAAAAGCCTTTCATGATT
ATAGTGCAGCAGCTGCCCCGAGCCCCGTGCTTGGCAACATTCCCCCAACGATGGGATGCCGGGAGGCCCCATCC
CGCCAGGTTTTCTTTCAGGGTCCTCCGGGGTCACAGCCCTCGCCGCACGCACAGCCTCCACCTCACAATCCTAGCA
GCATGATGGGACCCACAGTCAGCCTCCGGGAGGAGTTCTTGGGACACAGCCATTGCTGCCCAATTCTATGGATC
CCACACGACAACAAGGCCACCCCAACATGGGAGGATCAATGCAGAGAATGAACCCTCCCCGAGGCATGGGGCCCA
TGGGTCCCGGGCCACAGAATTACGGCAGCGGCATGAGACCACCACCAACTCCCTCGGCCCCGCCATGCCCGGGAT
TAACATGGGCCCCGGGAGCTGGCAGACCCTGGCCCAATCCTAACAGTGCTAACTCAATTCATATTCTCTCATC
ACCTGGTACCTATGTGGGACCCCCGGTGGTGGCGGCCCTCCAGGAACACCCATTATGCCCAGTCCCGCAGATTCA
ACAAATTCCAGTGACAACATCTACACAATGACCTGGCGGCAGGTCCAACCTCCCGATGGGTCCCGGCTCGGACGG
TCCGATGGGCGGCATGGGTGGCATGGAGCCACACCACATGAATGGATCATTAGGGTCAGGCGACATAGACGGACT
TCCAAAAAATTCTCCTAACAAACATAAGTGGCATTAGCAATCCTCCAGGCACCCCTCGAGATGACGGCGAGCTAGG
AGGGAGCTTCCTCCACTCCTTTCAGAATGACAATTATTCTCCAAGCATGACGATGAGTGTGTGATCCCCCTTCT
CCGAGACGCTGAGAGAGCCGGCATTGCAGGCGGGAAGACGCCAGAAATTATGCAAGAAGTGAGGTGTTATTATCC
AGGAGCTGGTGGGAGGGCATCTCCCTGCTCCCCTAAACCCCTCCCACCCCATCCACGCCCCCTACCTTTCCCA
ATTTTAGTTTTCATGCAATAAAAAGGCCAAACTTTTTATTCCATAAAAC

2454/6881
FIGURE 2257

MFAKGRGSAVPSDGQAWEKLASVVEYLLHVRVQKSAETFLSEIRWEKNITLGEPPGFLHSWWCVFGDLYCAAPQ
RRDTCEHSSEAKAFHDYSAAAAPSPVLGNIPPNDGMFGGPIPPGFFQPFMSPRYVGGPGPPIRMGNQPPGGVLGT
QPLLNSMDPTRQQGHPNMGGSMQRMNPPRGMGPMGPGPQNYGSGMRPPPNLSGPPCPGLTWARELADPGPILTV
LTQFHIPPHELLVPMWDPWWRPSSRNTHYAQSRRFNKFQ

2455/6881
FIGURE 2258

GGCGGGTTTCGCGCCCCGAAGGCTGAGAGCTGGCGCTGCTCGTGCCCTGTGTGCCAGACGGCGGAGCTCCGCGGCC
GGACCCCGCGGGCCCCGCTTTGCTGCCGACTGGAGTTTGGGGGAAGAACTCTCCTGCGCCCCAGAGGATTTCTTC
CTCGGCGAAGGGACAGCGAAAGATGAGGGTGGCAGGAAGAGAAGGGCGCTTTCTGTCTGCCGGGGTGCAGCGCG
AGAGGGCAGTGCCATGTTCTCTCCATCCTAGTGGCGCTGTGCCTGTGGCTGCACCTGGCGCTGGGCGTGCAGCGG
CGCGCCCCTGCGAGGCGGTGCGCATCCCTATGTGCCGGCACATGCCCTGGAACATCACGCGGATGCCCAACCACCT
GCACCACAGCACGCAGGAGAAGGCCATCCTGGCCATCGAGCAGTACGAGGAGCTGGTGGACGTGAACTGCAGCGC
CGTGCTGCGCTTCTTCTCTGTGCCATGTACGCGCCCATTTGCACCCTGGAGTTCTGCAGCACCTTATCAAGCC
GTGCAAGTCGGTGTGCCAACGCGCGCGGACGACTGCGAGCCCCCTCATGAAGATGTACAACCACAGCTGGCCCGA
AAGCCTGGCCTGCGACGAGCTGCCTGTCTATGACCGTGGCGTGTGCATCTCGCCTGAAGCCATCGTCACGGACCT
CCCGGAGGATGTTAAGTGGATAGACATCACACCAGACATGATGGTACAGGAAAGGCCTCTTGATGTTGACTGTAA
ACGCCTAAGCCCCGATCGGTGCAAGTGTAAGGTTGAAGCCAACCTTTGGCAACGTATCTCAGCAAAAACCTACAG
CTATGTTATTTCATGCCAAAATAAAAGCTGTGCAGAGGAGTGGCTGCAATGAGGTACACAACGGTGGTGGATGTAAA
AGAGATCTTCAAGTCTCATCACCCATCCCTCGAAGTCAAGTCCCGCTCATTACAAATTCCTTCTTGCCAGTGTCC
ACACATCCTGCCCCATCAAGATGTTCTCATCATGTGTTACGAGTGGCGCTCAAGGATGATGCTTCTTGAAAATTG
CTTAGTTGAAAAATGGAGAGATCAGCTTAGTAAAAGATCCATACAGTGGGAAGAGAGGCTGCAGGAACAGCGGAG
AACAGTTCAGGACAAGAAGAAAACAGCCGGGCGCACCAGTTCGTAGTAATCCCCCAAACCAAAGGGAAGCCTCC
TGCTCCCAAACCAGCCAGTCCCAAGAAGAACATTAAACTAGGAGTGGCCAGAAGAGAACAACCCGAAAAGAGT
GTGAGCTAACTAGTTTCCAAAGCGGAGACTTCCGACTTTCCTTACAGGATGAGGCTGGGCATTGCCTGGGACAGCC
TATGTAAGGCCATGTGCCCCCTTGCCCTAACAACTCACTGCAGTGCTCTTCATAGACACATCTTGACGATTTTTTC
TTAAGGCTATGCTTCAGTTTTTCTTTGTAAGCCATCACAAGCCATAGTGGTAGGTTTGCCCTTTGGTACAGAAGG
TGAGTTAAAGCTGGTGGAAAAGGCTTATTGCATTGCATTAGAGTAACCTGTGTGCATACTCTAGAAGAGTAGGG
AAAATAATGCTTGTTACAATTGACCTAATATGTGCATTGTAAAATAAATGCCATATTTCAAACAAAACACGTAA
TTTTTTTACAGTATGTTTTATTACCTTTTGATATCTGTTGTTGCAATGTTAGTGATGTTTTAAATGTGATCGAA
AAATATAATGCTTCTAAGAAGGAACAGTAGTGGAAATGAATGTCTAAAAGATCTTTATGTGTTTTATGGTCTGCAGAA
GGATTTTTGTGATGAAAGGGGATTTTTTGAAAAATCTAGAGAAGTAGCATATGGAAAACCTATAATGTGTCTTTTT
TACAATGACTTCAGCTCTGTTTTTAGCTAGAACTCTAAAAACAAAAATAATAATAAGAAAAATAATAAAAAAG
GAGAGGCAGACAATGTCTGGATTCCGTGTTTTTGGTTACCTGATTTTCATGATCATGATGCTTCTTGTCACACCC
TCTTAAGCAGCACCAGAAACAGTGAGTTTGTCTGTACCATTAGGAGTTAGGTACTAATTAGTTGGCTAATGCTCA
AGTATTTTTATACCACAAGAGAGGTATGTCATCTACTTCTTCCAGGACATCCACCCTGAGAATAATTTGACA
AGCTTAAAAATGGCCTTCATGTGAGTGCCAAATTTTGTCTTCTTCAATTTAAATATTTTCTTTGCCTAAATACATG
TGAGAGGAGTTAAATATAAATGTACAGAGAGGAAAGTTGAGGTTCCACCTCTGAAATGAGAATTACTTGACAGTT
GGGATACTTTAATCAGAAAAAAGAACTTATCTGCAGCATTTTATCAACAAATTCATAATTGTGGACAATTGG
AGGCATTTATTTTAAAAACAATTTTATTGGCCTTTTGCTAACACAGTAAGCATGTATTCTCTATAAGGCATTCA
ATAAATGCACAACGCCCAAAGGAAATAAAATCCTATCTAATCCTACTCTCCACTACACAGAGGTAATCACTATTA
GTATTTTGGCATATTATTCTCCAGGTGTTTCTTATGCACTTATAAAATGATTTGAACAAATAAACTAGGAACCT
GCTATACATGTGTTTCATAACCTGCCTCCTTTGCTTGGCCCTTTATTGAGATAAGTTTTCTGTCAAGAAAGCAG
AAACCATCTCATTTCTAACAGCTGTGTTATATTCCATAGTATGCATTACTCAACAACTGTTGTGCTATTGGATA
CTTAGGTGGTTTCTTCACTGACAATACTGAATAAACATCTCA

2456/6881
FIGURE 2259A

GCGTGTGCTGGGGCGAGCGGGAGCGGGCGAGGATGGGCACAGGATAGAGGCAGAGCCACCCACGCCGCCGCGGCC
CCACGCTGGGCGACAGAGCCTCCAGTTCCTTCAATGGTGGCGGGTCGCCGAGCTCTGATCGCCGGGAACCCCT
TGCCGCTGCTGTCTGCGACCCCAAGCAGGTATAGACACGTGTGGCCGTTTACGCTGTAGGATCCTCATTCCAC
TGGCTTTGAACATTTTGGGGACTTACAATGCCGCCACCCGCGGACATCGTCAAGGTGGCCATAGAATGGCCGGGC
GCCTACCCCAAACCTCATGGAAATTGATCAGAAAAAACCACTGTCTGCAATAATAAAGGAAGTCTGTGATGGGTGG
TCTCTTGCCAACCATGAATATTTTGCCTCCAGCATGCCGATAGTTCAAACCTTCTATATCACAGAAAAGAACCGC
AATGAGATAAAAAATGGCACTATCCTTCGATTAAACCACATCTCCAGCTCAGAACGCCAGCAGCTCCATGAACGA
ATCCAGTCTCGAGTATGGATGCCAAGCTGGAAGCCCTGAAGGACTTGGCCAGCCTCTCCCGGGATGTACAGTTT
GCCCAGGAGTTTATAAACCTGGACGGTATCTCTCTCTCACGCAGATGGTGGAGAGCGGCACTGAGCGATACCAG
AAATTGCAGAAGATCATGAAGCCTTGCTTTGGAGACATGCTGTCTTACCCTGACGGCCTTCGTGAGCTGATG
GACCATGGCATAGTGTCTGGGATACATTTTCGGTGGCGTTTCAATGAAGATAGCAAGTTTTGTGAACAAGTCA
GCCATAGACATCTCGATCCTGCAGCGGTCTTGGCCATTTTGGAGTCGATGGTGTCTCAATAGCCATGATCTCTAC
CAGAAAGTGGCGCAGGAGATCACCATCGGCCAGCTCATTCCACACCTGCAAGGGTCAGATCAAGAAATCCAAACC
TATACTATTGCAGTGATTAATGCGCTTTTCTGAAGGCTCTGATGAGAGGAGGCAGGAGATGGCGAATATTTTG
GCTCAGAAGCAACTGCGTTCCATCATTTTAAACACATGTCTCCGAGCCCAGCGGGCCATCAACAATGAGATGGCG
CACCAGCTGTATGTTTACAAGTGCTCACCTTTAACCTCCTGGAAGACAGGATGATGACCAAAATGGACCCCCAG
GACCAGGCTCAGAGGGACATCATATTTGAACTTCGAAGAATTGCTTTTGATGCTGAGTCTGAACCTAACACAGC
AGTGGCAGCATGGAGAAACGCAAGTCCATGTACACGCGAGATTATAAGAAGCTTGGGTTTCAATATCATGTCAAC
CCTGCCATGGACTTCACGCAGACTCCACCTGGGATGTTGGCTCTGGACAACATGCTGTACTTTGCCAAGCACCAC
CAAGATGCCTACATCCGATTGTGCTTGAGAACAGTAGTCGAGAAGACAAGCATGAATGTCCCTTTGGCCGCAGT
AGTATAGAGCTGACCAAGATGCTATGTGAGATCTTGAAAGTGGGCGAGTTGCCAGTGAGACCTGCAACGACTTC
CACCCGATGTTCTTACCCACGACAGATCCTTTGAGGAGTTTTTCTGCATCTGTATCCAGCTCCTGAACAAGACA
TGGAAGGAAATGAGGGCAACTTCTGAAGACTTCAACAAGGTAATGCAGGTGGTGAAGGAGCAGGTTATGAGAGCA
CTTACAACCAAGCCTAGCTCCCTGGACCAAGTTCAAGAGCAAACCTGCAGAACCTGAGCTACACTGAGATCCTGAAA
ATCCGCCAGTCCGAGAGGATGAACCAGGAAGATTTCCAGTCCCGCCCGATTTTGGAACTAAAGGAGAAGATTCAG
CCAGAAATCTTAGAGCTGATCAAAACAGCAACGCCCTGAACCGCCTTGTTGGAAGGGACCTGCTTTAGGAACTCAAT
GCCCGGCGGAGGCAAGACAAGTTTTGGTATTGTGCGCTTTCGCCAAATCACAAAGTCTGCAATTACGGAGACTTA
GAAGAGAGTCTCAGGGAGAAGTGCCCCACGATTCTTGAGGACAAACTGCCGGTGGCAGATATCAAAGCCGTG
GTGACGGGAAAGGACTGCCCTCATATGAAAAGAGAAAGGTGCCCTTAAACAAAACAAGGAGGTGCTTGAACCTGCT
TTCTCCATCTTGATGACTCAAACCTGCCAACTGAACCTCATCGCTCCTGACAAGCATGAGTACTGTATCTGGACG
GATGGACTGAATGCGCTACTCGGGAAGGACATGATGAGCGACCTGACGCGGAATGACCTGGACACCCTGCTCAGC
ATGGAAATCAAGCTCCGCCTCCTGGACCTGGAAAACATCCAGATCCCTGACGCACCTCCGCCGATTCCCAAGGAG
CCCAGCAACTATGACTTCGTCTATGACTGTAACCTGAAGTGGCCGGGCCAGACATGCCCTTCCAAAACCTGGAAC
ACCTAGCTAACAGGAGAGAGGAATGAAAACACACCCACGCCTTGGAACCGTCTTTGGTAAAGGGAAGCTGTGGG
TCCACATTCCCTTACGATCACCTCTAGCCCTGGCAACTTTCAGCCCTAGCTGGCATCTTGCTCACCGCCCTGA
TTCTGTTCCCTCGGCTCCACTGCTTCAGGTCACTTCCCATGGCTGCAGTCCACTGGTGGGACAAGAGCAAAGCCCA
CTGCCAGTAAGAAGGCCAAAGGGCCCTTCCATCCTAGCCCTCTGCAGGCATGCCCTTCCCTTCCCTTGGGCAGGAA
AGCCAGCAGCCCCAGACTGCCCAAAAACCTTGCCCAACAGACCAAGGGCAGTGCCCCAAGGCCCTGTCTGGAGGA
AATGGCCTAGCTATTTGATGAGAAGACCAAAACCCACATCCTCCTTTCCCTCTCTCTAGAATCATCTCGCACCA
CCAGTTACACTTGAATTAAGATCTGCGCTCAAATCTCCTCCACCTCTCTCCCTGCTTTTGCTTGTCTGTTC
TCTTTGGTCCCAAGAGCAGCAGCCGACGCTCCTCGTGATCCTCCCTAGCATAAATTTCCCAAAACAGTCCACAGG
TCCCATGCCCACCTTGCGTCTGCACTGTGATCGTGACAAATCTTCCCTCCTCACCAGCTAGTCTGGGGTTTCTCT
TCCCTGCCCCAGGCCAGAACTGCCTTCTTCATTTCCACCCACGCTCCAGCCTCTTAGCTGAAAGCACAAATGGT
GAAATCAGTAGTCTCGCTCCATCTCTAATAGACTAAACCTAAATGCCTCTAGGACGGACTGTTGCTATCCAAGCG
TTTGGTGTACCTTCTCCTGGGAGGTCTGCTGCAACTCAAGTTCCACAGGATGGTCAAGCTGTCAGACATCCAA
GTTTACATCATTGTAATTATTACTGGTATTTACAATTTGCAAGAGTTTTTGGGTTAGTTTTTTTTTTTTTTTGGT
TTGTTTTTGGACAAAAGAGTCTAACATTTTTTGGCAAACAGATATATATTTAATGAAAAGAAGAGATACATAAAT
GTGTGAATTTCCAGTTTTTTTTTTAATTATTTTAAATCCCAAACATCTTCCCTGAAAATAACATTCCCTTAAACATGC

2457/6881

FIGURE 2259B

TGTGGAATAAAATGGATTGTGATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

2458/6881
FIGURE 2260

CATTTAAAGGTGTGCGGCGGGTCTCTGTTACATGGCTCAACTGGAAACCTGTTTCATGAACAAGCTTACTCAGG
AACCATCTGGTGGTATTCCAGCACATTGTTCTTCAGGGGGACGACTCTAAGTCGCTTTGTGGTGGCAGCAGCTTA
GAATCAGTATTTGTGGTTGGGAAAGATGGACTTACGGGAGCTTGGTAAATGCAGGTGGTGAAGGAGCAGGTTATGA
GAGCACTTACAACCAAGCCTAGCTCCCTGGACCAGTTCAAGAGCAAACCTGCAGAACCTGAGCTACACTGAGATCC
TGAAAATCCGCCAGTCCGAGAGGATGAACCAGGAAGATTTCCAGTCCCGCCCGATTTTGGAACTAAAGGAGAAGA
TTCAGCCAGAAATCTTAGAGCTGATCAAACAGCAACGCCTGAACCGCCTTGTGGAAGGGACCTGCTTTAGGAAAC
TCAATGCCCCGGCGGAGGCAAGACAAGTTTTTGGTATTGTGCGCTTTTCGCCAAATCACAAAGTCCTGCATTACGGAG
ACTTAGAAGAGAGTCCCTCAGGGAGAAGTGCCCCACGATTCCCTTGCCAGGACAACTGCCGGTGGCAGATATCAAAG
CCGTGGTGACGGGAAAGGACTGCCCTCATATGAAAGAGAAAGGTGCCCTTAAACAAAACAAGGAGGTGCTTGAAC
TCGCTTTCTCCATCTTGTATGACTCAAACCTGCCAACTGAACTTCATCGCTCCTGACAAGCATGAGTACTGTATCT
GGACGGATGGACTGAATGCGCTACTCGGAAGGACATGATGAGCGACCTGACGCGGAATGACCTGGACACCCCTGC
TCAGCATGGAAATCAAGTCCGCCTCCTGGACCTGGAAAACATCCAGATCCCTGACGCACCTCCGCCGATTCCCA
AGGAGCCCAGCAACTATGACTTCGTCTATGACTGTAACTGAAGTGGCCGGGGCCAGACATGCCCTTCCAAAAC
GGAACACCTAGCTAACAGGAGAGAGGAATGAAAACACACCCACGCCTTGGAACCGTCCTTTGGTAAAGGGAAGCT
GTGGGTCCACATTCCCTTCAGCATCACCTCTAGCCCTGGCAACTTTCAGCCCCTAGCTGGCATCTTGCTCACCGC
CCTGATTCTGTTCCCTCGGCTCCACTGCTTCAGGTCACTTCCCATGGCTGCAGTCCACTGGTGGGACAAGAGCAAA
GCCCCACTGCCAGTAAGAAGGCCAAAGGGCCCTTCCATCCTAGCCCTCTGCAGGCATGCCCTTCCTTCCCTTGGGC
AGGAAAGCCAGCAGCCCCAGACTGCCCAAAAACCTTGCCCACCAGACCAAGGGCAGTGCCCCAAGGCCCTGTCTG
GAGGAAATGGCCTAGCTATTTGATGAGAAGACCAAACCCACATCCTCCTTCCCTCTCTCTAGAATCATCTCG
CACCACCAGTTACACTTGAATTAAGATCTGCGCTCAAATCTCCTCCCACCTCTCTCCCTGCTTTTGCTTGTCTCT
GTTCTCTTTGGTCCCAAGAGCAGCAGCCGCAGCCTCCTCGTGATCCTCCCTAGCATAAATTTCCCAAACAGTCC
ACAGGTCCCATGCCACTTTGCGTCTGCACTGTGATCGTGACAAATCTTCCCTCCTACCAGCTAGTCTGGGGTT
TCCTCTCCCTGCCCCAGGCCAGAACTGCCTTCTTCATTTCCACCCACGCTCCAGCCTCTTAGCTGAAAGCACAA
ATGGTGAAATCAGTAGTCTCGCTCCATCTCTAATAGACTAAACCTAAATGCCTCTAGGACGGACTGTTGCTATCC
AAGCGTTTGGTGTACCTTCTCCTGGGAGGTCTGCTGCAACTCAAGTTCCACAGGATGGTCAAGCTGTCAGACA
TCCAAGTTTACATCATTGTAATTATTACTGGTATTTACAATTTGCAAGAGTTTTGGGTTAGTTTTTTTTTTTTTT
TTGCTTTGTTTTTTGGACAAAAGAGTCTAACATTTTTTTGCCAAACAGATATATATTTAATGAAAAGAAGAGATACA
TAAATGTGTGAATTTCCAGTTTTTTTTTAATTATTTTAATCCCAAACATCTTCCTGAAAATAACATTCCCTTAAA
CATGCTGTGGAATAAAATGGATTGTGATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

2459/6881
FIGURE 2261

MQVVKEQVMRALTTKPSSLDQFKSKLQNLSTYTEILKIRQSERMNQEDFQSRPILELKEKIQPEILELIKQQRLNR
LVEGTCFRKLNARRRQDKFWYCRLSPNHKVLHYGDLEESPQGEVPHDSLQDKLPVADIKAVVTGKDCPHMKEKGA
LKQNKVLELAFSILYDSNCQLNFIAPDKHEYCIWTDGLNALLGKDMMSDLTRNDLDTLLSMEIKLRLLDLENIQ
IPDAPPPIPKEPSNYDFVYDCN

2460/6881
FIGURE 2262

GCACCCGGCAGCGGTCTCAGGCCAAGCCCCCTGCCAGCATGGCCAGCGAGTTCAAGAAGAAGCTCTTCTGGAGGG
CAGTGGTGGCCGAGTTCCTGGCCACGACCCTCTTTGTCTTCATCAGCATCGGTTCTGCCCTGGGCTTCAAATACC
CGGTGGGGAACAACCAGACGGCGGTCCAGGACAACGTGAAGGTGTCGCTGGCCTTCGGGCTGAGCATCGCCACGC
TGGCGCAGAGTGTGGGCCACATCAGCGGCGCCACCTCAACCCGGCTGTCACACTGGGGCTGCTGCTCAGCTGCC
AGATCAGCATCTTCCGTGCCCTCATGTACATCATCGCCAGTGCCTGGGGGCCATCGTCGCCACCGCCATCCTCT
CAGGCATCACCTCCTCCCTGACTGGGAACCTCGCTTGGCCGCAATGACCTGGCTGATGGTGTGAACCTCGGGCCAGG
GCCTGGGCATCGAGATCATCGGGACCCCTCCAGCTGGTGCTATGCGTGCTGGCTACTACCGACCGGAGGCGCCGTG
ACCTTGGTGGCTCAGCCCCCCTTGCCATCGGCCTCTCTGTAGCCCTTGGACACCTCCTGGCTATTGACTACACTG
GCTGTGGGATTAACCCTGCTCGGTCCTTTGGCTCCGCGGTGATCACACACAACCTTCAGCAACCCTGGATTTTCT
GGGTGGGGCCATTTCATCGGGGGAGCCCTGGCTGTACTCATCTACGACTTCATCCTGGCCCCACGCAGCAGTGACC
TCACAGACCGCGTGAAGGTGTGGACCAGCGGCCAGGTGGAGGAGTATGACCTGGATGCCGACGACATCAACTCCA
GGGTGGAGATGAAGCCCAATAGAAGGGGTCTGGCCCGGGCATCCACGTAGGGGGCAGGGGCAGGGGCGGGCGGA
GGGAGGGGAGGGGTGAAATCCATACTGTAGACACTCTGACAAGCTGGCCAAAGTCACTTCCCCAAGATCTGCCAG
ACCTGCATGGTCAAGCCTCTTATGGGGGTGTTTCTATCTCTTTCTTTCTTTCTGTTTCTTGGCCTCAGAGCTT
CCTGGGGACCAAGATTTACCAATTCACCCACTCCCTTGAAGTTGTGGAGGAGGTGAAAGAAAGGGACCCACCTGC
TAGTCGCCCCCTCAGAGCATGATGGGAGGTGTGCCAGAAAGTCCCCCTCGCCCCAAAGTTGCTCACCAGCTCACC
TGCGCAAGTGCCTGGGATTCTACCGTAATTGCTTTGTGCCTTTGGGCAGGCCCTCCTTCTTTTCTTACATGCAC
CTTGCTCCCAATGGTGCTTGGAGGGGGAAGAGATCCCAGGAGGTGCAGTGGAGGGGGCAAGCTTTGCTCCTTCAG
TTCTGCTTGCTCCCAAGCCCCCTGACCCGCTCGGACTTACTGCCTGACCTTGGAATCGTCCCTATATCAGGGCCTG
AGTGACCTCCTTCTGCAAAGTGGCAGGGACCGGCAGAGCTCTACAGGCCTGCAGCCCCTAAGTGCAAACACAGCA
TGGGTCCAGAAGACGTGGTCTAGACCAGGGCTGCTCTTTCCACTTGCCCTGTGTTCTTTCCCCAGGGGCATGACT
GTCGCCACACGCCTCTGCATATATGTCTCTTTGGAGTTGGAATTTATTATATGTTAAGAAAATAAAGGAAAATG
ACTTGTAAGGTC

2461/6881
FIGURE 2263

MASEFKKKLFWRAVVAEFLATTLFVFISIGSALGFKYPVGNNQTAVQDNVKVSLAFGLSIATLAQSVGHISGAHL
NPAVTLGLLLSCQISIFRALMYIIAQCVGAI VATAILSGITSSLTGNSLGRNDLADGVNSGQGLGIEIIGTLQLV
LCVLATTD RRRRLGGSAPLAIGLSVALGHLLAIDYTGCGINPARSFGSAVITHNFSNHWIFWVGPFFIGGALAVL
IYDFILAPRSSDLTDRVKVWTSGQVEEYDL DADDINSRVEMKPK

2462/6881

FIGURE 2264A

TCAGTCCCCGTGCACAGACCTGCACAAATGGCTGAGCCTCATCATTCCTGACAGCGAGGAGATCTTGGATGTGCC
AGGCCTAGTGAAAAGACCAACAATCTCACTGCAGGGCCCCGCCAGCCCCAGGGAAGGGGAGGAGTTCTTGCCGCGCC
GACGCCGCCGTGCCCACGGCAACGCGGCCATACTGCGCCGGACAGACCCAGTTGCCTGGTGCTGCGGCCCGGCGT
GGGCTCGTGGGCAGAGCCAGAGCCAGAGCCATGGACAGCCTCTTCGTGGAGGAGGTGGCCGCCTCCTTGGTTCAG
GGAGTTCCCTCAGCAGAAAGGGCTTAAAGAAGACATGTGTGACCATGGACCAGGAACGCCCACGCTCTGACCTCAG
CATAAACAACAGAAATGATCTTCGAAAGGTTTTGCATCTTGAATTTCTCTATAAGGAGAACAAGGCAAAGGAAAA
TCCTCTAAAAACAAGCCTTGAACCTCATCACCAGATACTTTCTGGATCACTTTGGAAATACGGCTAACAAATTCAC
TCAAGATACCCCAATCCCTGCACTCTCAGTTCCAAAGAAAAATAACAAAGTGCCATCAAGATGCTCAGAGACTAC
ACTGGTAAATATATATGACCTTTTCAGATGAAGATGCAGGATGGAGAACATCATTGTGAGAAACAAGCAAAGCCAG
ACATGACAATCTTGATGGAGATGTACTTGGTAATTTTGTATCATCTAAAAGGCCCCCGCACAAAAGTAAGCCCAT
GCAGACGGTCCCGGGTGAACCTCCTGTGTTGACTTCTGCATGGGAGAAGATAGACAAGCTTCACTCGGAGCCTTC
CTTGGATGTGAAGAGGATGGGAGAGAATTCCAGGCCAAAGTCTGGTCTGATTGTGCGAGGCATGATGTCTGGGCC
CATCGCCAGCTCCCCACAGGTGAGGAAATCAGGGACAGAGAAGTTAAGCAGCTTGCCACAGGTGACACAGTTGGT
AGGTGGTGTATGCAGACTGGAGCGACGGCTTCACCTGCTGCATGAACCTGCTCTCTGATTCTTTTCACAGACACTA
TCTGAGACGGTCCCTACCGTCAAGCAGCTCCACCCAACCCCAAGAAGAGAGCCGGAAGGTCCCTGAGCTCTTTGT
CTGCACCCAACAGGACATTCTGGCTTCGAGCAACAGCTCCCCCTCCAGGACCTCCCTGGGTTCAGCTTAGTGAAC
GACCGTAGAAAGGCAGAAAACCACTGCCAGCAGCCCTCCCCATCTGCCAGCAAACGGCTGCCCCCATGGGACAG
GGCCAGGCCGAGGGATCCCTCCGAGGACACCCAGCAGTGGACGGCAGCACAGACACGGACAGGATGCCCTTGAA
GCTCTACTTGCCCTGGTGGTAATTCCAGGATGACCCAGGAGAGGCTGGAAAGAGCGTTCAAACGGCAGGGCAGCCA
GCCCCGACCTGTTCAGGTATTACAGTAAAGATAAACTGCAAAGCCTGTCCCTGGATATCACCTTAGATGCATTGGA
TGCCCTGGGGGGAAAGTTTGCTGGTATCCCTGGGGTCTCATTCTAAAGACTGAAGCAGCTCTCTTGTCTTCCC
CAGCGTGTTTTTCTACGGCTGCATTGGGTTTTGCTGCATTTGCAGACATTTTTGGATAATGTACACTTATGGAA
AAATCAGTTGCTGCCGTCTGACAAGGTGGATGGTGAGCTGGGTGCCCTGCGGCTCGAGGATGTGGAGGATGAGTT
GATAAGGGAAGAGGTTCATCCTGTGCGCAGTCCCATCAGTGCTCAAGTTGCAGACAGCATCAAAACCAATTGACCT
CTCAGTAGCAAAGGCACCTTCAGATGTGGCTGGTGCAGCAAGAGCTGGGGAATAAGACCTCTGCTTTGGAGATGT
TAAATTTGAACATGGATTTAAGGAGCACTTGCTTCCCACTAGCCTTTGCCAATGTGTCCAGGAGTCAGATCCTG
TGCTAAGCCCCGTGATGCCTACAGAGATGAGCTCCTCAAGAAGCCTCTGCACCACAGGGGTGGTCCCTGCGGAGT
CCTGGCAGCTGTCCAAGGCTGTGTCTACAGAACTCCTGTTTTGAAGGAGATAGCAAAGCCGACTGTGCTCAGGG
ACTGCAGCCTTCAGATGCCACCGGACCCGCTGCCTCGTCTGCGCCCTCGCAGACATTGTGTGGCGGGCAGGGGG
CCGAGAGAGAGCCGTTGTTGCACTGGCTTCGAGAACACAGCAGTTTCAGTCCAACAGGGAAATACAAAGCAGATGG
AGTCTTAGAAACACTTACGCTTCACAGTTTGACCTGCTATGAGGACCTGGTGACTTTTCTTCAACAAAGCATTCA
TCAGAACTTTCCCAAAGACCTGAAGGCCTGGGCACAGCCCTGGGAAATGATCAGGCCCTGGCAGCACCAGATGT
CCCTTGGGTAGGCAATGGGGCCTACCCTAGGAACAAAAGGAGGCAGTTTGAAGTGGGCCCTATGGCTGCATCCT
GCTCACCCCTTTCTGCCATCCTGTCCAGGTCTACAGAGCTGGGCCTCTGCTGTGGATTGCGGGGAGGACAGTGGGG
GCTCTGTGGCCTCGTGCGCCAGGCTGCCTGCTGCTTCTGACCTTATTAAATGCGTACCAGAGCCAGGG
TGAGGACATCATGGACAGATGTAAACCTAGCCGAGTGCTGCCGACCACTGCCTGCCTGGCCACTTCATTGTCAGA
GGCCCCAAGAAGAGTCGAGAAACAGACCTTTGAGGGAGCTCTCACAAGCCCCAAGGATGCTCAGGGTCTGGGGT
CAGGACAGCTCTGAACCAGACCTGGGCAGCACTGAGCATGGGCTGCTCTGGTGCCCTCAGTGAGCACAGACCTGG
CCAGGTCAATTGAGGCCCTGAGAAGGGTCCAGTGTGACCCCCAGGGCCGTGTGTGCCCCAGGGTTGTGTGTACCC
CCCTGGGTTCAGGGGCCCTCAATGGACCTCACAGGGGGCAAAGAAGACCCCTGAGCACAGTTGCTTGTATCAGTCCT
CTCAGTCACCCAGGAACCTTGTCATCTGCTCCTGACTGGGAAAGCTGTGTCCAACGTTTTCAACGATGTGGTTGA
GCTGGATTCTGGGGATGGGAACATCACACTTCTCAGAGGCATTGCTGCACGCAGTGATATTGGCTTCTTATCTCT
CTTTGAGCATTACAACATGTGCCAGGTTGGCTGCTTCCTGAAGACCCCGAGGTTCCCCATCTGGGTGGTTTGCAG
TGAGAGCCACTTCAGCATCCTCTTTAGCCTGCAGCCGGGGCTCCTGCGTGACTGGAGGACTGAGAGGCTCTTTGA
CTTGTACTIONTACGATGGCCTGGCCAACCAGCAGGAGCAGATCCGGCTGACCATTGACACCACCCAAACCATCTC
TGAGGACACAGACAACGACCTTGTCCCACCCCTCGAGCTCTGCATCAGAAACCAAGTCTGTGTTCCATGTCTGCGA
GAACCTTGCTGACACCAGCTGCCTGCCTGTTCCACTTCCCCCATCAATCCCCCATCATGGTGGGTCCACCTTGGC
AGTTGTTCTTAGAAAAGCTGAGTGGGCTCTATCAGGCACCTTTTTCCCCATGAAAAACACTGGGTCCATCAACGT

2463/6881

FIGURE 2264B

TGAAAAGCAGTTAAGGCAGTATCAGCAATGGGCACTCACTGCCGAGGAGAAGTCTGACTTCACCAAGCCAAGCCA
GTTTGTCTCCAAATACGGCACCAGTGTCTCTTATTTGAGCAGTGAAGATGAACGCTCTGATATGGATAAATTCCA
TCAAAGTGGCTCAACCCCAAAACCCAATAGACTCCTCTGGATCTGCTTGACACACAGAAGCCCAGTAAATAGTCT
GAAGCACTTGGATAGCATAGAAGCACTTAATTCTTCCACATCCAATGGATTTCAAAAAGAAGATGAGAACATGCA
GAAGTGCGGTGGCCTGCTGATGAAGAAGGGGACCCCAGCAGCCTCTTCCCAAAGTGGCCTGCCTGCAGCC
TTCCCTGGTGTCTTTGATTACCTGGGTCTTGCCCTCTGGCTCCCCATGTCCATCTGTCAAATCCTACCCATC
CCACAAGGCCAGCTCCAAGGCCCTCCTCTAAGAAGCCCTCCTGGATTACCCAGCCGACAGTTCAAGTCCTCCCC
TCTGAGTGCTCACAGGACTCAATCACCTCCTCTTTCACAAGCCTAG

2464/6881
FIGURE 2265

GTCAC TCGTATAAAAAACCTATGCTTTGAAGGTTCTCGTGTGTCTCGGCCTGCAGGTCTCGCTCAGAGCTGTGTCC
CTGAACATCCACCCTGCTGGGGTGGCTTGACGCACTTCTGTGCAAATCTGTTTCGCTCGCAACCCTACCTACCTCT
CTCCCGAACC GGAGAAAACCTTCGGCGGGGTCTTCCGGGTTTTGTGTGCAATCTGCGGCGGCGACCCGGCGCCG
CGTCACGCGGTGGTGAATGTGCGGCAGTACGCGCGCCGCGTCTTTACGCGGCGATTTTCATCATGCTCCGAGCCG
GCGGCGCGCGCCGCTTCCGTCGCCACCCTCTCTGGACAGCCCAGGGCCGAGGCTCATGCCCTCTCCGCGTCCAG
TGCTGCTTAGAGGTGCTCGCGCCGCTCTGCTGCTGCTGCTGCCGCCCGGCTCTTAGCCCGACCCCTCGCTCCTCC
TCCGCCGGTCCCTCAGCGCGGCCTCTGCGCCCCGATCTCCTTGCCCCGCGCCGCTCTCCCGGAGCAGC**ATGG**ACG
GCGCGGGGGCTGAGGAGGTGCTGGCACCTCTGAGGCTAGCAGTGCGCCAGCAGGGAGATCTTGTGCGAAAACCTCA
AAGAAGATAAAGCACCCCAAGTAGACGTAGACAAAAGCAGTGGCTGAGCTCAAAGCCCCGAAGAGGGTTCTGGAAG
CAAAGGAGCTGGCGTTACAGCCCAAAGATGATATTGTAGACCGAGCAAAAATGGAAGATACCCTGAAGAGGAGGT
TTTTCTATGATCAAGCTTTTGTATTTATGGAGGTGTTAGTGGTCTGTATGACTTTGGGCCAGTTGGCTGTGCTT
TGAAGAACAATATTATTACAGACCTGGAGGCAGCACTTTATCCAAGAGGAACAGATCCTGGAGATCGATTGCACCA
TGCTCACCCCTGAGCCAGTTTTAAAGACCTCTGGCCATGTAGACAAATTTGCTGACTTCATGGTGAAAGACGTAA
AAAATGGAGAATGTTTTCTGTCTGACCATCTATTAAGCTCATTTACAGAAATTGATGTCTGATAAGAAGTGTT
CTGTGCAAAAAGAAATCAGAAATGGAAGTGTTTTGGCCAGCTTGATAACTATGGACAGCAAGAACTTGCGGATC
TTTTTGTGAACATAATGTAAAATCTCCATTACTGGAAATGATCTATCCCCTCCAGTGCTTTTAACTTAATGT
TCAAGACTTTTCATTGGGCCTGGAGGAAACATGCCTGGGTACTTGAGACCAGAACTGCACAGGGGATTTTCTTGA
ATTTCAAACGACTTTTGGAGTTCAACCAAGGAAAGTTGCCTTTTGCTGCTGCCAGATTGGAAATCTTTTAGAA
ATGAGATCTCCCCTCGATCTGGACTGATCAGAGTCAGAGAATTACAATGGCAGAAATTGAGCACTTTGTAGATC
CCAGTGAGAAAGACCACCCCAAGTTCCAGAATGTGGCAGACCTTCACCTTTATTTGTATTAGCAAAAGCCCAGG
TCAGCGGACAGTCCGCTCGGAAAATGCGCCTGGGAGATGCTGTTGAACAGGGTGTGATTAATAACACAGTATTAG
GCTATTTTCATTGGCCGCATCTACCTCTACCTCACGAAGGTTGGAATATCTCCAGATAAACTCCGCTTCCGGCAGC
ACATGGAGAATGAGATGGCCATTATGCCTGTGACTGTTGGGATGCAGAATCCAAAACATCCTACGGTTGGATTG
AGATTGTTGGATGTGCTGATCGTTCTGTTATGACCTCTCCTGTGATGCACGAGCCACCAAAGTCCCACTTGTAG
CTGAGAAACCTCTGAAAGAACCCAAAACAGTCAATGTTGTTTCAGTTTGAACCCAGTAAGGGAGCAATTGGTAAGG
CATATAAGAAGGATGCAAAACTGGTGATGGAGTATCTTGCCATTTGTGATGAGTGCTACATTACAGAAATGGAGA
TGCTGCTGAATGAGAAAGGGGAATTCACAATTGAACTGAAGGGAAAACATTTTCAGTTAACAAAAGACATGATCA
ATGTGAAGAGATTCCAGAAAACACTATATGTGGAAGAAGTTGTTCCGAATGTAATTGAACCTTCCTTCGGCCTGG
GTAGGATCATGTATACGGTATTTGAACATACATTCCATGTACGAGAAGGAGATGAACAGAGAACATTCTTCAGTT
TCCCTGCTGTAGTTGCTCCATTCAAATGTTCCGTCCTCCCACTGAGCCAAAACAGGAGTTTCATGCCATTTGTCA
AGGAATTATCGGAAGCCCTGACCAGGCATGGAGTATCTCACAAGTAGACGATTCTCTGGGTCAATCGGAAGGC
GCTATGCCAGGACTGATGAGATTGGCGTGGCTTTTGGTGTACCATTGACTTTGACACAGTGAACAAGACCCCC
ACACTGCAACTCTGAGGGACCGTGACTCAATGCGGCAGATAAGAGCAGAGATCTCTGAGCTGCCAGCATAGTCC
AAGACCTAGCCAATGGCAACATCACATGGGCTGATGTGGAGGCCAGGTATCCTCTGTTTGAAGGGCAAGAGACTG
GTAAAAAGAGACAATCGAGGA**TGAG**GACAATTTTGACAACCTTTTGACCATTGCGCTAATAAAAAAAAAAAAA
CTACTCTTATGTCCACTTTACAAAAGAAAACAGCATTGTGATTACTCCAGGGACCGTATTTTATCTTCAGTGGC
TGCCCTGATTTTACCCCCACAATTAAAGTTGAAGGAATCCTGA

2465/6881
FIGURE 2266

MDGAGAEVVLAPLRLAVRQQGDLVRKLKEDKAPQVDVDKAVAEKARKRVLEAKELALQPKDDIVDRAKMEDTLK
RRFFYDQAFAIYGGVSGLYDFGPVGCALKNNIIQTWRQHFIQEEQILEIDCTMLTPEPVLKTSGHVDKFADFMVK
DVKNGECEFRADHLLKAHLQKLMSDKKCSVEKKSEMESVLAQLDNYGQQELADLFVNYNVKSPITGNDLSPEVSFN
LMFKTFIGPGGNMPGYLRPETAQGIFLNFKRLLEFNQGKLPFAAAQIGNSFRNEISPRSGLIRVREFTMAEIEHF
VDPSEKDHPKFQNVADLHLYLSAKAQVSGQSARKMRLGDAVEQGVINNTVLGYFIGRIYLYLTKVGISPDKLRF
RQHMENEMAHYACDCWDAESKTSYGWIEIVGCADRSCYDLSCHARATKVPLVAEKPLKEPKTVNVVQFEPKSGAI
GKAYKKDAKLVMEYLAICDECYITEMEMLLNEKGEFTIETEGKTFQLTKDMINVKRFQKTLVVEEVVNVIEPSF
GLGRIMYTVFEHTFHVREGDEQRTFFSFPVAVAPFKCSVLPLSQNQEFMPFVKELSEALTRHGVSHKVDDSSGSI
GRRYARTDEIGVAFGVTIDFDTVNKTPHTATLRDRDSMRQIRAEISELPSIVQDLANGNITWADVEARYPLFEGQ
ETGKKETIEE

2466/6881
FIGURE 2267

ATGACAGATGCCGCTGTGTCCTTCGCCAAGGACTTCCTGGCAGGTGGAGTGGCCGAAGCCATCTCCAAGACAGCG
GTAGCGCCCATCGAGCAGGTCAAGCTGCTGCTGCAGGCTTTTAACTTCGCCTTCAAAGATAAATAACAAGCAGATC
TTCCTGGGTGGGAATCTGGCATCAGGAGGTGCCGCTGGGGCCACATACTTGTGTTTTGTGTACCCTCTTGATTTT
GCCCGTACCTGTCTAGCAGCTAATGTGGGTAAAGCTGAAGCTGAAAGGGAATTCCGAGGCCTCTGTGACTGCCTG
GTTAAGATCTACAAATCTGATGGGATTAAGGGCCTGTACCAAGGCTTTAACGTGTCTATGCAGGGTATTATCCGA
GCTGCCTACTTCGGTATCTATGACACCGCAAAGGGAATGCTTCCGGATCCCAAGGACACTCACATCGTCATCAGC
TGGATGACCACACAGACTGTCACTGCCTTTTCTGGGTTGACTTCCTATTTCATTGACATCTCAGGGCGCAAAGTA
ACTGACATCATGTACACAGGCACACTTGACTGCTGGAGGAAGATTGCTGGTGATGAAGGAGGCAAAGCTTTTTTC
AAGGGTTCATGGTCCAGTGTTCCTCAGAGGCATGGGTGGTGCTTTTGTGCTTGCTTTGTTTGATGAAATCAAGAAG
TACAGGTAA

2467/6881
FIGURE 2268

MTDAAVSFAKDFLAGGVAEAI SKTAVAPIEQVKLLLQAFNFAFKDKYKQIFLGGNLASGGAAGATYLCFVYPLDF
ARTCLAANVGKAEAEERFRLCDCLVKIYKSDGIKGLYQG FNVSMQGIIRAAYFGIYDTAKGMLPDPK DTHIVIS
WMTTQTVTAFSGLTSYSFDISGRKVTDIMYTGTLD CWRKIAGDEGGKAFFKGSWSSVLRGMGGAFVLVLFDEIKK
YR

2468/6881
FIGURE 2269

TCGGCGGGACGGCTCCCGGCTGCAGTCTGCCCCCGCCCGCGCGGGGGCCGAGTCGCGAAGCGCGCCTGCGAC
CCGGCGTCCGGGCGCGCTGGAGAGGACGCGAGGAGCCATGAGGCGCCAGCCTGCGAAGGTGGCGGCGCTGCTGCT
CGGGCTGCTCTTGGAGTGCACAGAAGCCAAAAAGCATTGCTGGTATTTTGAAGGACTCTATCCAACCTATTATAT
ATGCCGCTCCTACGAGGACTGCTGTGGCTCCAGGTGCTGTGTGCGGGCCCTCTCCATACAGAGGCTGTGGTACTT
CTGGTTCCCTTCTGATGATGGGCGTGCTTTTCTGCTGCGGAGCCGGCTTCTTCATCCGGAGGCGCATGTACCCCC
GCCGCTGATCGAGGAGCCAGCCTTCAATGTGTCTACACCAGGCAGCCCCCAAATCCCGGCCAGGAGCCCAGCA
GCCGGGGCCGCCCTATTACACCGACCCAGGAGGACCGGGGATGAACCCTGTGCGGAATTCCATGGCAATGGCTTT
CCAGGTCCCACCCAACTACCCCAGGGGAGTGTGGCCTGCCCCGCCCTCCAGCCTACTGCAACACGCCTCCGCC
CCCGTACGAACAGGTAGTGAAGGCCAAGTAGTGGGGTGCCACGTGCAAGAGGAGAGACAGGAGAGGGCCTTTCC
CTGGCCTTTCTGTCTTCGTTGATGTTCACTTCCAGGAACGGTCTCGTGGGCTGCTAAGGGCAGTTCTCTGATAT
CCTCAGCAAGCACAGCTCTCTTTCAGGCTTTCCATGGAGTACAATATATGAACTCACACTTTGTCTCCTCTGT
TGCTTCTGTTTCTGACGCAGTCTGTGCTCTCATATGGTAGTGTGGTGACAGTCCCCGAGGGCTGACGTCCTTACG
GTGGCGTGACCAGATCTACAGGAGAGAGACTGAGAGGAAGAAGGCAGTGCTGGAGGTGCAGGTGGCATGTAGAGG
GGCCAGGCCGAGCATCCCAGGCAAGCATCCTTCTGCCCGGTATTAATAGGAAGCCCCATGCCGGGCGGCTCAGC
CGATGAAGCAGCAGCCGACTGAGCTGAGCCAGCAGGTCATCTGCTCCAGCCTGTCTCTCGTCAGCCTTCCTCT
TCCAGAAGCTGTTGGAGAGACATTCAGGAGAGAGCAAGCCCCTTGTCATGTTTCTGTCTCTGTTCATATCCTAAA
GATAGACTTCTCCTGCACCGCCAGGGAAGGGTAGCACGTGCAGCTCTCACCGCAGGATGGGGCCTAGAATCAGGC
TTGCCCTGGAGGCCTGACAGTGATCTGACATCCACTAAGCAAATTTATTTAAATTCATGGGAAATCACTTCCTGC
CCCAAAGTGAGACATTGCATTTTGTGAGCTCTTGGTCTGATTTGGAGAAAGGACTGTTACCCATTTTTTTTGGTGT
GTTTATGGAAGTGATGTAGAGCGTCTGCCCTTTGAAATCAGACTGGGTGTGTGTCTTCCCTGGACATCACTGC
CTCTCCAGGGCATTCTCAGGCCCCGGGGTCTCCTTCCCTCAGGCAGCTCCAGTGGTGGGTCTGAAGGGTGCTTT
CAAAACGGGGCACATCTGGCTGGGAAGTCACATGGACTCTTCCAGGGAGAGAGACCAGCTGAGGCGTCTCTCTCT
GAGGTTGTGTTGGGTCTAAGCGGGTGTGTGCTGGGCTCCAAGGAGGAGGAGCTTGCTGGGAAAAGACAGGAGAAG
TACTGACTCAACTGCAGTGACCATGTTGTGCATAATTAGAATAAAGAAGAAGTGGTCGGAATGCACATTCCTGGA
TAGGAATCACAGCTCACCCCAGGATCTCACAGGTAGTCTCCTGAGTAGTTGACGGCTAGCGGGGAGCTAGTTCCG
CCGCATAGTTATAGTGTGATGTGTGAACGCTGACCTGTCTGTGTGCTAAGAGCTATGCAGCTTAGCTGAGGCG
CCTAGATTACTAGATGTGCTGTATCACGGGGAATGAGGTGGGGGTGCTTATTTTTTAATGAACTAATCAGAGCCT
CTTGAGAAATTGTTACTCATTGAACTGGAGCATCAAGACATCTCATGGAAGTGGAATACGGAGTGATTGGTGTCC
ATGCTTTTCACTCTGAGGACATTTAATCGGAGAACCTCCTGGGGAATTTTGTGGGAGACACTTGGGAACAAAACA
GACACCCTGGGAATGCAGTTGCAAGCACAGATGCTGCCACAGTGTCTCTGACCACCCTGGTGTGACTGCTGACT
GCCAGCGTGGTACCTCCCATGCTGCAGGCCTCCATCTAAATGAGACAACAAAGCACAAATGTTCACTGTTTACAAC
CAAGACAAGTGCCTGGGTCCAAACACTCCTCTTCCCTCCAGGTCAATTTGTTTTGCATTTTAAATGTCTTTATTTTT
TGTAATGAAAAAGCACACTAAGCTGCCCCCTGGAATCGGGTGCAGCTGAATAGGCACCCAAAAGTCCGTGACTAAA
TTTCGTTTGTCTTTTGTATAGCAAATTATGTTAAGAGACAGTGATGGCTAGGGCTCAACAATTTTGTATTCCCAT
GTTTGTGTGAGACAGAGTTTGTCTTCCCTTGAACCTGGTTAGAATTGTGCTACTGTGAACGCTGATCCTGCATAT
GGAAGTCCCACTTCGGTGACATTTCTGGCCATTCTTGTTTCCATTGTGTGGATGGTGGGTGTGCCCACTTCCT
GGAGTGAGACAGCTCCTGGTGTGTAGAATTCCCGGAGCGTCCGTGGTTCAGAGTAACTTGAAGCAGATCTGTGC
ATGCTTTTCTCTGCAACAATTGGCTCGTTTCTCTTTTTTGTCTCTTTTGTATAGGATCCTGTTTCCTATGTGTG
CAAAATAAAAATAAATTTGGGCA

2469/6881

FIGURE 2270

MRRQPAKVAALLLGLLLECTEAKKHCWYFEGLYPTYYICRSYEDCCGSRCCVRALSIQRLWYFWFLMMGVLFCC
GAGFFIRRRMYPPPLIEEPAFNVSYTRQPPNPGPGAQQPGPPYYTDPGGPGMNPVGNSMAMAFQVPFNSPQGSVA
CPPPPAYCNTPPPPYEQVVKAK

2470/6881
FIGURE 2271

GCCGCTCCTGGTGCTGCTTGTGTGCTCGTTTGGTGCGGACCTGGTACCTCTTTTGTGAAGTGGCAGCTGAGGAGA
CCGGCGCTCGCCATGGCCGACGAAAAGCCCAACCAAGGAGTCAAGTCGGAGAACAACGATCATACTAATTTGAAG
GTGGCGGGGCAGGATGGTTCTGTGGTGCAGTTTAAAGATTAAAGAGGCATACACCACTTAGTAACTAATGAAAGCC
TATTGTAAGCAACAGGGATTGTCAATGAGGCAGATCAGATTCCGATTTCGACGGGCAACCAATCAAGGAAACAGAC
ACACCTGCACAGTTGGAAATGGAGAATGAAGATACAATTGATGTGTTCCAACAGCAGACGGGAGGTGTCTACTTGA

AAAGGGAACCTGCTTCTTTACTCCAGAACTCTGTTTCCTTAAAGACCAAGATTACATTCTCAATTAGTCTTTCATT
TCCCCCTTCCCCATTCTTTATTGTACATAACTGGTATATGTGCACAAGCATATTGCATTTTTTTT

2471/6881
FIGURE 2272

MADEKPNQGVKSENNDHTNLKVAGQDGSVVQFKIKRHTPLSKLMKAYCKQQGLSMRQIRFRFDGQPIKETDTPAQ
LEMENEDTIDVFQQQTGGVY

2472/6881
FIGURE 2273

GGAGGAAAATTCTTCCAGCGATGGTCTCCCACTCAGAGCTGAGGAAGCTTTTCTACTCAGCAGATGCTGTGTGTT
TTGATGTTGACAGCACGGTCATCAGAGAAGAAGGAATCGATGAGCTAGCCAAAATCTGTGGCGTTGAGGACGCGG
TGTCAGAAAATGACACGGCGAGCCATGGGCGGGGCAGTGCCTTTCAAAGCTGCTCTCACAGAGCGCTTAGCCCTCA
TCCAGCCCTCCAGGGAGCAGGTGCAGAGACTCATAGCAGAGCAACCCCCACACCTGACCCCCGGCATAAGGGAGC
TGGTAAGTCGCCTACAGGAGCGAAATGTTTCAGGTTTTCTAATATCTGGTGGCTTTAGGAGTATTGTAGAGCATG
TTGCTTCAAAGCTCAATATCCCAGCAACCAATGTATTTGCCAATAGGCTGAAATTCTACTTTAACGGTGAATATG
CAGGTTTTGATGAGACGCAGCCAACAGCTGAATCTGGTGGAAAAGGAAAAGTGATTAACTTTTAAAGGAAAAAT
TTCATTTTAAGAAAATAATCATGATTGGAGATGGTGCCACAGATATGGAAGCCTGTCCTCCTGCTGATGCTTTCA
TTGGATTTGGAGGAAATGTGATCAGGCAACAAGTCAAGGATAACGCCAAATGGTATATCACTGATTTTGTAGAGC
TGCTGGGAGAACTGGAAGAATAACATCCATTGTCTGACAGCTCCAAACAACCTTCAGATGAATTTTTACAAGTTAT
ACAGATTGATACTGTTTGCTTACAGTTGCCTATTACAACCTTGCTATAGAAAGTTGGTACAAATGATCTGTACTTT
AAACTACAGTTAGGAATCCTAGAAAGATTGCTTTTTTTTTTTTTTTTAACTGTAGTTCCAGTATTATATGATGACTA
TTGATTTCTGGAGAGGTTTTTTTTTTTTTTTGGAGACAGAATCTTGCTCTGTTGCCAGGCTGGAGTGCAGTGGCG
CGGTCTCGGCTCACTGCAAGCTCTGCCTCCAGGTTACGCCATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGA
CTACAGGCACCCGCCACCACATCCGGCTAATTTTTTGTATTTTTTAGTAGAGACGGGGTTTGACCGTGTTAGCCAG
GATGGTCTTGATCTCCTGACCTTGTGATCCGCCTGCCTCAGCCTCCCAAAGTGCTGGGATTACAGGCTTGGGCCA
CCGCGCCCAGCCAATGTCCTAGAGAGTTTTGTGATCTGAATCTTTATGTATATTGTAGCTATATTTCATACAA
AGTGCTTTAAGTGTGGAGAGTCAATTAAACACCTTTACTCTTAGAAATACGGATTCCGGCAGCCTTCAGTGAATAT
TGGTTTCTCTTTGGTATGTCAATAAAAGTTTATCCGTATGTCAGAACGGATTTGTGG

2473/6881
FIGURE 2274

CGAGAAGACCCGGATAGTTCCTCCCGGCCACGCCGCGCCGGCTCTGGGCACTCAGCATCGTTTCCTTTTCCTCCG
CTGGAGCAGCTATGGCGGCGGTGAAGACCCTGAACCCCAAGGCCGAGGTGGCCCGAGCGCAGGCGGCGCTGGCGG
TCAACATCAGCGCAGCGCGGGGTCTGCAGGACGTGCTAAGGACCAACCTGGGGCCCAAGGGCACCATGAAGATGC
TCGTTTCTGGCGCTGGAGACATCAAACCTTACTAAAGACGGCAATGTGCTGCTTCACGAAATGCAAATTC AACACC
CAACAGCTTTCCTTAATAGCAAAGGTAGCAACAGCCCAGGATGATATAACTGGTGATGGTACGACTTCTAATGTCC
TAATCATTTGGAGAGCTGCTGAAACAGGCGGATCTCTACATTTCTGAAGGCCTTCATCCTAGAATAATCACTGAAG
GATTTGAAGCTGCAAAGGAAAAGGCCCTTCAGTTTTTGGAAGAAGTCAAAGTAAGCAGAGAGATGGACAGGGAAA
CACTTATAGATGTGGCCAGAACATCTCTTCGTACTAAAGTTCATGCTGAACTTGCAGATGTCTTAACAGAGGCTG
TAGTGGACTCCATTTTGGCCATTAAAAAGCAAGATGAACCTATTGATCTCTTCATGATTGAGATCATGGAGATGA
AACATAAATCTGAAACTGATACAAGCTTAATCAGAGGGCTTGTTTTGGACCACGGAGCACGGCATCCTGATATGA
AGAAAAGGGTGGAGGATGCATACATCCTCACTTGTAACGTGTCAATTAGAGTATGAGAAAAACAGAAGTGAATTCGT
GCTTTTTTTACAAGAGTGCAGAAGAGAGAGAAAACTCGTGAAAGCTGAAAGAAAATTCATTGAAGATAGGGTTA
AAAAAATAATAGAACTGAAAAGGAAAGTCTGTGGCGATTGAGATAAAGGATTTGTTGTTATTAATCAAAGGGAA
TTGACCCCTTTTCTTAGATGCTCTTCAAAGAAGGCATAGTCGCTCTGCGCAGAGCTAAAAGGAGAAATATGG
AGAGGCTGACTCTTGCTTGTGGTGGGGTAGCCCTGAATTCCTTTGACGACCTAAGTCCTGACTGCTTGGGACATG
CAGGACTTGTATATGAGTATACATTGGGAGAAGAGAAGTTTACCTTTATTGAGAAATGTAACAACCCCTCGTTCTG
TCACATTATTGATCAAAGGACCAAATAAGCACACACTCACTCAGATCAAAGATGCAGTGAGGGACGGCTTGAGGG
CTGTCAAAAATGCTATTGATGATGGCTGTGTGGTTCCAGGTGCTGGTGCCGTGGAAGTGGCAATGGCAGAAGCCC
TGATTAAACATAAGCCAGTGTAAGGGCAGGGCACAGCTTGGAGTCCAAGCATTGCTGATGCATTGCTCATTA
TTCCCAAGGTTCTTGCTCAGAACTCTGGTTTTGACCTTCAGGAAACATTAGTTAAAATTCAAGCAGAACATTGAG
AATCAGGTGAGCTTGTGGGTGTGGACCTGAACACAGGTGAGCCAATGGTGGCAGCAGAAGTAGGCGTATGGGATA
ACTATTGTGTAAAGAAACAGCTTCTTCACTCCTGCACTGTGATTGCCACCAACATTCTCTTGTTGATGAGATCA
TGCGAGCTGGAATGTCTTCTCTGAAAGGTTGAATTGAAGCTTCTCTGTATCTGAATCTTGAAGACTGCAAAGTG
ATCCTGAGGATTACAGCTGTGGAATTTTTGTCCAAGCTTCAAATAATTTTGAAAGAAATTTCCCATATGAAAAA
AGGAGAGAACTGGCATCTGTTGAAATTTGGAAGTTCTGAAATTATAGTATTTTTAAAAATTGCACTGAAGTGT
ATACACATAAAGCAGGTCTTTTATCCAGTGAACAGGATGTTTTGCTTTAGCAGCAGTGACATAAAATTCCATGTT
AGATAAGCATATGTTACTTACCTTGTATTAAATATTTCTTGAAAAGCAGGCCACGAAGG

2474/6881
FIGURE 2275

MAAVKTLNPKAEVARAQAALAVNISAAAGLQDVLRTNLGPKGTMKMLVSGAGDIKLTGDGNVLLHEMQIQHPTAS
LIAKVATAQDDITGDGTTSNVLIIGELLKQADLYISEGLHPRIITEGFEEAKEKALQFLEEVKVSREMDRETLID
VARTSLRTKVHAEADVLTEAVVDSILAIKKQDEPIDLFMIEIMEMKHKSETDTSILIRGLVLDHGARHPDMKKRV
EDAYILTCNVSLEYEKTEVNSGFFYKSAEEREKLVKAERKFIEDRVKKIIEELKRKVCGDSKGFVVINQKGIDPF
SLDALSKEGIVALRRAKRRNMERLTLACGGVALNSFDDLSPDCLGHAGLVYEYTLGEEKFTFIEKCNNPRSVTLL
IKGPNKHTLTQIKDAVRDGLRAVKNAIDDGCVVPGAGAVEVAMAEALIKHKPSVKGRAQLGVQAFADALLIIPKV
LAQNSGFDLQETLVKIQAEHSESGQLVGVDLNTGPEMVAAEVGVWDNYCVKKQLLHSCTVIATNILLVDEIMRAG
MSSLKG

2475/6881
FIGURE 2276

CAGACACACTGTGACGGCTGCCTGAAGCTAGTGAGTCGCGGCGCCGCGCACTGGTGGTTGGGTCAGTGCCGCGCG
CCGATCGGTCGTTACCGCGAGGCGCTGGTGGCCTTCAGGCTGGACGGCGCGGGTCAGCCCTGGTTCGCCGGCTTC
TGGGTCTTTGAACAGCCGCG**ATG**TCGATCTTCACCCCCACCAACCAGATCCGCCTAACCAATGTGGCCGTGGTAC
GGATGAAGCGTGCCGGAAGCGCTTCGAAATCGCCTGCTACAAAAACAAGGTCGTCGGCTGGCGGAGCGGCGTGG
AAAAAGACCTCGATGAAGTTCTGCAGACCCACTCAGTGTTTGTAATGTTTCTAAAGGTCAGGTTGCCAAAAAGG
AAGATCTCATCAGTGCGTTTGGAACAGATGACCAAACTGAAATCTGTAAGCAGATTTTGAATAAGGAGAAGTTC
AAGTATCAGATAAAGAAAGACACACAACTGGAGCAGATGTTTAGGGACATTGCAACTATTGTGGCAGACAAAT
GTGTGAATCCTGAAACAAAGAGACCATAACCGTGATCCTTATTGAGAGAGCCATGAAGGACATCCACTATTCGG
TGAAAACCAACAAGAGTACAAAACAGCAGGCTTTGGAAGTGATAAAGCAGTTAAAAGAGAAAAATGAAGATAGAAC
GTGCTCACATGAGGCTTCGGTTCATCCTTCCAGTCAATGAAGGCAAGAAGCTGAAAGAAAAGCTCAAGCCACTGA
TCAAGGTCATAGAAAGTGAAGATTATGGCCAACAGTTAGAAATCGTATGTCTGATTGACCCGGGCTGCTTCCGAG
AAATTGATGAGCTAATAAAAAAGGAACTAAAGGCAAAGGTTCTTTGGAAGTACTCAATCTGAAAGATGTAGAAG
AAGGAGATGAGAAATTTGAAT**TGA**CACCCATCAATCTCTTCACCTCTAAAACAC

2476/6881
FIGURE 2277

MSIFTPTNQIRLTNVAVVRMKRAGKRFEIACYKNKVVGWRSGVEKDLDEVLQTHSVFVNVSKGQVAKKEDLISAF
GTDDQTEICKQILTKGEVQVSDKERHTQLEQMFRDIATIVADKCVNPETKRPTYTVILIERAMKDIHYSVKTNKST
KQQALEVIKQLKEKMKIERAHMRLRFILPVNEGKKLKEKLKPLIKVIESEDYGQQLEIVCLIDPGCFREIDELIK
KETKGKGSLEVLNLKDVEEGDEKFE

2477/6881
FIGURE 2278

GACACTATCCGTGCGGCCAGGCGGAGACCCGGAGGACCGAAGCTTCCGGACGACGAGGAACCGCCCAACATGGCC
TCGGAGAGTGGGAAGCTTTGGGGTGGCCGGTTTGTGGGTGCAGTGGACCCCATCATGGAGAAGTTCAACGCGTCC
ATTGCCTACGACCGGCACCTTTGGGAGGTGGATGTTCAAGGCAGCAAAGCCTACAGCAGGGGCTGGAGAAGGCA
GGGCTCCTCACCAAGGCCGAGATGGACCAGATACTCCATGGCCTAGACAAGGTGGCTGAGGAGTGGGCCCAGGGC
ACCTTCAAACCTGAACCTCCAATGATGAGGACATCCACACAGCCAATGAGCGCCGCCTGAAGGAGCTCATTGGTGCA
ACGGCAGGGAAGCTGCACACGGGACGGAGCCGGAATGACCAGGTGGTCACAGACCTCAGGCTGTGGATGCGGCAG
ACCTGCTCCACGCTCTCGGGCCTCCTCTGGGAGCTCATTAGGACCATGGTGGATCGGGCAGAGGCGGAACGTGAT
GTTCTCTTCCCGGGGTACACCCATTTGCAGAGGGCCCAGCCCATCCGCTGGAGCCACTGGATTCTGAGCCACGCC
GTGGCACTGACCCGAGACTCTGAGCGGCTGCTGGAGGTGCGGAAGCGGATCAATGTCCTGCCCCTGGGGAGGTGG
GGCCATTGCAGGCAATCCCCTGGGTGTGGACCGAGAGCTGCTCCGAGCAGAACTCAACTTTGGGGCCATCACTCT
CAACAGCATGGATGCCACTAGTGAGCGGGACTTTGTGGCCGAGTTCCTGTTCTGGGCTTCGCTGTGCATGACCCA
TCTCAGCAGGATGGCCGAGGACCTCATCTCTACTGCACCAAGGAATTCAGCTTCGTGCAGCTCTCAGATGCCTA
CAGCACGGGAAGCAGCCTGATGCCCCAGAAGAAAACCCGACAGTTTGGAGCTGATCCGGAGCAAGGCTGGGCG
TGTGTTTGGGCGGTGTGCCGGGCTCCTGATGACCCTCAAGGGACTTCCCAGCACCTACAACAAAGACTTACAGGA
GGACAAGGAAGCTGTGTTTGAAGTGTGAGACACTATGAGTGCCGTGCTCCAGGTGGCCACTGGCGTCATCTCTAC
GCTGCAGATTACCAAGAGAACATGGGACAGGCTCTCAGCCCCGACATGCTGGCCACTGACCTTGCCTATTACCT
GGTCCGCAAAGGGATGCCATTCCGCCAGGCCCACGAGGCCTCCGGGAAAGCTGTGTTTCATGGCCGAGACCAAGGG
GGTCGCCCTCAACCAGCTGTCACTGCAGGAGCTGCAGACCATCAGCCCCCTGTTCTCGGGCGACGTGATCTGCGT
GTGGGACTACGGGCACAGTGTGGAGCAGTATGGTGCCCTGGGCGGCACTGCGCGCTCCAGCGTCGACTGGCAGAT
CCGCCAGGTGCGGGCGCTACTGCAGGCACAGCAGGCCTAGGTCCTCCACACCTGCCCCCTAATAAAGTGGGCGC
GAG

2478/6881
FIGURE 2279

MASESGKLWGGRFVGAVDPIMEKFNASIAYDRHLWEVDVQGSKAYSRGLEKAGLLTKAEMDQILHGLDKVAEEWA
QGTFKLNSNDEDIHTANERRLKELIGATAGKLHTGRSRNDQVVTDLRLWMRQTCSTLSGLLWELIRTMVDRAEAE
RDVLFPGYTHLQRAQPIRWSHWILRAIAGNPLGVDRELLRAELNFGAITLNSMDATSERDFVAEFLFWASLCMTH
LSRMAEDLILYCTKEFSFVQLSDAYSTGSSLMPQKKNPDSLELIRSKAGRVFGRGAGLLMTLKGLPSTYNKDLQE
DKEAVFEVSDTMSAVLQVATGVISTLQIHQENMGQALSPDMLATDLAYYLVRKGMPPFRQAHEASGKAVFMAETKG
VALNQLSLQELQTISPLFSGDVICVWDYGHSEVQYGALGGTARSSVDWQIRQVRALLQAQQA

2479/6881
FIGURE 2280

CTCTTTCCCATCTTGCAAGATGGCAGGTGAAAAAGTTGAGAAGCCAGATACTAAAGAGAAGAAACCCGAAGCCAA
GAAGGCTGATGCTGGTGGCAAGGTGCAAGAGGGTAATCTTAAAGTTAAAAAGCCCAAGAAGGGGAAGCCCTATTG
CAGCCACAACCCCTGTCCTTGTCAGAGGAAGTGGCAGGTATTCCCGATCTGCCATGTATTCTAGAAAGGCCATGTA
TAAGAGGAAGTACTCAGCCGCTAAATCAAAGATTGAAAAGAAAAAGGAGAAGGTTCTTGCAACTGTTACAAAACC
AGTTGGTGGTGACAAGAATGGTGGTACCCAGGTGGTTAAACTTCACAAAATGCCTAGATACTATCCTACCGAAGA
TGTACCTCGAAAGCTGTTGAGCCACAGCAAAAAACCCCTTCAGTCAGCATGTGAGAAAAGTGAAGCCAGCATTAC
CCCTGGGACCATTTCTGATCATCCTCACTGGATGCCACAGGGGGCAAGAGGGTGGTTTTCTGAAGCAGCTGGCTAG
TGGCTTGTTACTTGTGACTGGACCTCTGGTCCTCAATTGAGTTCTCTACGAGGAACACACCAGAAATTTGTCAT
TGCCACCTCAACCAAAATCGATATCAGCAATGTAAAAATCCCAAAACATCTTACTGATGCTTACTTCAAGAAGCA
GCAGCTGCGGAAGCCCAGACACCAGGAAGGCAACATCTTCGACACAGAAAAAGAGAAATATGAGATTACAGAGCA
GCGCAAGATTGATCAGAAAGCTGTGGACTCACAAATTTTACCAAAAGTCAAAGCTATTTCTCAGCTCCAGGGCTA
CCTGCGATCTGTGTTTGCCCTGACGAATGGAATTTATCCTCACAAATTGGTGTCTAAATGTCTTAAGAACCTAA
TTAAATAGCTAAGTAC

2480/6881
FIGURE 2281A

CGCTTCCTGCGCCTCTTCAGGTCACCGCTTGCTCTAGTTCCCAGGCTTTGGCCTCTAGTGGATGAGAATCACCGA
GTCTGCGGGGCTGGACGCTGACCGCCCGGGCCAGCACCTAGGCGGGCGGGAGCTGTGCGGGCCAGGGTTCGCGCG
GGCCGGGTAGAGGCTCGAGCCGGGACCCCCGAGCGTGAACCCCGGAGCCAGCGGCGCTGGGGCCAGAGGGGGCCAG
GCGGGAGGTGGTGGCGGAGGCGAAGGGGCGACGGGACCTGGGCCCTGGCCCGTGTGTGTCTCGGCGGCTGGCGC
CGGCCGTGCTGTACGGTGAGCCCCAGGGAGGCGGATCTGGGCCCCGAGAAGGACACCCGCCTGGATTTGCCCCG
TAGGCCCCGGCCGGGCCCCCTCGGGAGCAGAACAGCCTTGGTGAGGTGGACGGGAGGGGACTTCGCGAGCAGACGC
GCGCGCCAGCGACAGCAGCCCGCCCCGGCCTCTCGGGAGCCGTGGGGCAGAGGCTGCAGAGCCCCAGGAGGGGGC
CAGTGTCAATTCAAAGATGTGGCTGTGGATTTACCCAGGAGGAGTGGTGGCAACTGGACCCTGATGAGAAAGATAA
CATACGGGGATGTGATGTTGGAGAACTACAGCCATCTAGTTTCCCTGGCTTATGAGGTGGCAACATCTTGTACTT
CGGAGATCTGAAGCCGAGCAACTTGCCCAAGTCCTTCTTCTTTCCCATTAACAAGATATGATATCACCAAGCCA
AACGTCATCATTAAGTTGGAGCAGGGAGAGGAGCTGTGGATAACGGGAGGTGAATTTCCATGTCAACATAGTCCA
GCCCTTCACATCCTCAGCCGAAGATCTCACTTCCTCCCAGAGGCCCTTGCTGACTGACCCCTCAGGGATTGTGGG
ACTTTACCAAAATCGGTTTGTAAATAACACCTAGAAGACGCTATCCGATCCATCAGGCCCAGTATTCCTGTCTGGGG
GTACTTCCCACCGTGTGCTGGAATGGTTATCACAAGAAGGCTGTGCTGTCCCCTCGCAACTCCAGGATGGTGTGT
AGCCCAGTGACTGTGAGGATCGCCCTCCTGACAGAAGATTTTCGCGTTCTGCGATACCAGAGCAGATAATCAGC
TCAACACTGTCTCACCATCAAGTAACGCCCCAGACCCATGTGCAAAGGAGACAGTACTGAGTGCCCTCAAAGAG
AAGGAGAAGAAAAGGACAGTGGAGGAAGAAGACCAAATATTCCTTGATGGCCAGGAAAATAAAGAAGGCGCCAT
GATAGCAGTGGCAGTGGACATTTCAGCATTTGAGCCCCCTGGTGGCCAATGGAGTCCCGCTTCTTTTGTGCCTAAG
CCTGGGTCTCTGAAGAGAGGCCTCAATTCTCAGAGCTCAGATGACCACTTGAATAAGAGATCCCGAAGCTCTTCC
ATGAGCTCCTTGACAGGCGCTTACGCAAGTGGCATCCCTAGCTCCAGCCGCAATGCCATTACCAGTTCCTACAGC
TCCACTCGAGGCATCTCAGCTCTGGAAGAGAAATGGCCCCAGTTCATCACCTTCTCTAGCCCAGCCTCCTCC
CGCTCCCAGACACCGGAGAGGCCAGCAAAGAAAATAAGAGAAGAGGAGCTGTGTATCATTTCCAGTTCCTCAACT
CCATTGGCAGCAGACAGGGAGTCCCAGGGAGAAAAGGCTGCAGATACAACCCCAAGGAAGAAACAAAACCTCGAAT
TCTCAGTCTACACCTGGCAGCTCTGGGCAGCGTAAGCGGAAAGTTCAGCTGCTGCCTTCTCGGCGAGGGGAACAG
CTGACCTTGCTCCACCTCCCCAGCTTGCTATTTCGATCACTGCCGAGGACCTAGACTTAGAGAAGAAGGCTTCA
TTACAGTGGTTCAACCAGGCCTTGAGGACAAGAGCGATGCTGCCTCGAACTCTGTCACTGAGACCCACCTATC
ACTCAGCCTTCATTTACCTTTACCCTGCCTGCTGCTGCACCTGCCTCCCCACCCACCTCCCTCCTGGCCCCAAGC
ACCAACCCACTGTTAGAGAGCTTGAAGAAGATGCAGACTCCCCCGAGCCTGCCACCCTGCCAGAATCTGCTGGA
GCAGCAACCACTGAGGCCCTCTACCTCCAAAGACACCCAGCCTCCTACCCCGCTGGGTTTATCACAGTCAGGG
CCGCCAGGGCTGCTCCCCAGCCCTCCTTTGACTCCAAACCCCCGACCCTTTGCTGGGGCTGATCCCTGCTCCA
TCCATGGTACCAGCCACTGACACCAAGGCACCTCCAACCTTCAGGCAGAGACGGCTACCAAACCCCAAGCCACA
TCTGCCCCGTCCCCCGCCCCAAGCAAAGCTTCTGTTTGGAAACACAGAACACCTCACCTTCCAGCCCTGCCGCC
CCTGCTGCATCTTCAGCACCTCCCATGTTCAAGCCCATTTTCACGGCTCCACCCAAGAGTGAGAAGGAAGGCCCC
ACACCGCCTGGCCCTTCAGTCACAGCCACAGCGCCCTCCAGCTCCTCCCTCCCCACGACCACCAGCACCACAGCC
CCGACCTTCCAGCCTGTCTTTAGCAGCATGGGGCCACCTGCATCTGTGCCCTTGCTGCTCCCTTCTTCAAGCAG
ACAACCTACTCCCGCCACTGCTCCCACCACAACCTGCCCCGCTCTTCACTGGCCTGGCCAGCGCCACCTCTGCTGTG
GCTCCCATCACCTCTGCCAGTCCATCCACAGACTCTGCTTCGAAGCCTGCGTTTGGCTTTGGCATAAACAGTGTG
AGCAGCAGCAGTGTGAGTACCACGACCAGCACCGCCACTGCCGCCTCACAGCCTTTCTCTTCGGGGCGCCCCAG
GCCTCTGCTGCCAGCTTCACCCGGCCATGGGCTCCATATTCAGTTTGGCAAACCTCCTGCCTTGCCCCACAACC
ACCACAGTCACCACTTCAGCCAGTCCCTGCACACTGCCGTGCCAACGGCCACCAGCAGCAGCGCTGCCGACTTT
AGTGGTTTTTGGCAGCACCTTCGCCACCTCCGCCCGGCCACCAGCAGCCAGCCCACTCTGACGTTCAAGTAAACG
AGCACCCCAAGCTTCAACATTCCCTTTGGCTCAAGCGCCAAGTCCCCGCTCCCATCATATCCGGGAGCCAACCCC
CAGCCCGCATTTGGGGCCGCTGAGGGGACGCCACCGGGGGCCGCCAAGCCGGCCCTTGCCCCAGCTTTGGCAGC
TCTTTCACTTTTTGAAACTCTGCAGCCCCGGCTGCTGCACCCACACCTGCACCTCCGTCCATGATCAAGGTCGTG
CCTGCGTACGTGCCTACGCCCATCCATCCTATCTTTGGCGGTGCCACGCACTCGGCGTTTGGGTTGAAAGCCACG
GCTTCGGCCTTCGGCGCTCCCGCCAGCTCACAGCCCGCCTTTGGCGGCTCCACTGCTGTCTTCTTCGGTGCAGCC
ACCAGCTCCGGCTTTGGAGCCACCACCAGACCGCCAGCAGCGGGAGCAGCAGCTCGGTGTTTGGCAGCACAAACA
CCATCACCTTCACGTTTGGGGTTTCGGCAGCCCCCGCTGGCAGTGGGAGCTTTGGGATCAATGTGGCCACCCCA

2481/6881

FIGURE 2281B

GGCTCCAGCACCACCACCGGAGCTTTCAGCTTTGGAGCAGGACAGAGTGGGAGCACAGCCACCTCCACCCCCTTC
GCAGGGGGCTTAGGTCAGAACGCCCTGGGCACCACCGGCCAGAGCACACCGTTTGCCTTCAACGTGAGCAGCACA
ACTGAGAGCAAACCTGTGTTTGGAGGCACCGCCACCCCCACCTTTGGTCTGAACACCCCTGCGCCTGGAGTGGGC
ACATCAGGCAGCAGCCTCTCCTTTGGGGCATCCTCAGCACCCGCCCAAGGCTTTGTTGGTGTGACCTTTCGGC
AACACTTTTGTCTACCAGCAAGAACACAGCCCCGAGGAAGGGACCCAATAACCTTTCAAACGCAAACCTGCTGCCT
GCGGTGAGGGCCCCAGGGTCTTCCACGGAGAGGACAGGCATCTTCCTTTCCACCCAGGAAGGAGTGAGCCCGGAGC
CTCTGCTATGTGCAAGGCGGTGTGCAAGCACCGGCTGCAGCTTTTGTCTCTCTTTCTCTTTGGGGCTGGGCT
GGGTGTGCGTTCTGGTGTGATGCTTTGGCCTGTGAGGCTGAGCTAGAGAAATGTAGATGTTAGATGTGCCAGTA
CCATCCTGCGCCTCCCAAGCATGCCCCCACTCACTCACGTCGGCATCTCGACCCGTTCAATTACAGCAACGAAGA
AGCCACCGCTAAGCGTGGTCTTGGGGGAAGCCCGGAGGCAGTGCTCGGCACCCGGGAACGTGCTCAGGCCTCGGT
GGGGCCGGGCAGGCAGGGCGGGAGCTAGCCTGCAAGAGAAAACAGCCCCAATGCTGGGTAAGAGAGCAGTTACCC
CATCCCCCCTCCACGACCCTGGCGCACGCCCTGTACCTGAAGGCGCCCGGGTTCTGCTGCAGCGCATCTTGATC
CATGTCTTCATTCTCCTCCTGGCAGAGGGAGCACATGGAGTAGACGAGCCGCTGCAGGGAAGGGAAAAGTGAGCGC
GTGGCACAGGGCTCGCTGCTGGAACCCTGCCAGGGCATGCAGACGCACCGGGCTAGGTGTCCCTGCCCCGGGCTC
CTCCAGCTGTCTGCTCGGCATACCTAAGGAAAAGCGTGTCTCGGTTACACAGCTTACAGGGCTGCCTCAGTCTTG
AAATCCTCGCTCCTGAAATCCTCGCTTACAGAGGAGAACTTTTGCTCCAGGGTCCCAAGCCCATTAAAGTGTCA
GAACTAAGACCAAAACAGATGACTCCAGGTCTAAGCTGCTGTGGACCTCTGAGTCCCTCAGCCACGCCTTCTCAC
CATCTCACCCGAGCCACTGCAGGAAGGATCCAGCAGGACATAGTGACCTCACGATAGCGCGGATCTAAGGGGA
GACCGCCAGGAAGTCTCCTCAGCCAGCTCACAGCAGGAGACGCCAGCCAGGCCAGCAGCGTGGCCATGGATGC
CAGCCGCTTGGCATCCAGGTCAAAGGCAAAGATCTTCTAGGGCAGAGGGCAGAGCAGGGGTGAGCTGAGCATGC
ATGGAGCAGCTAAGGGCTGTACAGCTGACACAGACAACCAGAACATGCAGGTTAAGCCAGGACACACAATATT
GAAACAGCCTATATTTAAAGGGCCAGGGTCAGAGGTAAGTGGCTGGGGTCTCTGCCCCAAGGGCTAAGGGATC
CACATCTCACACCTGCAGTGGGGAAGCTTAGCTTGGGGCAAATACCGTGAAGTACTTTGGTGCAGCAGGAAAGA
GTTAAGCGAAAAGTCATCCTTTACGCTTCAATACCCACTGAAAGGCACAAAATCAAACCCCATGTCTCCTCCTC
CTCCTGTGGCACTCACCTTGGTTCTTCAAGAGCAGCCAAGTGACTGGTCTTTATTGCTGGGGTGGCACAGG
CATCCATGACATGGGAGCCTGGCGGGGTCCAGCAGCATGGCTGGGAGACAGCTGGCCTGGCAGGCAGAACACAG
GGGCCGGGTAAACAGAGACCCCAGGCTAGGCCCTTCCCGTGCCTACACATTCTTCCCTTTTCTATTCTCTTGCC
TACCCTGTCTGAGAAATGAGGTGTCCGGCCCGGTACAGTGGGTGTTTATGAGATCTGTCTGGGCGGGAAACAC
CAGCAGCTCCGGCATCAAGGGGTCCAGGAGAAAATGCTTCCCTTGAGGGCTCGTAAGTCATCGAGGCTGCCAGG
GAAGAACCATTTCATTCATTTTCTGAAATTTCTCCCTGCCAGGCCCTATTTCAACGGTCCATTTCATGCAACAA
TGTTACCACAGCTATGGAGAAATCAACAGGGTGATAAGGGAATCCGGGATCCGAGTTGAGGGAATGGGTTGTCA
AGCCAGACTTATGGGTGAGGAGCCCCCTCTACTGTTTACCAGCAGTGGGAGCCTGGGCAAGTGATTCAATCTCAA
GCCCCACTGGCATCTCTGTAAAATAGTAGGTGTGAGGATTCAATGAGCCAATATATCCAAGATACTTACGTGCCA
CAATTTAATAAATGTTAGCTATTCTGTGAAGCATAACCTTGAGAAAGGTTACTTTACAGGGGGGTGAGGAGT
GGGGAAGTGAGAGCTGAGCTCATTCTTGATGGATGAGGAGTTAGTCATGTGAGGCGCTTAGGTTAAACTACATT
CACTATAACTCAGTAAAGCAGTCCCGCCACTCTCCGACCCATGCAGAAATAGGCCTAGGGAGTCACATGTCTCA
GTTTCAAGAAATCTATCGAAGTGGCAGAGCTGGAATTCAAACACAAGCAGCCGTTCTCTGCTATTCCACCCTGGTGT
CCAAGCAACATGGTAGGGCAGAAGGAAGAGGATCTTACAAAGAGTAAGGGAAAGGGAGAGGGGCAGAGGCTGCTT
CTCAGAGCCACCAAAGGACAAAATAAGACAGGTGTGAGCCAGTGGAGGAGGCACGGGGCAGAGACCAGCCACTG
TTGCTGGCACGCTGGTGCACGTAGCACTGTGGCAGATGGACCTGGAGAGGAAGCAGGAGGGACAGCACAAATGGAG
CCAAGAAAGGACTTAGCATGGCCGGGCGCGGTGGTTCATGCCTGTAATCCCAGCATTTTGGGAGGCCAAGGTGGG
CAGATCACCTGAGGTGAGGAGTTTGGAGCAGCCTGGCCAACATGGAGAAATCCCGTCTCTACTAAAAATACAAA
ATTAGCCAGGCATGGTGTGCTGCAATCCTGTAGGGAAAAGAAAGAGAGATCAGACTGTTACTGTGTCTG
TGTAAGAAAGGGAAGACATAAGAAATTCATTTTGACCTGTACCTTGAACAATTGGTTGGCTGAGATGCTGTTAAT
TTGTGACTTTGCCCCAAATTTGAGCTCACAAAAACATGTGTTGTATGGAATCAAGGTTTAAAGGATCTAGGGCTG
TGCAGGACATGCCTTGTTAATAAAACGTTTACAAGC

2482/6881

FIGURE 2282

GCCAGGGAGCACTGGAGGGCCACCCAGTCATGGGGGACACCTTCATCCGTCACATCGCCCTGCTGGGCTTTGAGAA
GCGCTTCGTACCCAGCCAGCACTATGTACATGTTCCCTGGTGAAATGGCAGGACCTGTCGGAGAAGGTGGTCTACC
GGCGCTTCACCGAGATCTACGAGTTCCATAAAACCTTAAAAGAAATGTTCCCTATTGAGGCAGGGGCGATCAATC
CAGAGAACAGGATCATCCCCACCTCCCAGCTCCCAAGTGGTTTGACGGGCAGCGGGCCGCCGAGAACCACCAGG
GCACACTTACCGAGTACTGCGGCACGCTCATGAGCCTGCCACCAAGATCTCCCGCTGTCCCCACCTCCTTGACT
TCTTCAAGGTGCGCCCTGATGACCTCAAGCTCCCCACGGACAACCAGACAAAAAAGCCAGAGACATACTTGATGC
CCAAAGATGGCAAGAGTACCGCGACAGACATCACCGGCCCCATCATCCTGCAGACGTACCGCGCCATTGCCAACT
ACGAGAAGACCTCGGGCTCCGAGATGGCTCTGTCCACGGGGGACGTGGTGGAGGTCGTGGAGAAGAGCGAGAGCG
GTTGGTGGTTCTGTGTCAGATGAAAGCAAAGCGAGGCTGGATCCCAGCATCCTTCCTCGAGCCCCCTGGACAGTCCTG
ACGAGACGGAAGACCCTGAGCCCAACTATGCAGGTGAGCCATACGTCGCCATCAAGGCCTACACTGCTGTGGAGG
GGGACGAGGTGTCCCTGCTCGAGGGTGAAAGCTGTTGAGGTAATTACAAGCTCCTGGACGGCTGGTGGGTCTATCA
GGAAAGACGACGTACAGGCTACTTCCCGTCCATGTACCTGCAAAAGTCAGGGCAAGACGTGTCCCAGGCCCAAC
GCCAGATCAAGCGGGGGGCGCCGCCCGCAGGTTCGTCCATCCGCAACGTGCACAGCATCCACCAGCGGTTCGCGGA
AGCGCCTCAGCCAGGACGCCTATCGCCGCAACAGCGTCCGTTTTCTGCAGCAGCGACGCCGCCAGGCGCGGCCGG
GACCGCAGAGCCCCGGGAGCCCGCTCGAGGAGGAGCGGCAGACGCAGCGCTCTAAACCGCAGCCGGCGGTGCCCC
CGCGGCCGAGCGCCGACCTCATCCTGAACCGCTGCAGCGAGAGCACCAAGCGGAAGCTGGCGTCTGCCGTCTGAG
GCTGGAGCGCAGTCCCCAGCTAGCGTCTCGGCCCTTGCCGCCCGTGCCTGTATATACGTGTTCTATAGAGCCTG
GCGTCTGGACGCCGAGGGCAGCCCCGACCCCTGTCCAGCGCGGCTCCCGCCACCCTCAATAAATGTTGCTTGAG
TGGACCGAGGCTCTGCAGGAATGCAGGGAGGGCCGGGCTCCGCCCCAGGGTTATTTCTAAGTTGA

2483/6881
FIGURE 2283

MYMFLVKWQDLSEKVYRRFTEIYEFHKTLEMFPIEAGAINPENRIIPHLPAKWFQDQRAAENHQGTLTEYCG
TLMSLPTKISRCPHLLDFFKVRPDDLKLPDNTQTKKPETYLMFKDGKSTATDITGPIILQTYRAIANYEKTSQSE
MALSTGQVVEVVEKSESGWWFCQMKAKRGWIPASFLEPLDSPDETEDPEPNYAGEPYVAIKAYTAVEGDEVSLLE
GEAVEVIHKLLDGWWVIRKDDVTGYFPSMYLQKSGQDVSAQRQIKRGAPRRSSIRNVHSIHQSRKRLSQDAY
RRNSVRFLQQRRRQARPGPQSPGSPLEERQTQRSKPQPAVPPRPSADLILNRCSESTKRKLASAV

2484/6881
FIGURE 2284

CCCCGCGCTGCGCGGAGCAGGGACCAGGCGGTTGCGGCGGCGACAGCCATCGCCGCGCGCTGGCAGGTCTGGCC
GCGGGCTTGCAGGTCCCGCGGGTCGCGCCAGCCCAGACTCGGACTCGGACACAGACTCGGAGGACCCGAGTCTC
CGGCGCAGCGCGGGCGGCTTGCTCCGCTCGCAGGTCAATCCACAGCGGTCACTTCATGGTGTGCTCGCCGCACAGC
GACTCGCTGCCCCGGCGGCGCGACCAGGAGGGGTCCGTGGGGCCCTCCGACTTCGGGCCGCGCAGTATCGACCCC
ACACTCACACGCCTCTTCGAGTGCTTGAGCCTGGCCTACAGTGGAAGCTGGTGTCTCCCAAGTGGAAGAATTTT
AAAGGCCTCAAGCTGCTCTGCAGAGACAAGATCCGCCTGAACAACGCCATCTGGAGGGCCTGGTATATCCAGTAT
GTGAAGCGGAGGAAGAGCCCCGTGTGTGGCTTCGTGACCCCCCTGCAGGGGCTGAGGCTGATGCGCACCGGAAG
CCGAGGGCCGTGGTCTTGAGGGGAACTACTGGAAGCGGCGCATCGAGGTGGTGTGCGGGAATACCACAAGTGG
CGCATCTACTACAAGAAGCGGCTCCGTAAGCCCAGCAGGGAAGATGACCTCCTGGCCCCCTAAGCAGGCGGAAGGC
AGGTGGCCGCCCGCCGAGCAATGGTGCAAACAGCTCTTCTCCAGTGTGGTCCCGTGTCTGCTGGGGGACCCAGAG
GAGGAGCCGGGTGGGCGGCAGCTCCTGGACCTCAATTGCTTTTTGTCCGACATCTCAGACACTCTCTTACCATG
ACTCAGTCCGGCCCTTCGCCCCCTGCAGCTGCCGCTGAGGATGCCTACGTCGGCAATGCTGACATGATCCAGCCG
GACCTGACGCCACTGCAGCCAAGCCTGGATGACTTCATGGACATCTCAGATTTCTTTACCAACTCCCGCCTCCCA
CAGCCGCCCATGCTTCAAACCTTCCAGAGCCCCCAGCTTCAGCCCCGTGGTTGACTCCCTCTTCAGCAGTGGG
ACCCTGGGGCCAGAGGTGCCCCCGGCTTCTCGGCCATGACCCACCTCTCTGGACACAGCCGTCTGCAGGCTCGG
AACAGCTGCCCTGGCCCCCTTGACTCCAGCGCTTCTGAGTTCTGATTTCTCCTTCTGAAGACCCCAAGCCC
CGGCTCCCACCCCCCTCCTGTACCCCCACCTCTGCTGCATTACCCTCCCCCTGCCAAGGTGCCAGGCCTGGAGCCC
TGCCCCCACCTCCCTTCCCTCCCATGGCACCACTGCTTTGCTGCAGGAAGAGCCTCTCTTCTCTCCCAGG
TTTCCCTTCCCCACCGTCCCTCCTGCCCCAGGAGTGTCTCCGCTGCCTGCTCCTGCAGCCTTCCACCCACCCCA
CAGTCTGTCCCCAGCCCAGCCCCACCCCTTCCCCATAGAGCTTCTACCCTTGGGGTATTTCGGAGCCTGCCTTT
GGGCCTTGCTTCTCCATGCCCAGAGGCAAGCCCCCGCCTCATCCCCCTAGGGGACAGAAAGCCAGCCCCCTACC
TTAGCCCCCTGCCACTGCCAGTCCCCCACCCTGCGGGGAGCAACAACCCCTGCCTCACACAGCTGCTCACAGCA
GCTAAGCCGGAGCAAGCCCTGGAGCCACCCTTGTATCCAGCACCTCCTCCGGTCCCCAGGGTCCCCGCAGGAG
ACAGTCCCTGAATTCCCTGCACATTCTTCCCCGACCCCGGCCCTTACACCGCCCCGGCCACCTCCAGGCCCCG
GCCACATTGGCCCCCTTCCAGGCCCCCTGCTTGTCCCCAAAGCGGAGCGGCTCTCACCCCCAGCGCCAGCGGCAGT
GAACGGCGGCTGTACAGGGACCTCAGCTCCATGCCAGGCCCTGGGACTCTGAGCGTCCGTGTCTCTCCCCGCAA
CCCATCCTCAGCCGGGGCCGTCCAGACAGCAACAAGACCGAGAACCGGCGTATCACACACATCTCCGCGGAGCAG
AAGCGGCGCTTCAACATCAAGCTGGGGTTTGACACCTTCATGGGCTCGTGAGCACACTCAGTGCCAGCCCAGC
CTCAAGGTGAGCAAAGCTACCACGCTGCAGAAGACAGCTGAGTACATCCTTATGCTACAGCAGGAGCGTGCGGGC
TTGCAGGAGGAGGCCCAGCAGCTGCGGGATGAGATTGAGGAGCTCAATGCCGCCATTAACTGTGCCAGCAGCAG
CTGCCCGCCACAGGGGTACCCATCACACACCAGCGTTTTTGACCAGATGCGAGACATGTTTGATGACTACGTCCGA
ACCCGTACGCTGCACAACCTGGAAGTTCTGGGTGTTACGATCCTCATCCGGCCTCTGTTTGAGTCTTCAACGGG
ATGGTGTCCACGGCAAGTGTGCACACCTCCGCCAGACCTCACTGGCCTGGCTGGACCAGTACTGCTCTCTGCCC
GCTCTCCGGCCAACCTGTCTGAACCTCCCTACGCCAGCTGGGCACATCTACCAGTATCCTGACCGACCCGGGCCG
ATCCCTGAGCAAGCCACACGGGCAGTCACAGAGGGCACCTTGGCAAACCTTTATAGTCCTGGCCAGACCCTGCT
GCTCACTCAGCTGCCCTGGGGGCTGCTTTCCCTGGGCACGGGCTCCAGGGATCATCTCTGGGCACTCCCTTCTG
CCCCAGGCCCTGGCTCTGCCCTTCCCTGGGGGGTGGAGCAGGGTCCAGGTTTCACTTGCCACCTCCTGGAGGT
CAAGAAGAGCAGAGTCCCCGTCCCTGCTCTGCCACTGTGCTCCAGCACCGTGACCTTGGGTGACTCGTCCGCTGT
CTTTGGACCGCTGTGTTTCAATCTGCAAAAATGGGGATGGGGAAGGTTCAATCAGCAGATGACCCCCAGGCCTTGG
CAGCTGTGACATTGGGGGCTAGGCTGGCAACTCCGGGGGCTCAACGGTGGAAAGAGGAGGATGCTGTTTATCTG
TCACCTCCACTTGCTCCCCGACAGGTGGGGCACAGACCTCTGTTTCTGAGCAGAGAAGCAGAAAAGGAGGTTCCC
TCTCTCTGCTCCTTCACTGCTGACCCAGAGGGGCTGCAGGATGGTTTTCCCTGGGAGAGGCCAGGAGGGCCTGAT
CCCAGGAGACACCAGGGCCAGAGTGACCACAGCAGGGCAGGCATCATGTGTGTGTGTGTGTGTGGATGTGTGTGT
GTGGGTTTTGTAAAGAATTCTTGACCAATAAAAGCAAAACTGTCTGCTGGTTAAAAA

2485/6881
FIGURE 2285

MAGALAGLAAGLQVPRVAPSPDSDSDTDSEDP SLRRSAGGLLRSQVIHSGHFMVSSPHSDSLPRRRDQEGSVGPS
DFGPRSIDPTLTRLFECLSLAYSGKLVSPKWKNFKGLKLLCRDKIRLNNAIWRAWYIQYVKRRKSPVCGFVTPLQ
GPEADAHRKPEAVVLEGNWYKRRIEVVMREYHKWRIYYKKRLRKPSREDDLLAPKQAEGRWPPPEQWCKQLFSSV
VPVLLGDPEEEPGGRQLLDLNCFLSDISDTLFTMTQSGPSPLQLPPEDAYVGNADMIQPDLTPLQPSLDDFMDIS
DFFTNSRLPQPPMPSNFPPEPPSFSPVVD SLFSSGTLGPEVPPASSAMTHLSGHSRLQARNSCPGPLDSSAFLSSD
FLLPEDPKPRLPPPPVPPPLLHYPPPAKVPGLEPCPPPPFPPMAPPTALLQEEPLFSRFPFPFTVPPAPGV SPLP
APAAFPPTPQSVFSPAPTPFPIELLPLGYSEPAFGPCFSMPRGKPPAPSPRGQKASPPTLAPATASPPTTAGSNN
PCLTQLLTAAKPEQALEPPLVSSTLLRSPGSPQETVPEFFCTFLPPTPAPTTPRPPPGPATLAPSRPLLVPKAER
LSPPAPSGSERRLSGDLSSMPGPGTLSVRVSPPQPILSRGRPDSNKTENRRITHISAEQKRRFNIKLGFDTLHGL
VSTLSAQPSLKVSKATT LQKTA EYILMLQQERAGLQEEAQQLRDEIEELNAAINLCQQQLPATGVPI THQRFDQM
RDMFDDYVRTRTLHNWKFVFSILIRPLFESFNGMVSTASVHTLRQTS LAWLDQYCSLPALRPTVLNSLRQLGTS
TSILTDPGRIPEQATRAVTEGTLGKPL

2486/6881
FIGURE 2286

CCCCGCGCTGCGCGGAGCAGGGACCAGGCGGTTGCGGCGGCGACAGCC**ATG**GCCGGCGCGCTGGCAGGTCTGGCC
GCGGGCTTGCAAGTCCCGCGGGTCGCGCCAGCCCAGACTCGGACTCGGACACAGACTCGGAGGACCCGAGTCTC
CGGCGCAGCGCGGGCGGCTTGCTCCGCTCGCAGGTCAACACAGCGGTCACTTCATGGTGTCTCGCCGCACAGC
GACTCGCTGCCCCGGCGGCGCGACCAGGAGGGGTCCGTGGGGCCCTCCGACTTCGGGCGCGCAGTATCGACCCC
ACACTCACACGCCTCTTCGAGTGCTTGAGCCTGGCCTACAGTGGAAGCTGGTGTCTCCCAAGTGAAGAATTC
AAAGGCCTCAAGCTGCTCTGCAGAGACAAGATCCGCTGAACAACGCCATCTGGAGGGCCTGGTATATCCAGTAT
GTGAAGCGGAGGAAGAGCCCCGTGTGTGGCTTCGTGACCCCCCTGCAGGGGCTGAGGCTGATGCGCACCCGAAG
CCGGAGGCCGTGGTCTTGAGGGGAACTACTGGAAGCGGCGCATCGAGGTGGTGTGATGCGGGAATACCACAAGTGG
CGCATCTACTACAAGAAGCGGCTCCGTAAGCCCAGCAGGGAAGATGACCTCCTGGCCCCCTAAGCAGGCGGAAGGC
AGGTGGCCGCCCGCGGAGCAATGGTGCAAACAGCTCTTCTCCAGTGTGGTCCCCGTGCTGCTGGGGGACCCAGAG
GAGGAGCCGGGTGGGCGGCAGCTCCTGGACCTCAATTGCTTTTTGTCCGACATCTCAGACACTCTCTTCACCATG
ACTCAGTCCGGCCCTTCGCCCCCTGCAGCTGCCGCTGAGGATGCCTACGTGCGCAATGCTGACATGATCCAGCCG
GACCTGACGCCACTGCAGCCAAGCCTGGATGACTTCATGGACATCTCAGATTTCTTTACCAACTCCGCGCTCCCA
CAGCCGCCCATGCTTCAAACCTTCCCAGAGCCCCCAGCTTCAGCCCCGTGGTTGACTCCCTCTTCAGCAGTGGG
ACCCTGGGCCCAGAGGTGCCCCCGGCTTCCTCGGCCATGACCCACCTCTCTGGACACAGCCGTCTGCAGGCTCGG
AACAGCTGCCCTGGCCCCCTTGACTCCAGCGCCTTCCTGAGTTCTGATTTCTCCTCCTTGAAGACCCCAAGCCC
CGGCTCCCACCCCTCCTGTACCCCCACCTCTGCTGCATTACCCTCCCCCTGCCAAGGTGCCAGGCCTGGAGCCC
TGCCCCCACCTCCCTTCCCTCCCATGGCACCACCCACTGCTTTGCTGCAGGAAGAGCCTCTCTTCTCTCCCAGG
TTTCCCTTCCCCACCGTCCCTCCTGCCCCAGGAGTGTCTCCGCTGCCTGCTCCTGCAGCCTTCCACCCACCCCA
CAGTCTGTCCCCAGCCCAGCCCCACCCCTTCCCCATAGAGCTTCTACCCTTGGGGTATTTCGGAGCCTGCCTTT
GGGCTTGCTTCTCCATGCCCAGAGGCAAGCCCCCGCCCCATCCCTAGGGGACAGAAAGCCAGCCCCCCTACC
TTAGCCCCTGCCACTGCCAGTCCCCCACCCTGCGGGGAGCAACAACCCCTGCCTCACACAGCTGCTCACAGCA
GCTAAGCCGGAGCAAGCCCTGGAGCCACCCTTGATCCAGCACCCCTCCTCCGGTCCCCAGGGTCCCCGCAGGAG
ACAGTCCCTGAATTCCCTTGCACATTCTTCCCCCGACCCCGGCCCTACACCGCCCCGGCCACCTCCAGGCCCCG
GCCACATTGGCCCCCTTCCAGGCCCTGCTTGTCCCCAAAGCGGAGCGGCTCTCACCCCCAGCGCCAGCGGCAGT
GAACGGCGGCTGTGAGGGGACCTCAGTCCATGCCAGGCCCTGGGACTCTGAGCGTCCGTGTCTCTCCCCGCAA
CCCATCCTCAGCCGGGGCGCTCCAGACAGCAACAAGAACCGGCGTATCACACACATCTCCGCGGAGCAGAAGCGG
CGCTTCAACATCAAGCTGGGGTTTGACACCCCTTCATGGGCTCGTGAGCACACTCAGTGCCCGCCAGCCAGCTCAAG
GTGAGCAAAGCTACCACGCTGCAGAAGACAGCTGAGTACATCCTTATGCTACAGCAGGAGCGTGCGGGCTTGCAG
GAGGAGGCCAGCAGCTGCGGGATGAGATTGAGGAGCTCAATGCCGCCATTAACTGTGCCAGCAGCAGCTGCCC
GCCACAGGGGTACCCATCACACACCAGCGTTTTTGACCAGATGCGAGACATGTTTGATGACTACGTCCGAACCCGT
ACGCTGCACAACCTGGAAGTTCTGGGTGTTTACGATCCTCATCCGGCCTCTGTTTGAGTCTTCAACGGGATGGTG
TCCACGGCAAGTGTGCACACCCTCCGCCAGACCTCACTGGCCTGGCTGGACCAGTACTGCTCTCTGCCCCGCTCTC
CGGCCAACTGTCTGAACTCCCTACGCCAGCTGGGCACATCTACCAGTATCCTGACCGACCCGGGCGCATCCCT
GAGCAAGCCACACGGGCAGTCACAGAGGGCACCCCTTGCCAAACCTTTA**TAG**TCTGGCCAGACCCTGCTGCTCAC
TCAGCTGCCCTGGGGGCTGCTTTCCCTGGGCACGGGCTCCAGGGATCATCTCTGGGCACTCCCTTCTGCCCCAG
GCCCTGGCTCTGCCCTTCCCTGGGGGTGGAGCAGGGTCCAGGTTTCACACTTGCCACCTCCTGGAGGTCAAGAA
GAGCAGAGTCCCCGTCCCTGCTCTGCCACTGTGCTCCAGCACCGTGACCTTGGGTGACTCGTCCGCTGTCTTTGG
ACCGCTGTGTTTCAATCTGCAAAATGGGGATGGGGAAGGTTCAATCAGCAGATGACCCCCAGGCCTTGGCAGCTG
TGACATTGGGGGCTAGGCTGGCAACTCCGGGGGCTCAACGGTGGAAGAGGAGGATGCTGTTTATCTGTACCT
CCACTTGCTCCCCGACAGGTGGGGCACAGACCTCTGTTCTGAGCAGAGAAGCAGAAAAGGAGGTTCCCTCTCTC
TGCTCCTTCACTGCTGACCCAGAGGGGCTGCAGGATGGTTTCCCTGGGAGAGGCCAGGAGGGCCTGATCCCAGG
AGACACCAGGGCCAGAGTGACCACAGCAGGGCAGGCATCATGTGTGTGTGTGTGTGTGGATGTGTGTGTGTGGT
TTTGTAAGAATTCTTGACCAATAAAAGCAAAACTGTCTGCTGGTTAAAAAAAAAAAAA

2487/6881
FIGURE 2287

MAGALAGLAAGLQVPRVAPSPDSDSDTSEDPSLRRSAGGLLRSQVIHSGHFMVSSPHSDSLPRRRDQEGSVGPS
DFGPRSIDPTLTRLECLSLAYSGKLVSPKWKNFKGLKLLCRDKIRLNNAIWRAWYIQYVKRRKSPVCGFVTPLQ
GPEADAHRKPEAVVLEGNYWKRIEVMREYHKWRIYYKKRLRKPSREDDLLAPKQAEGRWPPPEQWCKQLFSSV
VPVLLGDPEEEPGGRQLLDLNCFLSDISDTLFTMTQSGPSPLQLPPEDAYVGNADMIQPDLTPLQPSLDDFMDIS
DFFTNSRLPQPPMPSNFPPEPPSFSPVVDSLFSSTGLGPEVPPASSAMTHLSGHSRLQARNSCPGPLDSSAFLSSD
FLLPEDPKPRLPEPPVPPPLHYPPPAKVPGLEPCPPPFPPMAPPTALLQEEPLFSRFPFPTVPPAPGVSPLP
APAAFPPTPQSVSPAPTFFPIELLPLGYSEPAFGPCFSMPRGKPPAPSPRGQKASPPTLAPATASPPTTAGSNN
PCLTQLLTAAKPEQALEPPLVSSTLLRSPGSPQETVPEFFCTFLPPTPAPTTPRPPPGPATLAPSRPLLVPKAER
LSPPAPSGSERRLSGDLSSMPGPGTLSVRVSPPQPILSRGRPDSNKNRRITHISAEQKRRFNKLGFDTLHGLVS
TLAQPSLVSKATTLOKTAEYILMLQGERAGLQEEAQQLRDEIEELNAAINLCQQQLPATGVPIHQRFDQMRD
MFDDYVRTRLHNWKFWVFSILIRPLFESFNGMVSTASVHTLRQTSALWLDQYCSLPALRPTVLNSLRQLGTSTS
ILTDPGRIPEQATRAVTEGTLGKPL

2488/6881
FIGURE 2288

GACGGCAAATGCGGGA CTTCGACACCTACGACGATCGGGCCTACAGCAGCTTCGGCGGCGGCAGAGGGTCCCGCG
GCAGTGCTGGTGGCCATGGTTCCCGTAGCCAGAAGGAGTTGCCACAGAGCCCCCTACACAGCATACGTAGGAA
ATCTACCTTTCAATACGGTTCAGGGCGACATAGATGCTATCTTTAAGGATCTCAGCATAAGGAGTGACGGCTAG
TCAGAGACAAAGACACAGATAAATTTAAAGGATTCTGCTATGTAGAATTCGATGAAGTGGATTCCCTTAAGGAAG
CCTTGACATACGATGGTGCACCTGTTGGGCGATCGGTCACTTCGTGTGGACATTGCAGAAGGCAGAAAACAAGATA
AAGGTGGCTTTGGATTTCAGAAAAGGTGGACCAGATGACAGAGGAATGGGTAGCTCTCGAGAATCTAGAGGTGGAT
GGGATTCCCGGGATGACTTCAATTCTGGCTTCAGGGATGACTTCTTAGGGGGCAGGGGAGGTAGTCGCCCAGGCG
ACCGGCGAACAGGCCCCCCCATGGGCAGCCGCTTCAGAGATGGCCCTCCCTCCGTGGATCCAACATGGATTTC
GAGAACCCACAGAAGAGGAAAGAGCACAGAGACCACGACTCCAGCTTAAACCTCGAACAGTCGCGACGCCCTCA
ATCAAGTAGCCAATCCCACTCTGCTATCTTCGGGGGTGCCAGGCCTAGAGAGGAAGTCGTTCAAAGGAGCAAG
AATGAGCCTGCGGTTGGGAGGGAATGGGGCGTGGGGGGTTAGAGCAGGACCACAGCCTGGTGAGTCCCGGGCAG
CCGTCTGCAGCCGCCACTCCTGCGCCTGCCATTGGCCTCCTCACAGCGGAAACACAGCTTGTGAGTGCATGTCA
GCTGTTAACAAGTGGTTTTTTAGTACATTCTGGGCTTTGCTGTATCTATCTAGTGCCTGTTTGTGCGTTTTTTCT
TTCTTCCGCTGCTTCCCCATTTTCTTCTGTCTTTTTCTCCTGCTCCTTGTTTTCCAGCAGCACATGGGGTTC
CTCGGAGGAGCAGAGGTGGCCGCCGTGGGGGGCGTTTTGGGCTGCGGTGCTGCGTCATTTTTCTTTGCTTTCTC
TTTACTTTAGACACTGGCCCACTCCAGGCGTTTCTTTTCACTCCCTCAGTGCCTTCTCTCTGACCTGCATGTTG
AGTTCTGTATTGCTGGGGCTTCCAACAAAACCAGAGTCACTGACAGAGGGAACAGCAGAGACCTTGTGTTGATT
CAGCTGTGATGGATATAGAGAATCAGAGGCACCTTGTTTTCACTAGGATAAAAATATCTGCAGGGTCTTTTC
CATTCTATTTAGAGGGAGTCTGGCTCCATGACCCCTCCCGAGTGGACTGTCCAAGCAGATAGGCTCACACGA
GAAACAGTGAGGCTGAAAGGGGGGGCTATGGAAGAGCGGTAGGGAGTCCACGGAGAAGATGCAGTGAATGCTTGC
ATGCATTACACGCTGTGTGTGTCCAGCTAGTTCACTCCTTTGCGCGTGCGTGGTGGAGGCTGGCCTCTCTGGCT
GGGTGCAGTGAATGGCCAGCGGGTTTTCTTTCTGCTGGGCCAAGGCGCTTTGGGGGTGGAGGGGGTGGTGCTGGT
GCTGCACTGGGCTGACTGCGGCGCTGACGCAGCGTTTTCCCCCATCCCTGTTGCCTGTGTGTTGTGTGGATCTGT
TCCTAGTATAGGCAACATAATGAGATACTGTGCTTCCACCTCCCCTTCAGTTCAGAGCCAAAATGGGTCTAGAA
TCTGGCACTTTACTCATTTTCTTTTGATAAATTGTACTATGCAGAGCTGTCAGGAACCTTCAGATAGCAGTAGAGG
ACTGCAGCTGTCTAGGTCTGCGGCCACATCTTGGGGACACACTGGACTGTTCCCATGTGCAGGGTTCAGCAGTTA
TGTGGGAGTGCTAGGGGTTAGGCTTTTGAGCTTGAACGCCTGCGTGTGAACAGATGAAAAATCCTTCAGTACCCA
AGTCCCAGTCTGTCTATGGGGAGCAGTTTGGGGGCGGCCGGCAGCAGGAGCCTGGGAAAGAGGCCCTCGCCAGG
TGATGGCAGGGCCAGGGTGGCCTGGGGCACCCAGCGGAATGTGCTTAGTATTTGGTCACCAGCGTCATCCTGGG
CTTTTCTTACTGTGTCTTGTACAAGGCCTCAGCAATCCACAGAATCTCTCTCCTTCCCTTCCACCTGTGAGCTT
CTCTGCTTCTGAGATAAGAACCATTTGTGTAAACCAACACTTAACTTCAGAAAAGACATGCATTATGTGGTGTA
TCAAACCCGATGCTTTTCAGATGACCTACTTACATCTTCAATGTGGATAAGATAAAGAACAAAACACATGCATCTA
AACTGCTGGGCAATCCAGTTGACTTTTAAATGTAAGAATGGAATTCCAAACACTTAACACATTGAGCTATATGAC
AGAAAGTAAATCTATGGATATGCTATTTTGTGAATGATCTTTTAAATAAAAGAAAACCTTACGTAATATTT

2489/6881
FIGURE 2289

MADFDTYDDRAYSSFGGGRGSRGSAGGHGSRSQKELPTEPPYTAYVGNLPFNTVQGDIDAIFKDLSIRSVRLVRD
KDTDKFKGFCYVEFDEVDSLKEALTYDGALLGDRSLRVDIAEGRKQDKGGFGFRKGGPDDRGMGSSRESRGGWDS
RDDFNSGFRDDFLGGRGGSRPGRRTGPPMGSRFRDGPPLRGSNMDFREPTEEERAQRPRQLKPRTVATPLNQV
ANPNSAIFGGARPREEVVQKEQE

2490/6881
FIGURE 2290

GACGGCAAATGGCGGACTTCGACACCTACGACGATCGGGCCTACAGCAGCTTCGGCGGCGGCAGAGGGTCCCGCG
GCAGTGCTGGTGGCCATGGTTCCCGTAGCCAGAAGGAGTTGCCACAGAGCCCCCTACACAGCATAACGTAGGAA
ATCTACCTTTCAATACGGTTCAGGGCGACATAGATGCTATCTTTAAGGATCTCAGCATAAGGAGTGTACGGCTAG
TCAGAGACAAAGACACAGATAAATTTAAAGGATTCTGCTATGTAGAATTCGATGAAGTGGATTCCCTTAAGGAAG
CCTTGACATACGATGGTGCACCTGTTGGGCGATCGGTCACTTCGTGTGGACATTGCAGAAGGCAGAAAACAAGATA
AAGGTGGCTTTGGATTTCAGAAAAGGTGGACCAGATGACAGAGGCTTCAGGGATGACTTCTTAGGGGGCAGGGGAG
GTAGTCGCCCAGGCGACCGGCGAACAGGCCCCCCCCATGGGCAGCCGCTTCAGAGATGGCCCTCCCTCCGTGGAT
CCAACATGGATTTTCAGAGAACCCACAGAAGAGGAAAGAGCACAGAGACCACGACTCCAGCTTAAACCTCGAACAG
TCGCGACGCCCCCTCAATCAAGTAGCCAATCCCAACTCTGCTATCTTCGGGGGTGCCAGGCCTAGAGAGGAAGTCG
TTCAAAGGAGCAAGAATGAGCCTGCGGTTGGGAGGGAATGGGGCGTGGGGGGTTAGAGCAGGACCACAGCCTGG
TGAGTCCCCGGGCAGCCGTCTGCAGCCGCCACTCCTGCGCCTGCCATTGGCCTCCTCACAGCGGAAACACAGCT
TGTGAGTGCATGTCAGCTGTTAACAAGTGGTTTTTGTAGTACATTCTGGGCTTTGCTGTATCTATCTAGTGCCTGTT
TGTGCGTTTTTTTCTTTCTTCCGCTGCTTCCCCATTTTCTTCTGTCTTTTTCTCCTGCTCCTTGTTTTCCAG
CAGCACATGGGGTTCTCTCGGAGGAGCAGAGGTGGCCGCCGTGGGGGGCGTTTTGGGCTGCGGTGCTGCGTCATTT
TTCCTTTGCTTTCTCTTTACTTTAGACACTGGCCCAACTCCAGGCGTTTTCTTTTATTCCCTCAGTGCTTCTCTT
CTGACCTGCATGTTGAGTTCTGTATTGCTGGGGCTTCCAACAAAACCAGAGTCACTGACAGAGGGAACAGCAGA
GACCTTGTTGGTATTTCAGCTGTGATGGATATAGAGAATCAGAGGCACCTTGTTTTCACTAGGATAAAAATAT
CTGCAGGGTCCCTTCCATTCTATTTAGAGGGAGTCTTGCTCCATGACCCCTCCCGAGTGGACTGTCCAAGCA
GATAGGCTCACACGAGAAACAGTGAGGCTGAAAGGGGGGGCTATGGAAGAGCGGTAGGGAGTCCACGGAGAAGAT
GCAGTGAATGCTTGCAATGCATTACACGTGTGTGTGTCCCAGCTAGTTCACTCCTTTCCCGTGCGTGGTGGAGG
CTGGCCTCTCTGGCTGGGTGCAGTGAATGGCCAGCGGGTTTCTTTCTGCTGGGCCAAGGCGCTTTGGGGGTGGA
GGGGGTGGTGTGCTGCTGCACTGGGCTGACTGCGGCGCTGACGCAGCGTTTCCCCCATCCCTGTTGCCTGTGT
GTTGTGTGGATCTGTTCTAGTATAGGCAACATAATGAGATACTGTGCTTCCACCTCCCTTCAGTTCAGAGCC
AAAATGGGTCTAGAATCTGGCACTTTACTCATTTCCTTTGATAAATTGTACTATGCAGAGCTGTCAGGAACCTTC
AGATAGCAGTAGAGGACTGCAGCTGTCTAGGTCTGCGGCCACATCTTGGGGACACACTGGACTGTTCCCATGTGC
AGGGTTTCAGCAGTTATGTGGGAGTGCTAGGGGTTAGGCTTTTGAGCTTGAACGCCTGCGTGTGAACAGATGAAAA
ATCCTTCAGTACCCAAGTCCAGTCTGTCTATGGGGAGCAGTTTGGGGCGGCGGCAGCAGGAGCCTGGGAAA
GAGGCCCTCGCCAGGTGATGGCAGGGCCAGGGTGGCCTGGGGCACCCAGCGGAATGTGCTTAGTATTTGGTCACC
AGCCGTCATCCTGGGCTTTTCTACTGTGTCTTGTACAAAGGCCTCAGCAATCCACAGAACTCTCTCTCCTTCTT
TCCACCTGTCAGCTTCTCTGCTTCTGAGATAAGAACCATTGTGTAAACCAACACTTAACTTCAGAAAGACATG
CATTATGTGGTGTAAATCAAACCCGATGCTTTCAGATGACCTACTTACATCTTCAATGTGGATAAGATAAAGAACA
AAACACATGCATCTAACTGCTGGGCAATCCAGTTGACTTTTAAATGTAAGAATGGAATTCCAAACACTTAACAC
ATTCAGCTATATGACAGAAAGTAAATCTATGGATATGGTATTTTGTGAATGATCTTTTAAATAAAAGAAAACCTT
ACGTAATATTT

2491/6881
FIGURE 2291

MADFDTYDDRAYSSFGGGRGSRGSAGGHGSRSQKELPTEPPYTAYVGNLPFNTVQGDIDAIKDL SIRSVRLVRD
KDTDKFKGFCYVEFDEVDSLKEALTYDGALLGDRSLRVDIAEGRKQDKGGFGFRKGGPDDRGFRDDFLGGRGGS
PGDRRTGPPMGSRFRDGPPLRGSNMDFREPTEEERAQRPLQLKPRTVATPLNQVANPNSAIFGGARPREEVVK
EQE

2492/6881
FIGURE 2292

GGGAAGAGGAGGCGCGAGAATGGAGGTGGAGGCCGTCTGTGGTGGCGCGGGCGAGGTGGAGGCCAGGACTCTGA
CCCTGCCCCCTGCCTTCAGCAAGGCCCGGCGAGCGCCGGCCACTACGAACTGCCGTGGGTGAAAAATATAGGCC
AGTAAAGCTGAATGAAATTGTCGGGAATGAAGACACCGTGAGCAGGCTAGAGGTCTTTGCAAGGGAAGGAAATGT
GCCCCAACATCATCATTGCGGGCCCTCCAGGAACCGGCAAGACCACAAGCATTCTGTGCTTGGCCCCGGGCCCTGCT
GGGCCCAGCACTCAAAGATGCCATGTTGGAAGTCAATGCTTCAAATGACAGGGGCATTGACGTTGTGAGGAATAA
AATTAAAATGTTTGCTCAACAAAAAGTCACTCTTCCCAAAGGCCGACATAAGATCATCATTCTGGATGAAGCAGA
CAGCATGACCGACGGAGCCCAGCAAGCCTTGAGGAGAACCATGGAAATCTACTCTAAAACCACTCGCTTCGCCCT
TGCTTGTAATGCTTCGGATAAGATCATCGAGCCCATTCACTCCCGCTGTGCAGTCCTCCGGTACACAAAGCTGAC
CGACGCCCAGATCCTCACCAGGCTGATGAATGTTATCGAGAAGGAGAGGGTACCCTACACTGATGACGGCCTAGA
AGCCATCATCTTCACGGCCCAGGGAGACATGAGGCAGGCGCTGAACAACCTGCAGTCCACCTTCTCAGGATTTGG
CTTCATTAACAGTGAGAACGTGTTCAAGGTCTGTGACGAGCCCCACCCACTGCTGGTAAAGGAGATGATCCAGCA
CTGTGTGAATGCCAACATTGACGAAGCCTACAAGATTCTTGCTCACTTGTGGCATCTGGGCTACTCACCAGAAGA
TATCATTGGCAACATCTTTCGAGTGTGTAAACTTTCCAAATGGCAGAATACCTGAAACTGGAGTTTATCAAGGA
AATTGGATACACTCACATGAAAATAGCGGAAGGAGTGAAGTCTCTTTTGCAGATGGCAGGCCTCCTGGCAAGGCT
GTGTGAGAAGACAATGGCCCCGGTGGCCAGTTAGAGCAGAGACTTCACTGACTGACTTACAGGTGCCCTATTCTG
AGGTACAGGAGCCGCGGCTTTCTGATGGGGGAAAATGCCGCTTAGGCTGGAGCCAACATGACTGTCTTTAAAC
TCCAGTGGCTGGCCAGGCACGGTAGCTCAGCCTGTAATCCCAACACTTTGGGAGGCCGAGGCAGGTGGATCACC
TGAGGTGAGAAGTTCAAGACCAGCCTGGCCAACATGGGGAAACCCTGTCTTTACTAAAAATATAAAAATTAGCTG
GGTGTGGTGGCGGGCACCTGTAATCCAGCTACTCGGGAGGCTGTGGCAGGAGAATCGCTTGAACCCAGGAGGTG
GAGGTTGCAGTGAGCCAAGATCACACCATTGCACTCCAGCCTGGGCGACAGAGTCTCCATCTGGGGAAAAAAATT
AAATAAATAAACTCCCG

2493/6881
FIGURE 2293

TAAATGGCAGCCAATGGAGGGTGGTGTGCGCGGGGCTGGGATTAGGGCCGGGGCGAATGGCTGGCAATCTTACT
GGGATTACAGAACAAAGAGCCTCCCCGCGCTCCCGCTCTCCGCTCCTCTCCCCGCGCCGCCCCGCCCTCCGCCGC
AGCCCCGCGCCGGGGGTGGGGGCGCCGAGCGCCAGCCCCCGGCCGGCCGATTCCCCCCCCGCGCCCCCTCCCCG
CGCCTCCCTCCCCGCCCTCGCCGCGCCGCCGTCTCGCTCCCTCTGCCTCTCCTTCCCCCATCTCCCGGATTA
ATTAAGGAGGCAGCGGCAGGAGGCTGAGTCCTGGCCGCGGGCCGGGGCCGGGGCGCCGCTGGCAGGAGCGCTTGG
GGATCCTCCAAGGCGACC**ATGG**CCTTGCTGGGTAAAGCGCTGTGACGTCCCCACCAACGGCTGCGGACCCGACCGC
TGGAATCCGCGTTACCCGCAAAGACGAGATCATCACCAGCCTCGTGTCTGCCTTAGACTCCATGTGCTCAGCG
CTGTCCAAACTGAACGCCGAGGTGGCCTGTGTGCGCCGTGCACGATGAGAGCGCCTTTGTGGTGGGCACAGAGAAG
GGGAGAATGTTCTGAATGCCCGGAAGGAGCTACAGTCAGACTTCCTCAGGTTCTGCCGAGGGCCCCCGTGGAAG
GATCCGGAGGCAGAGCACCCCAAGAAGGTGCAGCGGGGCGAGGGTGGAGGCCGTAGCCTCCCTCGGTCTCCCTG
GAACATGGCTCAGATGTGTACCTTCTGCGGAAGATGGTAGAGGAGGTGTTTGATGTTCTTTATAGCGAGGCCCTG
GGAAGGGCCAGTGTGGTGCCACTGCCCTATGAGAGGCTGCTCAGGGAGCCAGGGCTGCTGGCCGTGCAGGGGCTG
CCCGAAGGCCTGGCCTTCCGAAGGCCAGCCGAGTATGACCCCAAGGCCCTCATGGCCATCCTGGAACACAGCCAC
CGCATCCGCTTCAAGCTCAAGAGGCCACTTGAGGATGGCGGGCGGGACTCGAAGGCCCTGGTGGAGCTGAACGGT
GTCTCCCTGATTCCCAAGGGGTACAGGGACTGTGGCCTGCATGGCCAGGCCCCCAAGGTGCCACCCAGGACCTG
CCCCCAACCGCCACCTCCTCCTCCATGGCCAGCTTCCTGTACAGCACGGCGCTCCCCAACCCACGCCATCCGAGAG
CTCAAGCAGGAAGCACCTTCTGCCCCCTTGCCCCCAGCGACCTGGGCCTGAGTCGGCCCATGCCAGAGCCCAAG
GCCACCGGTGCCAAGACTTCTCCGACTGTTGTGGACAGAAGCCCACTGGGCCTGGTGGGCCTCTCATCCAGAAC
GTCCATGCCTCCAAGCGCATTCTCTTCTCCATCGTCCATGACAAGTCAGAGAAGTGGGACGCCTTCATAAAGGAA
ACCGAGGACATCAACACGCTCCGGGAGTGTGTGCAGATCCTGTTTAACAGCAGATATGCGGAAGCCCTGGGCCTG
GACCACATGGTCCCCGTGCCCTACCGGAAGATTGCCTGTGACCCGGAGGCTGTGGAGATCGTGGGCATCCCGGAC
AAGATCCCCCTCAAGCGCCCCCTGCACTTATGGAGTCCCCAAGCTGAAGCGGATCCTGGAGGAGCGCCATAGTATC
CACTTCATCATTAAGAGGATGTTTGATGAGCGAATTTTCACAGGGAACAAGTTTACCAAAGACACCACGAAGCTG
GAGCCAGCCAGCCCGCCAGAGGACACCTCTGCAGAGGTCTCTAGGGCCACCGTCCTTGACCTTGCTGGGAATGCT
CGGTGAGACAAGGGCAGCATGTCTGAAGACTGTGGGCCAGGAACCTCCGGGGAGCTGGGCGGGCTGAGGCCGATC
AAAATTGAGCCAGAGGATCTGGACATCATTAGGTACCCGTCCAGACCCCTCGCCAACCTCTGAGGAAATGACA
GACTCGATGCCTGGGCACCTGCCATCGGAGGATTCTGGTTATGGGATGGAGATGCTGACAGACAAAGGTCTGAGT
GAGGACGCGCGGCCGGAGGAGAGGCCCGTGGAGGACAGCCACGGTGACGTGATCCGGCCCCCTGCGGAAGCAGGTG
GAGCTGCTCTTCAACACACGATACGCCAAGGCCATTGGCATCTCGGAGCCCGTCAAGGTGCCGTACTCCAAGTTT
CTGATGCACCCGGAGGAGCTGTTTGTGGTGGGACTGCCTGAAGGCATCTCCCTCCGAGGCCCAACTGCTTCGGG
ATCGCCAAGCTCCGGAAGATTCTGGAGGCCAGCAACAGCATCCAGTTTGTATCAAGAGGCCCGAGCTGCTCACT
GAGGGAGTCAAAGAGCCCATCATGGATAGTCAAGGAACTGCCTCCTCACTTGGCTTCTCTCCCCCTGCCCTGCC
CCAGAGAGGGATTCCGGGGACCTCTGGTGGACGAGAGCCTGAAGAGACAGGGCTTTCAAGAAAATTATGACGCG
AGGCTCTCACGGATCGACATCGCCAACACACTAAGGGAGCAGGTCCAGGACCTTTTCAATAAGAAATACGGGGAA
GCCTTGGGCATCAAGTACCCGGTCCAGGTCCCCTACAAGCGGATCAAGAGTAACCCCGGCTCCGTGATCATCGAG
GGGCTGCCCCCAGGAATCCCGTTCCGAAAGCCCTGTACCTTCGGCTCCCAAGCCTGGAGAGGATTCTTGCTGTG
GCTGACAAGATCAAGTTCACAGTCACCAGGCCCTTCCAAGGACTCATCCCAAGCCTGATGAAGATGACGCCAAC
AGACTCGGGGAGAAGGTGATCCTGCGGGAGCAGGTGAAGGAACTCTTCAACGAGAAATACGGTGAGGCCCTGGGC
CTGAACCGGCCCGGTGCTGGTCCCTTATAAACTAATCCGGGACAGCCAGACGCGTGGAGGTACGGGTCTGCCT
GATGACATCCCCCTCCGGAACCCCAACACGTACGACATCCACCGGTGGAGAAGATCCTGAAGGCCCGAGAGCAT
GTCCGCATGGTCATCATTAAACAGCTCCAACCCCTTGCAGAAATCTGCAATGATGCCAAGGTGCCAGCCAAAGAC
AGCAGCATTCCAAGCGCAAGAGAAAGCGGGTCTCGGAAGGAAATTCGCTCTCCTCTCTCCTCCTCGTCTCCTCT
TCCTCGTCTCTAACCCGGATTCAAGTGGCATCGGCCAACAGATCTCACTCGTGCAATGGCCAATGTACATGGTG
GACTATGCCGGCCTGAACGTGCAGCTCCCGGGACCTCTTAATTAC**TAG**ACCTCAGTACTGAATCAGGACCTCACT
CAGAAAGACTAAAGGAAATGTAATTTATGTACAAAATGTATATTCGGATATGTATCGATGCCTTTTAGTTTTTCC
AATGATTTTTTACACTATATTCTGCCACCAAGGCCTTTTTAAATAAGTAAAAAAAAAAAAAAAAAAAAA

2494/6881
FIGURE 2294

MALLGKRCDVPTNGCGPDRWNSAFTRKDEIITSLVSALDSMCSALSKLNAEVACVAVHDESAFVVGTEKGRMFLN
ARKELQSDFLRFRCRGPWWDPEAEHPKKVQRGEGGGRSLPRSSLEHGSDVYLLRKMVEEVFDVLYSEALGRASVV
PLPYERLLREFGLLAVQGLPEGLAFRRPAEYDPKALMAILEHSHRIRFKLRPLEDGGRDSKALVELNGVSLIPK
GSRDCGLHGQAPKVPPQDLPTATSSSMASFLYSTALPNHAIRELKQEAPSCPLAPSDLGLSRPMPEPKATGAQD
FSDCCGQKPTGPGGPLIQNVHASKRILFSIVHDKSEKWDAFIKETEDINTLRECVQILFNSRYAEALGLDHMPV
PYRKIACDPEAVEIVGIPDKIPFKRPCTYGVPKLKRILEERHSIHFI IKRMFDERIFTGNKFTKDTTKLEPASPP
EDTSAEVS RATVLDLAGNARSDKGSMSEDCGPGTSGELGGLRPIKIEPEDLDIIQVTVPDPSPTSEEMTDSMPGH
LPSEDSGYGMEMLTDKGLSEDARPEERPVEDSHGDVIRPLRKQVELLFNTRYAKAIGISEPVKVPYKFLMHPEE
LFVVGLPEGISLRRPNCFGIAKLRKILEASNSIQFVIKRPPELLTEGVKEPIMDSQGTASSLGFSPPALPPERDSG
DPLVDESLKRQGFQENYDARLSRIDIAN TLREQVQDLFNKKYGEALGIKYPVQVPYKRIKSNPGSVIIEGLPPGI
PFRKPCTFGSQNLERILAVADKIKFTVTRPFQGLIPKPDEDDANRLGEKVILREQVKELFNEKYGEALGLNRPVL
VPYKLIRDSPDAVEVTGLPDDIPFRNPNTYDIHRLEKILKAREHVRMVIINQLQPF AEICNDAKVP AKDSSIPKR
KRKRVS EGN SVSSSSSSSSSSSSSNPDSVASANQISLVQWPMY MVDYAGLNVQLPGPLNY

2495/6881
FIGURE 2295A

AGGAGGAGGAGGGTGAGAGAGAAGCTGGGAGAGCAGAGAAAAGGGGCCACCGGTGCGCCCCCGCTTCCCCGCAC
GCGCTCTCCAGCCGCGGCCCGCCCTGCCGCGGTACCCCGGCCTCTGCCTCTGTCCCCCAGTGATCGGATCAA
GGCGCTGAGCGAGGCCCTGCCTGCGGGGCGGCCATGCGGCGGTGACAGGAGCGCGACCGACACGCACGGGCCCT
CGCCCCCTCTCGCTCCCGTCCGCTCGCCAGCTCCCCCTCAGCCGAGGCTGCTCCGCGGCGGCCGAGCCCGCGCG
CGGCCACACTCGCTCCCTCGGCACCCCGGCCCGGAGCTGCCTGGAGGCGGCCGCACTCGGGGATC**ATG**GC
CCAAGTTGCAATGTCCACCCTCCCGTTGAAGATGAGGAGTCCCTCGGAGAGCAGGATGGTGGTGACATTTCCTCAT
GTCAGCTCTCGAGTCCATGTGTAAAGAACTGGCCAAGTCCAAAGCCGAAGTGGCCTGCATTGCAGTGTATGAAAC
AGACGTGTTTGTCTCGGAACTGAAAGAGGACGTGCTTTTGTCAATACCAGAAAGGATTTTCAAAAAGATTTTGT
AAAATATTGTGTTGAAGAAGAAGAAAAAGCTGCAGAGATGCATAAAATGAAATCTACAACCCAGGCAAATCGGAT
GAGTGTAGATGCTGTAGAAATTGAAACACTCAGAAAAACAGTTGAGGACTATTTCTGCTTTTGGTATGGGAAAGC
TTTAGGCAAATCCACAGTGGTACCTGTACCATATGAGAAGATGCTGCGAGACCAGTGGCTGTGGTAGTGACAGGG
GCTTCCGGAAGGTGTTGCCTTTAAACACCCCGAGAAGTATGATCTTGCAACCCTGAAATGGATTTTGGAGAACAA
AGCAGGGATTTTATTATCATTAAAGAGACCTTTTTTAGAGCCAAAGAAGCATGTAGGTGGTCTGTGTATGGTAAC
AGATGCTGACAGGTCAATACTATCTCCAGGTGGAAGTTGTGGCCCCATCAAAGTGAAAACCTGAACCCACAGAAGA
TTCTGGCATTTCCCTGGAAATGGCAGCTGTGACAGTAAAGGAAGAATCAGAAGATCCTGATTATTATCAATATAA
CATTCAAGCAGGCCCTTCTGAACTGATGATGTTGATGAAAAACAGCCCTATCGAAGCCTTTGCAAGGAAGCCA
CCATTCTTCAGAGGGCAATGAAGGCACAGAAATGGAAGTACCAGCAGAAGATTCTACTCAACATGTCCCTTCAGA
AACAAGTGAGGACCCTGAAGTTGAGGTGACTATTGAAGATGATGATTATTCTCCACCGTCTAAGAGACCAAGGC
CAATGAGCTACCGCAGCCACCAGTCCCGGAACCCGCCAATGCTGGGAAGCGGAAAGTGAGGGAGTTCAACTTCGA
GAAATGGAATGCTCGCATCACTGATCTACGTAAACAAGTTGAAGAATTGTTTGAAAGGAAATATGCTCAAGCCAT
AAAAGCCAAAGGTCCGGTGACGATCCCGTACCCTCTTTCCAGTCTCATGTTGAAGATCTTTATGTAGAAGGACT
TCCTGAAGGAATTCTTTTGAAGGCCATCTACTTACGGAATTCTCGCCTGGAGAGGATATTACTTGCAAAGGA
AAGGATTCGTTTTGTGATTAAGAAACATGAGCTTCTGAATTCAACACGTGAAGATTTACAGCTTGATAAGCCAGC
TTCAGGAGTAAAGGAAGAATGGTATGCCAGAATCACTAAATTAAGAAAGATGGTGGATCAGCTTTTCTGCAAAAA
ATTTGCGGAAGCCTTGGGGAGCACTGAAGCCAAGGCTGTACCGTACCAAAAATTTGAGGCACACCCGAATGATCT
GTACGTGGAAGGACTGCCAGAAAACATTCTTTCCGAGTCCCTCATGGTATGGAATCCCAAGGCTGGAAAAAT
CATTCAAGTGGGCAATCGAATTAAATTTGTTATTAAAAAGACCAGAATCTGACTCACAGTACCACTGAAGTTAC
TCAGCCAAGAACGAATACCCAGTCAAGGAAGATTGGAATGTCAGAATTACCAAGCTACGGAAGCAAGTGGAAGA
GATTTTTTAATTTGAAATTTGCTCAAGCTCTTGGACTCACCGAGGCAGTAAAAGTACCATATCCTGTGTTTGAATC
AAACCCGGAGTTCTTGTATGTGGAAGGCTTGCCAGAGGGGATTCCCTTCCGAAGCCCTACCTGGTTTGGAAATTC
ACGACTTGAAAAGGATCGTCCGCGGGAGTAATAAAATCAAGTTCGTTGTTAAAAAACCTGAACTAGTTATTTCTTA
CTTGCCCTCCTGGGATGGCTAGTAAATAAAACACTAAAGCTTTGCAGTCCCCAAAAGACCACGAAGTCTTGGGAG
TAATTCAAAGGTTCTGAAATTGAGGTACCCGTGGAAGGCCCTAATAACAACAATCCTCAAAACCTCAGCTGTTTCG
AACCCCGACCCAGACTAACGGTTCTAACGTTCCCTTCAAGCCACGAGGGAGAGAGTTTTCTTTGAGGCCTGGAA
TGCCAAAATCACGGACCTAAACAGAAAGTTGAAAATCTCTTCAATGAGAAATGTGGGAAGCTCTTGCCCTTAA
ACAAGCTGTGAAGGTGCCGTTTCGCGTTATTTGAGTCTTTCCCGGAAGACTTTTATGTGGAAGGCTTACCTGAGGG
TGTGCCATTCCGAAGACCATCGACTTTTGGCATTCCGAGGCTGGAGAAGATACTCAGAAACAAAGCCAAAATTAA
GTTTCATCATTA AAAAGCCCGAAATGTTTGAGACGGCGATTAAGGAGAGCACCTCCTCTAAGAGCCCTCCAGAAA
AATAAATTCATCACCCAATGTTAATACTACTGCATCAGGTGTTGAAGACCTTAACATCATTAGGTGACAATTCC
AGATGATGATAATGAAAGACTCTCGAAAGTTGAAAAAGCTAGACAGCTAAGAGAACAAGTGAATGACCTCTTTAG
TCGGAAATTTGGTGAAGCTATTGGTATGGGTTTTCTGTGAAAGTTCCCTACAGGAAAATCACAATTAACCCTGG
CTGTGTGGTGGTTGATGGCATGCCCCGGGGGTGTCCTTCAAAGCCCCAGCTACCTGGAAATCAGCTCCATGAG
AAGGATCTTAGACTCTGCCGAGTTTATCAAATTCACGGTCATTAGACCATTTCCAGGACTTGTGATTAATAACCA
GCTGGTTGATCAGAGTGAGTCAGAAGGCCCGTGATACAAGAATCAGCTGAACCAAGCCAGTTGGAAGTTCCAGC
CACAGAAGAAATAAAAGAGACTGATGGAAGCTCTCAGATCAAGCAAGAACCAGACCCACGTGGT**TAG**ACCTCTTC
CCTCCTAGGCTTAAAGTATCAGTGGTTGAGAAGAGCTTTTCCGACCTGTTACTACCCCAAGCTGTGTAATATACT
TGTATAACAGAAATACCTTCTATACAAACCTTTTTTTCTACTTTTAGATAGAAATGTCTACTTTTTTCAGCAGTTC
TGTGAATTAAGAGCAGAGTGACTGTGGGTCTGGAATGGCTGGTGTACTTGGAATGTACTATCAGGATTTTACA

2496/6881
FIGURE 2295B

GCAATGCTGGGAAATGACAGGGAAATGACAGGAATGAATCTCACCAGATTTTTTATGTACTCAGCAGAGCCTTG
AGTTACGGTGTTTATTTTCCAATCAAGTGAAGATATCTCCTACTTCTCCTACTGGAACATCTCAGCTTCTGCAGT
GAAGAAAAATTCCTGTGATAGTTCAGTTCTTTAGTTTTTCTATTTGAAAAAAAAAATCATTAAATGATCCTTT
GTTACGGCTCTCCTTAATGACTGAGTGAACAGTTCCTATCTGTATATTTGACTAAACCTTTTCCTAAGCTATCT
CTCATGGTTCCTATGTTTTTTATCATAATTAAGCAAAACCATCTGGATCACCTAACAGTCAGAGGTCAGTAT
CTCAGCGTGTGAATTATAGAGGAAATACAGAGAGAACCTCTTCCACTTTTACTTTTCGTCCAAATAAAATGCATG
GTGTACCAGAAAGTTGAAGATCGGGTTGAGGATTGGGGCTAGCTCGATGACACTAAGGCCCCAACATCGCGGGACC
TGCTGTGGCGCGGATTCTTAGGAACGCTGTTCTAGCCGGCCCCCTCTCCAGGGGTCGCGTGGCCGGCATTATTTT
CTAGTTCTTCTTGTAAACCCTGAGGTGCCAGCGCGGGGAGTGAGGAGGGGTCAGGGGGCTAAGGATGCAACCTCTG
ACGTTCTGCGCCTTCCTAGGAGAGTCTTACATGTGTTGAGATTTTACAAGCAATGCGAGTTGTAAAAATACCAGCT
CTACAAGAAGCTAGGCTCTGTGACGGCATAGTTTTTCTAGTCTTTATCACAATATTACAAATGGAGAATTATATG
ACATGGTAGCAGAAATAGGCCCTTTTATGTGTTGCTTCTATTTTACCTCAAATTGTAGATATAGGGTAATCAATA
AAATCCATCCATGCCTTTCACACACTAAAAAGTCGGA

2497/6881
FIGURE 2296

MAQVAMSTLPVEDEESSES RMVVTFLMSALES MCKELAKSKAEVACIAVYETDVFVVGTERGRAFVNTRKDFQKD
FVKYCVEEEEKAAEMHKMKSTTQANRMSVDAVEIETLRKTVEDYFCFCYKALGKSTVVPVPYEKMLRDQSAVVV
QGLPEGVAFKHPENYDLATLKWILENKAGISFI IKRPFLEPKKHVGGRMVTDADRSILSPGGSCGPIKVKTEPT
EDSGISLEMAAVTVKEESED PDYYQYNIQAGPSETDDVDEKQPLSKPLQGSHHSSEGNEGTEMEVPAEDSTQHVP
SETSEDPEVEVTIEDDDYSPPSKRPKANELPQPPVPEPANAGKRKVREFNF EKWNARITDLRKQVEELFERKYAQ
AIKAKGPVTIPYPLFQSHVEDLYVEGLPEGIPFRRPSTYGIPRLERILLAKERIRFVIKKHELLNSTREDLQLDK
PASGVKEEWYARITKLRKMVDQLFCCKFAEALGSTEAKAVPYQKFEAHPNDLYVEGLPENIPFRSPSWYGIPRLE
KIIQVGNRIKFVIKRPELLTHSTTEVTQPRNTFPVKEDWNVRITKLRKQVEEIFNLKFAQALGLTEAVKVPYPVF
ESNPEFLYVEGLPEGIPFRSPTWFGIPRLERIVRGSNKIKFVVKKPELVISYLP PGMASKINTKALQSPKRPRSP
GSNSKVPEIEVTVEGPNNNNPQTSAVRTPTQTNGSNVPFKPRGREFSFEAWNAKITDLKQKVENLFNEKCGEALG
LKQAVKVPFALFESFPEDFYVEGLPEGVPFRRPSTFGIPRLEKILRNKAKIKFIKKPEMFETAIKESTSSKSP
RKINSSPNVNTTASGVEDLNIIQVTIPDDDNERLSKVEKARQLREQVNDLFSRKFGEAIGMGFPVKVPYRKITIN
PGCVVVDGMPGVSFKAPSYLEISSMRRIILDSAEFIKFTVIRPFPGLVINNLVDQSESESGPVIQESAEPSQLEV
PATEEIKETDGSSQIKQEPDPTW

2498/6881
FIGURE 2297

GCGACTTCCTCTTTCCAGTGCATTTAAGGCGCAGCCTGGAAGTGCCAGGGAGCACTGGAGGCCACCCAGTCA**ATGG**
GGGACACCTTCATCCGTCACATCGCCCTGCTGGGCTTTGAGAAGCGCTTCGTACCCAGCCAGCACTATGTGTACA
TGTTCTGGTGAAATGGCAGGACCTGTCTGGAGAAGGTGGTCTACCGGCGCTTCACCGAGATCTACGAGTTCCATA
AAACCTTAAAAGAAATGTTCCCTATTGAGGCAGGGGCGATCAATCCAGAGAACAGGATCATCCCCACCTCCCAG
CTCCCAAGTGGTTTGACGGGCAGCGGGCCGCCGAGAACCGCCAGGGCACACTTACCGAGTACTGCGGCACGCTCA
TGAGCCTGCCCACCAAGATCTCCCGCTGTCCCCACCTCCTCGACTTCTTCAAGGTGCGCCCTGATGACCTCAAGC
TCCCCACGGACAACCAGACAAAAAAGCCAGAGACATACTTGATGCCCAAAGATGGCAAGAGTACCGCGACAGACA
TCACCGGCCCCATCATCCTGCAGACGTACCGCGCCATTGCCAACTACGAGAAGACCTCGGGCTCCGAGATGGCTC
TGTCACGGGGGACGTGGTGGAGGTCGTAGAGAAGAGCGAGAGCGGTCAGACCTCCACCTTACGGGGCTCCTTC
CCCTGGTGCTCAGGAACCCACAGCCACAAGCCCCCTGCCAAGGCTCAGGCAGCCTTGCCCCCTGGGAGGACTCCGG
CTCTGTTAGGGGCCCTAAATGTCCTCCCCACACTGTGGGTGCGCTTCTGTCTTAGTGTGCACCTGTGGTGGCTG
TGGGCATCTGTGCTTGGCAGGCCGGGGCGGGGCATGTCTGCGTGTTCTGTCTGGATGGGTATGGGACCGTCTGTT
CATTAT**TGA**AGTGGGCTCAGAGCTGTGATTCTGTGAGCATGTGTGCATGCATGCATGTGACCTCATTGTCCGGTGT
GGTGAAGGTGACATTTCCAAATCTGAGCATTGGACATCAGTGTGTCTGTGTCCCTGTGTCTCACCATCCCTGAT
GGCTGCAGGGAGCCGCTGGGCCCTGCCCTCAGTCACATTCCCGCACCTCTGGCACAGGTTGGTGGTTCTGTCAG
ATGAAAGCAAAGCGAGGCTGGATCCCAGCGTCCTTCTCGAGCCCCCTGGACAGTCCTGACGAGACGGAAGACCT
G

2499/6881
FIGURE 2298

MGDTFIRHIALLGFEKRFVPSQHYVYMFLVKWQDLSEKVYRRFTEIYEFHKTLKEMFPIEAGAINPENRIIPHL
PAPKWFDGQRAAENRQGTLTEYCSLMSLPTKISRCPHLLDFFKVRPDDLKLPTDNQTKKPETYLMPKDGKSTAT
DITGPIILQTYRAIANYEKTSGSEMALSTGDVVEVVEKSESGQTSHLTGLLPLVLRNPQPQAPCQSGSGLAPGRT
PALLGALNVLPTLWVAFCLSVHPVAVGICAWQAGAGHVCVFCLDGYGTVCSL

2500/6881
FIGURE 2299A

GAGCCCCAGGGAGGCGGATCTGGGCCCCGAGAAGGACACCCGCCTGGATTGCCCCGTAGGCCCGGCCGGGGCCC
CTCGGGAGCAGAACAGCCTTGGTGAGGTGGACAGGAGGGGACCTCGCGAGCAGACGCGCGGCCAGCGACAGCAG
CCCCCCCCGGCCTCTCGGGAGCCGTGGGGCAGAGGCTGCGGAGCCCCAGGAGGGGGCCAGTGTCAATCAAAGATG
TGGCTGTGGATTTCACCCAGGAGGAGTGGCGGCAACTGGACCCTGATGAGAAGATAACATACGGGGATGTGATGT
TGGAGAACTACAGCCATCTAGTTTCTTGGCTTATGAGGTGGCAACATCTTGTACTTCGGAGATTCTGAAGCCGA
GCAACTTGCCCAAGTCCTTCTTCTTTTCCCATTAACAAGATATGATATCACCAAGCCAAACGTCATCATTAAAGTT
GGAGCAGGGAGAGGAGCTGTGGATAACGGGAGGTGAATTTCCATGTCAACATAGTCCAGCCCCCTCACATCCTCAG
CCGAAGATCTCACTTCGTCCCAGAGGCCTTTGCTGACTGACCCCTCAGGGATCGTGGGACTTTACCAGATCGGTT
TGTAATAACACCTCGAAGACGCTATCCGATCCATCAGACCCAGTATTCTGTCCGGGGGTACTTTCCACAGTGTG
CTGGAATGGTTATCACAGAAGGCTGTGCTGTCCCCTCGCAACTCCAGGATGGTGTGTAGCCAGTGAAGTGTGAG
GATCGCCCCCTCCTGACAGAAGATTTTACGTTCTGCGATACCAGAGCAGATAATCAGCTCAACACTGTGCTCACC
ATCAAGTAATGCCCCAGACCCATGTGCAAAGGAGACTGTACTGAGTGCCCTCAAAGAGAAGAAGAAGAAAAGGAC
AGTGGAGGAAGAAGACCAAATATTCCTTGATGGCCAGGAAAATAAAAGAAGGCGCCATGATAGCAGTGGCAGTGG
ACATTACGATTTGAGCCCCCTGGTGGCCAGTGGAGTCCCCGCTTCTTTTGTGCCTAAGCCTGGGTCTCTGAAGAG
AGGCCTCAATTCTCAGAGCTCAGATGACCACTTGAATAAGAGATCCCGAAGCTCTTCCATGAGCTCCTTGACAGG
CGCTTACACAAGTGGCATCCCTAGCTCCAGCCGCAATGCCATTACCAGTTCCTACAGCTCCACTCGAGGCATCTC
ACAGCTCTGGAAGAGAAAATGGCCCCAGTTCATACCCCTTCTCTAGCCCAGCCTCATCCGCTCCCAGACACCCGA
GAGGCCAGCAAAGAAAATAAGAGAAGAAGAGCTGTGTATCATTTCCAGTTCTTCAACTCCATTGGCAGCAGACAA
GGAGTCCCAGGGAGAAAAGGCTGCAGATACAACCCCAAGGAAGAAACAAAACCTCGAATTCTCAGTCTACACCTGG
CAGCTCTGGGCAGCGTAAGCGGAAAGTTTCACTGCTGCCTTCTCGGCGAGGGGAACAGCTGACCTTGCCTCCACC
TCCCCAGCTTGGCTATTTCGATCACTGCCGAGGACCTAGACTTAGAGAAGAAGGCTTCATTACAGTGGTTCAACCA
GGCCTTGGAGGACAAGAGTGATGCTGCCTCGAACTCTGTCACTGAGACCCACCTACCACTCAGCCTTCATTTAC
CTTIACCCTGCCTGCTGCTGCAACTGCCTCCCCACCCACCTCCCTCCTGGCCCCAAGCACCAACCCACTGTTAGA
GAGCTTGAAGAAGATGCAGACTCCCCCGAGCCTGCCACCCTGCCAGAATCTGCTGGAGCAGCAACCACTGAGGC
CCTCTCACCTCCAAAGACACCCAGCCTCCTACCCCCGCTGGGTTTATCACAGTCAGGGCGGCCAGGGCTGCTCCC
CAGCCCCCTCCTTTGACTCCAAACCCCGACCACTTTGCTGGGGCTGATCCCTGCTCCATCCATGGTACCAGCCAC
TGACACCAAGGCACCTCCAACCTTCAAGCAGAGACGGCTACCAAACCCCAAGCCACATCTGCCCGCTCCCCCGC
CCCCAAGCAAAGCTTCTGTTTGGAAACACAGAACACCTCACCTTCCAGCCCTGCCGCCCCCTGCTGCATCTTCAGC
ATCTCCCATGTTCAAGCCCATTTTACGGCTCCACCCAAGAGTGAGAAGGAAGGCCCCACACCGCCTGGCCCTTC
AGTCACAGCCACAGCGCCCTCCAGCTCCTCCCTCCCCACGACCACCAGCACCACAGCCCCGACCTTCCAGCCTGT
CTTTAGCAGCATGGGGCCACCTGCATCTGTGCCCTTGCTGCTCCCTTCTTCAAGCAGACAACACTACTCCCGCCAC
TGCTCCCAACCAACTGCCCGCTCTTCACTGGCCTGGCCAGCGCCACCTCTGCTGTGGCTCCCATCACCTCTGC
CAGTCCATCCACAGACTCTGCTTCGAAGCCTGCGTTTGGCTTTGGCATAAACAGTGTGAGCAGCAGCAGTGTGAG
TACCACGACCAGCACCGCCACTGCCGCTCACAGCCTTTCCTCTTCGGGGCGCCCCAGGCCTCTGCTGCCAGCTT
CACCCCGGCCATGGGCTCCATATTCAGTTTGGCAAACCTCCTGCCTTGCCACAACCACCACAGTCACCACTT
CAGCCAGTCCCTGCCCACTGCCGTGCCAACGGCCACCAGCAGCAGCGCTGCCGACTTTAGTGGTTTTGGCAGCAC
CCTCGCCACCTCCGCCCCGGCCACCAGCAGCCAGCCACTCTGACGTTCAAGTAACACGAGCAACCCACGTTCAA
CATTCCTTTGGCTCAAGCGCCAAGTCCCCGCTCCCATCATATCCGGGAGCCAACCCCAAGCCGCAATTTGGGGC
CGCTGAGGGGCAGCCACCGGGGGCGCCAAAGCCAGCCCTTACCCCAAGCTTTGGCAGCTCTTCACTTTTGGAAA
CTCTGCAGCCCCGGCCCCGGCTACTGCACCCACACCTGCACCTGCGTCCACGATCAAGATCGTGCCTGCGCACGT
GCCTACGCCCATCCAGCCTACCTTTGGCGGTGCCACGCACTCGGCGTTTGGATTGAAAGCCACGGCTTCCGCCTT
CGGCGCTCCCGCCAGCTCACAGCCCGCCTTTGGCGGTCCACTGCTGTCTTCTCCTTCGGTGCAGCCACCAGCTC
CGGCTTTGGAGCCACCACCCAGACCGCCAGCAGCGGAGCAGCAGCTCGGTGTTTGGCAGCACAAACACCATCACC
CTTCAGTTTGGGGGTTTCGGCAGCCCCCGCTGGCAGTGGGAGCTTTGGGATCAACGTGGCCACCCCAAGGCTCCAG
CGCCACCACCGGAGCTTTTCACTTTGGAGCAGGACAGAGTGGGAGCACAGCCACCTCCACCCCTTTCACAGGGGG
CTTAGGTCAGAACGCCCTGGGCACCACCGGCCAGAGCACACCGTTTGCCTTCAACGTGGGCAGCACAACTGAGAG
CAAACCTGTGTTTGGAGGCACCGCCACCCCACTTTGGTTCAGAACACCCCTGCGCCTGGAGTGGGCACATCGGG
CAGCAGCCTCTCCTTTGGGGCATCTTCAGCACCCGCCCAAGGCTTTGTTGGTGTGGACCGTTTCGGCAACACTTT

2501/6881
FIGURE 2299B

TGCTCACCAGCAAGAACACAGCCCCGAGGAAGGGACCCAATAACCTTTCAAAATGCAAACCTGCTGCCTGCGGTGAG
GGCCCAGGGTCTCTCCACGGAGAGGACAGGCATCTTCTTTCCCACCAGGAAGGAGTCAGCCTGGAGCCTCTGCTA
TGTGCAAGGCGGTGTGCAAGCACCGGCTGCGGCTCTTTGCTGTCTCTTCTTTCTCTTTGGGGCTGGGCTGGGTGT
GCGTTCTGGTGCTGATGCTTTGGCCTGTGAGGCTGAGCTAGAGAAGTGTAGATGTTAGATGTGCCAGTACCATCC
TGCGCCTCCCAAGCATGCCCCACTCACTCACGTGCGCATCTCGACCCGTTCAATTACAGCAACGAAGAAGCCAC
CGCTAAGCGTGGTCTTGGGGGAAGCCCGGAGGCAGTGCTCGGCACCCGGGAACGTGCTCAGGCCTCGGTGGGGCC
GGGCAGGCAGGGCGGGAGCTAGCCTGCAAGAGAAACAGCCCCAATGCTGGGTAAAGAGAGCAGTTACCCCCATCCC
CCCCCTCCACGACCCTGGCGCCCGCCCTGTACCTGAAGGCGCCCGGGTCTGCTGCAGCGCATCTGGTACCATGT
CTTCATTCTCCTCCTGGCAGAGGGAGCACATGGAGTAGACGAGCCGCTGCAGGGAAGGGAAAGTGAGCGCGTGGC
ACAGGGCTCGCTGCTGGAACCTGCCAGGGCATGCAGACGCACCGGGCTAGGTGTCCCTGCCCGGGATCCTCCA
GCTGTCTGCTCGGCATACCTAAGGAAAAGCGTGTCTCGGTTACACAGCTTCACAGGCTGCCTCAGTCCTGAAATC
CTCGCTCCTGAAATCCTTGCTCACAGAGGAGAACTTTTGCTCCAGGGTCCCAAGCCCATTAAAGTGTCAGAACT
AAGACCAAAACAGATGACTCCAGGTCTAAGCTGCTGTGGACCTCCGAGTCCCTCAGCCACGCCTTCTCACCATCT
CACCCGAGCCACTGCAGGAAGGATCCAGCAGGACATAGTGGACCTCACGATAGCGCGGATCTAAGGGGGAGACCG
CCAGGAAGTCCTCCTCAGCCAGCTCACAGCAGGAGACGCCAACCCAGGCCAGCAGCGTGGCCATGGATGCCAGCC
GCITGGCATCCAGGTCAAAGGCAAAGATCTTCTAGGGCAGAGGGCAGAGCAGGGGTGAGCTGAGCATGCACGGA
GCAGCTAAGGGGCTGTACAGCTGACACAGACAACCAGAACATGCAGGTTAAGCCAGGACACACAATATTGAAAC
GGCCTATATTTAAAGGGCCCAGGGTCAGAGGTAAGTGGCCTGGGGTCTCTGCCCCAAGGGCTAAGGGATCCACAT
CTCACACCTGCAGTGGGGAAAGCTTAGCTTGGGGCAAATACCGTGAACCTACTTTGGTACAGCAGGAAAGAGTTAA
GCGAAAGTCATCCTTTAGCCCTTTATTACCCACTGAAAGGCACAAAATCAAACCCCATGTCCTCCTCCTCCTCCT
CCTGTGGCACTACCCCTTGGTTCTTCAGAAGAGCAGCCAAGTGAAGTGGTCTTATTGCCTGGGGCGGCACAGGCAT
CGATGACATGGGAGCCTGGCGGGGGTCCAGCAGCATGGCTGGGAGACAGCTGGCCTGGCAGGCAGAGCACAGGGG
CCGGGTAAACAGAGACCCAGGCTAGGCCCTTCCCGTGCCTACACATTCTTCCCTTTTCTATTCTCTTGCTAC
CCTGTCTGCAGAATGAGGTGTCCGGCCCGGTACAGTGGGTGTTTCATGCAGATCTGTCTGGGCGGGAAACACCAG
CAGCTCCGGCATCAAGGAGTCCAGGAGAAAATGCTTCCCCTTGAGGGCTTGTAAAGTCATCAAGGCTGCCAGGGAA
GAACCATTCAATTCATTTCTGAATTTCTCCCTGCCAGGCCCTATTTCAACGGTCCATTTCATGCAACAAATGTTAC
CACAGCTATGGAGAAATCAACAGGGTGATAAGGGAATCCGGGATCCGCAGTTGAGGGAATGGGTGTCAAGCCAG
ACTGATGGGTGAGGAGCCCCCTCTACTGTTTACCAGCAGTGGGAGCCTGGGCAAGTGATTCAATCTCAAGCCCCA
CTGGCATCTCTGTAAAATAGTAGGTGTGAGGATTCAATGAGCCAATATATCCAAGATACTTACGTGCCACAATTT
AATAAATGTTAGCTATTCTGTGAAGCATAACCTTGAGAGAAAGGTTACTTTACAGGGGGGTGAGGAGTGGGGAA
GTGAGAGCTGAGCTCATTCTTGATGGATGAGGAGTTAGTCATGTGAGGCGCTTAGGTTAAACTACATTCACTAT
AACTCAGTAAAGCAGTCCCGCCCACTCTCCGACCCATGCAGAAATAGGCCTAGAGAGTCACATGTCTCAGTTCAG
AAATCTATCGAAGTGGCAGAGCTGGAATTCAAACACAAGCAGCCGTTCTCTGCTATTCCACCCTGGTGTCCAAGC
AACATGGTAGGGCAGAAGGAAGAGGATCTTACAAAGAGTAAGGGAAAGGGAGAGGGGCAGAGGCTGCTTCTCAGA
GCCACCAAAGGACAAAATAAGACAGGTGTGAGCCAGTGGAGGAGGCACGGGGCAGAGACCAGCCACTGTTGCTG
GCACGCTGGTGCACGTAGCACTGTGGCAGATGGACCTGGAGAGGAAGCAGGAGGGACAGCACAAATGGAGCCAAGA
AAGGACTTAGCATGGCCGGGCGCGGTGGTTTCATGCCTGTAATCCAGCATTTTGGGAGGCCAAGGTGGGCAGATC
ACCTGAGGTGAGGAGTTTGAGACCAGCCTGGCCAACATGGAGAAATCCCGTCTCTACTAAAAATACAAAATTAGC
CAGGCATGGTGTGCTGCATGCCTGCAATCCTGTAGGGAAAAGAAAGAGAGATCAGACTGTTACTGTGTCTGTGTAGA
AAGGGAAGACATAAGAAATTCATTTGACCTGTACCTTGAACAATTGGTTGGCTGAGATGCTGTTAATTTGTGA
CTTTGCCCCAAATTTGAGCTCACAAAACATGTGTTGTATGGAATCAAGGTTTAAAGGATCTAGGGCTGTGCAGG
ACATGCCTTGTTAATAAAACGTTTACAAGC

2502/6881
FIGURE 2300A

CAGCATCAATAAGGCCATTAATACGCAGGAAGTGGCTGTAAAGGAAAAACAGCCAGAACGTGCATACTGGGCAC
CCACCATGAGAAAGGGGCACAGACCTTCTGGTCTGTTGTCAACCGCTGCCTCTGTCTAGCAACGCAGTGCTCTG
CTGGAAGTTCTGCCATGTGTTCCACAACTCCTCCGAGATGGACACCCGAACGTCCTGAAGGACTCTCTGAGATA
CAGAAATGAATTGAGTGACATGAGCAGGATGTGGGGCCACCTGAGCGAGGGGTATGGCCAGCTGTGCAGCATCTA
CCTGAAACTGCTAAGAACCAAGATGGAGTACCACACCAAAAAATCCCAGGTTCCCAGGCAACCTGCAGATGAGTGA
CCGCCAGCTGGACGAGGCTGGAGAAAGTGACGTGAACAACTTTTTCCAGTTAACAGTGGAGATGTTTGACTACCT
GGAGTGTGAACTCAACCTCTTCCAAACAGTATTCAACTCCCTGGACATGTCCCGCTCTGTGTCCGTGACGGCAGC
AGGGCAGTGCCCGCTCGCCCCGCTGATCCAGGTCATCTTGGACTGCAGCCACCTTTATGACTACACTGTCAAGCT
TCTCTTCAAACTCCACTCCTGCCTCCCAGCTGACACCCTGCAAGGCCACCGGGACCGCTTCATGGAGCAGTTTAC
AAAGTTGAAAGATCTGTTCTACCGCTCCAGCAACCTGCAGTACTTCAAGCGGCTCATTCAAGATCCCCCAGCTGCC
TGAGAACCCACCCAACTTCTGCGAGCCTCAGCCCTGTGAGAACATATCAGCCCTGTGGTGGTGATCCCTGCAGA
GGCCTCATCCCCCGACAGCGAGCCAGTCCAGAGAAAGGATGACCTCATGGACATGGATGCCTCTCAGCAGAAATTT
ATTTGACAACAAGTTTGTATGACATCTTTGGCAGTTTCAATTCAGCAGTGATCCCTTCAATTTCAACAGTCAAAAATGG
TGTGAACAAGGATGAGAAGGACCCTTAATTGAGCGACTATACAGAGAGATCAGTGGATTGAAGGCACAGCTAGA
AAACATGAAGACTGAGAGCCAGCGGGTTGTGCTGCAGCTGAAGGGCCACGTCAGCGAGCTGGAAGCAGATCTGGC
CGAGCAGCAGCACCTGCGGCAGCAGGCGGCCGACGACTGTGAATTCCTGCGGGCAGAACTGGACGAGCTCAGGAG
GCAGCGGGAGGACACCGAGAAGGCTCAGCGGAGCCTGTCTGAGATAGAAAGGAAGCTCAAGCCAATGAACAGCG
ATATAGCAAGCTAAAGGAGAAGTACAGCGAGCTGGTTTCAAGAACGCTGACCTGGTGCAGGAAGAATGCAGAGGT
GACCAAAACAGGTGTCCATGGCCAGACAAGCCAGGTAGATTTGGAACGAGAGAAAAAAGAGCTGGAGGATTTCGT
GGAGCGCATCAGTGACCAGGGCCAGCGGAAGACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGAAGCAGGAAC
TGCCACAAGCCAACGGGAGCTTCAGGTTCTGCAAGGCAGCCTGAAACTTCTGCCCAGTCAGAAGCAAACCTGGGC
AGCCGAGTTTCGCCGAGCTAGAGAAGGAGCGGGACAGCCTGGTGAGTGGCGCAGCTCATAGGGAGGAGGAATTATC
TGCTCTTCGGAAGAAGCTGCAGGACACTCAGCTCAAACCTGGCCAGCACAGAGGAATCTATGTCCAGCTTGCCAA
AGACCAACGAAAAATGCTTCTGGTGGGGTCCAGGAAGGCTGCGGAGCAGGTGATACAAGACGCCCTGAACCAGCT
TGAAGAACCTCCTCTCATCAGCTGCGCTGGGTCTGCAGATCACCTCCTCTCCACGGTCACATCCATTTCCAGCTG
CATCGAGCAACTGGAGAAAAGCTGGAGCCAGTATCTGGCCTGCCCAGAAGACATCAGTGGACTTCTCCATTCCAT
AACCCTGCTGGCCCACTTGACCAGCGACGCCATTGCTCATGGTGGCCACCACCTGCCTCAGAGCCCCACCTGAGCC
TGCCGACTCACTGACCAGGCCCTGTAAGCAGTATGGCAGGGAAACCTCGCCTACCTGGCCTCCCTGGAGGAAGA
GGGAAGCCTTGAGAATGCCGACAGCACAGCCATGAGGAAGCTGCCTGAGCAAGATCAAGGCCATCGGCGAGGAGCT
CCTGCCCAGGGGACTGGACATCAAGCAGGAGGAGCTGGGGGACCTGGTGGACAAGGAGATGGCGGCCACTTCAGC
TGCTATTGAAACTGCCACGGCCAGAATAGAGGAGATGCTCAGCAAAATCCCAGCAGGAGACACAGGAGTCAAATTT
GGAGGTGAATGAAAGGATCCTTGGTTGCTGTACCAGCCTCATGCAAGCTATTCAGGTGCTCATCGTGGCCTCTAA
GGACCTCCAGAGAGAGATTGTGGAGAGCGGAGGGGTACAGCATCCCCCTAAAGAGTTTTATGCCAAGAAGCTCTCG
ATGGACAGAAGGACTTATCTCAGCCTCCAAGGCTGTGGGCTGGGGAGCCACTGTCATGGTGGATGCAGCTGATCT
GGTGGTACAAGGCAGAGGGAAATTTGAGGAGCTAATGGTGTGTTCTCATGAAATTGCTGCTAGCACAGCCCAGCT
TGTGGCTGCATCCAAGGTGAAAGCTGATAAGGACAGCCCCAACCTAGCCAGCTGCAGCAGGCCTCTCGGGGAGT
GAACCAGGCCACTGCCGGCGTTGTGGCCTCAACCATTTCGGCAAATCACAGATCGAAGAGACAGACAACATGGA
CTTCTCAAGCATGACGCTGACACAGATCAAACGCCAAGAGATGGATTCTCAGGTTAGGGTGCTAGAGCTAGAAAA
TGAATTGCAGAAGGAGCGTCAAAAACCTGGGAGAGCTTCGGAAAAAGCACTACGAGCTTGCTGGTGTGCTGAGGG
CTGGGAAGAAGGAACAGAGGCATCTCCACCTACACTGCAAGAAGTGTTAACCAGAAAAAGAAATAGAGCCAAACCAA
CACCCCATATGTCAAGTGTAAATCCTTGTTACCTATCTCGTGTGTGTTATTTCCCCAGCCACAGGCCAAATCCTTG
GAGTCCCAGGGGCAGCCACACCACTGCCATTACCCAGTGCCGAGGACATGCATGACACTTCCAAAGACTCCCTCC
ATAGCGACACCCTTTCTGTTTGGACCATGGTTCATCTCTGTTCTTTTCCCGCCTCCCTAGTTAGCATCCAGGCTG
GCCAGTGCTGCCCATGAGCAAGCCTAGGTACGAAGAGGGGTGGTGGGGGGCAGGGCCACTCAACAGAGAGGACCA
ACATCCAGTCCCTGCTGACTATTTGACCCCCACAACAATGGGTATCCTTAATAGAGGAGCTGCTTGTGTGTTTGTG
ACAGCTTGGAAGGGGAAGATCTTATGCCTTTTCTTTTCTGTTTTCTTCTCAGTCTTTTCAGTTTTCATCATTTGCA
CAAACCTGTGAGCATCAGAGGGCTGATGGATTCCAAACCAGGACACTACCTGAGATCTGCACAGTCAGAAGGAC
GGCAGGAGTGTCTGGCTGTGAATGCCAAAGCCATTCTCCCCCTCTTTGGGCAGTGCCATGGATTTCCACTGCTT

2503/6881
FIGURE 2300B

CTTATGGTGGTTGGTTGGGTTTTTGGTTTTGTTTTTTTTTTTAAAGTTTCACTCACATAGCCAACCTCTCCCAAAG
GGCACACCCCTGGGGCTGAGTCTCCAGGGCCCCCAACTGTGGTAGCTCCAGCGATGGTGCTGCCAGGCCTCTC
GGTGCTCCATCTCCGCCTCCACACTGACCAAGTGCTGGCCCACCCAGTCCATGCTCCAGGGTCAGGCGGAGCTGC
TGAGTGACAGCTTTCTCAAAAAGCAGAAGGAGAGTGAGTGCCTTTCCCTCCTAAAGCTGAATCCCGGCGGAAAG
CCTCTGTCCGCCTTTACAAGGGAGAAGACAACAGAAAGAGGGACAAGAGGGTTACACAGCCCAGTTCCCGTGAC
GAGGCTCAAAAACCTTGATCACATGCTTGAATGGAGCTGGTGAGATCAACAACACTACTTCCCTGCCGGAATGAAC
TGTCGGTGAATGGTCTCTGTCAAGCGGGCCGTCTCCCTTGGCCCAGAGACGGAGTGTTGGGAGTGATTCCCAACTC
CTTTCCTGCAGACGTCTGCCTTGGCATCCTCTTGAATAGGAAGATCGTTCCACCTTCTACGCAATTGACAAACCCG
GAAGATCAGATGCAATTGCTCCCATCAGGGAAGAACCCTATACTTGGTTTGCTACCCCTAGTATTTATTACTAAC
CTCCCTTAAGCAGCAACAGCCTACAAAGAGATGCTTGGAGCAATCAGAACTTCAGGTGTGACTCTAGCAAGGCTC
ATCTTTCTGCCCGGCTACATCAGCCTTCAAGAATCAGAAGAAAGGCCAAGGTGCTGGACTGTTACTGACTTGGAT
CCCAAAGCAAGGAGATCATTTGGAGCTCTTGGGTGAGAGAAAATGAGAAAAGGACAGAGCCAGCGGCTCCAACCTC
TTTCAGCCACATGCCCCAGGCTCTCGCTGCCCTGTGGACAGGATGAGGACAGAGGGCACATGAACAGCTTGCCAG
GGATGGGCAGCCCAACAGCACTTTTCTCTTCTAGATGGACCCAGCATTAAAGTGACCTTCTGATCTTGAAAA
ACAGCGTCTTCTTCTTTATCTATAGCAACTCATTGGTGGTAGCCATCAAGCACTTCCCAGGATCTGCTCCAACA
GAATATTGCTAGGTTTTGCTACATGACGGGTGTGAGACTTCTGTTTGATCACTGTGAACCAACCCCATCTCCC
TAGCCACCCCCCTCCCCAACTCCCTCTCTGTGCATTTTCTAAGTGGGACATTCAAAAACTCTCTCCCAGGACC
TCGGATGACCATACTCAGACGTGTGACCTCCATACTGGGCTAAGGAAGTATCAGCACTAGAAATTGGGCAGTCTT
AATGTTGAATGCTGCTTTCTGCTTAGTATTTTTTTGATTCAAGGCTCAGAAGGAATGGTGCGTGGCTTCCCTGTC
CCAGTTGTGGCAACTAAACCAATCGGTGTGTTCTTGATGCGGGTCAACATTTCCAAAAGTGGCTAGTCCTCACTT
CTAGATCTCAGCCATTCTAACTCATATGTTCCCAATTACCAAGGGGTGGCCGGGCACAGTGGCTCACGCCTGTAA
TCCCAGCACTTTGAGAGGCTGAGGTGGTAGGATCACCTGAGGTGAGGAGTCAAGACCAGCCTGTCCAACATGGT
GAAACCCCATCTCTACTAAAAATACCAAAAATTAGCCGAGCGTAGTGACGGGTGCCCGTAATCCCAGCTACTCA
GGAGGCTGAGACAGGAGAATCACCTGAACCCAGAGGCAGAGGTTGCAGTGAGCTGAGATCACGCCATTGTACTC
CAGCCTGGGCAACAAGAGCAAAAACCTCCGTCTCAAAAAAAAAAAAAAAAAATTACAAATGGGGCAACAGTCTAGTGTA
ATGGATCAAAATTAAGATTCTCTGCCCAGCCGGGCACAGTGGCGCATGCCTGTAATCCCAGAACTTTGGGAGGCCA
AGACGGGATGATTGCTTGAGCTCAGGAGTTTGAGACCAGGCTGGGCATCATAGCAAGACCTCATCTCTACTAAAA
TTCAAAAACAAAATTAGCCGGGCATGATGGTGCATGCCTGTAGTCTCAGCTAGTTGGGGAGCTAAGGTGGGAGAA
TTGCTTGAGCTTGGGAAGTCGAGGCTGCAGTCAGCCCTGATTGTGCCAGTGCCTCCGGCCTGGGTGACAGAGTG
AGACCCTGTCTCAAAAAAAAAAAGATTCTGTGTGAGAGCCAGCCAGGAGTTTGAGGCTGCAATGAGCCATGAT
TTCCCACTGCACTCCAGCCTGAGTGACAGAGCGAGACTCCATCTCTTTAAAAACAAACAAAAAATTATCTGAATG
ATCCTGTCTCTAAAAAGAAGCCACAGAAATGTTTAAAAACTTCATCGACTTAGCCTGAGTCATAACGGTTAAGAA
AGCACTTAAACAGAAGCAGAGGCTAATTCAGTGTACATGAGGAAGTAGCTGTGAGATGTACATAATTACTTTC
GTAATAGCTCAGATTAGAATGGCTACCCCATCTCTAGACAAAATCAAATGTCTCTATTGTGACTCTTCTAAAAA
TGAAGATGAAGAGCTATTTAATGACACACCTTGATTAAACGGGAATCACATCTTAAAGCTAAAAATGAACCTG
CAAGCCTTCTAAATGAGTCACTGAGCATCACTAGTGACAAGTCTCGGGTGAGCGTAAATGGGTGATGACAAGATG
GGACAGCAACAAAATCATGGCTTAGGATCGACAAGAAGTTAAAAAACAGCTGCATCTGTACTTAAAGTTTGTAAG
ACAGTGGCCTGAGACCTCTAGAGAAAAGATGTTTGTTTACATAAGAGAAAGAGGCCAGACATGGTGTCTCACACG
TTTAATCCCAGCACTTTGGGAGGCAGGGCGGGTGGATCACCTGAGGTGAGGAGTTCAAGACTAGCCTGGCCAAC
ATGGTGAACCCCGTCTCTACTAAAAATACAAAATTAGCCGGGCATGGTGGCAGGCGCTATAATCCCAGCTAC
TGGGGAGGCTGAGGCAGGAGAATC

2504/6881
FIGURE 2301

ATGGGGCGGGGCCTCTGGGAGGCGTGGCCTCCGGCCGGCTCCTCTGCTGTTGCCAAGGGAAACTGCCGCGAGGAG
GCGGAAGGAGCAGAGGACCGGCAGCCGGCGTCGAGGCGGGGCGCGGGAACGACGGCGGCCATGGCGGCCTCGGGG
CCCGGGTGTGCGAGCTGGTGCTTGTGTCCCGAGGTGCCATCCGCCACCTTCTTCACTGCGCTGCTCTCGCTGCTG
GTTTCCGGGCCTCGCCTGTTCTGCTGCGAGCAGCCCCTGGCGCCCTCGGGCCTCACGCTGAAGTCCGAGGCCCTT
CGCAACTGGCAAGTTTACAGGCTGGTAACCTACATCTTTGTCTACGAGAATCCCATCTCCCTGCTCTGCGGCGCT
ATCATCATCTGGCGCTTTGCTGGCAATTTGAGAGAACCGTGGGCACCGTCCGCCACTGCTTCTTACCGTGATC
TTCGCCATCTTCTCCGCTATCATCTTCTGTCTTCGAGGCTGTGTTCATCACTGTCAAAGCTGGGGGAAGTGGAG
GATGCCAGAGGTTTACCCCCAGTGGCCTTTGCCATGCTGGGAGTCAACACCGTCCGTTCTCGGATGAGGCGGGCC
CTGGTGTGTTGGCATGGTTGTGCCCTCAGTCCTGGTTCCGTGGCTCCTGCTGGGTGCCTCGTGGCTCATTCCCCAG
ACCTCTTTCCTCAGTAATGTCTGCGGGCTGTCCATCGGGCTGGCCTATGGCCTCACCTACTGCTATTCCATCGAC
CTCTCAGAGCGAGTGGCACTGAAGCTCGATCAGACCTTCCCCTTCAGCCTGATGAGGAGGATATCCGTGTTCAAG
TACGTCTCAGGGTCTTCAGCCGAGAGGAGGGCAGCCAGAGCCGGAAACTGAACCCGGTGCCTGGCTCCTACCCC
ACACAGAGCTGCCACCCTCACCTGTCCCAAGCCACCCTGTGTCCAGACGCAGCACGCCAGTGGTCAGAAGCTG
GCCTCCTGGCCCTCCTGCACCCCGGGCACATGCCACCTTGCCTCCGTACCAGCCTGCCTCCGGCCTGTGCTAT
GTGCAGAACCCTTTGGTCCAAACCCACCTCCTCCAGTGTCTACCCAGCTTCTGCGGGCACCTCCCTGGGCATC
CAGCCCCCACGCCTGTGAACAGCCCTGGCACGGTGTATTCTGGGGCCTTGGGCACACCAGGGGCTGCAGGCTCC
AAGGAGTCCTCCAGGGTCCCCATGCCCTGAGAGAATTTCTAGGGAAGTCATCTCACTTGGCCTTCTGAAGGTCTT
CCCTAAGAGTCTCCTGACAAAAGTTACTTATTGA

2505/6881
FIGURE 2302

GTTCATGATCAACATGGGAGACTCCCACGTGGACACCAGCTCCACCGTGTCCGAGGCGGTGGCCGAAGAAGTAT
CTCTTTTCAGCATGACGGACATGATTCTGTTTTCGCTCATCGTGGGTCTCCTAACCTACTGGTTCTCTTCAGAA
AGAAAAAGAAGAAGTCCCCGAGTTCACCAAAATTACAGACATTGACCTCCTCTGTGAGAGAGAGCAGCTTTGTGG
AAAAGATGAAGAAAACGGGGAGGAACATCATCGTGTCTACGGCTCCCAGACGGGGACTGCAGAGGAGTTTGCCA
ACCGCTGTCCAAGGACGCCCACCGCTACGGGATGCGAGGCATGTGAGCGGACCCCTGAGGAGTATGACCTGGCCG
ACCTGAGCAGCCTGCCAGAGATCGACAACGCCCTGGTGGTTTTCTGCATGGCCACCTACGGTGAGGGAGACCCCA
CCGACAATGCCCAGGACTTCTACGACTGGCTGCAGGAGACAGACGTGGATCTCTCTGGGGTCAAGTTGCGGGTGT
TTGGTCTFTGGGAACAAGACCTACGAGCACTTCAATGCCATGGGCAAGTACGTGGACAAGCGGCTGGAGCAGCTCG
GCGCCCAGCGCATCTTTGAGCTGGGGTTGGGCGACGACGATGGGAACTTGGAGGAGGACTTCATCACCTGGCGAG
AGCAGTTCTGGCCGGCCGTGTGTGAACACTTTGGGGTGGGAAGCCACTGGCGAGGAGTCCAGCATTGCCAGTACG
AGCTTGTGGTCCACACCGACATAGATGCGGCCAAGGTGTACATGGGGGAGATGGGCCGGCTGAAGAGCTACGAGA
ACCAGAAGCCCCCTTTGATGCCAAGAATCCGTTTCTGGCTGCAGTCAACCACCAACCGGAAGCTGAACCAGGGAA
CCGAGCGCCACCTCATGCACCTGGAATTGGACATCTCGGACTCCAAAATCAGGTATGAATCTGGGGACCACGTGG
CTGTGTACCCAGCCAACGACTCTGCTCTCGTCAACCAGCTGGGCAAAATCCTGGGTGCCGACCTGGACGTCGTCA
TGTCCCTGAACAACCTGGATGAGGAGTCCAACAAGAAGCACCCATTCCCGTGCCCTACGTCTACCGCACGGCCC
TCACCTACTACCTGGACATCAACAACCCGCCGCGTACCAACGTGCTGTACGAGCTGGCGCAGTACGCCTCGGAGC
CCTCGGAGCAGGAGCTGCTGCGCAAGATGGCCTCCTCCTCCGGCGAGGGCAAGGAGCTGTACCTGAGCTGGGTGG
TGGAGGCCCCGAGGCACATCCTGGCCATCCTGCAGGACTGCCCCTCCCTGCGGCCCCCATCGACCACCTGTGTG
AGCTGCTGCCGCGCCTGCAGGCCCCGCTACTACTCCATCGCCTCATCTCCAAGGTCCACCCCAACTCTGTGCACA
TCTGTGCGGTGGTTGTGGAGTACGAGACCAAGGCTGGCCGCATCAACAAGGGCGTGGCCACCAACTGGCTGCGGG
CCAAGGAGCCTGCCGGGGAGAACGGCGGCCGTGCGCTGGTGCCCATGTTCTGTGCGCAAGTCCCAGTTCCGCTGC
CCTTCAAGGCCACCACGCCTGTCTATCATGGTGGGCCCCGGCACCGGGGTGGCACCCCTTCATAGGCTTCATCCAGG
AGCGGGCCTGGCTGCGACAGCAGGGCAAGGAGGTGGGGGAGACGCTGCTGTACTACGGCTGCCGCCGCTCGGATG
AGGACTACCTGTACCGGGAGGAGCTGGCGCAGTTCCACAGGGACGGTGCCTCAGCTCAACGTGGCCTTCT
CCCGGGAGCAGTCCCACAAGGTCTACGTCCAGCACCTGCTAAAGCAAGACCGAGAGCACCTGTGGAAGTTGATCG
AAGGCGGTGCCACATCTACGTCTGTGGGGATGCACGGAACATGGCCAGGGATGTGCAGAACACCTTCTACGACA
TCGTGGCTGAGCTCGGGGCCATGGAGCACGCGCAGGCGGTGGACTACATCAAGAACTGATGACCAAGGGCCGCT
ACTCCCTGGACGTGTGGAGCTAGGGGCCCTGCCTGCCCCACCCACCCACAGACTCCGGCCTGTAATCAGCTCTCC
TGGCTCCCTCCCGTAGTCTCCTGGGTGTGTTTGGCTTGGCCTTGGCATGGGCGCAGGCCCAGTGACAAAGACTCC
TCTGGGCCTGGGGTGCATCCTCCTCAGCCCCAGGCCAGGTGAGGTCCACCGGCCCTGGCAGCACAGCCCAGGG
CCTGCATGGGGGCACCGGGCTCCATGCCTCTGGAGGCCTCTGGCCCTCGGTGGCTGCACAGAAGGGCTCTTTCTC
TCTGCTGAGCTGGGCCCAGCCCCCTCCACGTGATTTCCAGTGAGTGTAATAATTTTAAATAACCTCTGGCCCTTG
GAATAAAGTTCTGTTTTCTGT

2506/6881
FIGURE 2303

MTDMILFSLIVGLLTYWFLFRKKKEEVPEFTKIQTLTSSVRESSFVEKMKKTGRNIIVFYGSQTGTAEEFANRLS
KDAHRYGMRGMSADPEEYDLADLSSLPEIDNALVVFCMATYGEDPTDNAQDFYDWLQETDVDLSGVKFAVFGLG
NKTYEHFNAMGKYVDKRLEQLGAQRIFELGLGDDDGNNLEEDFITWREQFWPAVCEHFGVEATGEESSIRQYELVV
HTDIDAAKVYMGEMGRLKSYENQKPPFDAKNPFLAAVTTNRKLNQGTERHLMHLELDISDSKIRYESGDHVAVYP
ANDSALVNQLGKILGADLDVMSLNNLDEESNKKHPFPCPTSYRTALTYLDITNPPRTNVLYELAQYASEPSEQ
ELLRKMASSSGEGKELYLSWVVEARRHILAILQDCPSLRPPIDHLCCELLPRLQARYYSIASSSKVHPNSVHICAV
VVEYETKAGRINKGVATNWLRAKEPAGENGGRALVPMFVRKSQFRLPFKATTPVIMVGP GTGVAPFIGFIQERAW
LRQQGKEVGETLLYYGCRSDDEDYLYREELAQFHRDGALTQLNVAFSREQSHKVYVQHLLKQDREHLWKLI EGGA
HIYVCGDARNMARDVQNTFYDIVAELGAMEHAQAVDYIKKLMTKGRYSLDVWS

2507/6881
FIGURE 2304

GAGGAGCCTCGGGTGGGCCGGGGTTGCTGCGCCGTCCTCCACTACTGGCTACTGGCGCTGCAGCCATGCAGCCCC
CGCCCCCGGGCCCGCTGGGCGACTGCCTGCGGGACTGGGAGGATCTACAGCAGGACTTCCAGAACATCCAGGAGA
CCCATCGGCTCTACCGCCTGAAGCTGGAGGAGCTGACCAAACCTTCAGAACAAATTGCACCAGCTCCATCACGCGGC
AGAAGAAGCGGCTCCAGGAGCTGGCCCTCGCCCTGAAGAAATGCAAACCCTCCCTCCCAGCAGAGGCCGAGGGGG
CCGCACAGGAGCTGGAGAACCAGATGAAAGAGCGCCAAGGCCTCTTCTTTGACATGGAGGCCTATTTGCCTAAGA
AGAATGGATTGTACCTGAGCCTGGTTCTGGGGAACGTCAACGTACGCTCCTGAGCAAGCAGGCTAAGTTTGCT
ACAAGGACGAGTATGAGAAGTTCAAGCTCTACCTCACCATCATCCTCATCTCCTTCACTTGCCGCTTCC
TGCTCAACTCCAGGGTGACAGATGCTGCCTTCAACTTCCTGCTGGTCTGGTACTACTGCACCCTGACCATCCGGG
AGAGCATCCTCATCAACAACGGCTCCCGGATCAAAGGCTGGTGGGTGTTCCATCACTACGTGTCCACCTTCCTGT
CGGGAGTCATGCTGACGTGGCCCGACGGTCTCATGTACCAGAAATTCCGGAACCAATTCCTCTCCTTTTCCATGT
ACCAGAGCTTCGTGCAGTTTCTCCAGTACTACTACCAGAGCGGCTGCCTCTACCGCCTGCGGGCGCTGGGCGAGC
GGCACACCATGGACCTCACTGTGGAGGGCTTCCAGTCCTGGATGTGGCGGGGCCTCACCTTCCTGCTGCCTTTTC
TTTTCTTTGGACACTTCTGGCAGCTTTTTTAACGCGCTGACGTTGTTCAACCTGGCCCAGGACCCTCAGTGCAAGG
AGTGGCAGGTGCTTATGTGCGGCTTTCCTTCCTCCTCCTTTTCTCGGCAATTTCTTCACCACCCTGAGGGTTG
TGCACCACAAGTTTACAGTCAGCGGCACGGGAGCAAGAAGGATTGAGGCTGGGCCTTCCCCTGCCGGCCAGAG
GGGCTTCTGTCCTGTGTGTTGTGGGAGGGGATGGGAGGCGCCCCTCGAGTGTGCGTGTATCAGGGGGTCTCTTCT
ATTCTCCCTTGGGTTTTATGGGCGCTGTGGGCCCTGAAGGAAGACCTGGGCCCAGTGCCCTCAATAAAGAGAGGC
CCAGAAA

2508/6881
FIGURE 2305

MQPPPPGPLGDCLRDWEDLQQDFQNIQETHRLYRLKLEELTKLQNNCTSSITRQKKRLQELALALKKCKPSLP
AEGAAQELNQMKERQGLFFDMEAYLPKKNGLYLSVLGNVNVTLSSKQAKFAYKDEYEKFKLYLTIILILISFT
CRFLNLSRVTDAAFNFLVWYYCTLTIREILINNGSRIKGWWVFHHYVSTFLSGVMLTWPDGLMYQKFRNQFLS
FSMYQSFVQFLQYYYQSGCLYRLRALGERHTMDLTVEGFQSWMWRGLTFLLPFLFFGHFWQLFNALTFLNLAQDP
QCKEQVLMCGFPFLLLFLGNFFTTLRVVHHKFHSQRHGSKKD

2509/6881
FIGURE 2306

GGCGCTGGGCAGTGTGGAGGTCGTTGGAGTCACTTCCGCGTCACCAGCTCCTGTGCCTGCCAGTCGGTGCCCCCTC
CCGCTCCAGCC**ATG**CTCTCCGCCCTCGCCCGGCCTGCCAGCGCTGCTCTCCGCCGCAGCTTCAGCACCTCGGCCC
AGAACAATGCTAAAGTAGCTGTGCTAGGGGCCTCTGGAGGCATCGGGCAGCCACTTTCCTTCTCTGAAGAACA
GCCCCTTGGTGAGCCGCTGACCCCTCTATGATATCGCGCACACACCCGGAGTGCCGCAGATCTGAGCCACATCG
AGACCAAAGCCGCTGTGAAAGGCTACCTCGGACCTGAACAGCTGCCTGACTGCCTGAAAGGTTGTGATGTGGTAG
TTATTCCGGCTGGAGTCCCCAGAAAGCCAGGCATGACCCGGGACGACCTGTTCAACACCAATGCCACGATTGTGG
CCACCCTGACCGCTGCCTGTGCCCAGCACTGCCCAGGAAGCCATGATCTGCGTCATTGCCAATCCGGTTAATTCCA
CCATCCCCATCACAGCAGAAAGTTTCAAGAAGCATGGAGTGTACAACCCCAACAAAATCTTCGGCGTGACGACCC
TGGACATCGTCAGAGCCAACACCTTTGTTGCAGAGCTGAAGGGTTTGGATCCAGCTCGAGTCAACGTCCCTGTCA
TTGGTGGCCATGCTGGGAAGACCATCATCCCCCTGATCTCTCAGTGACCCCCCAAGGTGGACTTTCCCCAGGACC
AGCTGACAGCACTCACTGGGCGGATCCAGGAGGCCGGCACGGAGGTGGTCAAGGCTAAAGCCGGAGCAGGCTCTG
CCACCCTCTCCATGGCGTATGCCGGCGCCCGCTTTGTCTTCTCCCTTGTGGATGCAATGAATGGAAAGGAAGGTG
TTGTGGAATGTTCCCTTCGTTAAGTCACAGGAAACGGAATGTACCTACTTCTCCACACCGCTGCTGCTTGGGAAAA
AGGGCATCGAGAAGAACCTGGGCATCGGCAAAGTCTCCTCTTTTGAGGAGAAGATGATCTCGGATGCCATCCCCG
AGCTGAAGGCCTCCATCAAGAAGGGGAAGATTTTCGTGAAGACCTGAAG**TGA**GCCGCTGTGACGGGTGGCCAGT
TTCCTTAATTTATGAAGGCATCATGTCACTGCAAAGCCGTTGCAGATAAACTTTGTATTTTAATTTGCTTTGGTG
ATGATTACTGTATTGACATCATCATGCCTTCCAAATTGTGGGTGGCTCTGTGGGCGCATCAATAAAAGCCGTCCT
TGATTTTATTTTCAAGGTCCCTTCTGTAAAAA

2510/6881
FIGURE 2307

MLSALARPASAALRRSFSTSAQNNAKVAVLGASGGIGQPLSLLLKNSPLVSRLTLYDIAHTPGVAADLSHIETKA
AVKGYLGPEQLPDCLKGCDVVVIPAGVPRKPGMTRDDLFNTNATIVATLTAACAQHCPEAMICVIANP VNSTIPI
TAEVFKKHGVYNPNKIFGVTTLDIVRANTFVAELKGLDPARVNVFVIGGHAGKTIIP LISQCTPKVDFFQDQLTA
LTGRIQEAGTEVVKAKAGAGSATLSMAYAGARFVFSLVDAMNGKEGVVECSFVKSQETECTYFSTPLLLGKKGIE
KNLGIGKVSSFEEKMISDAIPELKASIKKGEDFVKTLK

2511/6881
FIGURE 2308

CTCAAACACCGCCTGCTAAAAATACCCGACTGGAGGAGCATAAAAGCGCAGCCGAGCCAGCGCCCCGCACTTTT
CTGAGCAGACGTCCAGAGCAGAGTCAGCCAGCATGACCGAGCGCCGCGTCCCCTTCTCGCTCCTGCGGGGCCCCA
GCTGGGACCCCTTCCGCGACTGGTACCCGCATAGCCGCTCTTCGACCAGGCCTTCGGGCTGCCCCGGCTGCCGG
AGGAGTGGTCGCAGTGGTTAGGCGGCAGCAGCTGGCCAGGCTACGTGCGCCCCCTGCCCCCGCCGCCATCGAGA
GCCCCGCAGTGGCCGCGCCCGCCTACAGCCGCGCGCTCAGCCGGCAACTCAGCAGCGGGGTCTCGGAGATCCGGC
ACACTGCGGACCGCTGGCGCGTGTCCCTGGATGTCAACCACTTCGCCCCGGACGAGCTGACGGTCAAGACCAAGG
ATGGCGTGGTGGAGATCACCGGCAAGCACGAGGAGCGGCAGGACGAGCATGGCTACATCTCCCGGTGCTTCACGC
GGAAATACACGCTGCCCCCGGTGTGGACCCACCCAAGTTTCCTCCTCCCTGTCCCCTGAGGGCACACTGACCG
TGGAGGCCCCCATGCCCAAGCTAGCCACGCAGTCCAACGAGATCACCATCCCAGTCACCTTCGAGTCGCGGGCCC
AGCTTGGGGGCCCAGAAGCTGCAAAATCCGATGAGACTGCCGCCAAGTAAAGCCTTAGCCTGGATGCCACCCCT
GCTGCCGCCACTGGCTGTGCCTCCCCGCCACCTGTGTGTTCTTTTGATACATTTATCTTCTGTTTTTCTCAAAAT
AAAGTTCAAAGCAACCACCTGTAAAAAAAAAAAAAAAAAAAA

2512/6881
FIGURE 2309

MTERRVPFSLLRGPSWDPFRDWYPHSRLFDQAFGLPRLPEEWSQWLGGSSWPGYVRPLPPAAIESPAVAAPAYSR
ALSRQLSSGVSEIRHTADRWVRVSLDVNHFAPDELTVKTKDGVVEITGKHEERQDEHGYISRCFTRKYTLPPGVDP
TQVSSSLSPGTLTVEAPMPKLATQSNEITIPVTFESRAQLGGPEAAKSDETAAK

2513/6881
FIGURE 2310

ATAAAAGCGCAGCCGAGCCCAGCGCCCCGCACTTTTCTGAGCAGACGTCCAGAGCAGAGTCAGCCAGCATGACCG
AGCGCCGCGTCCCCCTTCTCGCTCCTGCGGGGCCCCAGCTGGGACCCCTTCCGCGACTGGTACCCGCATAGCCGCC
TCTTCGACCAGGCCTTCGGGCTGCCCCGGCTGCCGGAGGAGTGGTCGCAGTGGTTAGGCGGCAGCAGCTGGCCAG
GCTACGTGCGCCCCCTGCCCCCGCCGCCATCGAGAGCCCCGAGTGGCCGCGCCCGCCTACAGCCGCGCGCTCA
GCCGGCAACTCAGCAGCGGGGTCTCGGAGATCCGGCACACTGCGGACCGCTGGCGCGTGTCCCTGGATGTCAACC
ACTTCGCCCCGGACGAGCTGACGGTCAAGACCAAGGATGGCGTGGTGGAGATCACCGGTGAGCCCCCTGCTCCT
GCAGGGGAGAGGAGGAGGCTAGCAGGGCGGGCAGGGCCGGGGGCGTGCGGTTGAAACGGGGGTCCCGGGGGCCTG
GGGAGTTAAACGTTGGCCCAGCACCGGGAAAAACAGGACTCCTGATTCCCTTGCTCAGGAATTGGGAGTGCGGGT
CGCTTCTAAGGGCGCTTTCTGCTCTGTAATCCCAGCGCTTTGGGAGGCCGAGACGGGAGGATCGCTTGAGGCCAG
GAGTTCAAGACTAGCCTGGGGCAACATAGCGAGACGCGCCCCCGCCCCGACCCGCGCCATTAC

2514/6881
FIGURE 2311

CAGAGTCAGCCAGCATGACCGAGCGCCGCGTCCCCTTCTCGCTCCTGCGGGGCCCCAGCTGGGACCCCTTCCGCG
ACTGGTACCCGCATAGCCGCCTCTTCGACCAGGCCTTCGGGCTGCCCCGGCTGCCGGAGGAGTGGTCGCAGTGGT
TAGGCGGCAGCAGCTGGCCAGGCTACGTGCGCCCCCTGCCCCCGCCGCCATCGAGAGCCCCGCAGTGGCCGCGC
CCGCCTACAGCCGCGCGCTCAGCCGGCAACTCAGCAGCGGGGTCTCGGAGATCCGGCACACTGCGGACCGCTGGC
GCGTGTCCCTGGATGTCAACCACTTCGCCCCGGACGAGCTGACGGTCAAGACCAAGCTAGCCACGCAGTCCAACG
AGATCACCATCCCAGTCACCTTCGAGTCGCGGGGCCAGCTTGGGGGCCCAGAAGCTGCAAAATCCGATGAGACTG
CCGCCAAGTAAAGCCTTAGCCCGGATGCCCACCCCTGCTGCCGCCACTGGCTGTGCCTCCCCGCCACCTGTGTG
TTCTTTTGATACATTTATCTTCTGTTTTTCTCAAATAAAGTTCAAAGCAACC

2515/6881
FIGURE 2312A

GGACTGCGAAAGGAGCAGGGTTGCGGAGCTAGGGCTCCAGCCTGCGGCCGCGCATTCTTGCGTCTGGCCAGCCGC
GAGCTCTAAGGGTCGGCCCCGCGGTCGCCCCCGCGGCTCCCTGCCAGGCTCTCGCGGGCGCGCTCGGGGTGG
GGCCTCGCGGCTGGCGGAGATGCGGCCGGGGCTGCGCGGTGGTGATGCGAGCCTGCAGGGCGGCGCGCCGGGGCA
GCCGGAGCCGCGCGCCGCGGGCGCTGTAATCGGACACCAAGAGCGCTCGCCCCCGGCTCCGGCCACTTTCCATTCT
ACTCCGAGGTGCTTGATTGAGCGACGCGGAGAAAGAGCTCCGGGTGCCGCGGCACTGCAGCGCTGAGATTCTTTA
CAAAGAACTCAGAGGACCGGGAAGAAAAGAAATTTACCTTTGCGACGTGCTAGAAAAATAAGGTCGTCTGGGAAAA
GGACTGGAGACACAAGCGCATCCAACCCCGGTAGCAAACCTGATGACTTTTCCGTGCTGATTTCTTTCAACCTCGG
TATTTTCCCTTGATATTAACCTTGCATATCTGAAGAAATGGCATTCCGGACAATTTGCGTGTTGGTTGGAGTATT
TATTTGTTCTATCTGTGTGAAAGGATCTTCCCAGCCCCAAGCAAGAGTTTATTTAACATTTGATGAACCTTCGAGA
AACCAAGACCTCTGAATACTTCAGCCTTTCCCACCATCTTTAGACTACAGGATTTTATTAATGGATGAAGATCA
GGACCGGATATATGTGGGAAGCAAGATCACATTCTTTCCCTGAATATTAACAATATAAGTCAAGAAGCTTTGAG
TGTTTTCTGGCCAGCATCTACAATCAAAGTTGAAGAATGCAAAATGGCTGGCAAGATCCCACACACGGCTGTGG
GAACCTTTGTCCGTGTAATTCAGACTTTCAATCGCACACATTTGTATGTCTGTGGGAGTGGCGCTTTTCAGTCCTGT
CTGTACTTACTTGAACAGAGGGAGGAGATCAGAGGACCAAGTTTTTCATGATTGACTCCAAGTGTGAATCTGGAAA
AGGACGCTGCTCTTTCAACCCCAACGTGAACACGGTGTCTGTTATGATCAATGAGGAGCTTTTCTCTGGAATGTA
TATAGATTTTCATGGGGACAGATGCTGCTATTTTTTCGAAGTTTAACCAAGAGGAATGCGGTGAGAACTGATCAACA
TAATTCCAAATGGCTAAGTGAACCTATGTTTGTAGATGCACATGTCTATCCAGATGGTACTGATCCAAATGATGC
TAAGGTGACTTCTTCTTCAAAGAAAAACTGACTGACAATAACAGGAGCACGAAACAGATTCAATCCATGATTGC
TCGAATATGTCCTAATGACACTGGTGGACTGCGTAGCCTTGTCAACAAGTGGACCACTTTCTTAAAGGCGAGGCT
GGTGTGCTCGGTAACAGATGAAGACGGCCCAAGAACACACTTTGATGAATTAGAGGATGTGTTTCTGCTGGAAAC
TGATAACCCGAGGACAACACTAGTGTATGGCATTTTTACAACATCAAGCTCAGTTTCAAAGGATCAGCCGTGTG
TGTGTATCATTTATCTGATATACAGACTGTGTTAATGGGCCTTTTGCCACAAAGAAGGGCCCAATCATCAGCT
GATTTCTTATCAGGGCAGAATTCCATATCCTCGCCCTGGAACCTTGTCCAGGAGGAGCATTTACACCCAATATGCG
AACCACCAAGGAGTTCCAGATGATGTTGTCATTTTATTCGGAACCATCCTCTCATGTACAATTCCATCTACCC
AATCCACAAAAGGCCTTTGATTGTTTCGTATTGGCACTGACTACAAGTATACAAAGATAGCTGTGGATCGAGTGAA
CGCTGCTGATGGGAGATACCATGTCTGTTTCTCGGAACAGATCGGGGTACTGTGCAAAAAGTGGTTGTTCTTCC
TACTAACAACCTCTGTCACTGGCGAGCTCATTCTGGAGGAGCTGGAAGTCTTTAAGAATCATGCTCCTATAACAAC
AATGAAAATTTTCATCTAAAAAGCAACAGTTGTATGTGAGTTCCAATGAAGGGGTTCCTCAGGTATCTCTGCACCG
CTGCCACATCTATGGTACAGCCTGTGCTGACTGCTGCCTGGCGCGGGACCCCTATTGCGCCTGGGATGGCCATTC
CTGTTCCAGATTCTACCCAACTGGGAAACGGAGGAGCCGAAGACAAGATGTGAGACATGGAACCCCACTGACTCA
ATGCAGAGGATTTAATCTAAAAAGCATAACAGAAATGCAGCTGAAATTGTCCAGTATGGAGTAAAAAATAACACCAC
TTTTCTGGAGTGTGCCCCAAGTCTCCGCAGGCATCTATCAAGTGGCTGTTACAGAAAGACAAAGACAGGAGGAA
AGAGGTTAAGCTGAATGAACGAATAATAGCCACTTCACAGGGACTCCTGATCCGCTCTGTTTCAGGGTTCTGACCA
AGGACTTTTATCACTGCATTGCTACAGAAAATAGTTTCAAGCAGACCATAGCCAAGATCAACTTCAAAGTTTTAGA
TTCAGAAATGGTGGCTGTTGTGACGACAAATGGTCCCATGGACCTGGGCCAGCTCTGTGAGGGCTTTACCCTT
CCACCCGAAGGACATCATGGGGGCATTCAGCCACTCAGAAATGCAGATGATTAACCAATATTGCAAAGACACTCG
GCAGCAACATCAGCAGGGAGATGAATCACAGAAAATGAGAGGGGACTATGGCAAGTTAAAGGCCCTCATCAATAG
TCGAAAAGTAGAAACAGGAGGAATCAGTTGCCAGAGTCATAATATTTCTTATGTGGGTCTTATGCTTCCATTA
ACAAATGCTCTGTCTTCAATGATCAAATTTTGAAGCAAGAACTTGTGCTTTACCAAGGGGAATTACTGAAAAAG
GTGATTACTCCTGAAGTGAGTTTACACGAACTGAAATGAGCATGCATTTTCTTGATGATAGTGACTAGCACTA
GACATGTCATGGTCTCATGGTGCATATAAATATATTTAACTTAACCCAGATTTTATTTATATCTTTATTACCT
TTTCTTCAAATCGATATGGTGGCTGCAAACTAGAATTGTTGCATCCCTCAATTGAATGAGGGCCATATCCCTG
TGGTATTCCTTTCTGCTTTGGGGCTTTAGAATTCTAATTGTCACTGATTTTGTATATGAAAACAAGTTCCAAAT
CCACAGCTTTTACGTAGTAAAAGTCATAAATGCATATGACAGAATGGCTATCAAAAGAAATAGAAAAGGAAGACA
GCATTTAAAGTTGTATAAAAAACATGAGTTATTCATAAAGAGAAAATGATGAGTTTTTATGGTTCCAATGAAATAT
GTTGGGGTTTTTTTTAAGATTGTAAAAATAATCAGTTACTGGTATCTGTCACTGACCTTTGTTTCTTATTTCAGGA
AGATAAAAATCAGTAACCTACCCCATGAAGATATTTGGTGGGAGTTATATCAGTGAAGCAGTTTGGTTTATATTC
TTATGTTATCACCTTCCAAACAAAAGCACTTACTTTTTTTTGAAGTTATTTATTTTAGACTCAAAGAATATAATC

2516/6881
FIGURE 2312B

TGGCACTACTCAGTTATTACTGTTTGTCTCTTATTCCCTAGTCTGTGTGGCAAATTAAACAATATAAGAAGGAA
AAATTTGAAGTATTAGACTTCTAAATAAGGTGTGAAATCATCAAAAAGAAAAATCAAAGTAGAACTACTAATTT
TTTAAGAGGAATTTATAACAAATATGGCTAGTTTTCAACTTCAGTACTCAAATTCAATGATTCTTCTTTTTATTA
AAACCAGTCTCAGATATCATACTGATTTTTAAGTCAACACTATATATTTTATGATCTTTTCAGTGTGATGGCAAG
GTGCTTGTTATGTCTAGAAAGTAAGAAAACAATATGAGGAGACATTCTGTCTTTCAAAAGGTAATGGTACATACG
TTCCTGGTCTCTAAGTGTAAAAGTAGTAAATTTTGTGATGAATAAAATAATTATCTCCTAATTGTATGTTAGAA
TAATTTTATTAGAATAATTTTCTACTGAAATTTTCTCCAAATAAAAATTAGATGGAAAAATGTGAAAAAAT
TATTCATGCTCTCATATATATTTTTAAAAACACTACTTTTGCTTTTTTATTTACCTTTTAAGACATTTTCATGCTT
CCAGGTAAAAACAGATATTGTACCATGTACCTAATCCAAATATCATATAAACATTTTATTTATAGTTAATAATCT
ATGATGAAGGTAATTAAAGTAGATTATGGCCTTTTTTAAGTATTGCAGTCTAAAACCTTCAAAAACATAAATCATTG
TCAAAATTAATATGATTATTAATCAGAATATCAGAATATGATTCACTATTTAAACTATGATAAATTATGATAATA
TATGAGGAGGCCTCGCTATAGCAAAAATAGTTAAAAATGCTGACATAACACCAAACCTTCATTTTTTAAAAAATCTG
TTGTTCCAAATGTGTATAATTTTAAAGTAATTTCTAAAGCAGTTTATTATAATGGTTTGCTTAAAAGGTAT
AATTAACTTCTTTTCTCTTCTACATTGACACACAGAAATGTGTCAATGTAAAGCCAAAACCATCTTCTGTGTTT
ATGGCCAATCTATTCTCAAAGTTAAAAGTAAAATTGTTTCAGAGTCACAGTTCCCTTTATTTTACATAAGCCCAA
ACTGATAGACAGTAACGGTGTTTAGTTTTATACTATATTTGTGCTATTTAATTCTTTCTATTTTACAAATTATTA
AATTGTGTACACTTTCATTACTTTTAAAAATGTAGAAATCTTCATGAACATAACTCTGCTGAATGTAAAAGAAA
ATTTTTTTTCAAAAATGCTGTAAATGTATACTACTGGTGGTTGATTGGTTTTATTTTATGTAGCTTGACAATTCA
GTGACTTAATATCTATTCCATTTGTATTGTACATAAAATTTCTAGAAATACACTTTTTTCCAAAGTGTAAAGTTT
GTGAATAGATTTTAGCATGATGAACTGTCATAATGGTGAATGTTCAATCTGTGTAAGAAAACAACTAAATGTA
GTTGTCACACTAAAATTTAATTGGATATTGATGAAATCATTGGCCTGGCAAAATAAAACATGTTGAATTCCCC

2517/6881
FIGURE 2313

CTTTCTGTCTTGATGACCTGTCTAGTGCTATAAATGAACACCTTTCTGCCCCGTGGACGCCGCCGAAGAAGCATCG
TTAAAGTCTCTCTTCTCCCTGCCGTCATGTCTAAGTCAGAGTCTCCTAAAGAGCCCAAACAGCTGAGGAAGCTCT
TCATTGGAGGGTTGAGCTTTGAAACAACCAATGAGAGTCTGAGGAGCCATTTTGAGCAATGGGGAACGCTCATGG
ACTGTGTGGTAATGAGAGATCCAAACACCAAGTGCTCCAGGGGCTTTGGGTTTGTACATATGCCACTGTGGAGG
AGGTGGATGCAGCTATGAATGCAAGGCCACACAAGGTGGATGGAAGAGTTGTGGAATCAAAGAGAGCTGTTTCAA
GAGAAGATTCTCAAAGACCAGGTGCCACTTAACTGTGAAAAAGATATTTGTTGGTGGCATTAAAGAAGACACCA
AAGAACATCACCTAAGAGATTATTTTGAACAGTATGGAAAAATTGAAGTGATTGAAATCATGACTGACCGAGGCA
GTGGCAAGAAAAGGGGCTTTGCCTTTGTAAACCTTTGACGACCATGACTCTGTGGATAAGATTGTCATTTCAGAAAT
ACCATACTGTGAATGGCCACATCTGTGAAGTTAGGAAAGCCCTGTCAAAGCAAGAGATGGCGAGTACTTCATCCA
GCCAAAGAGGTCAAAGTGGTTCTGGAACTTTAGTGGTGGTCTGGAGGTGGTTTCAGTGGGAATGACAACTTTG
GTCATGGAGGAACTTCAGTGGTCGTGGTGGCTTTGGTGGCAGCCGTGGTGCTGGTGGATATGGTGGCAGTGGGG
ATGGCTATAATGGATTTGGTAATGATGGAAGCAATTTTGGAGGTGGTGGAGCTACAATGATTTTGGCAATTACA
ACAATCAGTCTTCAAAATTTTAGACCCATGAAGGGAGGAAATTTTGGAGGCAGAAGCTCTGGCCCCTATGGCGGTG
GAGGCAATACTTTGCAAAACCAAGGTGGCTATGGCAGTTCCAGCAGCAGCAGTAGCTATGGCAGTGGCAGAAGAT
TTTAATTAGGAAACAAAGCTTAGCAGGAGAGGAGAGCCAGAGAAGTGACAGGGAAGCTACAGGTTACAAGAGATT
TGTGAACTCAGCCAAGCACAGTGGTGGCAGGGCCTAGCTGCTACAAAGAAGACGTGTTTTAGACACATACTCATG
TGTATGGGCAAAAACTCGAGGACTGTATTTGTGACTAGCTGTATAACAGGTTATTTTAATTTCTATTCTGCGGA
AAGTGTAAGCATTCCAACAAAGGGTTTTAATGTAGTTTTTTTTTGCACCCATGCTGTTGATTATTAAATGTAA
TAGTCTGATTGTGACACTGAATAAATGTCTTTTTT

2518/6881
FIGURE 2314

MSKSESPKEPKQLRKLFIGGLSFETTNESLRSHFEQWGTLMDCVVMRDPNTKCSRGFGFVITYATVEEVDAAMNAR
PHKVDGRVVESKRAVSREDSQRPGAHLTVKKIFVGGIKEDTKEHHLRDYFEQYGKIEVIEIMTDRGSGKKRGFAF
VTFDDHDSVDKIVIQKYHTVNGHICEVRKALSKQEMASTSSSRGQSGSGNFVVEATMILAITTISLQILDP

2519/6881
FIGURE 2315

CCTTTCTGCCCCGTGGACGCCGCCGAAGAAGCATCGTTAAAGTCTCTCTTCTCCCTGCCGTGTCATGTCTAAGTCAGA
GTCTCCTAAAGAGCCCCAAACAGCTGAGGAAGCTCTTCATTGGAGGGTTGAGCTTTGAAACAACCAATGAGAGTCT
GAGGAGCCATTTTGAGCAATGGGGAACGCTCATGGACTGTGTGGTAATGAGAGATCCAAACACCAAGTGCTCCAG
GGGCTTTGGGTTTGTACATATGCCACTGTGGAGGAGGTGGATGCAGCTATGAATGCAAGGCCACACAAGGTGGA
TGAAGAGTTGTGGAATCAAAGAGAGCTGTTTCAAGAGAAGATTCTCAAAGACCAGGTGCCCACTTAAGTGTGAA
AAAGATATTTGTTGGTGGCATTAAAGAAGACACCAAAGAATCACCTAAGAGATTATTTTGAACAGTATGTGGA
AGCAATTTTGGAGGTGGTGAAGCTACAATGATTTTGGCAATTACAACAATCAGTCTTCAAATTTTAGACCCATG
AAGGGAGGAAATTTTGGAGGCAGAAGCTCTGGCCCCCTATGGCGGTGGAGGCAATACTTTGCAAAACCAAGGTGGC
TATGGCAGTTCCAGCAGCAGCAGTAGCTATGGCAGTGGCAGAAGATTTTAATTAGGAAACAAAGCTTAGCAGGAG
AGGAGAGCCAGAGAAGTGACAGGGAAGCTACAGGTTACAAGAGATTTGTGAACTCAGCCAAGCACAGTGGTGGCA
GGGCCTAGCTG

2520/6881
FIGURE 2316

AAGTCTCTCTTCTCCCTGCCGTCATGTCTAAGTCAGAGTCTCCTAAAGAGCCCAAACAGCTGAGGAAGCTCTTCA
TTGGAGGGTTGAGCTTTGAAACAACCAATGAGAGTCTGAGGAGCCATTTTGAGCAATGGGGAACGCTCATGGACT
GTGTGGTAATGAGAGATCCAAACACCAAGTGCTCCAGGGGCTTTGGGTTTGTACATATGCCACTGTGGAGGAGG
TGGATGCAGCTATGAATGCAAGGCCACACAAGGTGGATGGAAGAGTTGTGGAATCAAAGAGAGCTGTTTCAAGAG
AAGATTCTCAAAGACCAGGTGCCCCACTTAACTGTGAAAAAGATATTTGTTGGTGGCATTAAAGAAGACACCAAAG
AACATCACCTAAGAGATTATTTTGAACAGTATGGAAAAATTGAAGTGATTGAAATCATGACTGACCGAGGCAGTG
GCAAGAAAAGGGGCTTTGCCTTTGTAACTTTGACGACCATGACTCTGTGGATAAGATTGTCATTTCAGAAATACC
ATACTGTGAATGGCCACATCTGTGAAGTTAGGAAAGCCCTGTCAAAGCAAGAGATGGCGAGTACTTCATCCAGCC
AAAGAGGTCAAAGTGGTTCTGGAACTTTAGTGGTGGTCGTGGAGGTGGTTTCAGTGGGAATGACAACTTTGGTC
ATGGAGGAACTTCAGTGGTCGTGGTGGCTTTGGATGGCTATAATGGATTTGGTAATGATGGAAGCAATTTTGGA
GGTGGTGGAAAGCTACAATGATTTTGGCAATTACAACAATCAGTCTTCAAATTTTAGACCCATGAAGGGAGGAAAT
TTTGGAGGCAGAAGCTCTGGCCCCTATGGCGGTGGAGGCAATACTTTGCAA

2521/6881
FIGURE 2317

CCCTGCCGTCATGTCTAAGTCAGAGTCTCCTAAAGAGCCCAAACAGCTGAGGAAGCTCTTCATTGGAGGGTTGAG
CTTTGAAACAACCAATGAGAGTCTGAGGAGCCATTTTGAGCAATGGGGAACGCTCATGGACTGTGTGGTAATGAG
AGATCCAAACACCAAGTGCTCCAGGGGCTTTGGGTTTGTACATATGCCACTGTGGAGGAGGTGGATGCAGCTAT
GAATGCAAGGCCACACAAGGTGGATGGAAGAGTTGTGGAATCAAAGAGAGCTGTTTCAAGAGAAGATTCTCAAAG
ACCAGGTGCCCCTTAACTGTGAAAAAGATATTTGTTGGTGGCATTAAAGAAGACACCAAAGAACATCACCTAAG
AGATTATTTTGAACAGTATGGAAAAATTGAAGTGATTGAAATCATGACTGACCGAGGCAGTGGCAAGAAAAGGGG
CTTTGCCCTTTGTAACCTTTGACGACCATGACTCGGTGGCTTTGGTGGCAGCCGTGGTGCTGGTGGATATGGTGGC
AGTGGGGATGGCTATAATGGATTTGGTAATGATGGAAGCAATTTTGGAGGTGGTGGGAAGCTACAATGATTTTGGC
AATTACAACAATCAGTCTTCAAATTTTAGACCCATGAAGGG

2522/6881
FIGURE 2318

ATGCCAACTATGTCACCTTTACGGATACCAAACAATTGATTAGTGATACTCCAAATAATCAAGTTCCAATGAAC
CGTGCCAGCATGGCTTTTGATGCCAAATGTCTGACTGGATGCAGATTTGATGATGCCATTGTCCAGTTTGATATG
ACATATTGGCCTTTCACGGTGGTAAATGATGCTGGCAGGCCCAAGGTCCAAGTAGAGTATGAGAGAGACAAAAAG
CTGCTACCCATAGGAGGTGTCTTCTATGGTTCTGACAAAGATGAAGGAAATTGCAAAAGTCTACCTTGGGAAGAC
TGTTACCAATGCTGTGGTCACAGTGCCAGCTTACTTGAATGA

2523/6881
FIGURE 2319A

GTAACAACCGTCACCCTGGGTCCCGACTGCCACCTCCTCCTCCTCCCCCTCCCCCAACAACAACAACAAC
AACTCCAAGCACACCGGCCATAAGAGTGCCTGTGTCCCAACATGACCGAACGAAGAAGGGACGAGCTCTCTGAA
GAGATCAACAACCTTAAGAGAGAAGGTCATGAAGCAGTCGGAGGAGAACAACAACCTGCAGAGCCAGGTGCAGAAG
CTCACAGAGGAGAACACCACCCTTCGAGAGCAAGTGGAACCCACCCCTGAGGATGAGGATGATGACATCGAGCTC
CGCGGTGCTGCAGCAGCTGCTGCCCCACCCCTCCAATAGAGGAAGAGTGCCCAAGACCTCCAGAGAAGTTC
GATGGCAACCCAGACATGCTGGCTCCTTTTCATGGCCAGTGCCAGATCTTCATGGAAAAGAGCACCAGGGATTTC
TCAGTTGATCGTGTCCGTGTCTGCTTCGTGACAAGCATGATGACCGGCCGTGCTGCCCGTTGGGCCTCAGCAAAG
CTGGAGCGCTCCCACTACCTGATGCACAACCTACCAGCTTTTCATGATGGAAATGAAGCATGTCTTTGAAGACCCT
CAGAGGCGAGAGGTTGCCAAACGCAAGATCAGACGCCTGCGCCAAGGCATGGGGTCTGTCTATCGACTACTCCAAT
GCTTTCCAGATGATTGCCAGGACCTGGATTGGAACGAGCCTGCGCTGATTGACCAGTACCACGAGGGCCTCAGC
GACCACATTCAGGAGGAGCTCTCCACCTCGAGGTGCGCAAGTCGCTGTCTGCTCTGATTGGGCAGTGCATTAC
ATTGAGAGAAGGCTGGCCAGGGCTGCTGCAGCTCGCAAGCCACGCTCGCCACCCCGGGCGCTGGTGTGCTCAGC
ATTGCAAGCCACCACCAGGTAGATCCAACCGAGCCGGTGGGAGGTGCCCCGATGCGCCTGACGCAGGAAGAAAAA
GAAAGACGCAGAAAGCTGAACCTGTGCCTCTACTGTGGAACAGGAGGTCACTACGCTGACAATTGTCTGCCAAG
GCCTCAAAGTCTTCGCCGGCGGGAAACTCCCCGGCCCCGCTGTTAGAGGGACCTTCAGCGACCGGGCCAGAAATAA
TAAGGTCCCCACAAGATGATGCCTCATCTCCACACTTGCAAGTGATGCTCCAGATTTCATCTTCGGGCAGACACA
CCCTGTTTCGTCCGAGCCATGATCGATTCTGGTGCTTCTGGCAACTTCATTGATCAGGAATATGTTGCTCAAAATG
GAATTCCTCTAAGAATCAAGGACTGGCCAATACTTGTGGAAGCAATTGATGGGCGCCCCATAGCATCGGGCCAG
TTGTCCACGAAACTCAGACCTGATAGTTGACCTGGGAGATCACCGAGAGGTGCTGTCAATTTGATGTGACTCAGT
CTCCATTCTTCCCTGTCTGCTCCTAGGGGTTGCTGGCTGAGCACACATGATCCCAATATCACATGGAGCACTCGAT
CTATCGTCTTTGATTCTGAATACTGCCGCTACCACTGCCGATGTATTCTCCAATACCACCATCGCTCCCACCAC
CAGCACCACAACCGCCACTCTATTATCCAGTAGATGGATACAGAGTTTACCAACCAGTGAGGTATTACTATGTCC
AGAATGTGTACACTCCAGTAGATGAGCACGTCTACCCAGATCACCGCCTGGTTGACCCTCACATAGAAATGATAC
CTGGAGCACACAGTATTCCCAGTGGACATGTGTATTCACTGTCCGAACCTGAAATGGCAGCTCTTCGAGATTTTG
TGGCAAGAAATGTAAAAGATGGGCTAATTACTCCAACGATTGCACCTAATGGAGCCCAAGTTCTCCAGGTGAAGA
GGGGGTGGAAACTGCAAGTTTCTTATGATTGCCGAGCTCCAAACAATTTTACTATCCAGAATCAGTATCCTCGCC
TATCTATTCCAAATTTAGAAGACCAAGCACACCTGGCAACGTACACTGAATTCGTACCTCAAATACCTGGATACC
AAACATACCCACATATGCCGCTACCCGACCTACCCAGTAGGATTGCCTGGTACCCAGTGGGACGAGACGGAC
AAGGAAGATCACTATATGTACCTGTGATGATCACTTGAATCCACACTGGTACC GCCAGCCTCCGGTACCACAGT
ACCCGCCGCCACAGCCGCCCTCCACCACCACCACCGCCGCCCTCCATCTTACAGTACCCTGTAAATACCTG
TCATGTCCTTCAGGATCTCTGCCCTCAAATTTTATTCCTGTTTACGCTTCTCAATCAGTGACTGTGTGCTAAATTT
TAGGCTACTGTATCTTCAGGCCACCTGAGGCACATCCTCTCTGAAACGGCTATGGAAGGTTAGGGCCACTCTGGA
CTGGCACACATCCTAAAGCACCAAAAGACCTTCAACATTTTCTGAGAGCAACAGAGTATTTGCCAATAAATGATC
TCTATTTTTTCCACCTTGACTGCCAATCTAACTAAAATAATTAATAAGTTTACTTTCCAGCCAGTCTGGAAGTC
TGGGTTTTTACCTGCCAAAACCTCCATCACCATCTAAATTATAGGCTGCCAAATTTGCTGTTTAAATTTACAGAG
AAGCTGATACAAACGCAGGAAATGCTGATTTCTTTATGGAGGGGAGACGAGGAGGAGGAGGACATGACTTTTCT
TGCGGTTTTCGGTACCTCTTTTTAAATCACTGGAGGACTGAGGCCTTATTAAGGAAGCCAAAATTATCGGTGCAG
TGTTGAAAGGCTTCCGTGATCCTCTCGCTGCACCTTAGAACTTCACCGTCTTCAAACCTCATTTCATGGTTC
TGTTAATTCTCAAGGAGCAGCAACTCGACTGGTTCTCCAGGAGCAGGAAAAACCTTGTGACATGAAACATCTC
AGCCTGAAAAGAAAGTGCTCTCTCAGATGGACTCTTGATGTTAAGACTATGTCTTCACATCATGGTGCAAATC
ACATGTACCCAATGACTCCGGCTTTGACACAACACCTTACCATCATCATGCCATGATGGCTTCACAAAGCATT
AACCTGGTAACCAGAGATTACTGGTGGCTCCAGCGTTGTTAGATGTTTCATGAAATGTGACCACCTCTCAATCACC
TTTGAGGGCTAAAGAGTAGCACATCAAAGGACTCCAAAATCCCATACCCAACCTCTTAAGAGATTTGTCTGGTA
CTTCAGAAAGAATTTTCATGAGTGTTCTTAATTGGCTGGAAAAGCACCAGCTGACGTTTTGGAAGAATCTATCCA
TGTGTCTGCCTCCATATGCATCTGGGCATTTTCATCTTCAGTCCCCTCATTAGACTGTAGCATTAGGATGTGTGGA
GAGAGGAGAAATGATTTAGCACCCAGATTCACACTCCTATGCCTGGAAGGGGGACATCTTTGAAGAAGAGGAATT
AGGGCTGTGGACACTGTCTTGAGGATGTGGACTTCCTTAGTGAGCTCCACATTACTTGATGGTAACCACTTCAA
AGGATCAGAATCCACGTAATGAAAAAGGTCCTCTAGAGGATGGAGCTGATGTGAAGCTGCCAATGGATGAAAAG

2524/6881

FIGURE 2319B

CCTCAGAAAGCAACTCAAAGGACTCAAAGCAACGGACAACACAAGAGTTGTCTTCAGCCCAGTGACACCTCTGAT
GTCCCTTGGAAGCTTTGTGCTAACCTGGGACTGCCTGACTTCCTTTAGCCTGGTCCCTTGCTACTACCTTGAAC
GTTTTATCTAACCTCTCTTTTTCTGTTTAATTCTTTGCTACTGCCATTGACCCTGCTGCAGGATTTGTGTCATTT
TCCTGCCTGGTTGCTGAGACTCCATTTTGCTGCCACACACAGAGATGTAAGAGGCAGGCTTTAATTGCCAAAGCA
CAGTTTGAGCAGTAGAAAAACAACATGGTGTATATCTCAAATTGCCTGACATGAAGAGGAGTCTAACGGTGAAGTT
TCACTTTTCATCAGCATCATCTTTCACATGTTTATTATCATCCGCTCTTATTCTTGTCATGTTTAAACACTTAAAA
TTTTTAGTATAATTTTAGTGTGTTTTGAAGTGGTGACTAGGCTTTCAAAAACCTTCCATTGAATTACAAAGCACT
ATCCAGTTCTTATTGTTAAACTAAGTAAAAATGATAAGTAACATAGTGTAATAATTCTTTACTGTGAACCTCT
TACAATGCTGTGAATGAGAGGCTCCTCAGAACTGGAGCATTTGTATAATAATTATCCTGTTTCATCTTCAATTTT
AACATCATATATAATTTCAATTCTATCAATTGGGCCTTTAAAAATCATATAAAAGGATATAAAATTTGAAAAGAG
AAACCTAATTGGCTATTTAATCCAAAACAACCTTTTTTTTTTCTTCAATGGAATCAGAAAGCTTGTCAATCACTC
ATGTGTTTTAGAGTAATTACTTTTTAAATGGTGCATTTGTGCTTCTGAACTATTTTGAAGAGTCACTTCTGTTTA
CCTCAAGTATCAATTCATCCTCCATACATTTGAATTCAAGTTGTTTTTGTCAAATTTACAGTTGTCAATTGATC
TTCAAGCTGCAGGGTGCTAGAAATGGGCCGTTGTCTGTAGCCCTGGCATGTGCACACGGACATTTGCCACCACT
GCAAGCAAAAGTCTGGAGAAGTTACCAACGACAAGAACGATTAGGGAAAATATGCTGCTGTGGGTTAACAACCTC
AGAAAGTCCCTGATCCACATTTGGCTGTTTACTAAAGCTTGTGATTAACTTTTTTGGCAGTGTGTACTATGCTCTA
TTGCTATATATGCTATCTATAAATGTAGATGTTAAGGATAAGTAATTCATAATTTATTATTCTATAGTTTTGAAG
TTTGGTTAAGTTTCCTTTCCTCAATTGATTTATTTTGTGTTAATCAAATTTATGTTAATTGGATCCTTTAAAT
TTTTTTTGGCATTTCCTCAACAAAAATGGCTTTATTATATAAGAAAGGAAAAAATCAATGGAATTTGATATCTAAA
GAAGTTAGAAAGGGAGCAAAATAAAAAACATAAAGGAGATAGATGAATTAGTAAGCAAATCAGTAGTCGAGTTTT
TCAAACITGGCAAAATTAATTAATTGACTTTTAGCCCAAATTTACATTGTTAATTAAATCAAGAAGGAAGAAGATC
TAAGAGCTCCCATTTGATAGGCAAGCCTAGAGAGAAGTCTAAATTTATCATGCTAGGATATTGAAACACAGAAA
GTTTACATACATTTATGAAGGGTCAATTTAGTTTGGACAGTGAGGTATTTGTCTTAGTGGAAAAAGGAGAATTA
GTCTGATCAAATCGTGAAGTAATACAGTGAACCTGCAGGTGCACAAAATAAGAGGGCCACATCTATATGGTGCAG
TCTGGAATTTCTGTTAAGTTTGTAGGTACCTCTTGGACTTCTGAATTGATCCAGTTGTCATCCACCACAGACATC
TCACATCAGATACAGACAGTTCCAAGATTGACAACAGAGAACAACCTGCTGGAAAGACCTGGGCAGAAATGGAGA
GCCCTGCGGGAACCATGCTACATTTTCATCTAAAGAGAGAATGCACATCTGATGAGACTGAAAGTTCTTTGTTGT
TTTAGATTGTAGAATGGTATTGAATTGGTCTGTGGAAAATTGCATTGCTTTTATTTCTTTGTGTAATCAAGTTTA
AGTAATAGGGGATATATAATCATAAGCATTTTAGGGTGGGAGGGACTATTAAGTAATTTTAAGTGGGTGGGGTTA
TTTAGAATGTTAGAATAATATTATGTATTAGATATCGCTATAAGTGGACATGCGTACTTACTTGTAACCTTTTAC
CCTATAATTGCTATCCTTAAAGATTTCAAATAAACTCGGAGGGAACTGCAGGGAGACCAACTTATTTAGAGCGAA
TTGGACATGGATAAAAAACCCAGTGGGAGAAAGTTCAAAGGTGATTAGATTAATAATTTAATAGAGGATGAGTGA
CCTCTGATAAATTACTGCTAGAATGAACCTGTCAATGATGGATGGTAAATTTTCATGGAAGTTATAAAAGTGATA
AATAAAAACCCCTTGCTTTTACCCCTGTCAGTAGCCCTCCTCCTACCACTGAACCCCATGCCCCCTACCCCTCCTT
CTAAGTTTATTGCTGTATTCTCTTCACTCTATATTTCTCTCTATTTGCTAATATTGCATTGCTGTTACAATAAAA
ATTCAATAAAGATTTAGTGGTTAAGTGC

2525/6881
FIGURE 2320

MTERRRDELSEEINNLREKVMKQSEENNNLQSQVQKLTEENTTLREQVEPTPEDEDDDIELRGAAAAAAPPPIE
EECPEDLPEKFDGNPDMLAPFMAQCQIFMEKSTRDFSVDVRVRCFVTSMMTGRAARWASAKLERSHYLMHNYPAF
MEMKHVFEDPQRREVAKRKIRRLRQGMGSVIDYSNAFQMIQDLWNEPALIDQYHEGLSDHIQEELSHLEVAK
SLSALIGQCIHIERRLARAAAARKPRSPPRALVLPFIASHHQVDPTEPVGGARMRLTQEEKERRRKLNLCLYCGT
GGHYADNCPAKASKSSPAGNSPAPL

2526/6881
FIGURE 2321A

AGCACACGGCAGCAGGAGGTTTCGGCTAAGTTGGAGGTACTGGCCACGACTGCATGCCCGCGCCCCGCCAGGTGA
TACCTCCGCGGTGACCCAGGGGCTCTGCGACACAAGGAGTCTGCATGTCTAAGTGCTAGACATGCTCAGCTTTG
TGGATACGCGGACTTTTGTGTGCTTGCAGTAACCTTATGCCTAGCAACATGCCAATCTTTACAAGAGGAAACTG
TAAGAAAGGGCCCAGCCGGAGATAGAGGACCACGTGGAGAAAGGGGTCCACCAGGCCCCCAGGCAGAGATGGTG
AAGATGGTCCACAGGCCCTCCTGGTCCACCTGGTCCCTCCTGGCCCCCTGGTCTCGGTGGGAACCTTTGCTGCTC
AGTATGATGGAAGAGGAGTTGGACTTGGCCCTGGACCAATGGGCTTAATGGGACCTAGAGGCCACCTGGTGCA
CTGGAGCCCCAGGCCCTCAAGGTTTCCAAGGACCTGCTGGTGAGCCTGGTGAACCTGGTCAAACCTGGTCCCTGCAG
GTGCTCGTGGTCCAGCTGGCCCTCCTGGCAAGGCTGGTGAAGATGGTCACCTGGAAAACCCGGACGACCTGGTG
AGAGAGGAGTTGTTGGACCACAGGGTGCTCGTGGTTTCCCTGGAACTCCTGGACTTCTGGCTTCAAAGGCATTA
GGGGACACAATGGTCTGGATGGATTGAAGGGACAGCCCGGTGCTCCTGGTGTGAAGGTGAACCTGGTGCCCCCTG
GTGAAAATGGAATCCAGGTCAAACAGGAGCCCGTGGGCTTCTGGTGAGAGAGGACGTGTTGGTGCCCCCTGGCC
CAGCTGGTGCCCCGTGGCAGTGATGGAAGTGTGGGTCCCGTGGGTCTGCTGGTCCCATTGGGTCTGCTGGCCCTC
CAGGCTTCCCAGGTGCCCTGGCCCCAAGGTGAAATTGGAGCTATTGGTAACGCTGGTCCCTGCTGGTCCCCGCCG
GTCCCCGTGGTGAAGTGGGTCTTCCAGGCCTCTCCGGCCCCGTGGACCTCCTGGTAATCCTGGAGCAAACGGCC
TTACTGGTGCCAAGGGTGCTGCTGGCCTTCCCGGCGTTGCTGGGGCTCCCGGCCTCCCTGGACCCCGCGGTATT
CTGGCCCTGTTGGTGCTGCCGGTGCTACTGGTGCCAGAGGACTTGTGGTGAGCCTGGTCCAGCTGGCTCCAAAG
GAGAGAGCGGTAAACAAGGTGAGCCCGGCTCTGCTGGGCCCCAAGGTCTCCTGGTCCCAGTGGTGAAGAAGGAA
AGAGAGGCCCTAATGGGGAAGCTGGATCTGCCGGCCCTCCAGGACCTCCTGGGCTGAGAGGTAGTCTGGTTCTC
GTGGTCTTCTGGAGCTGATGGCAGAGCTGGCGTCATGGGCCCTCCTGGTAGTCGTGGTGCAAGTGGCCCTGCTG
GAGTCCGAGGACCTAATGGAGATGCTGGTCGCCCTGGGGAGCCTGGTCTCATGGGACCCAGAGGTCTTCTGGTT
CCCCTGGAAATATCGGCCCGCTGGAAAAGAAGGTCTGTGGCCCTCCTGGCATCGACGGCAGGCCTGGCCCAA
TTGGCCCCGTGGAGCAAGAGGAGAGCCTGGCAACATTGGATTCCCTGGACCCAAAGGCCCCACTGGTGACCCTG
GCAAAAACGGTGATAAAGGTCATGCTGGTCTTGTGGTGCTCGGGGTGCTCCAGGTCTGATGGAACAATGGTG
CTCAGGGACCTCCTGGACCACAGGGTGTTCAAGGTGGAAGAGGTGAACAGGGTCCCGCTGGTCTCAGGCTTCC
AGGGTCTGCCTGGCCCCCTCAGGTCCCGCTGGTGAAGTTGGCAAACCAGGAGAAAGGGGTCTCCATGGTGAGTTTG
GTCTCCCTGGTCTGCTGGTCCAAGAGGGGAACGCGGTCCCCCAGGTGAGAGTGGTGCTGCCGGTCTACTGGTG
CTATTGGAAGCCGAGGTCTTCTGGACCCCAAGGCCTGATGGAACAAGGGTGAACCTGGTGTGGTTGGTGCTG
TGGGCACTGCTGGTCCATCTGGTCTAGTGGACTCCCAGGAGAGAGGGGTGCTGCTGGCATACTGGAGGCAAGG
GAGAAAAGGGTGAACCTGGTCTCAGAGGTGAAATTGGTAACCTGGCAGAGATGGTGCTCGTGGTGCTCATGGTG
CTGTAGGTGCCCTGGTCTGCTGGAGCCACAGGTGACCGGGGCGAAGCTGGGGCTGCTGGTCTGCTGGTCTCTG
CTGGTCTCGGGGAAGCCCTGGTGAACGIGGCGAGGTGGTCTGCTGGCCCCAACGGATTTGCTGGTCCGGCTG
GTGCTGCTGGTCAACCGGGTGCTAAAGGAGAAAGAGGAGGCAAAGGGCTAAGGGTGAAAACGGTGTTGTTGGTC
CCACAGGCCCGTTGGAGCTGCTGGCCAGCTGGTCCAAATGGTCCCCCGGTCTGCTGGAAGTCGTGGTGATG
GAGGCCCCCTGGTATGACTGGTTTCCCTGGTGCTGCTGGACGGACTGGTCCCCCAGGACCTCTGGTATTTCTG
GCCCTCCTGGTCCCCCTGGTCTGCTGGGAAAGAAGGGCTTCGTGGTCTCCTGGTGACCAAGGTCCAGTTGGCC
GAACTGGAGAAGTAGGTGCAGTTGGTCCCCCTGGCTTCGCTGGTGAGAAGGTCCCTCTGGAGAGGCTGGTACTG
CTGGACCTCCTGGCACTCCAGGTCTCAGGTCTTCTTGGTGCTCCTGGTATTCTGGGTCTCCCTGGCTCGAGAG
GTGAACGTGGTCTACCTGGTGTGCTGGTGCTGTGGGTGAACCTGGTCTCTTGGCATTGCCGGCCCTCCTGGGG
CCCGTGGTCTCCTGGTGCTGTGGGTAGTCTGGAGTCAACGGTGCTCCTGGTGAAGCTGGTCTGATGGCAACC
CTGGGAACGATGGTCCCCCAGGTGCGATGGTCAACCCGGACACAAGGGAGAGCGGGTTACCCTGGCAATATTG
GTCCCGTTGGTGCTGCAGGTGCACCTGGTCTCATGGCCCCGTGGGTCTGCTGGCAAACATGGAACCCGTGGTG
AACTGGTCTCTTCTGGTCTGTGGTCTGCTGGTGCTGTTGGCCCAAGAGGTCTAGTGGCCCAACAGGCATTC
GTGGCGATAAGGGAGAGCCCGGTGAAAAGGGGCCAGAGGTCTTCTGGCTTCAAGGGACACAATGGATTGCAAG
GTCTGCCTGGTATCGCTGGTCACCATGGTGATCAAGGTGCTCCTGGTCCGTGGGTCTGCTGGTCTAGGGGCC
CTGCTGGTCTTCTGGCCCTGCTGGAAAAGATGGTGCACCTGGACATCCTGGTACGGTTGGACCTGCTGGCATTC
GAGGCCCTCAGGGTCAACCAAGGCCCTGCTGGCCCCCTGGTCCCCCTGGCCCTCCTGGACCTCCAGGTGTAAGCG
GTGGTGGTTATGACTTTGGTTACGATGGAGACTTCTACAGGGGTGACCAGCCTCGCTCAGCACCTTCTCTCAGAC
CCAAGGACTATGAAGTTGATGCTACTCTGAAGTCTCTCAACAACCAGATTGAGACCCTTCTTACTCCTGAAGGCT

2527/6881
FIGURE 2321B

CTAGAAAGAACCCAGCTCGCACATGCCGTGACTTGAGACTCAGCCACCCAGAGTGGAGCAGTGGTTACTACTGGA
TTGACCCCAACCAAGGATGCACTATGGAAGCCATCAAAGTATACTGTGATTTCCCTACCGGCGAAACCTGTATCC
GGGCCCCAACCTGAAAACATCCCAGCCAAGAACTGGTATAGGAGCTCCAAGGACAAGAAACACGTCTGGCTAGGAG
AAACTATCAATGCTGGCAGCCAGTTTGAATATAATGTTGAAGGAGTGACTTCCAAGGAAATGGCTACCCAACTTG
CCTTCATGCGCCTGCTGGCCAACTATGCCTCTCAGAACATCACCTACCACTGCAAGAACAGCATTGCATACATGG
ATGAGGAGACTGGCAACCTGAAAAAGGCTGTCAATCTACAGGGCTCTAATGATGTTGAACTTGTTGCTGAGGGCA
ACAGCAGGTTCACTTACACTGTTCTTGTAGATGGCTGCTCTAAAAAGACAAATGAATGGGGAAAGACAATCATTG
AATACAAAACAAATAAGCCATCACGCCTGCCCTTCCTTGATATTGCACCTTTGGACATCGGTGGTGCTGACCATG
AATTCTTTGTGGACATTGGCCCCAGTCTGTTTCAAATAAATGAACTCAATCTAAATTAAGAAAGAAATTTGA
AAAAACTTTCTCTTTGCCATTTCTTCTTCTTCTTTTAACTGAAAGCTGAATCCTTCCATTTCTTCTGCACATC
TACTTGCTTAAATTGTGGGCAAAAGAGAAAAAGAAGGATTGATCAGAGCATTGTGCAATACAGTTTCATTAACTC
CTTCCCCCGCTCCCCCAAAAATTGAATTTTTTTTTTCAACACTCTTACACCTGTTATGGAAAAATGTCAACCTTTG
TAAGAAAACCAAAATAAAAAATTGAAAAATAAAAAACCATAAACATTTGCACCACTTGTGGCTTTTGAATATCTTCC
ACAGAGGGAAGTTTTAAACCCAAACTTCCAAAGGTTTAAACTACCTCAAAACACTTTCCCATGAGTGTGATCCAC
ATTGTTAGGTGCTGACCTAGACAGAGATGAACTGAGGTCCTTGTTTTGTTTTGTTTCATAATACAAAGGTGCTAAT
TAATAGTATTTTCAATACTTGAAGAATGTTGATGGTGCTAGAAGAATTTGAGAAGAAATACTCCTGTATTGAGTT
GTATCGTGTGGTGTATTTTTTAAAAAATTTGATTTAGCATTTCATATTTTCCATCTTATTCCCAATTAAGATG
CAGATTATTTGCCCAAAGTTGTCCTCTTCTTCAGATTTCAGCATTGTGTTCTTTGCCAGTCTCATTTTTCATCTTCTT
CCATGGTTCACAGAAGCTTTGTTTCTTGGGCAAGCAGAAAAATTAAATTGTACCTATTTTGTATATGTGAGATG
TTTAAATAAATTGTGAAAAAATGAAATAAAGCATGTTTGGTTTTTCCAAAAGAACATAT

2528/6881
FIGURE 2322

ATTTAACTTTTAAATGCTTTTTCTACAATATGCTATAAATATAAGAAAAATTAAAATTCACATAACAGCAAGACTAC
ATACCCACCCAGGTCCCGCTCCCAAAGACACACATAGAGGGACATACACACAACAATCCTAAAAATGACTTTGTA
GAGATAGGTCACTTGGAAATGTGTGTTGAAATGTTGTTGGTTTTTTTTGGTTGGTTTGTGTTGTTGTTTTTTGTTAG
ACTGATAGGGAGCCCCCTCCCACTAAAGACACCCTTGATACTGTTATTTCAAGGATGAACTTATTTATCTGGGACA
GACATCTTCAGAATGACACATGCCAAACAGTGGTTCTTATTAAATCAAAGGTTGAGATATTATCAGATTCAGAAA
TAGTGATGCTTTGTGTATCTATTTTCTTCTCTTTAAACAGAAAAAGACAAATGAATGGGGAAAGACAATCATTGA
ATACAAAACAAATAAGCCATCACGCCTGCCCTTCCTTGATATTGCACCTTTGGACATCGGTGGTGCTGACCATGA
ATTCTTTGTGGACATTGGCCCAGTCTGTTTCAAATAAATGAACTCAATCTAAATTAAAAAGAAAGAAATTTGGA
GAAAAAGAAGGATTGATCAGAGCATTGTGCAATACAGTTTCATTAACCTCCTTCCCCCGCTCCCCCAAAATTTGA
ATTTTTTTTTTCAACACTCTTACACCTGTIATGGAATGTCAACCTTTGTAAGAAAACCAAATAAAAAATTGAAA
AATAAAAACCATAAAACATTTGCACCACTTGTGGCTTTTGAATATCTTCCACAGAGGGAAGTTTAAAACCCAACT
TCCAAAGGTTTAAACTACCTCAAAACACTTCCCATGAGTGTGATCCACATTGTTAGGTGCTGACCTAGACAGAG
ATGAACTGAGGTCTTGTGTTTGTGTTTCATAATACAAAGGTGCTAATTAATAGTATTTAGATACTTGAAGAA
TGTTGATGGTGCTAGAAGAATTTGAGAAGAAATACTCCTGTATTGAGTTGTATCGTGTGGTGATTTTTTTAA

2529/6881
FIGURE 2323

CATCCGTGGACTTGGAGGCTGGCTCGGGCCCCGCACCTCCCATCCCCAGCTGCCCGCAACCCCCAGTGA CT CGGGA
TCCCCCGGAGAGCCCTCCCCCTCTCGGCAGGAGGGGGCTGACTCAGGGAGAAAATGGCAGTTT AGGGCCTAGGGGGC
CACGTGACCCTCCCCCAGGAATGTGGTGACGTATCGGAGGCGTGGTTCGTCCCCAAAATTAGGGAGGAAGAGGAA
AAAAAAAAGCCAGAAAAAGTTTTCTTTTCTGGAGTCCCAAACGAGGTGCGGGACGGAAGAGGGGGTGAAGGCCAG
AGGCTCGGGGCTTCAAGACCGCTGTCTGGAGTCCCCCTTTCCAGGCCATGTGCGGGGCCACCTGGCTGCCCCCGA
AGCAGCCGGAGCCCGCCAGAGCCCCCTCAGGGGAGGGCGATCCCCCGCGGCACCCCGGGGCCACCACGGCCCCACG
GAGCAGCACTCCAGCCCCACCCAGGGTCAATTTTTGCCCCCTTCCATCTGAGCAGTGTTACCAGGCCCCAGGGG
GACCGGAGGATCGGGGGCCGGCGTGGGTGGGGTCCCATGGAGTACTCCAGCACACGCAGGGGCTCCCTGCAGACA
GGGGGGGCCTTCGCCCTGGAAGCCTGGACGCCGAGATAGACTTGCTGAGCAGCACGCTGGCCGAGCTGAATGGGG
GTCGGGGTCA TGCGTCACGGCGACCAGACCGACAGGCATATGAGCCCCCGCCACCTCCTGCCTACCGCACGGGCT
CCCTGAAGCCAAATCCAGCCTCGCCGCTCCCAGCGTCTCCCTATGGGGGGCCCCACTCCAGCCTCTTACACTACCG
CCAGCACCCCGGCTGGCCCCAGCCTTCCCCGTGCAAGTGAAGGTGGCACAGCCAGTGAGGGGCTGCGGGCCACCCA
GGCGGGGAGCCTCTCAGGCCTCTGGGCCCCCTCCCGGGCCCCCACTTTCTCTCCCAGGCCGAGGTGAAGTCTGGG
GGCCTGGCTATAGGAGCCAGAGAGAGCCAGGGCCAGGGGCCAAAGAGGAAGCTGCTGGGGTCTCTGGCCCTGCAG
GAAGAGGAAGAGGAGGCGAGCACGGGCCCCAGGTGCCCTGAGCCAGCCTCCAGAGGATGAGCTGGATAGGGCTGA
CGAAGAAGCTGGTTACGACATGAACCACCCGCCCAGCGGGGAGTACTTTGGCCAGTGTGGTGGCTGCGGAGAAG
ATGTGGTTGGGGATGGGGCTGGGGTTGTGGCCCTTGATCGCGTCTTTACGTGGGCTGCTTTGTATGTTCTACAT
GCCGGGGCCAGCTTCGCGGCCAGCATTTCTACGCCGTGGAGAGGAGGGCATATTGCGAGGGCTGCTACGTGGCCA
CCCTGGAGAAATGTGCCACGTGCTCCCAGCCCATCCTGGACCGGATCCTGCGGGCTATGGGGAAGGCCTACCACC
CTGGCTGCTTACCTGCGTGGTGTGTACCGCGGCCTCGACGGCATCCCCCTTCACAGTGGATGCTACGAGCCAGA
TCCACTGCATTGAGGACTTTCACAGGAAGTTTGCCCCAAGATGCTCAGTGTGCGGTGGGGCCATAATGCCTGAGC
CAGGT CAGGAGGAGACTGTGAGAATTGTTGCTCTGGATCGAAGTTTTACATTGGCTGTTACAAGTGCGAGGAGT
GTGGGCTGCTGCTCTCCTCTGAGGGCGAGTGT CAGGGCTGCTACCCGCTGGATGGGCACATCTTGTGCAAGGCCT
GCAGCGCCTGGCGCATCCAGGAGCTCTCAGCCACCGTCA CCACTGACTGCTGAGTCTTCCTAGAAGTACCTGCTG
GGTTCTCAGTTCCAGTTCCCATCCTTTGATTGATCACTCTCCCTGACATCCACCTGTATGACTTTGTACCAAAAT
GCTGTCTTCTCTTTCTCCAATCAAGAAATAATAATCCCTCGAGTTTACAAAACACTTCCAAGTCTGTTGTCTCAT
CTGATTCTCCAGTAGCCCATTACAGGCCCCAGTCATTGTT

2530/6881
FIGURE 2324

MSGPTWLPPKQPEPARAPQGRAIPRGTPGPPPAHGAALQPHPRVNFCELPSEQCYQAPGGPEDRGPAWVGSHGVL
QHTQGLPADRGGLRPGSLDAEIDLLSSTLAELNGGRGHASRRPDRQAYEP PPPPAYRTGSLKPNPASPLPASPYG
GPTPASYYTASTPAGPAFPVQVKVAQPVRGCGPFRRGASQASGPLPGPHFFLPGRGEVWGPGYRSQREFGPGAKE
EAAGVSGPAGRGRGGEHGPQVPLSQPPEDELDRLTKKLVHDMNHPPSGEYFGQCGGCGEDVVG DGAGVVALDRV F
HVGCFVCSTCRAQLRGQHFYAVERRAYCEGCVATLEKCATCSQPILDRILRAMGKAYHPGCFTCVVCHRG LDGI
PFTVDATSQIHCIEDFHRKFAPRCSVCGGAIMPEPGQEETVRIVALDRSFHIGCYKCEECGLLLSSEGE CQGCYP
LDGHILCKACSAWRIQELSATVTTDC

2531/6881
FIGURE 2325

GTCTTTTCCGGCCCCCGTGCACTCTCCGCCCGAGCGGAGCCCCCGGCTCGCGGGGATCGCCCCGAGCGCTGCG
TCCTGCGGGTCACCTAACCATTGTGGCTTCCTCTACCTGTGCTCAGCCATGGCCAGCGAGAGCTCACCTCTGC
TGGCCTACCGGCTCCTGGGGGAGGAGGGGGTTGCCCTCCCTGCCAATGGGGCCGGGGTCTGGAGGGGCGTCTG
CCCGGAAGCTGTCCACCTTCCTGGGTGTGGTGGTGCCACTGTCTGTCCATGTTACAGCATAGTTGTTTTTCTGA
GGATTGGGTTCGTGGTGGGTCATGCTGGGCTACTGCAGGCCCTGGCCATGCTGCTGGTTGCCTACTTCATCCTGG
CACTCACCGTCTCTCTGTCTGTGCCATCGCCACCAATGGAGCCGTGCAGGGGGGCGGAGCCTACTTCATGATCA
GCCGCACACTGGGGCCCGAGGTCGGGGGCAGCATTGGGCTCATGTTCTACCTGGCTAACGTCTGTGGCTGTGCCG
TCTCCCTCCTGGGGCTGGTGGAGTCTGTGCTTGATGTCTTCGGGGCCGATGCCACAGGGGCCAGTGGGCTCCGGG
TCCTGCCCCAGGGCTACGGCTGGAACCTGCTGTATGGCTCCCTGCTGCTGGGCCCTTGTGGGTGGGGTCTGCACCC
TGGGAGCCGGCCTCTATGCCCGGGCCTCATTCCTCACATTCCCTGCTGGTCTCTGGCTCCCTGGCCTCTGTGCTCA
TCAGTTTTGTGGCTGTGGGGCCGAGGGACATCCGCTTGACTCCTAGGCCTGGCCCCAATGGCTCCTCCCTGCCGC
CCCGGTTTGGCCACTTCACCGGCTTCAACAGCAGTACCCTGAAGGACAACCTTGGGCGCTGGCTATGCTGAGGACT
ACACCACGGGAGCCGTGATGAATTTTGCCAGCGTCTTTGCTGTCTCTTTAACGGCTGTACAGGCATCATGGCTG
GGGCCAACATGTAGGGGAGCTGAAGGACCCAGCCGGGCGATCCCTCTGGGCACGATCGTCGCCGTGCCTACA
CCTTCTTCGTCTATGTCTGCTTTTCTTTCTCTCCAGCTTCACTTGTGACAGGACCCTGCTGCAGGAAGACTATG
GGTTCCTCCGCGCCATCAGCCTGTGGCCCCACTGGTGTGATCGGAATCTATGCCACAGCGCTCTCAGCGTCCA
TGAGCTCGCTCATTGGTGCTCCCGCATCCTCCATGCCCTGGCCCCGGGATGACCTCTTTGGCGTGATCTTGGCAC
CGGCCAAGGTTGTGTCCCGAGGGGAAACCCCTGGGCAGCTGTACTTTATCTTGGGGCCTGGTGCAGCTGGTGC
TCCTGGCTGGGAAGCTGAACACACTGGCTGCTGTGGTCACTGTCTTCTACCTGGTGGCCTATGCTGCCGTGGACC
TGCTCTGCCTGAGCCTGGAGTGGGCCTCGGCCCCCAACTTCGCCCCACCTTCAGCCTGTTCTCCTGGCACACCT
GCCTGCTGGGGGTGGCCTCCTGCCTGCTCATGATGTTCTCATCAGTCTGCGCGGGCTGGTGGCTCCCTGCTCC
TCATGGGTCTGCTGGCTGCCCTGCTCACCGCGCGAGGAGGCCCCAGTAGCTGGGGCTATGTCAGCCAGGCCTTGC
TTTTCCACCAGGTGCGTAAGTATCTGCTTCGGCTGGACGTCCGGAAGGATCACGTGAAGTTCTGGCGGCCCCAGC
TGCTGCTCCTGGTGGGGAACCCCCGGGGCGCCCTGCCTCTGCTGCGGTTGGCCAACCAGCTTAAGAAGGGGGGGC
TGATGTGCTGGGCCACGTACCCCTGGGAGACCTCGACTCCCTGCCCTCGGACCCTGTACAGCCGCGAGTATGGGG
CATGGCTCAGCCTGGTGGACCGTGCCAGGTGAAGGCTTTTGTGGATCTAACCTCTCACCTCCGTGCGCCAGG
GGGCTCAGCATCTGCTGCGAATCTCCGGCCTCGGTGGCATGAAGCCCAACACGTTGGTCTTAGGTTTCTACGATG
ACGCTCCACCGCAGGACCATTTCTGACGGACCCGGCTTTCTCTGAGCCTGCAGACAGCACCAGGGAGGGCAGTT
CCCCAGCTCTGAGCACCTGTTCCCTCCTCCCGGGCTCCTGGGAGCCCCCGGGCCCTCAATCCCCAGGACTATG
TGGCCACGGTGGCCGACGCCCTCAAGATGAACAAGAATGTGGTGTGGCCCCGGGCCAGCGGGCCTTGCCCCCTG
AGCGGCTGAGCCGGGGTCTGGGGGCACCTCTCAGCTGCACCATGTGGACGTGTGGCCCCTCAACCTGCTGCGGC
CCCGGGGTGGGCCCGGCTATGTGGATGTCTGCGGCCTCTTCTGCTGCAGATGGCAACCATCTTGGGCATGGTGC
CCGCTTGGCATAGCGCCCGGCTCCGGATCTTCTGTGCTGGGGCCTCGGGAGGCGCCTGGGGCGGCCGAGGGGC
GGCTGCGGGCACTGCTGAGCCAACCTGAGGATCCGGGCTGAGGTGCAGGAGTGGTGTGGGGCGAGGGGGCCGGGG
CTGGGGAACCCGAGGCGGAGGAGGAAGGGGACTTTGTGAACAGTGGGCGGGGAGACGCAGAGGCAGAGGCCCTGG
CACGCAGCGCCAACGCCCTGGTTCGGGCCCAGCAGGGGCGCGGCACAGGAGGAGGGCCGGGTGGGCCGGAGGGTG
GGGATGCTGAGGGCCCCATCACAGCCCTCACCTTCTGTACTTGCCCTCGGCCGCCAGCCGATCCCGCCCGATAACC
CCCGCTACCTGGCGCTACTGGAGACTCTAACCCGAGACCTGGGCCCCACGCTGCTGGTTCATGGGGTCACTCCAG
TCACCTGCACTGATCTGTGATGCCCTGCCTCCAGGGCTAGGTAGAGAGGGCCCAGGCAGGCGGCCTATCCTGAT
CCTTGGAGGAGGAGGAAGAGGAGGCCACTGTGGCCCGTGGCCCTGCCCTTGGGACGTGGAGCCAGGGGAGGTTT
GAAGGGGATCCTGGGCTTGGGCATCACGCCACCTCCTTTGGCAGAGGGACCCAGCACACTAACTCTGGGTGGC
TGTCCCCACCGTGCAGGGGAGGGAGTCCGCAGCCTCCCTTCACTGGTGCCTTGATGCTAGGGGCCAGGCCTCCTC
TGTGACTCTGGGCTACCTCAGTTTCCCCATTTTGGCCAGACTACCCGGCCCACTGGGGTGGTGATGTTTTCTGTT
TGTTTTATTTTCTAACTCTGCTGACCATGAATAAAAGACCAAAACAC

2532/6881
FIGURE 2326

GCGCGGGCAGGGCCGCACGAGCTGGCTGGCTGCTTGCACCCACATCCTTCTTTCTCTGGGACCTGGGGTCGCGGT
TACTTGGGCTGGCCGGCGAACCCTTGAGTGGCCTGGCGGGGAGCGGGCCTCGCGCGCCTGGAGGGCCCTGTGGAA
CGAAGAGAGGCACACAGCATGGCAGAAAACCGAGAGCCCCGCGGTGCTGTGGAGGCTGAACTGGATCCAGTGGAA
TACACCCTTAGGAAAAGGCTTCCCAGCCGCTTGCCCCGAGACCCAATGACATTTATGTCAACATGAAGACGGAC
TTTAAGGCCCAGCTGGCCCGCTGCCAGAAGCTGCTGGACGGAGGGGGCCCGGGGTCAGAACGCGTGCTCTGAGATC
TACATTCACGGCTTGGGCCTGGCCATCAACCACGCCATCAACATCGCGCTGCAGCTGCAGGCGGGCAGCTTCGGG
TCCTTGCAAGTGGCTGCCAATACCTCCACCGTGGAGCTTGTTGATGAGCTGGAGCCAGAGACCGACACACGGGAG
CCACTGACTCGGATCCGCAACAACCTCAGCCATCCACATCCGAGTCTTCAGGGTCACACCCAAGTAATTGAAAAGA
CACTCCTCCACTTATCCCCCTCCGTGATAIGGCTCTTCGCATGCTGAGTACTGGACCTCGGACCAGAGCCATGTAA
GAAAAGGCCTGTTCCCTGGAAGCCCAAAGGACTCTGCATTGAGGGTGGGGGTAAATTGTCTCTTGGTGGCCCAGTT
AGTGGGCCTTCCTGAGTGTGTGTATGCGGTCTGTAACATTGCCATATAAATAAAAAATCCTGTTGCACTAGTGT
CCTGCCAAA

2533/6881
FIGURE 2327

MAENREPRGAVEAELDPVEYTLRKRLPSRLPRRPNDIYVNMKTDFKAQLARCQKLLDGGARGQNACSEIYIHGLG
LAINHAINIALQLQAGSFGSLQVAANTSTVELVDELEPETDTREPLTRIRNNSAIHIRVFRVTPK

2534/6881
FIGURE 2328

GGAGGAAGACAGCGCCGCCCGCGCACCGCCAGCGACCTCCGCCGCAGAGTCCCACCGCCACAGGCCTCGGGCCAG
CGGCCAGGAGCTGCCTCCCCAGCCCCCGTCCCGCGGGCCCCAGCCGCCCCCAACCCTGCCCCACGGGCCCCGGCG
CCATGAGTGAGCTGGAGCAACTGAGACAGGAGGCCGAGCAGCTCCGGAACCAGATCCGGGATGCCGAAAAGCAT
GTGGGGACTCAACACTGACCCAGATCACAGCTGGGCTGGACCCAGTGGGGAGAATCCAGATGAGGACCCGGAGGA
CCCTCCGTGGGCACCTGGCAAAGATCTATGCCATGCACTGGGGGACCGACTCAAGGCTGCTGGTCAGCGCCTCCC
AGGATGGGAAGCTCATCATCTGGGACAGCTACACCACCAACAAGGTCCACGCCATCCCGCTGCGCTCCTCCTGGG
TAATGACCTGTGCCTACGCGCCCTCAGGGAACCTTGTGGCCTGTGGGGGGTTGGACAACATCTGCTCCATCTACA
GCCTCAAGACCCGCGAGGGCAACGTCAGGGTCAGCCGGGAGCTGCCTGGCCACACTGGGTACCTGTCGTGTTGCC
GCTTCCTGGATGACAACCAAATCATCACCAGCTCTGGGGATAACCACCTGTGCCCTGTGGGACATTGAGACAGGCC
AGCAGACAGTGGGTTTTGCTGGACACAGTGGGGATGTGATGTCCCTGTCCCTGGCCCCGATGGCCGCACGTTTG
TGTCAGGCGCCTGTGATGCCTCTATCAAGCTGTGGGACGTGCGGGATTCCATGTGCCGACAGACCTTCATCGGCC
ATGAATCCGACATCAATGCAGTGGCTTTCTTCCCCAACGGCTACGCCTTCACCACCGGCTCTGACGACGCCACGT
GCCGCTCTTCGACCTGCGGGCCGATCAGGAGCTCCTCATGTACTCCCATGACAACATCATCTGTGGCATCACCT
CTGTTGCCTTCTCGCGCAGCGGACGGCTGCTGCTCGCTGGCTACGACGACTTCAACTGCAACATCTGGGATGCCA
TGAAGGGCGACCGTGCAGGAGTCCTCGCTGGCCACGACAACCGCGTGAGCTGCCTCGGGGTCACCGACGATGGCA
TGGCTGTGGCCACGGGCTCCTGGGACTCCTTCCTCAAGATCTGGAACATAATGGCCCCACCCCCACTGGGCCAGG
CCAGGAGGGGCCCTGCCCATGCCACACTACAGGCCAGGGCTGCGGGGCTGGCGCAATCCAGCCCCCTTCCCCG
GGCCACGGGGCCTTGGGTCCCTGCCCTCCACCCAGGTTTGGTTCCCTCCCGGGGCCCCCACTGTGGAGATAAGAA
GGGGATGGAATGGGGGAAGAGGAGGAGCAGGAGGCCCTCATCCTTCTGCTGCCCTGGGGTTGGGGCCTCACCCCT
CTGGAGGGCCGGAGGCAGGAGGTGGAACCCAGGGGCTGGCTTTTTTAAACTGGTTTTATTTTAATTTTTATT
ATATTTTCAGTTTTTCCATAAAGGAGCCAATTCCAACCTCTGT

2535/6881
FIGURE 2329

ATCCTGCTGCTGCCGCCACCGCTGCTGCTGCTCTGCAAAATTGAGCTGCTGCCTCTGTCTTGAGGACCCCAGCGC
CTTTCCCCCGGGGCCATGCTGCCTGCAGCCACAGCCTCCCTCCTGGGGCCCCCTCCTCACTGCCTGCGCCCTGCTG
CCTTTTGCCCAAGGGCCAGACCCCCAACTACACCAGACCCGTGTTTCTGTGCGGAGGGGATGTGAAGGGGGAATCA
GGTTACGTGGCAAGTGAGGGGTTCCTCAACCTCTACCCCCCTAATAAGGAGTGATCTGGACCATAACGGTCCCC
GAGGGCCAGACTGTGTCCCTCTCATTCCGAGTCTTCGACCTGGAGCTGCACCCCGCTGCCGCTACGATGCTCTG
GAGGTCTTCGCTGGGTCTGGGACTTCCGGCCAGCGGCTCGGACGCTTTTGTGGGACCTTCCGGCCTGCGCCCCTA
GTCGCCCCCGGCAACCAGGTGACCCTGAGGATGACGACGGATGAGGGCACAGGAGGACGAGGCTTCCTGCTCTGG
TACAGCGGGCGGGCCACCTCGGGCACTGAGCACCAATTTTGCGGGGGCGGCTGGAGAAGGCCAGGGAACCCTG
ACCACGCCCAACTGGCCCCGAGTCCGATTACCCCCCGGGCATCAGCTGTTCTTGGCACATCATCGCGCCCCCGGAC
CAGGTCATCGCGCTGACCTTCGAGAAGTTTGACCTGGAGCCGGACACCTACTGCCGCTATGACTCGGTGAGCGTG
TTCAACGGAGCCGTGAGCGACGACTCCCGGAGGCTGGGGAAGTTCTGCGGCGACGCAGTCCCGGGCTCCATCTCC
TCCGAAGGGAATGAACTCCTCGTCCAGTTCGTCTCAGATCTCAGTGTCACCGCTGATGGCTTCTCAGCCTCCTAC
AAGACCCTGCCGCGGGGCACTGCCAAAGAAGGGCAAGGGCCCCGGCCCCAAACGGGGAAGTGAAGCTAAAGTCAAG
CTGCCCCCAAGTCCCAACCTCCGGAGAAAACAGAGGAATCTCCTTCAGCCCCCTGATGCACCCACCTGCCCAAAG
CAGTGCCGCGGACAGGCACCTTGCAGAGCAACTTCTGTGCCAGCAGCCTTGTGGTGACTGCGACAGTGAAGTCC
ATGGTTCGGGAGCCAGGGGAGGGCCTTGCCGTGACTGTCAGTCTTATTGGTGCTTATAAACTGGAGGACTGGAC
CTGCCTTCTCCACCCACTGGTGCTCCCTGAAGTTTACGTGCCTTGCAAGCAGTCCCCCCCCATGAAGAAAGGA
GTCAGTTATCTGCTGATGGGCCAGGTAGAAGAGAACAGAGGCCCCGTCCTTCCTCCAGAGAGCTTTGTGGTTCTC
CACCGGCCCAACCAGGACCAGATCCTCACCAACCTAAGCAAGAGGAAGTGGCCCTCTCAACCTGTGCGGGCTGCT
GCGTCCCAGGACTTGAGACGACGAGGCCAGCCCCGGCCCCCTAGCCCTCAGGCCTTCTTTCTTATCCAAATAAATGTTT
CTTAATGA

2536/6881
FIGURE 2330

MLPAATASLLGPLLTAALLPFAQGQTPNYTRPVFLCGGDVKGESGYVASEGFPNLYPPNKECIWTITVPEGQTV
SLSFRVFDLELHPACRYDALEVFAAGSGTSGQRLGRFCGTFRPAPLVAPGNQVTLRMTTDEGTGGRGFLLWYSGRA
TSGTEHQFCGGRLEKAQGTLTTPNWPESDYPPGISCSWHIIAPPDQVIALTFEKFDLEPDITYCRYDSVSVFNGAV
SDDSRRLGKFCGDAVPGSISSEGNELLVQFVSDLSVTADGFSASYKTLPRGTAKGQGPGRGTPEPKVKLPKPS
QPPEKTEESPSAPDAPTCPKQCRRTGTLQSNFCASSLVVTATVKSMVREPGEGLAVTVSLIGAYKTGGDLDPSP
TGASLKFYVPCKQCPPMKKGVSYLLMGQVEENRGPVLPPEFVVLHRPNQDQILTNLSKRKCPSQPVRAAASQD

2537/6881
FIGURE 2331

GGAGAGGCAGAGACCCAGGGGAGCCGAGGAGCGGAGACACGGACCCAGCAGGGTCACGCGGGAGGAGACTCGGGA
CACCCACTCGCTGGCTGCCACCGGGAGCAGAGGGGGGCTCGGCCGCCCTCCACATCAGTCTCCAGACCCCTG
GGGCTTCAGAGGCCGCTCCTAGGCTCCTCGGAGGAGGCGCGGGTTTCTTCTTTTCCGGAGAGCAAACCTTCTCG
GAGATGCCTGGCAGGATGAGCCGCGGCCCGGAGAGGACGGGACAGCCTCTGATCGCCGCTGCGTGCCCCGCC
ACTGCCCATGGCCAGGAGGCCCCAGGGAACGGACAGCCCGACCTCTTAGGCGCCGGGACCCCTCAGGCTCAGATCA
GTGGCCGAGGCCCCAGAGTTTGCAAACCTCAGCTCTGGAGTTCAGCAGCAACAGCAGCAGGAAAAACCTGCCCCTG
CTCCCCCTCCCCGCCACCTCCCCCTCTCCTCTTCTCCCCCTACCCAGCAGGCACCCCCGGTTCCCGCCAGGCCCTC
CTGCCATGTGCGGACCCAGACGTCCCCAGGGGCTCGGATGTCCCCGCCATGTGGCCCCCTTGTTCCAGGGGTGCCT
GAGCCCCCTTCAAGGAGCCCCAACCCACCCCAACCTTGGCCCCAGCCCTGAGCCCCAGGGACC**ATG**AGCGGGGGCA
AGAAGAAGAGTAGTTTTCCAAATCACCAGCGTCACCACGGACTATGAGGGCCCTGGGAGCCCAGGGGCTTCGGATC
CCCCACCCACAGCCCCAACCGGGCCCCCGCCCCGCTGCCCAATGGGGAGCCCAGCCCCGATCCGGGGGGCA
AGGGCACCCCCCGGAATGGCTCCCCACCACCTGGGGCCCCCTTCCCTCCCGTTTCCGGGTGGTGAAGCTGCCCCACG
GCCTGGGAGAGCCTTATCGCCGCGGTGCGTGGACGTGTGTGGATGTTTATGAGCGAGACCTGGAGCCCCACAGCT
TCGGCGGACTCCTGGAGGGAATTCGAGGGGCCTCAGGGGGCGCCGGGGGCAGATCTTTGGATTCCAGGTTGGAGC
TGGCCAGCCTCGGCCTGGGCGCCCCACCCACCGTCAGGCCTGTCTCAGGGCCCCACCTCCTGGCTCCGTCCAC
CCCCACCTCTCCTGGACCTCAGGCCGCTCCTTCACTGGGGGACTGGGCCAGCTGGTGGTGCCAGCAAAGCCA
AGGCAGAGAAACCCCCACTGTGCGCCTCCTACCCAGCAGCGCCCCCAGAGCCTGAGACCGGTGAGAGTGCGG
GCACATCCCGGGCTGCCACGCCCTGCCCTCTCTGAGGGTGGAAGCGGAGGCTGGGGGCTCAGGGGCCAGGACCC
CTCCACTGTCCCGGAGGAAAGCTGTAGACATGCGGCTGCGGATGGAGTTGGGTGCTCCAGAAGAGATGGGGCAGG
TGCCCCCACTTGACTCTCGCCCCAGCTCCCCAGCCCTCTACTTCACCCACGATGCCAGCCTGGTTCACAAATCTC
CAGACCCCTTCGGAGCAGTAGCAGCTCAGAAGTTCAGCCTGGCCCCACTCCATGTTGGCCATCAGTGGTACCTAG
ACAGCGACGATGATAGTGGCTCCGGAAGCCTGGTTGGCATTGACAACAAAATCGAGCAAGCCATGGACTTGGTGA
AGTCCCACCTCATGTTTGCGGTCCGGGAGGAGGTGGAGGTGCTGAAGGAGCAGATCCGGGAACCTGGCGGAGCGGA
ACGCTGCGCTGGAGCAGGAGAATGGGCTGCTGCGCGCCCTGGCCAGCCCGGAGCAGCTGGCTCAGCTGCCCTCCT
CGGGGGTCCCACGGCTTGGGGCCCCCTGCGCCCAATGGGCCCTCCGTCT**AG**AGCCTCCCTTCCCTTACAATGTGCCT
TTGGGGCTGCCCCGCCCTTGCCTCAGCCGCTGCCCCCTCTTCTATGCAGCTTTAATGTCCCCGTGTCCCCGGGG
TGGGAGTTCAAGGCTCAGTAATGGCCTGGTCCCCCGGCCCTGCCCCATCTCCTCATCATCCCCAGCCTTGATGG
AGGAGGGAGGGCTTCAGGACGGGGCGTCAGAGGGAGCCCCCTCTGGGAGGGAACCAACCCCCACCTCCCTCCTG
GGACCCCCCAGCAGTAGACGGCTTGGGGGAGTCGGAGGCTCCCCGGCAGACACCCACCCCATCTTGTTCCCTT
GAGGTGCCTCCTCTCCTCTGCCAGGGGAGGGAGTGTGGACAGTATCTGGAAGTTCTGGGATTACAGGTTGTTATT
AAAATAATAATAATAATTAAAACTCTGAAGAAAAAAAAAAAAAAAAAAAAA

2538/6881
FIGURE 2332

MSGGKKKSSFQITSVTTDYEGPGSPGASDPFTPQPPTGPPRLPNGEPSDPDGGKGTPRNGSPPPGAPSSRFRVV
KLPHGLGEPYRRGRWTCVDVYERDLEPHSFSGGLEGIRGASGGAGGRSLDSRLELASLGLGAPTPPSGLSQGPTS
WLRPPPTSPGPQARSFTGGLGQLVVPSKAKAEKPPLSASSPQQRPEPETGESAGTSRAATPLPSLRVEAEAGGS
GARTPPLSRRKAVDMRLRMELGAPEEMGQVPPLDSRPSSPALYFTHDASLVHKSPDPFGAVAAQKFSLAHSMIAI
SGHLDSDDDSGSGSLVGIDNKIEQAMD LVKSHLMFAVREEVEVLKEQIRELAERNAALEQENGLLRALASPEQLA
QLPSSGVPRLGPPAPNGPSV

2539/6881
FIGURE 2333

ATTTAAACTCCCAGAGCCGTTAAGTTGGTTCGTAGTCTGATGCGCGCGCAACCAGGGTGGTGGCGGAGTGCGCAT
GCGTGGTTCCGGGGCGAAGGGAACGCGCGCTCACCGTGCGCGCTCGCGGCCGGGTGGTAGTGGCGGAGGAGAAAG
GGGTCGGCGCACGCGCGGTTGAGTCTTCAGTAGTTCCGGTCTCGCGGGCCTCTTGTTTTGGTCTCGCGGGCTAG
TAGGGCGCACTTGGCGGGGAGGCGCTTGGGCGCGAGACTAGGCGTGAAGAGCAGAGCTGCGCGCGCACTCGGGAA
AGGGGGGAAGGGAGCAGGGTCCAGGCAGGGGGGGTTAGGCCCCCTGATCCCCCTCGTTACCCCGACTGGCACGGA
ATAAGGGGAGGAAATGATCGAGATGGCGGCGGAGAAGGAGCCGTTTCTGGTGCCGGCCCCGCCGCCGCCGCTCAA
AGATGAGTCGGGCGGAGGGGGCGGCCACCGTGCCACCACCAAGAGGCCGCTCTGGGGAGCTCCGCGGCGG
GACGGAGCGTGGTCCGGGTCGTTGCGCGCCATCTGCGGGGTCCCCAGCCGCTGCGGTGGTTCGGGAAAGCCCCGG
GGCCGCGGCCACCTCCTCCAGTGGTCCCCAGGCGCAGCAGCACCGAGGGGGCGGCCCCAGGCGCAGTCGCATGG
GGAGGCCCGCCTGTTCGGATCCCCCGGGGCGAGCCGCTCCCCCGGACGTGGGGGAGGAGCGCCGGGGAGGGGGCGG
GACAGAGCTGGGTCCCCCTGCTCCTCCTCGACCCCGCAATGGCTATCAGCCCCACCGGCCACCTGGGGGGGGCGG
GGGCAAGAGGAGAAATAGCTGTAATGTAGGGGGAGGCGGGGGAGGCTTCAAACATCCGGCCTTCAAGAGGCGCAG
GCGGGTGAATTCGGACTGTGACTCTGTGTTACCTTCCAACCTTCCCTCCTGGGGGGCAATATCTTTGATCCCCCTGAA
CCTGAATAGCCTCCTGGATGAGGAAGTGAGCCGCACTCTCAACGCGGAGACCCCTAAGTCATCCCCCTTCCGGC
CAAAGGGCGAGATCCGGTGGAGATCCTCATCCCCAAGATATTACTGACCCGCTCAGTCTCAATACTTGCAGTGA
TGAGGGCCATGTAGTTCTTGCTTCGCCACTCAAGACTGGTCCGAAGCGGCATAGACACCGGGGACAGCACCACCA
GCAGCAGCAGGCAGCCGGAGGGAGTGAGAGCCACCCCGTGCCGCCACAGCCCTCTCACCCCTTACTCCACGG
GGAGGGCGCCTCACAGCAGCCGCGGCACAGGGGCCAGAACC GGATGCCCCCAACCCTATGAACCAACACAGC
CATCAACTGCAGGGATGAAGTGGTGTCTCCCCTTCCATCTGCTCTGCAGGGTCCCTCAGGCTCCCTATCAGCCCC
TCCAGCTGCCTCAGTTATCTCTGCACCCCATCTTCTCCTCCCGACATCGCAAACGTGCGAGGACTTCCAGCAA
GTCGGAGGCAGGGGCTAGGGGTGGAGGCCAGGGTTCCAAGGAAAAGGGCCGAGGGAGTTGGGGAGGCCGCCACCA
CCACCACCACCCACTGCCTGCAGCAGGCTTCAAAAAGCAACAGCGCAAGTTCCAGTATGGGAATTATTGCAAATA
CTATGGGTACCGCAATCCTTCCCTGTGAGGATGGGCGCCTTCGGGTGTTGAAGCCTGAGTGGTTTTCGGGGCCGGGA
CGTCCTAGATCTGGGCTGCAATGTGGGCCATCTGACCCTGAGCATTGCCTGCAAGTGGGGCCCGTCCCGCATGGT
GGGCTGGATATCGATTCCCGGCTCATCCATTCTGCCCCGCAAAACATCCGACACTACCTTTCCGAGGAGCTGCG
TCTCCCACCCAGACTTTGGAAGGGGACCCGGGGGAGAGGGGTGAGGAAGGGACCACCACCGTTGAAAGAGGAG
CTGCTTCCAGCCTCGCTGACTGCCAGCCGGGTCCCATCGCTGCCCCCAAGTGCCCTTGGATGGAGCGGACAC
ATCAGTCTTCCCCAACAAATGTTGTCTTCGTACGGGTAATTATGTGCTGGATCGAGATGACCTGGTGGAGGCCCA
AACACCTGAGTATGATGTGGTGTCTGCCTCAGCCTCACCAAGTGGGTGCATCTGAACCTGGGGAGACGAGGGCCT
GAAGCGCATGTTTCGCCGGATCTACCGGCACCTACGCCCTGGGGGCATCCTGGTCTAGAGCCCCAACCTGGTCT
GTCGTATGGCAAGAGAAAAGACTCTTACAGAAACGATCTACAAGAACTACTACCGAATCCAATTGAAGCCAGAGCA
GTTTCAAGTTCTACCTGACATCCCCAGACGTGGGCTTCTCCAGCTATGAGCTTGTGGCCACACCCACAACACCTC
TAAAGGCTTCCAGCGTCCCTGTGTACCTGTTCCACAAGGCCCGATCCCCAGCCACTAAGTGGCCCCCTAAACAGA
AAGTGTGAAGAGGCTGCCCTCGCTGCTCATAAGGACCTGGGGGAAGAGGAAAGTGTCCCAAGGTCTTTCTTTCT
GACTCCAAAAATAGTTTCCTTTCTTGATCTGCAAAGAAAGCTTTTCTTCCGTCGCTGCCTCAGCCTCCTCCCTA
TGCCTCTGGCACCTGCGCAGCAAGGCTGGCTGTGCTGGAGTCACCATCATCTTCTCTCCCCAGCCTCCAGGC
CTTTCTCCTATTCTCTAGCCCTTCTATTCTCCCAAGGAGAGAGATTCCCATTTCTCCTCGGCCATTGTACCTAG
CTCTTGTCCCTAGCTGCATTTTCAAGTGGACCATGGATAGAGGGACTGAGGGTTAGACGGAGAAGACTGGCAGGGAG
GCACGCAGGTACTGTGAAAATCCTTCCCTTTGCCCTCCCCCAGTGGGAGAGGGGGTTGGGTTTTCAATGTGAGAA
CAGCACAATAAACTTGATGTCTAGGGCAGTGGCCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAA

2540/6881
FIGURE 2334

MVGLDIDSRLIHSARQNIRHYLSEELRLPPQTLEGDPGAEGEETTVRKRSCTFASLTASRGPIAAPQVPLDGA
DTSVFPNNVVFVTIGNYVLD RDDLVEAQTPEYDVLCLSLTKWVHLNWGDEGLKRMFRIYRHLRPGGILVLEPQP
WSSYGKRKTLTETIYKNYYRIQLKPEQFSSYLTPDVGFSSYELVATPHNTSKGFQRPVYLFHKARSPSH

2541/6881
FIGURE 2335

GGCACGAGGGGAAGTGGCTGTTTGGCTGCTGACAACATGAAGACTTCCTGCGATGAGAACAGAGGCACAGGTGCC
GGCCCTGCAGCCCCCAGAACCTGGACTGGAGGGGGCCATGGGGCACCGGACCCTGGTCCTGCCCTGGGTGCTGCT
GACCTTGTGTGTCACTGCGGGGACCCCGGAGGTGTGGGTTCAGTTTCGGATGGAGGCCACCGAGCTCTCGTCCTT
CACCATCCGTTGTGGGTTCCTGGGGTCTGGCTCCATCTCCCTGGTGACTGTGAGCTGGGGGGGCCCCGACGGTGC
TGGGGGGACCACGCTGGCTGTGTTGCACCCAGAACGTGGCATCCGGCAATGGGGCCCCTGCTCGCCAGGCCCCGCTG
GGAAACCCAGAGCAGCATCTCTCTCATCCTGGAAGGCTCTGGGGCCAGCAGCCCCCTGCGCCAACACCACCTTCTG
CTGCAAGTTTTCGCTCCTTCCCTGAGGGCTCCTGGGAGGCCTGTGGGAGCCTCCCGCCCAGCTCAGACCCAGGGCT
CTCTGCCCCGCCGACTCCTGCCCCCATTCCTGCGGGCAGACCTGGCCGGGATCTTGGGGGTCTCAGGAGTCCTCCT
CTTTGGCTGTGTCTACCTCCTTCATCTGCTGCGCCGACATAAGCACCGCCCTGCCCTAGGCTCCAGCCGTCCCCG
CACCAGCCCCCAGGCACCGAGAGCACGAGCATGGGCACCAAGCCAGGCCTCCCAGGCTGCTCTTCACGTCCCTTA
TGCCACTATCAACACCAGCTGCCGCCAGCTACTTTGGACACAGCTCACCCCCATGGGGGGCCGTCCTGGTGGGC
GTCACCTCCCCACCCACGCTGCACACCGGCCCCAGGGCCCTGCCGCCTGGGCCTCCACACCCATCCCTGCACGTGG
CAGCTTTGTCTCTGTTGAGAATGGACTCTACGCTCAGGCAGGGGAGAGGCCTCCTCACACTGGTCCCGGCCTCAC
TCTTTTCCCTGACCCTCGGGGGCCCAGGGCCATGGAAGGACCCCTTAGGAGTTCGATTGAGAGAGACCATGAGGCCA
CTGGGCTTTCCCCCTCCCAGGCCTCCTGGGTGTCTATCCCTTACTTTAATTCTTGGGCCTCCAATAAGTGTCCCA
TAGGTGTCTGGCCAGGCCACCTGCTGCGGATGTGGTCTGTGTGCGTGTGTGGGCACAGGTGTGAGTGTGTGAGT
GACAGTTACCCCATTTAGTCATTTCTGCTGCAACTAAGTCAGCAACACAGTTTCTCTGAAAAAAAAAAAAAAAA
AAAA

2542/6881
FIGURE 2336

MRTEAQVPALQPPEPGLEGAMGHRTLVLFPWVLLTLCVTAGTPEVWVQVRMEATELSSFTIRCGLGSGSISLVTV
SWGGPDGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCKFASFPEGSWEACGSL
FPSSDPGLSAPPTPAPILRADLAGILGVSGVLLFGCVYLLHLLRRHKHRPAPRLQPSRTSPQAPRARAWAPSQAS
QAALHVPYATINTSCRPATLDTAHPHGGPSWWASLPTHAAHRPQGPAAWASTFIPARGSFVSVENGLYAQAGERP
PHTGPGLTLFPDPRGPRAMEGPLGVR

2543/6881
FIGURE 2337

AAGGGTCTAGGATACAGTCTTTGTAGATGAGCGGGTCCCCCTTGGAGGACAGAATGAAGAATTGGGAAATCATGG
CCGTTCTGGAGAGTAGACAAGAAGACGGCGAAAGTCGGGCCTGCCCCGCCCTGCGGCCCCGGAACAAAAGAACGC
GTGTGCGCTGGCCCTTTAAGAGCGATTCTCCTCCGCCCCGCGCCAGCTCGGACCGCGGGAAACCCGGCGCCTGCAC
TACCCCGCCCCGGAGATTCCCTTCCGACGCCCCGACCGCCTCCCCGTCACTCATTCTAGGCCCGCACGGTGATTGG
CTTGCGGCTAGCGGGAGGTGAAGAAGGCCGCCTTGTCCGATTGGCCCCGCACGCAGTGGCGCCGGTCACGTGGGGG
GCGACGTTTCGCGCCAATTTCCGTTGGCCGGCCACAGTCCACCGCGCGGAGATTCTCAGCTTCCCCAGGAGCAAG
ACCTCTGAGCCCCGCCAAGCGCGGCCGCACGGCCCTCGGCAGCGATGGCACTGAAGGACTACGCGCTAGAGAAGGA
AAAGGTTAAGAAGTTCTTACAAGAGTTCTACCAGGATGATGAACTCGGGAAGAAGCAGTTCAAGTATGGGAACCA
GTTGGTTTCGGCTGGCTCATCGGGAACAGGTGGCTCTGTATGTGGACCTGGACGACGTAGCCGAGGATGACCCCGA
GTTGGTGGACTCAATTTGTGAGAATGCCAGGCGCTACGCGAAGCTCTTTGCTGATGCCGTACAAGAGCTGCTGCC
TCAGTACAAGGAGAGGGAAGTGGTAAATAAAGATGTCTGGACGTTTACATTGAGCATCGGCTAATGATGGAGCA
GCGGAGTCGGGACCCCTGGGATGGTCCGAAGCCCCCAGAACCAGTACCCCTGCTGAACCTCATGCGCAGATTGTGAGT
GGTCTCTGTGCGGAAAGATGTAGGGATTGGTTCTCCAGGATCTTGTTTGTGACTGTTTTCTCCCCTTAGTGAGCT
GTATTTTCAAGGCCCTAGCAGCAACAAGCCTCGTGTGATCCGGGAAGTGCGGGCTGACTCTGTGGGGAAAGTTGGT
AACTGTGCGTGGAATCGTCACTCGTGTCTCTGAAGTCAAACCCAAGATGGTGGTGGCCACTTACACTTGTGACCA
GTGTGGGGCAGAGACCTACCAGCCGATCCAGTCTCCCACCTTTCATGCCTCTGATCATGTGCCAAGCCAGGAGTG
CCAAACCAACCGCTCAGGAGGGCGGCTGTATCTGCAGACACGGGGCTCCAGATTCATCAAATTCCAGGAGATGAA
GATGCAAGAACATAGTGATCAGGTGCCTGTGGGAAATATCCCTCGTAGTATCACGGTGCTGGTAGAAGGAGAGAA
CACAAGGATTGCCAGCCTGGAGACCACGTACGCGTCACTGGTATTTTCTTGCCAATCCTGCGCACTGGGTTCG
ACAGGTGGTACAGGGTTTACTCTCAGAAACCTACCTGGAAGCCCATCGGATTGTGAAGATGAACAAGAGTGAGGA
TGATGAGTCTGGGGCTGGAGAGCTCACCAGGGAGGAGCTGAGGCAAATTGCAGAGGAGGATTTCTACGAAAAGCT
GGCAGCTTCAATCGCCCCAGAAATATACGGGCATGAAGATGTGAAGAAGGCACTGCTGCTCCTGCTAGTCGGGGG
TGTGGACCAGTCTCCTCGAGGCATGAAAATCCGGGGCAACATCAACATCTGTCTGATGGGGGATCCTGGTGTGGC
CAAGTCTCAGCTCCTGTGCATACATTGATCGACTGGCGCCTCGCAGCCAGTACACAACAGGCCGGGGCTCCTCAGG
AGTGGGGCTTACGGCAGCTGTGCTGAGAGACTCCGTGAGTGGAGAAGTACCTTAGAGGGTGGGGCCCTGGTGCT
GGCTGACCAGGGTGTGTGCTGCATTGATGAGTTCGACAAGATGGCTGAGGCCGACCGCACAGCCATCCACGAGGT
CATGGAGCAGCAGACCATCTCCATTGCCAAGGCCGGCATTCTCACCACACTCAATGCCCGCTGCTCCATCCTGGC
TGCCGCCAACCCTGCCTACGGGCGCTACAACCCTCGCCGCAGCCTGGAGCAGAACATACAGCTACCTGCTGCACT
GCTCTCCCGGTTTGACCTCCTCTGGCTGATTGAGGACCGGCCCCGACCGAGACAATGACCTACGGTTGGCCCAGCA
CATCACCTATGTGCACCAGCACAGCCGGCAGCCCCCTCCCAGTTTGAACCTCTGGACATGAAGCTCATGAGGCG
TTACATAGCCATGTGCCGCGAGAAGCAGCCCATGGTGCCAGAGTCTCTGGCTGACTACATCACAGCAGCATACGT
GGAGATGAGGCGAGAGGCTTGGGCTAGTAAGGATGCCACCTATACTTCTGCCCGGACCCTGCTGGCTATCCTGCG
CCTTTCCACTGCTCTGGCACGTCTGAGAATGGTGGATGTGGTGGAGAAAGAAGATGTGAATGAAGCCATCAGGCT
AATGGAGATGTCAAAGGACTCTCTTCTAGGAGACAAGGGGCAGACAGCTAGGACTCAGAGACCAGCAGATGTGAT
ATTTGCCACCGTCCGTGAACTGGTCTCAGGGGGCCGAAGTGTCGGTTCTCTGAGGCAGAGCAGCGCTGTGTATC
TCGTGGCTTCACACCCGCCAGTTCCAGGCGGCTCTGGATGAATATGAGGAGCTCAATGTCTGGCAGGTCAATGC
TTCCCGGACACGGATCACTTTTGTCTGATTCCAGCCTGCTTGCAACCCTGGGGTCCTCTTGTTCCTGCTGGCCT
GCCCCCTTGGGAAGGGGCAGTGATGCCTTTGAGGGGAAGGAGGAGCCCCCTTTTCTCCCATGTGCACTTACTCCT
TTTGCTAATAAAAGTGTGTTGTAGATTGTATCTTCTAGCCTGGGCCTGACTTCCATTAAACAGGGTTTGTGCG
TTTTTTAGATTCCGTGTTGTTTTATGCTATTTCTAGCCTGGGCCTGACTTCCATTAAACAGGGTTTGTGCG
CAGGCCCCCAGTATAGACACTGGGGATGCGGCAAGGACTAAGCGGTCCCTGCTGTTTGGAGATACTTAAGATGG
GCTCCACTTTTTTGAGCCCCCGACTCCCT

2544/6881
FIGURE 2338

GGCACGAGGGGAAAATGGCGGCGGCGGCGGCGGCGGCTGCAGCTACGAACGGGACCGGAGGAAGCAGCGGGATGG
AGGTGGATGCAGCAGTAGTCCCCAGCGTGATGGCCTGCGGAGTGACTGGGAGTGTTCCGTCGCTCTCCATCCCC
TTGTCATTCTCAACATCTCAGACCACTGGATCCGCATGCGCTCCCAGGAGGGGCGGCCTGTGCAGGTGATTGGGG
CTCTGATTGGCAAGCAGGAGGGCCGAAATATCGAGGTGATGAACTCCTTTGAGCTGCTGTCCACACCGTGGAAG
AGAAGATTATCATTGACAAGGAATATTATTACACCAAGGAGGAGCAGTTTAAACAGGTGTTCAAGGAGCTGGAGT
TTCTGGGTTGGTATACCACAGGGGGGCCACCTGACCCCTCGGACATCCACGTCCATAAGCAGGTGTGTGAGATCA
TCGAGAGCCCCCTCTTTCTGAAGTTGAACCCTATGACCAAGCACACAGATCTTCCTGTCAGCGTTTTTTGAGTCTG
TCATTGATATAATCAATGGAGAGGCCACAATGCTGTTTGCTGAGCTGACCTACACTCTGGCCACAGAGGAAGCGG
AACGCATTGGTGTAGACCACGTAGCCCGAATGACAGCAACAGGCAGTGGAGAGAACTCCACTGTGGCTGAACACC
TGATAGCACAGCACAGCGCCATCAAGATGCTGCACAGCCGCGTCAAGCTCATCTTGAGTACGTCAAGGCCTCTG
AAGCGGGAGAGGTCCCCTTTAAATCATGAGATCCTGCGGGAGGCCTATGCTCTGTGTCACTGTCTCCCGGTGCTCA
GCACAGACAAGTTCAAGACAGATTTTTATGATCAATGCAACGACGTGGGGCTCATGGCCTACCTCGGCACCATCA
CCAAAACGTGCAACACCATGAACCAGTTTGTGAACAAGTTCAATGTCCTCTACGACCGACAAGGCATCGGCAGGA
GAATGCGCGGGCTCTTTTTCTTGATGAGGGTACTTGAAGGGCTGATGGACAGGGGTCAGGCAACTATCCCAAAGGG
GAGGGCACTACACTTCCTTGAGAGAAACCGCTGTCATTAATAAAAGGGGAGCAGCCCCTGAGCACCAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

2545/6881
FIGURE 2339

MACGVTGSVSVALHPLVILNISDHWIRMRSQEGRPVQVIGALIGKQEGRNIEVMNSFELLSHTVEEKIIDKEYY
YTKEEQFKQVFKELEFLGWYTTGGPPDPSDIHVHKQVCEIIESPLFLKLNPMTKHTDLPVSVFESVIDIINGEAT
MLFAELTYTLATEEAERIGVDHVARMTATGSGENSTVAEHLIAQHSIAKMLHSRVKLILEYVKASEAGEVPFNHE
ILREAYALCHCLPVLSTDKFKTDFYDQCNDVGLMAYLGTITKTCNTMNQFVNKFNVLYDRQGIGRRMRGLFF

2546/6881
FIGURE 2340

GCTTCCGGCACGGGATGTTTTCGGTTGTTTGACCGAGAGAGTTGTAGGCGCAAAGCTGAGGAAAGGAGAGTGTGG
AGAGGGGCGCTGGTGTGGTGGGGCCCGGTGTTTGGGACCGGAGGGTGTGACGGCTGATGAGTTCCTTGGGTTTGC
TCTTTCTTCACCTGAAAAGAAGACTCCAGGAAGGGCAGCACATGCCGGAGAAAAGATGAATTGCAGCTTGACCGCC
CAGAGGCGCGGCAGTGACGCCGAGTTGGGACCCTGGGTGATGGCTGCGAGGTCCAAGGACGCGGCGCCGTCCCAA
CGCGACGGACTTTTGCCCGTGAAAGTGGAGGAAGACTCACCCGGAAGTTGGGAGCCCAACTATCCCGCGGCTTCG
CCGGACCCCGAACTTCTCGACTGCACCTTTAGGCAGCTGCGTTACCAGGAGGTGGCTGGACCGGAAGAGGCGCTG
AGCCGGCTCCGAGAACTCTGTCTGTCGGTGGCTGAGACCCGAGCTGCTCTCCAAGGAGCAGATCCTGGAGCTGCTG
GTGCTGGAGCAGTTCCTCACCATCCTGCCCCGAGGAGCTTCAAGCCTGGGTGCGAGAGCACTGCCCAGAGAGCGGG
GAGGAGGCGGTGGCCGTGGTGC GGCTCTGCAGCGAGCGCTCGATGGAACCTCATCCCAGGGGATGGTGACTTTC
GAGGACACGGCTGTGTCTCTAACTGGGAGGAGTGGGAGCGCCTGGACCCAGCACGGAGGGACTTCTGCAGAGAG
AGTGCGCAGAAGGATTCCGGGAGCACAGTTCGCCCGAGTTTGGAAAGCAGAGTGGAGAACAAAGAGTTGATTCCA
ATGCAACAAATTTTAGAAGAAGCGGAGCCACAGGGGCAACTACAAGAAGCGTTCCAGGGGAAGCGCCCCCTGTTT
TCTAAGTGTGGCAGTACCCATGAGGACAGGGTGGAAAAGCAGTCCGGAGACCCCTTGCCCCGTGAAACTTGAAAA
TCTCCTGAAGCAGAAGGACTCAACAGCATCTCAGATGTCAATAAGAATGGTTCCATAGAAGGGGAAGACTCTAAA
AATAATGAATTGCAGAACAGTGCCAGGTGTTCCAACCTTGTTCTATGTCAGCACATCCCGAAAGCAGAGAGGCCC
ACTGACAGTGAGGAACACGGGAACAAGTGCAAGCAAAGTTTCCACATGGTGACGTGGCACGTGCTGAAACCTCAC
AAGTCTGACAGTGGAGACAGTTTCCATCATTCCAGCCTTTTTGAGACCCAGAGGCAGCTCCATGAAGAAAGACCT
TATAAATGTGGTAACTGTGGGAAGAGTTTCAAACAACGCTCTGACCTCTTTAGACACCAGAGAATCCACACAGGT
GAGAAACCCCTATGGCTGCCAAGAATGTGGGAAAAGCTTCAGCCAGAGTGCTGCCCTGACCAAGCACCAGAGGACA
CACACAGGCGAGAAGCCGTACACCTGTCTGAAATGTGGGGAGCGCTTCAGGCAGAATTCACACCTAAATCGTCAT
CAAAGTACCCACAGTAGAGACAAACATTTTAAATGTGAGGAATGCGGGGAAACCTGTCAATTTTCCAACCTTTTT
AGACATCAGAGACTACATAAAGGGGAAAGACCCTATAAGTGTGAAGAATGCGAGAAGAGCTTCAAACAGCGCTCT
GACCTCTTTAAACACCACAGAATCCCACTGGGGAGAAGCCCTATGGATGTTCCGTCTGTGGGAAACGCTTCAAT
CAGAGTGCAACCCTCATTAAACACCAGAGAATTCACACTGGGGAAAAGCCTTACAAATGTCTTGAATGTGGGGAA
AGATTTAGACAAAGTACACACCTTATCCGACACCAAAGAATTCATCAAAATAAAGTGCTGTGCGCTGGGCGTGGT
GGCTCACGCCTATTAATCCCAGCACTTTGGGAGGCCAAGGCAGGCAGATCATTTGAGATCAGGAGTTTGAAACCAG
CCTGGCCAACATGGTGAAATTCTGTCTCTACTAAAAATACAAAAATGAGCCGGGCATGGTGGTGCATGCCTGTAA
GCCCAGCTATTCCGGGAGGCTGAGGTAGGAGAATCACTTGAACCCAGGAGGCGGAAGTTGCAGTGAGCTGAGATCA
TGCCACTGCACTCCAGCCTGGGCAACAGAGCGAGACTCCATCTCAAAAAAGAAATAAAGTGCTGTCAATTTTGAT
ATGTT

2547/6881
FIGURE 2341

MNCSLTAQRRGSDAELGPWVMAARSKDAAPSQRDGLLPVKVEEDSPGSWEPNYPASPDPETSRLHFRQLRYQEV
AGPEEALSRLRELCRRWLRPELLSKEQILELLVLEQFLTILPEELQAWVREHCPESGEEAVAVVRALQRALDGT
SQGMVTFEDTAVSLTWEWERLDPARRDFCRESAQKDSGSTVPPSLESRVENKELIPMQQILEEAEPQGQLQEAF
QGKRPLFSKCGSTHEDRVEKQSGDPLPLKLENSPEAEGLNSISDVNKNGSIEGEDSKNNELQNSARCSNLVLCQH
IPKAERPTDSEEHGNKCKQSFHMTWHVLKPHKSDSGDSFHHSSLFETQORQLHEERPYKCGNCGKSFKQRSDLFR
HQRIHTGEKPYGCQECGKSFSQSAALTKHQRTHTGEKPYTCLKCGERFRQNSHLNRHQSTHSRDKHFKCEECGET
CHISNLFRHQLHKGGERPYKCEECEKSFKQRSDLFKHHRIHTGEKPYGCSVCGKRFNQSATLIKHQRIHTGEKPY
KCLECGERFRQSTHLIRHQRIHQNKVLSAGRGG SRL

2548/6881
FIGURE 2342

GGGCACAGCGGACACCAGGACTCCAAAATGGCGTCAGTTGGTGAGTGTCCGGCCCCAGTACCAGTGAAGGACAAG
AAACTTCTGGAGGTCAAAC TGGGGGAGCTGCCAAGCTGGATCTTGATGCGGGACTTCAGTCCTAGTGGCATTTTC
GGAGCGTTTCAAAGAGGTTACTACCGGTACTACAACAAGTACATCAATGTGAAGAAGGGGAGCATCTCGGGGATT
ACCATGGTGCTGGCATGCTACGTGCTCTTTAGCTACTCCTTTTCCTACAAGCATCTCAAGCACGAGCGGCTCCGC
AAATACCACTGAAGAGGACACACTCTGCACCCCCCACCCACGACCTTGGCCCGAGCCCCCTCCGTGAGGAACAC
AATCTCAATCGTTGCTGAATCCTTTCATATCCTAATAGGAATTAACCTCAAATAAAACATGACTGGTAAAAAAA
AA

2549/6881
FIGURE 2343

MASVGECPAPVPVKDKKLEVKLGELPSWILMRDFSPSGIFGAFQGGYYRYN KYINVKKGSISGITMVLACYVL
FSYSFSYKHLKHERLRKYH

2550/6881
FIGURE 2344

TCGCTCGCTCCTCCTTCGCTTCGCCTCGCCGCCGCCATGCAGGAAATCATCGCCAGCGTGGACCACATCAAGTTT
GACTTGGAGATCGCGGTGGAGCAGCAGCTGGGGGCGCAGCCGCTGCCCTTCCCCGGCATGGACAAGTCGGGCGCT
GCTGTCTGTGAATTCTTTTGAAGCTGCCTGCGGCAAAGGGGGCATGTGTCCGTTTCGCCACATCAGTGGTGAG
AAGACAGTTGTGTGCAAACTGGCTGCGTGGCCTATGCAAGAAAGGGGACCAGTGTGAGTTCCTGCATGAGTAT
GACATGACCAAGATGCCCCGAGTGCTACTTCTACTCCAAGTTCGGGGAGTGCAGCAACAAGGAATGTCCCTTCCTG
CACATCGACCCCCGAGTCCAAGATCAAGGACTGTCCTTGGTATGACCGCGGCTTCTGCAAGCACGGTCCCCTCTGC
AGGCACCGGCACACACGGAGAGTCATCTGTGTGAATTACCTCGTGGGATTCTGCCCGGAGGGGCCCTCGTGTA
TTCATGCACCCTCGATTTGAACTGCCCATGGGAACCCGAGCAGCCCCACTGCCACAGCAGACACAGCCTCCA
GCAAAGCAAAGTAACAATCCGCCATTACAAAGGTGCTCCTCCTTGATCCAGTTAACGAGTCAGAACTCTTCTCCC
AATCAGCAGAGAACCCCGCAGGTCATCGGGGTCATGCAGAGTCAAAAACAGCAGCGCGGGCAACCGGGGACCCCGG
CCACTGGAGCAGGTCACCTGTTACAAGTGTGGCGAGAAAGGACACTACGCCAACAGATGCACCAAAGGGCACTTG
GCCTTTCTCAGTGGACAGTTGACAGCAGCTGGAGCCAGCTCCGAGCAGCCCGGGGGCCCCGCTGTTGGGAGTGTGC
ATTTAACTGTTTCATGCGCTTGTTGGCGCGACTGTGGCTCGAGCTGGCCCGCAGACACGTGGGTTTTCATCACTCT
GAGGGGCCACGTCTGTTAGTTTCTTATCATTTTGGCGTAGTATTTTTTGAAAAAGGGACATGTGTCTGTGGGTC
CCTGCAGTCGACATCATGTTTGGCTGGGCATCGATGCCTCCTTCTGGGACTCCCGGCACAACCTCCCCTCATCCA
GGGAGGGAGGCAGCTGCTGGGGAGGGGCTTGGCTAGGTAGTTCTGTGTGGCGGTGGTCATTCCCCTCATTAAACA
CCAGTTCTTGGTGACGCCAGGGGCTGGTAGGTCAATCAAAGCTGTGGCCAGCTCACGCCTGCTTCCTCCCTCCCT
GCCCTGCTGAATCCTAAAGCTGTGCCTATATCTGTGATTTGAATGAGGGAGCCCTTGGGGCAAATTCAGGTGCC
CCCATTGCCTCAGGCTGGCCCTGGTCCCAGGTGGCAGCGGTTGAGGAGGGGTACAGGGCTCTCAAGCCTGAGGTT
TTCTTCTCTGGGCTTAATTTTCTCTTGGGGTACGTGCCTGACAGTGTTTAAGGTGTCCGTTGAACTGGAGTTGCA
GACTTTTAAATAGATGACCCCTTCAGATCATCTGTGCCTACCTCCTGCCCATCAGGCGTCTACACTGTCACTCAG
ACACCTGTGGCATGTGGAGGAGACTGCCCTGTCCTGAGCCTGGAAAATGTGAACTGTCTCCTGCAACCTGCTGG
GCATGTGGGCCTGGCTGTGTTCAATTGCAAGAACAATTTTTATGAAATGGATTAAAGCTTGTTTTTT

2551/6881
FIGURE 2345

MQEIIASVDHIKFDLEIAVEQQQLGAQPLPFPMDKSGAAVCEFFLKAACGKGGMCPFRHISGEKTVVCKHWLRGL
CKKGDQCEFLHEYDMTKMPECYFYSKFGECSNKECPFLHIDPESKIKDCPWYDRGFCKHGPLCRHRHTRRVICVN
YLVGFCPEGPSCKFMHPRFELPMGTTEQPPLPQQTPPAKQSNNPFLQRSSSLIQLTSQNSSPNQQRTPOVIGVM
QSQNSSAGNRGPRPLEQVTCYKCGEKGHYANRCKGHLAFLSGQ

2552/6881
FIGURE 2346

CTGAGGCGGGAGACCGGTGGTCTGCACCGTCCTGGAGGGAGATATGAGTGGCTGGACTCTCAGCCAGCCACTGGG
ATGTGTTCTGGGCTTTGGACCTTGAGGCCGGAGAGAGCTCCCGAGAGGAGGCGGCCACGTTTCGTTCTTCTGAGG
GGACGGTAGATTTGGGGGTTTTCTCTAGGATTCTCGCGCCGTTTCCTCTGAAGAAACAGGACCAGAGAGGGGAAG
GTGACCTGAAAGTCACAGAATAATTTTTTAGAGCTGAACAAGAATCCAAGCCTGCAACTGCAGAGACGAGAGATC
TTTCTGCTGTCTATACTCTTGGAAGCACATCCTAAGATCTTTGCAGATTATCCTGTGGAAGGAAAATGCCTAAA
GTCAAAGAAGCCGGAAAGCACCCCCAGATGGCTGGGAGTTGATTGAGCCAACACTGGATGAATTAGATCAAAAG
ATGAGAGAAGCTGAAACAGAACCGCATGAGGGAAAGAGGAAAGTGGAATCTCTGTGGCCCATCTTCAGGATCCAC
CACCAGAAAACCCGCTACATCTTCGACCTCTTTTACAAGCGGAAAGCCATCAGCAGAGXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXACAAAACCTGATTGCAAAATGGAAAAAGCAAGGATATGAGAACTTGTGCTGCCTG
CGGTGCATTTCAGACACGGGACACCAACTTCGGGACGAACTGCATCTGCCGCGTGCCAAAAGCAAGCTGGAAGTG
GGCCGCATCATCGAGTGCACACACTGTGGCTGTCTGTGGCTGCTCTGGCTGAGGCTGGCGCGCTCCACCCTGGACT
CTGGACTTCGCAGGTTCTGCCTGTCACGCCACCCCTTCCTGGGAGCAGCGAGCAGTGCCCCAGGCCCCGAGTTG
GAGCACGGTCTCTATGGGGAAGGCTTCGCTGTCTATCAGCTGTGATTTGTAAAAATAAAATCTTTAAATCTCTCG

2553/6881
FIGURE 2347

MPKVKRSRKAPPDGWELIEPTLDELDQKMREAETEPHEGKRKVESLWPIFRIHHQKTRYIFDLFYKRKAISRXXX
XXXXXXXXXXKNLIAKWKKGQYENLCCLRCIQTRDTNFGTNCICRVPKSKLEVGRIEEECTHCGCRGCSG

2554/6881
FIGURE 2348

GGCACGAGGGAGCCCAGAGCCGGTTCGGCGCGTCTGACTGCCCAGAGTCCGCGGCCGGGGCGCGGGAGGAGCCAAG
CCGCC**ATG**GCCTACCACAGCTTCCTGGTGGAGCCCATCAGCTGCCACGCCTGGAACAAGGACCGCACCCAGATTG
CCATCTGCCCCAACCAACCATGAGGTGCATATCTATGAAAAGAGCGGTGCCAAATGGACCAAGGTGCACGAGCTCA
AGGAGCACAAACGGGCAGGTGACAGGCATCGACTGGGCCCCCGAGAGTAACCGTATTGTGACCTGCGGCACAGACC
GCAACGCCTACGTGTGGACGCTGAAGGGCCGCACATGGAAGCCCACGCTGGTCATCCTGCGGATCAACCGGGCTG
CCCGCTGCGTGCGCTGGGCCCCCAACGAGAACAAGTTTGCTGTGGGCAGCGGCTCTCGTGTGATCTCCATCTGTT
ATTTGAGCAGGAGAATGACTGGTGGGTTTGCAAGCACATCAAGAAGCCCATCCGCTCCACCGTCTCAGCCTGG
ACTGGCACCCCAACAATGTGCTGCTGGCTGCCGGCTCCTGTGACTTCAAGTGTGCGATCTTTTCAGCCTACATCA
AGGAGGTGGAGGAACGGCCGGCACCCACCCCGTGGGGCTCCAAGATGCCCTTTGGGGAAGTATGTTTGAATCCA
GCAGTAGCTGCGGCTGGGTACATGGCGTCTGTTTCTCAGCCAGCGGGAGCCGCGTGGCCTGGGTAAGCCACGACA
GCACCGTCTGCCTGGCTGATGCCGACAAGAAGATGGCCGTGCGGACTCTGGCCTCTGAAACACTACCACTGCTGG
CGCTGACCTTCATCACAGACAACAGCCTGGTGGCAGCGGGCCACGACTGCTTCCCGGTGCTGTTACCTATGACG
CCGCCGCGGGGATGCTGAGCTTCGGCGGGCGGCTGGACGTTCTTAAGCAGAGCTCGCAGCGTGGCTTGACGGCCC
GCGAGCGCTTCCAGAACCTGGACAAGAAGGCGAGCTCCGAGGGTGGCACGGCTGCGGGCGCGGGCCTAGACTCGC
TGCACAAGAACAGCGTCAAGCAGATCTCGGTGCTCAGCGCGGCAAGGCCAAGTGTGCGAGTTCTGCACCACTG
GCATGGATGGCGGCATGAGTATCTGGGATGTGAAGAGCTTGGAGTCAGCCTTGAAGGACCTCAAGATCAAA**TGAC**
CTGTGAGGAATATGTTGCCTTCATCCTAACTGCTGGGGAAGCGGGGAGAGGGGTGAGGGAGGCTAATGGTTGCTT
TGCTGAATGTTTCTGGGGTACCAATACGAGTTCCCATAGGGGCTGCTCCCTCAAAAAGGGAGGGGACAGATGGGG
AGCTTTTCTTACCTATTCAAGGAATACGTGCCTTTTTCTTAAATGCTTTCATTTATTGAAAAAAAAAAAAAAAAA
AAA

2555/6881
FIGURE 2349

MAYHSFLVEPISCHAWNKDRTQIAICPNNHEVHIYEKSGAKWTKVHELKEHNGQVTGIDWAPESNRIVTCGTDRN
AYVWTLKGRTWKPTLVILRINRAARCVRWAPNENKFAVGSGSRVISICYFEQENDWWVCKHIKKPIRSTVLSLDW
HPNNVLLAAGSCDFKCRIFSAYIKEVEERPAPTPWGSKMPPFGELMFESSSSCGWVHGVCFSASGSRVAWVSHDST
VCLADADKKMAVATLASETLPLLALTFITDNSLVAAGHDCFPVLFTYDAAAGMLSFGGRLDVPKQSSQRGLTARE
RFQNLDDKKASSEGGTAAGAGLDSLHKNSVSQISVLSGGKAKCSQFCTTGMDGGMSIWDVKSLESALKDLKIK

2556/6881
FIGURE 2350

CAGCTTTCTCTCCTTTGAAAACACTAAGAATAATGTCACTGCATCAGTTTTTACTAGAGCCAATCACCTGTCATG
CCTGGAACAGGGATCGTACTCAGATTGCCCTCAGTCCCAATAATCACGAAGTGCACATCTATAAGAAGAACGGGA
GCCAGTGGGTGAAAGCTCATGAACTCAAGGAGCACAAACGGACACATCACAGGTATTGACTGGGCTCCCAAGAGCG
ACCGCATTGTCACTTGTGGGGCAGACCGCAATGCCTATGTCTGGAGTCAGAAAGATGGTGTGTTGGAAGCCAACCC
TGGTGATCCTGAGAATTAATCGCGCAGCTACTTTTGTGAAGTGGTCCCCCTAGAGAACAAATTTGCTGTGGGAA
GTGGAGCACGACTCATTTCTGTTTGTACTTTGAGTCTGAAAATGACTGGTGGGTGAGCAAGCACATTAAAAAGC
CGATTGCTCCACAGTCCCTCAGCTTGGATTGGCATCCCAACAACGTTTTGCTGGCAGCAGGATCATGTGACTTCA
AATGCAGAGTGTTTTCTGCCTACATTAAAGAAGTGGATGAAAAGCCAGCCAGCACGCCCTGGGGCAGCAAGATGC
CTTTTGGGCAGCTGATGTCAGAGTTTGGTGGCAGTGGCACTGGTGGCTGGGTCCACGGGGTAAGCTTCTCTGCCA
GTGGGAGCCGCTGGCCTGGGTGAGCCACGACAGCACCGTGTCTGTTGCTGATGCCTCAAAAAGTGTGCAGGTCT
CGACTCTGAAGACAGAGTTCTTGCCGCTCCTAAGTGTGTCAATTTGTCTCAGAGAACAGCGTCGTGGCTGCTGGCC
ATGACTGCTGCCCCAATGCTCTTTAACTACGATGACCGCGGCTGCCTGACCTTCGTCTCCAAGTTAGATATTCCAA
AACAGAGCATCCAACGCAACATGTCTGCCATGGAACGCTTCCGCAACATGGACAAGAGAGCCACAACCTGAGGACC
GCAACACGGCCTTGGAGACGCTGCACCAGAATAGCATCACTCAAGTCTCTATTTATGAGGTGGACAAGCAAGATT
GTCGCAATTTTGCCTACTTGGCATCGATGGAGCCATGACAATTTGGGATTTCAAGACCCTCGAGTCTTCCATCC
AGGGCCTCCGGATAATGTGAAGCTGAGTG

2557/6881
FIGURE 2351A

CTCCTCTGCTCCTCGAAGAAGGCCAGGGCGGCGCTGCCGCAAGTTTTGACATTTTCGCAGCGGAGACGCGCGCGG
GCACTCTCGGGCCGACGGCTGCGGCGGCGGCCGACCCCTCCAGAGCCCCTTAGTCGCGCCCCGGCCCTCCCGCTGC
CCGGAGTCCGGCGGCCACGAGGCCAGCCGCGTCTCCCGCGCTTGCTCGCCCGGCGGCCGAGCCATGTCCCGG
GGGCCCCGAGGAGGTGAACCGGCTCACGGAGAGCACCTACCGGAATGTTATGGAACAGTTCAATCCTGGGCTGCGA
AATTTAATAAACCTGGGGAAAAATTATGAGAAAGCTGTAAACGCTATGATCCTGGCAGGAAAAGCCTACTACGAT
GGAGTGGCCAAGATCGGTGAGATTGCCACTGGGTCCCCCGTGTCAACTGAACTGGGACATGTCTCATAGAGATT
TCAAGTACCCACAAGAACTCAACGAGAGTCTTGATGAAAATTTTAAAAAATTCCACAAAGAGATTATCCATGAG
CTGGAGAAGAAGATAGAACTTGACGTGAAATATATGAACGCAACTCTAAAAAGATACCAAACAGAACACAAGAAT
AAATTAGAGTCTTTGGAGAAATCCCAAGCTGAGTTGAAGAAGATCAGAAGGAAAAGCCAAGGAAGCCGAAAACGCA
CTCAATATGAACACAAAAGAAATTGAGTATGTGGAGACCGTTACTTCTCGTCAGAGTGAAATCCAGAAAATTCATT
GCAGATGGTTGCAAGAGGGCTCTGCTTGAAGAGAAGAGGGCGCTTCTGCTTTCTGGTTGATAAGCACTGTGGCTTT
GCAAACCACATACATTATTATCAGTTACAGTCTGCAGAACTACTGAATTCCAAGCTGCCTCGGTGGCAGGAGACC
TGTTGTTGATGCCATCAAAGTGCCAGAGAAAATCATGAATATGATCGAAGAAATAAAGACCCCCAGCCTCTACCCCC
GTGCTCTGGAACCTCCTCAGGCTTACCCATGATCGAGAGAAGCAATGTGGTTAGGAAAGATTACGACACCCCTTTCT
AAATGCTCACCAAAGATGCCCCCGCTCCTTCAGGCAGAGCATATACCAGTCCCTTGATCGATATGTTTAATAAC
CCAGCCACGGCTGCCCCGAATTCACAAAGGGTAAATAATTCAACAGGTACTTCCGAAGATCCAGTTTACAGCGA
TCAGTTTTCGGTTGCAACGGGACTGAACATGATGAAGAAGCAGAAAGTGAAGACCATCTTCCCGCACACTGCGGGC
TCCAACAAGACCTTACTCAGCTTTGCACAGGGAGATGTCATCACGCTGCTCATCCCCGAGGAGAAGGATGGCTGG
CTCTATGGAGAACACGACGTGTCCAAGGCGAGGGGTTGGTTCCCGTCTGTCGTACACGAAGTTGCTGGAAGAAAAT
GAGACAGAAGCAGTGACCGTGCCACGCCAAGCCCCACACCAGTGAGAAGCATCAGCACCGTGAACCTGTCTGAG
AATAGCAGTGTGTCTATCCCCCACCAGCTACTTGAATGCTTGTCCATGGGGGAGCTGCCGACAGGAGAGCA
GATTCGGCCAGGACGACATCCACCTTTAAGGCCCCAGCGTCCAAGCCCCGAGACCGCGGCTCCTAACGATGCCAAC
GGGACTGCAAAGCCGCCTTTTCTCAGCGGAGAAAACCCCTTTGCCACTGTGAACTCCGCCCGACTGTGACGAAT
GATCGCTCGGCACCCATCATTTCGATGAGAGGACAGCCAAGGACTCTCCCGGGCCTCTCCGGTTCTCCCTTGCGGA
ATGATGGGCGCATCCTGTCTGCCACGTGCTGACGGTCGGGAAGCTTCAGTGGAGAGGCCTAACTCTAATGTGCC
TGCTTAAGCAAATCATGCTTCTCTGTTTACGTAGTTGGGTTGACAAGTTTCTGCCTTTAAGATAAATGAGTAAT
AGTCTAATGACCAGCTCAGCCATTTAAATATTTTCTTCTTCTGTTCAAGAAACAGTAACTTGGTTTCAAT
CTTTACTGTATTTTTTAAATGAATTTTTCTCTTAATAACAGCCAGAATAAGGGATAGTCTATGCTTTCAGGACTG
GCTTCTGCACCTGATATGAATGAGACCAGTTTTATTTTATAAAGCATGTGCTCTTAATAGCATTATGTCTAAAG
AAGATATCACGTAAGTTTGCATCTTAGCATGCAAATCATAATTTTAAAGCAATATAAATTATGAAAATACTATATA
AATGTAATTTAACTTAAAAATGTTTAAGTGTAGAGCTTCCAGAGATGGAGAAACCCCCACCCTCCCTCCAACCACG
CCAGAGCTGTAGAGTGCTAAGACGCTTTGCCTGCCCTTATCACAGCCACACGTAGCACTCGACGAAATCTCCTCC
GAGAGCTCCTTTTCTTGGTAGTTAGGAGTCGCCAACGGATTGCTGCACACGGCCCATCCAGGACACAGGCCTGG
GCGTCGGAGTACGGCTCCTTGTGTTCTCACTCAGCTAGTTGGCCAAAGCTGCATCCATTACCAGTACACTCAAA
CTGCTCGGGGTCCTGGTTTCTCCGTGTTTGAATCAGGTACAGACTCTCAAAGGATACGTGTAAAGCCAGGATGAC
CTCTGGTGCTGGAGAAGGGCGGGTTTTTCAGCCTAGCAGCCATGATGCCCTCGGAACCTGGCCCTATGGTATGG
ATGTGAGGACTACGCACTGGCTGCCCTGAGCCCGGGGCTGGAAATCATCTTTGGCTGCCAAGGATCTGGACCTAT
TTTGGAGTGGAGAGTCATGGTTAAATTTCCAGCCCGGCCAGGTACGGGAATCCAGCATTTTGTGAGGCCGAG
GCAGGGGGATCACCTGAGGTCAGGAGTCTCTACTAAAAATACAAAAATTAGACAGGTGTGGTGGTGGGCGCCACT
CAGGAGGCTGAGGCAGGAGAATCACTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCAGATCATGCTGCTGCACT
CCAGCCCGGCCGCTCACCGTGTGTGTTGCTGGGTGCTGGGGCTGTGACTTATCCCTCTCCTTTAGCCTTGCCAT
AAGTGTAGTATCCTATGAGGCTGAGATTGGGAAAGGTTACATGCAGGTAAGCCAGTGGACGTGGCCGATGCTTCA
GGCTCCTTCCAGCCAGGTCCAGCAGTGTTACCATCTGCTTCTCCTGGGAGGACAAACCAGGCACCCCCACCATGA
AGGGGCTGCAGGCACCATGAACTATGTTAACAACCCAGTCTGTACTACAGAAAGGGCTGCAGCCACATGAGAAT
TCAGTCCACACAAGCCCCATGGCCGTGTTCCCACTTCAGCCACAGGGCTCAGGGAGCCCCATCTGGCGCTAAGG
GGAAGTGTGGGGTGTGGGTGACACCTGGCCTTTGGCGTTCTGCCTTGGGGAGGTTTCTGGTTTTGTACGGGGT
GGAAGAATAGGACCTGGGGGTCTCGGATGCAACCTGCAGACCCCGTGGCTCACCCAACCCAGGTTCTGCCTCCC
AGACCAGAACGGGCATGGCCTGGTCTTGGCACCGAGGTGCCTGCTCTGTAAATATCAAGGGATTACAACTTTAA

2558/6881
FIGURE 2351B

TAATAAAGCAGAACTTG

5

2559/6881
FIGURE 2352

GGCGGTTGGCAAGAACAAGCGCCTTACGAAAGGCGGC AAAAAGGGAGCCAAGAAGAAAGTGGTTGATCCATTTTC
TAAGAAAGATTGGTATGATGTGAAAGCACCTGCTATGTT CAGTATAAGAAATATTGGAAAGACGCTCGTCACCAG
GACCCAAGGAACCAAAAATTGCATCTGATGGTCTCAAGGGTCGTGTGTTGAAGTGAGTCTTGCTGATTTGCAGAA
TGATGAAGTTGCATTTAGAAAATTCAGGCTGATTACTCTTCGTCTGTTCTGTGTTGGTTTTACTAAAAACGCAA
CAATCAGATACGGAAGACCTCTTATGCTCAGCACCAACAGGTCCGCCAAATCCGGAAGAAGATGATCGAAATCAT
GACCCGAGAGGTGCAGACAAATGACTTGAAAGAAGTGGTCAATAAAATTGATTCCAGACAGCATTGGAAAAGACAT
AGAAAAGGCTTGCCAGTCTATTTATCCTCTCCATGATGTCTTCGTTAGAAAAGTAAAAATGCTGAAGAAGCCCAA
GTTTGAATTGGGAAAGCTCATGGAGCTTCATGGTGAAGGCAGTAGTTCTGGAAAAGCCACTGGGGACGAGACAGG
TGCTAAAGTTGAACGAGCTGATGGATATGAACCACCAGTCCAAGAATCTGTTTAAAGTTCAGACTTCAAATAGTG
GCAAATAAAGAGTGCTATTTGTGAAAAAAAAAACAAAAAAAAA

2560/6881
FIGURE 2353A

CGCAGTGCTGCTGGGGCATTGCCTGTGACAACCAGGTCTACGTGTATGTGTGTGCCAGCGATGTCCCCATCCGCC
GCCGAGAGGAGGCCTATGAGAATCAGCGCTGGAATCCCATGGGCGGCTTCTGTGAGAAGCTCCTGTGAGTGACC
GCTGGGGGTGGAGTGACGTGAGTGGGCTCCAGCACCGGCCGCTGGACAGGGTGGCACTGCCCTCGCCGCACTGGG
AGTGGGAGTCTGACTGGTACGTGGATGAGAATTTTGGAGGTGAACCCACTGAGAAAGGGGGGTGGACGTACGCCA
TCGACTTTCCCGCCACCTACACGAAAGACAAGAAGTGAATTTCTTGTGTGCGGCGCCGGAAGTGGATCCGGTACA
GGAGATACAAGTCCCGGGACATCTGGGCCAAGATCCCCTCGAAGGATGACCCCAAGGAGCTGCCCCGACCCCTTCA
ACGACCTCTCTGTAGGGGGCTGGGAGATCACGGAGGAGCCTGTGGGCCGCTGTCTAGTGTGGGCTGTGTCTCTGC
AGGGCAAGGTGTGGTACAGAGAGGACGTACGCCACTCCAACCCGAAGGGTCCTCCTGGTCCCTGCTGGACACCC
CCGGGGAGGTGGTTTACAGATCAGCTGTGGGCCCCACGACCTCCTGTGGGCCACACTCTGGGAGGGACAGGCCCTGG
TCCGGGAAGGAATCAACAGGAGCAATCCCAAAGGAAGTTCTGGTCCATCGTGGAGCCTCCTGGATCTGAAAACG
GGGTCAATGCACATCTCGGTGGGAGTCAGCGTGGTCTGGGCTGTACCAAGGACTGGAAGGTGTGGTTCCGAAGAG
GCGTCAACTCTCACAATCCCTGCGGCACCAGTTGGATTGAGATGGTTGGTGGATGACGATGGTGAACGTGGGAA
TGAACGACCAGGTGTGGGGCATTGGCTGTGAGGACCGAGCCGTGTACTTCCGGCAGGGTGTACCCCCAGCGAGC
TCAGTGGGAAGACCTGGAAGCCATCATCGCGGCCCGAGAGTGTGACCGGTACACTCTGGCAGCTCGTCTAGTC
TCCTCAGTGCCGGCTGCTTCTTCGGTGATGAGGTGAGGGGTAGTGGCGAGTCTGCCCCAGCGACACCGATGCCT
CCTCGGAAGTCGAGAGACCAGGGCCTGGCCAGATTCTCCCTGCAGAACCTCTAGACGATTCCAAGAATGCCACAG
GGAACTCAGCCTCAGGCCTGGGGCTGGCAGGACCGCAGAAGATACCGTGGAAGATGCCTGCCAGCCGAGGGCA
GCAGGGAGGCCAGACCCAACACGCACCCCGGCCCGGCCCCACCCCGGCCGAGCTGCCCTGGACCAATATTGACC
TCAAGGAGGCCAAGAAAGTGGCCAGCCACTCGGCCGCTGGCTTCCCCGAGACCACCAGCCTCTCCTCTCTGGGGC
TCCTCCCACTGGGCTTGGAGGAGCCGTATGGGGTGGATGACCACCCGCTGTGGGCCCTGGGTGTGCGGAGGCGGCT
GCGTGGTGGAGGCATGTGCCATGCCAGATGGTTCACTGTCCAGGCGGGCCTGTCTCTCCTGGTACACATGCTGT
CCCTGTCCATCACGCCGCCCCAGACCGCTGCCTGGAGGAAGCAGATCTTCCAGCAGCTCACGGAAGGACCAAGC
GGGAGCTGGAGAACTTCAGACACTACGAGCAGGCCGTGGAGCAGTCGGTGTGGGTGAAGACCGGGGCGCTGCAGT
GGTGGTGCAGCTGGAAGCCCCACAAGTGGGTGGACGTGCGCTTGGCCCTGGAGCAGTTCACGGGGCACGACGGCG
TCCGGGACAGCATCCTCTTCATCTACTATGTGGTCCACGAGGAGAAGAAGTACATCCACATATTCTGAATGAGG
TGGTGGCGCTGGTCCCAGTGCTGAACGAGACCAAGCACTCCTTTGCCCTGTACACCCCTGAGCGGACACGGCAGA
GGTGGCCGGTGCCTGTGGCTGTGCCACCGAGCAGGACATGAATGACTGGCTCGCCCTGCTCAGCCTGTCTTGCT
GCGAGAGCCGGAAGGTGCAGGGCCGCCCCGTCCCCGAGGCCATCTGGTCCATCACCTGCAAGGGGGACATCTTCG
TGAGCGAGCCAGCCAGACCTGGAGGCCACGAGCACCCCTGCCCTGCGACCAGATGTTTTGGCGGCAGATGG
GAGGCCACCTGCGGATGGTGGAGGCCAACAGCCGGGGCGTGGTGTGGGGCATCGGCTATGACCACACGGCCTGGG
TATACACAGGCGGCTATGGAGGCGGCTGCTTCCAAGGCCTGGCCAGCAGCACCAGTAACATCTACACGCAGTCAG
ACGTGAAGTGTGTTACATCTATGAGAACCAGCGCTGGAACCCCGTCACAGGCTACACCAGCAGGGGTCTGCCCCA
CGGACCGGTACATGTGGAGCGATGCCTCGGGGCTGCAGGAGTGCACGAAGGCTGGCACGAAGCCCCCGTCCCTGC
AGTGGGCCTGGGTTTCCGACTGGTTCTGTGATTTTACGCGTTCCGGGGGGCACGGACCAGGAGGGGTGGCAGTATG
CCAGCGACTTCCCTGCCTCATACCATGGGTCCAAAACGATGAAGGATTTTGTGAGGAGGAGGTGCTGGGCCAGAA
AATGCAAGCTGGTGACCAAGTGGGCCCTGGCTGGAGGTGCCCCCATCGCCCTCAGGGACGTGTCCATCATCCCGG
AGAGCCCGGTGCCGAGGGGAGTGGGCACAGCATCGCCCTCTGGGCCGTACGCGACAAGGGGGATGTGCTGTGCC
GCCTGGGCGTGTGCGAGCTCAACCTGCGGGCTCCTCCTGGCTGCACGTTGGCACCGACCAGCCCTTCGCCTCCA
TCTCCATCGGGGCTGTACCAAGTGTGGGCCGTGGCAAGGGACGGCTCCGCCTTCTACCGGGGATCCGTGTACC
CCTCGCAGCCAGCCGGTGACTGCTGGTACCACATCCCGTCCCCACCGAGACAGAGGCTGAAGCAGGTGTCCGCGG
GGCAGACGTGGTGTATGCCCTGGATGAGAATGGAACCTGTGGTATCGCCAAGGGATCACGCCCAGCTACCCGC
AGGGCTCCAGCTGGGAGCACGTGTCCAACAACGTGTGCCAGTGTCCGTGGGGCCCTGGACCAGGTCTGGGTGA
TCGCCAACAAGTGCAGGGCAGCCACAGCTGAGCCGGGGGACAGTGTGTATCGCACCGGCGTGCAGCCTCACG
AGCCCAAGGGCCACGGCTGGGACTACGGCATCGGGGAGGCTGGGACCATATCTCTGTCCGGGCCAATGCCACCA
GGGCCCCCGGAGCTCGTCCAGGAGCAGGAGCCGAGTGCCCCACCGAGGGCCATGGCCCCGTCTGCTGTGAG
GCCCCCCCACACACCTACATGCAGGGACGGTGGCCAGTTTGGGGGATCAAGGCTGAGCCATTCTTGTGCTGGAGT
GTGCACCGTGGGAGCAATGTGGCCAGGTGGACTCAGGAGGGAACCTGGCCCCAAGGCTGCGGCCACTTCAGAGG
CACTGGCTGAGACGGCCCTGAAATGTGAAGCTCCGCGGACACTCCACACGTGTCCCGCTCTGCGAGGAGTCCCC

2561/6881
FIGURE 2353B

GGGTGTGGGGCATGGGGTGGGGCTGCACCTCCCAGAGGCCCCCTCCCACCCTTCCCTTCCCCTCTCCCTTCTGCCT
TTCCAGGACTAGAACCGGGAACCTGGAGCCCTCCGGGAACGCCGGCCCTGGGGCAGCAGAGCCAGGATGGAGCCC
TCCTGAGCTGGCATCTCAGACAGCACCCGGGCCCCGCCACCCCTCACCAAGAGAGATGGCCATGGGGCTCAGGGCC
TCTTTACCATGTGCAGTGACCATTCTCAGAGCAGGACTTGCAAAGAGGCTTTAATTTCAAAGTGAAGGAAGGA
GGCCAGGCGCCGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGGCAGATCACCTAGGTCAAGA
GTTTCAAACCAGACGGGCCAACATGGTGAAACCCCATCTCTGCTAAAAATACAAAAAAAAAAAAATTAGCTGGGC
ATGGTGGTGGGTGCCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATCGTTTGAACCCGGGAGGCGGAG
GCTGCAGTGAGCCGAGATCATGCCACTGCACTCCAGCCTGGGCGACAGAGACTCCATCTC

2562/6881
FIGURE 2354

MGWGCTSORPLPPFFPSPLPSAFFGLEPGTWSPPGTPALGQSQDGALLSWHLRQHFGPPPLTKRDGHGAQGLFTM
CSDHFSEQDLQRGFNFKSEGRRPGAVAHACNPSTLGG

2563/6881
FIGURE 2355

AAACTTCCCGCACGCGTTACAGGAGCCAGGTCGGTATAAGCGCCAGCGGCCTCGCCGCCCGTCAAGCTGTCCACA
TCCCTGGCCTCAGCCCCGCCACATCACCTGACCTGCTTACGCCCAGATTTTCTTCAATCACATCTGAATAAATCA
CTTGAAGAAAGCTTATAGCTTCATTGCACC**ATGT**GTGGCATTGTTGGGCGCTGTTTGGCAGTGATGATTGCCTTTCT
GTTCAAGTGTCTGAGTGCTATGAAGATTGCACACAGAGGTCCAGATGCATTCCGTTTTGAGAATGTCAATGGATAC
ACCAACTGCTGCTTTGGATTTACCGGTTGGCGGTAGTTGACCCGCTGTTTGGAAATGCAGCCAATTCGAGTGAAG
AAATATCCGTATTTGTGGCTCTGTTACAATGGTGAAATCTACAACCATAAGAAGATGCAACAGCATTTTGAATTT
GAATACCAGACCAAAGTGGATGGTGAGATAATCCTTCATCTTTATGACAAAGGAGGAATTGAGCAAACAATTTGT
ATGTTGGATGGTGTGTTTGCATTTGTTTTACTGGATACTGCCAATAAGAAAAGTGTTCTGGGTAGAGATACATAT
GGAGTCAGACCTTTGTTTTAAAGCAATGACAGAAGATGGATTTTTGGCTGTATGTTTCTGAGAAGCTAAAGGTCTTGTT
ACATTGAAGCACTCCGCGACTCCCTTTTTTAAAGTGGAGCCTTTTCTTCTGACACTATGAAGTTTTGGATTTA
AAGCCAAATGGCAAAGTTGCATCCGTGGAAATGGTTAAATATCATCACTGTCGGGATGAACCCCTGCACGCCCTC
TATGACAATGTGGAGAAACTCTTCCAGGTTTTGAGATAGAAACTGTGAAGAACAACCTCAGGATCCTTTTTTAAT
AATGCTGTAAAGAAACGTTTGATGACAGACAGAAGGATTGGCTGCCTTTTATCAGGGGGCTTGGACTCCAGCTTG
GTTGCTGCCACTCTGTTGAAGCAGCTGAAAGAAGCCCAAGTACAGTATCCTCTCCAGACATTTGCAATTGGCATG
GAAGACAGCCCCGATTTACTGGCTGCTAGAAAGGTGGCAGATCATATTGGAAGTGAACATTATGAAGTCCTTTTT
AACTCTGAGGAAGGCATTCAGGCTCTGGATGAAGTCATATTTTCTTGAAACTTATGACATTACAACAGTTCGT
GCTTCAGTAGGTATGTATTTAATTTCCAAGTATATTCGGAAGAACACAGATAGCGTGGTGATCTTCTCTGGAGAA
GGATCAGATGAACCTTACGCAGGGTTACATATATTTTACAAGGCTCCTTCTCCTGAAAAGCCGAGGAGGAGAGT
GAGAGGCTTCTGAGGGAACCTCTATTTGTTTGATGTTCTCCGCGCAGATCGAACTACTGCTGCCCATGGTCTTGAA
CTGAGAGTCCCATTTCTAGATCATCGATTTTCTTCTTATTACTTGCTCTGCCACCAGAAATGAGAATTCCAAAG
AATGGGATAGAAAAACATCTCCTGAGAGAGACGTTTGAGGATTCCAATCTGATACCCAAAGAGATTCTCTGGCGA
CCAAAAGAAGCCTTCAGTGATGGAATAACTTCAGTTAAGAATTCTGGTTTAAGATTTTACAGGAATACGTTGAA
CATCAGGTTGATGATGCAATGATGGCAAATGCAGCCCAGAAATTTCCCTTCAATACTCCTAAAACCAAAGAAGGA
TATTACTACCGTCAAGTCTTTGAACGCCATTACCCAGGCCGGGCTGACTGGCTGAGCCATTACTGGATGCCCAAG
TGGATCAATGCCACTGACCTTCTGCCCCGACGCTGACCCACTACAAGTCAGCTGTCAAAGCT**TAG**GTGGTCTTT
ATGCTGTAATGTGAAAGCAAATATTTCTTCGTGTTGGATGGGGACTGTGGGTAGATAGGGGAACAATGAGAGTCA
ACTCAGGCTAACTTGGGTGTGAAAAAATAAAAGTCCTAAATCT

2564/6881
FIGURE 2356

MCGIWALFGSDDCLSVQCLSAMKIAHRGPDAFRFENVNGYTNC CFGHRLAVVDPLFGMQPIRVKKYPYLWLCYN
GEIYNHKKMQQHFEFEYQTKVDGEIILHLYDKGGIEQTICMLDGVFAFVLLDTANKKVFLGRDTYGVRPLFKAMT
EDGFLAVCSEAKGLVTLKHSATPFLKVEPFLPGHYEVLDLKPNGKVASVEMVKYHHCRDEPLHALYDNVEKLFPG
FEIETVKNNLRILFNNAVKKRLMTDRRIGCLLSGGLDSSLVAATLLKQLKEAQVQYPLQTFAIGMEDSPDLLAAR
KVADHIGSEHYEVLFNSEEGIQALDEVIFSLETYDITTVRASVGMYLISKYIRKNTDSVVIFS GEGSDELTQGYI
YFHKAPSPEKAEESERLLRELYLFDVLRADRTTAAHGLELRVPFLDHRFSSYYLSLPPEMRIPKNGIEKHLRE
TFEDSNLIPKEILWRPKEAFSDGITSVKNSWFKILQEYVEHQVDDAMMANAAQKFPFNTPKTKEGYYYRQVFERH
YPGRADWL SHYWM PKWINATDPSARTLTHYKSAVKA

CCTTTCTGTCTCTGGTTCCCTGAAGCATCGAGAGGAAACCGCGCGGACGCCAGGCCGAGGAGGAGGCA
 GCGGCAGTTTGAGCCCTGTAAATGTTATATGTGTACTTTTTTTTTACTATGTGGCGTCTGAAGCCTGTGGACATTT
 TCGCGGTCCGGGTCCCTGCGGCGGACGGGTCCGATCGTGCTCGTGGCCAGGGCGCAGTCAGGTGTCTGCGTGGTCC
 TGATCTAGGAAGAGACTGCGGCCCTTATCACCGTCTCGGTGTCTGCTTTACCTTCAACTGCCCCCTCCTCACCT
 GGACCGCTCACCTCCTCCTCCCCCTCTACCCCGCCATCCCCACCAGTCCCCACCTGTCTCTGTAGACTGCAAGA
 CTCATCAAGTGACTTGCTGAGCAAACCTGCCGAGAAGAGATTTTCTTCAATCACATCTGAATAAATCACTTGAA
 GAAAGCTTATAGCTTCATTGCACCATGTGTGGCATTGTGGCGCTGTTTGGCAGTGATGATTGCCTTTCTGTTTCA
 TGTCTGAGTGCTATGAAGATTGCACACAGAGGTCCAGATGCATTCCGTTTTGAGAATGTCAATGGATACACCAAC
 TGCTGCTTTGGATTTACCGGTTGGCGGTAGTTGACCGCTGTTTGGGAATGCAGCCAATTCGAGTGAAGAAATAT
 CCGTATTTGTGGCTCTGTTTACAATGGTGAATCTACAACCATAAGAAGATGCAACAGCATTTTGAATTTGAATAC
 CAGACCAAAGTGGATGGTGAGATAATCCTTCATCTTTATGACAAAGGAGGAATTGAGCAAACAATTTGTATGTTG
 GATGGTGTGTTTGCATTTGTTTTACTGGATACTGCCAATAAGAAAGTGTTCTGGGTAGAGATACATATGGAGTC
 AGACCTTTGTTTAAAGCAATGACAGAAGATGGATTTTGGCTGTATGTTTCTGAGAAGCTAAAGGTCTTGTTACATTG
 AAGCACTCCGCGACTCCCTTTTTTAAAGTGGAGCCTTTTCTTCTGGACACTATGAAGTTTGGATTTAAAGCCA
 AATGGCAAAGTTGCATCCGTGGAAATGGTTAAATATCATCACTGTCTGGGATGAACCCCTGCACGCCCTCTATGAC
 AATGTGGAGAAACTCTTTCCAGGTTTTGAGATAGAACTGTGAAGAACAACCTCAGGATCCTTTTTAATAATGCT
 GTAAAGAAACGTTTGATGACAGACAGAAGGATTGGCTGCCTTTTATCAGGGGGCTTGGACTCCAGCTTGGTTGCT
 GCCACTCTGTTGAAGCAGCTGAAAAGAAGCCCAAGTACAGTATCCTCTCCAGACATTTGCAATTGGCATGGAAGAC
 AGCCCCGATTTACTGGCTGCTAGAAAAGGTGGCAGATCATATTGGAAGTGAACATTATGAAGTCCTTTTTTAACTCT
 GAGGAAGGCATTACAGGCTCTGGATGAAGTCATATTTTCTTGGAACTTATGACATTACAACAGTTCGTGCTTCA
 GTAGGTATGTATTTAATTTCCAAGTATATTTCGGAAGAACACAGATAGCGTGGTGATCTTCTCTGGAGAAGGATCA
 GATGAACCTTACGCAGGGTTACATATATTTTACAAAGGCTCCTTCTCTGAAAAAGCCGAGGAGGAGAGTGAGAGG
 CTTCTGAGGGAACCTCTATTTGTTTGATGTTCTCCGCGCAGATCGAACTACTGCTGCCCATGGTCTTGAAC TGAG
 GTCCCATTTCTAGATCATCGATTTTCTTCCCTATTACTTGTCTCTGCCACCAGAAATGAGAATTCCAAAGAATGGG
 ATAGAAAAACATCTCCTGAGAGAGACGTTTGAGGATTCCAATCTGATACCCAAAGAGATTCTCTGGCGACCAAAA
 GAAGCCTTCAGTGATGGAATAACTTCAGTTAAGAATTCTCGGTTTAAAGATTTTACAGGAATACGTTGAACATCAG
 GTTGATGATGCAATGATGGCAAATGCAGCCCAGAAATTTCCCTTCAATACTCCTAAAACCAAAGAAGGATATTAC
 TACCGTCAAGTCTTTGAACGCCATTACCCAGGCCGGGCTGACTGGCTGAGCCATTACTGGATGCCCAAGTGGATC
 AATGCCACTGACCTTCTGCCCGCACGCTGACCCACTACAAGTCAGCTGTCAAAGCTTAGGTGGTCTTTATGCTG
 TAATGTGAAAGCAAATATTTCTTCGTGTTGGATGGGGACTGTGGGTAGATAGGGGAACAATGAGAGTCAACTCAG
 GCTAACTTGGGTGTGAAAAAATAAAAGTCTTAAATCTAAAAA
 AAAAAAAAAAAAAAAAAAAAAA

2566/6881
FIGURE 2358

MCGIWALFGSDDCLSVQCLSAMKIAHRGPDAFRFENVNGYTNC CFGFHR LAVVDPLFGMQPIRVKKYPYLWLCYN
GEIYNHKKMQQHFEFEYQTKVDGEIILHLYDKGGIEQTICMLDGVFAFVLLDTANKKVFLGRDTYGVRPLFKAMT
EDGFLAVCSEAKGLVTLKHSATPFLKVEPFLPGHYEVL DLKPNGKVASVEMVKYHHRDEPLHALYDNVEKLFPG
FEIETVKNNLRILFNNAVKKRLMTDRRIGCLLSGGLDSSLVAATLLKQLKEAQVQYPLQTFAIGMEDSPDLLAAR
KVADHIGSEHYEVLFNSEEGIQALDEVIFSLETYDITTVRASVGMYLISKYIRKNTDSVVIFSGEGSDELTQGYI
YFHKAPSPEKAEESERLLRELYLFDVLRADRTTAAHGLELRVPFLDHRFSSYYLSLPPEMRIPKNGIEKHLRE
TFEDSNLIPKEILWRPKEAFSDGITSVKNSWFKILQEYVEHQVDDAMMANAAQKFPFNTPKTKEGYYYRQVFERH
YPGRADWLSHYWMPKWINATDPSARTLTHYKSAVKA

2567/6881
FIGURE 2359

CCTGGCTGGGACGGAAGTTGCACCACAAGTACAATTAGTTTCAGTTTTGTTTCTTTTCCAGGCACCCAGCAACGG
CGGCCTCCAGGCCTCAGGCCCCCTCACCATCCTAGAGGTCAAGATCAGCTCTGGCTAGTTCTCACAGGTCTGACC
CAACAAGTAGCACTGACATTTTTACGTTTGCTGGATGTACACACGGAAGTGGAGGAGGAGGAGAGAAGGAGGAG
GGCAGCTCCTTAGCTCAAGAGCAAGTGGCCCAAGGCCTCAGAAGACTAGAAGGAAGTTCTTGCCATTTCAGCATG

GTTTCCCACGGGTCTCGCCCTCCCTCCTGGAGGCCCTGAGCAGCGACTTCCTGGCCTGTAAATCTGCCTGGAG
CAGCTGCGGGCACCCAAGACACTGCCCTGCCTGCATACCTACTGCCAAGACTGCCTGGCACAGCTGGCGGATGGC
GGCCGCGTCCGCTGCCCCGAGTGCCGCGAGACAGTGCCTGTGCCGCCCGAGGGTGTGGCCTCCTTCAAGACCAAC
TTCTTCGTCAATGGGCTGCTGGACCTGGTGAAGGCCCGGGCCTGTGGAGACCTGCGTGCCGGGAAGCCAGCCTGT
GCCCTGTGTCCCCTGGTGGGTGGCACCAGCACCGGGGGGGCCGGCCACGGCCCGGTGCCTGGACTGTGCCGATGAC
TTGTGCCAGGCCTGTGCCGACGGGCACCGCTGCACCCGCCAGACCCACACCCACCGCGTGGTGGACCTGGTGGGC
TACAGGGCCGGGTGGTATGATGAGGAGGCCCGGGAGCGCCAAGCGGCCAGTGTCCCCAGCACCCCGGGGAGGCA
CTGCGCTTCCTGTGCCAGCCCTGCTCACAGTTGCTGTGCAGAGAGTGCCGCCTAGACCCCCACCTGGACCACCCC
TGCCTGCCTCTGGCTGAAGCTGTGCGTGCCCGGAGGCGGGCCTGGAGGGACTGCTGGCCGGTGTGGACAATAAC
CTGGTGGAGCTGGAGGCAGCGCGGAGGGTGGAGAAGGAGGCGCTAGCCCGGTGCGGGAGCAGGCGGCCCGGGTG
GGGACTCAGGTGGAGGAGGCGGCTGAGGGCGTCTCCGGGCCCTGCTGGCCAGAAGCAGGAGGTGCTGGGGCAG
CTACGAGCCACGTGGAGGCTGCCGAAGAAGCTGCTCGGGAGAGGCTGGCGGAGCTTGAGGGCCGGGAGCAGGTG
GCCAGGGCCGAGCCGCTTCGCCCGCCGGGTACTCAGCCTGGGGCGAGAGGCCGAGATCCTCTCCCTGGAAGGG
GCGATCGCACAGCGGCTCAGGCAGCTGCAGGGCTGCCCTGGGCACCAGGCCCGGCCCTGCCTGCTCCACAG
CTGGAGCTCCATCCTGGGCTCCTGGACAAGAAGTGCACCTTCTTCGGCTGTCTTTGAGGAGCAGCAGCCCCAG
AAGGATGGTGGGAAAGACGGAGCTGGTACCCAGGGAGGTGAGGAGAGCCAGAGCCGGAGGGAGGATGAGCCGAAG
ACTGAGAGACAGGGTGGAGTCCAGCCCCAGGCTGGAGATGGAGCCAGACCCCAAAGAGGAAAAAGCCCAGACA
ACCCGAGAAGAGGGAGCCCAGACCTTGAGGAGGACAGGGCCAGACACCCACAGGATGGAGGACCCCAGCCC
CACAGGGGTGGCAGACCCAACAAGAAGAAAAAGTTCAAAGGCAGGCTCAAGTCAATTTCCCGGGAGCCCAGCCCA
GCCCTGGGGCCGAATCTGGACGGCTCTGGCCTCCTCCCCAGACCCATCTTTTACTGCAGTTTCCCCACGCGGATG
CCTGGAGACAAGCGGTCCCCCGGATACCCGGGCTCTGTCCCTTCGGTCCCCGGGAGATCCTGGTGGCGGATGAG
CAGAACCGGGCACTGAAAACGCTTCTCCCTCAACGGCGACTACAAGGGCACCGTGCCGGTCCCTGAGGGCTGTCC
CCTTGACAGCTGGCCGCCCTGCAGAGCGCGGTGGCCTTCTCCGCTAGCGCACGGCTCTATCTCATCAACCCCAAC
GGCGAAGTGCAGTGGCGCAGGGCCCTGAGCCTCTCCAGGCCAGCCACGCGGTGGCGGCACTGCCTAGCGGGGAC
CGCGTGGCTGTGAGCTGGCGGGCCACGTGGAGGTGTACAATATGGAAGGCAGCCTGGCCACCCGGTTTATTCTCT
GGAGGCAAGGCCAGCCGGGGCCTGCGGGCGCTGGTGTCTTGACCACCAGCCCCAGGGGCATTTTCGTGGGGTCG
GACTGGCAGCAGAATAGTGTGTAATCTGTGATGGGCTGGGCCAGGTGGTTGGGGAGTACAAGGGGCCAGGCCTG
CATGGCTGCCAGCCGGGCTCCGTGTCTGTGGATAAGAAGGGCTACATCTTTCTGACCCTTCGAGAAGTCAACAAG
GTGGTGATCCTGGACCCGAAGGGGTCCCTCCTTGAGACTTCTGACAGCCTACCACGGCCTGGAAGGCCCGG
GTTACCACCATGGTGGATGGCAGGTACCTGGTGTGTCCTCAGTAACGGGACCATCCACATCTTTCGGGTCCGT
TCTCCGGACAGTTAAAGGGGCTAGGACTAGGGTGAGAGGGAGTGGGGAGGGAGAGGGCAGGAAGGAGGCAGAGCT
GTCCGTGGGAGGTGGAGGCCGAGGACATTTTCTGAAGGGCAGGGCTGGCAACTTTTCAACATGGAGTGCCAAA
CTGCTAACCCGTCTTCTAGTGTGTGAGAATAGGGACCAAGGTGGTGGCGTGACCTTAACCTCAGAAGCAGAGGA
GGCAGGTGGGTGGAGGGGGATGCTGGGAGTTACCTGCCTCTTGCTTTTGTGGGTGGCTGCTGCCACCACCGCC
GCTGCTATATAGTTTAGGTTTCTGAGGTTTGTGAGCCTGTCTGCTTTTGCACTTCTCAAACCATTCCTGATAGA
GTAGCCGAGGGAGAGTCTTGGGGCCAAGAAGGGCCAGGGTGGGTGAGCGTGTGCACTGTGGAACAGAGCTGAG
ACCCCGGCCCCCTTGACTGGCACAGGTCTTACAGAGTCAGAGGAGGCCCTGAGATTTCAATGGGCAGTGAAT
GGCCTCTTCTGCCAGCCACAGGCAGGATGCTCCTTGATCACGGCATCCCCCGCGGTAGTACAGGGTGAGCTTGC
AGGAGGGTCTGCAAGTGCAGACAGCAGCTGGGGCCAAAGAGGTGTTAGGTTCAAAGGCTGCGAAGAGAATAGGCT
ACTGGAAAACCAACCCAACAGAATTACGTCCAAAATCCACATTCTCCATCGCTTCTCAGCCTTTTGGCTAAG
ATTAAGTATTAATAAAAAAACAGGCTCTGCCAGGCGCAGTGGCTCATGCCTATAATCCCGGCACTTTGGGAGTCT
GTGGCAGGAGGATTGCTTGAGGCCAGGAGTTTGAGACCAGCCTGGGCAACATAGCGAGACCCCATCTCTACAAAA
GATTAATAATTAGCTGCGTGTAGTAGCATATGCCTTTCAACGTAGCTACTCAGGAGGCTGAGGTGGGAGGATCCC
TTGAGCCGAGGAGTTTGAGTCTGCAGTGAGCTATGATCGCACCACTGCATTCCAGACCCCATCTCG

2568/6881
FIGURE 2360

MVSHGSSPSLLEALSSDFLACKICLEQLRAPKTLPCCLHTYCQDCLAQLADGGRVRCPECRETVPVPPEGVASFKT
NFFVNGLLDLVKARACGDLRAGKPACALCPLVGGTSTGGPATARCLDCADDLCQACADGHRCTRQTHTHRVDLV
GYRAGWYDEEARERQAAQCPQHPGEALRFLCQPCSQLLCRECRLDPHLDHFCPLPLAEAVRARRPGLEGLLAGVDN
NLVELEAARRVEKEALARLREQAARVGTQVEEAAEGVLRALLAQKQEVLGQLRAHVEAAEEAARERLAELEGREQ
VARAAAFARRVLSLGREAEILSLEGAIAQRLRQLQGCPWAPGPAPCLLPQLELHPGLLDKNCHLLRLSFEEQQP
QKDGGKDGAGTQGGEESSSRREDEPKTERQGGVQPQAGDGAQTPKEEKAQTTREEGAQTLEEDRAQTPHEDGGPQ
PHRGGRPNNKKKFKGRLKSISSREPSALGPNLDGSGLLPRPIFYCSFPTRMPGDKRSPRITGLCPFGPREILVAD
EQNRALKRFSLNGDYKGTVPVPEGCSPCSVAALQSAVAFSASARLYLINPNGEVQWRRALSLSQASHAVAALPSG
DRVAVSVAGHVEVYNMEGSLATRFIPGGKASRGLRALVFLTTSPQGHFVGSDWQQNSVVICDGLGQVVGEYKGP
LHGCQPGSVSVDKKGYIFLTLREVNVVILDPKGSLLGDFLTAYHGLEKPRVTTMVDGRYLVVSLSNGTIHIFRV
RSPDS

2569/6881
FIGURE 2361

GAATTCTGCAGCTCAGCAGCCGCCGCCAGAGCAGGACGAACCGCCAATCGCAAGGCACCTCTGAGAACTTCAGG
ATGCAGATGTCTCCAGCCCTCACCTGCCTAGTCCTGGGCCTGGCCCTTGTCCTTGGTGAAGGGTCTGCTGTGCAC
CATCCCCATCCTACGTGGCCACCTGGCCTCAGACTTCGGGGTGAGGGTGTTTCAGCAGGTGGCGCAGGCCTCC
AAGGACCGCAACGTGGTTTTCTCACCTATGGGGTGGCCTCGGTGTTGGCCATGCTCCAGCTGACAACAGGAGGA
GAAACCCAGCAGCAGATTCAAGCAGCTATGGGATTCAAGATTGATGACAAGGGCATGGCCCCCGCCCTCCGGCAT
CTGTACAAGGAGCTCATGGGGCCATGGAACAAGGATGAGATCAGCACCACAGACGCGATCTTCGTCCAGCGGGAT
CTGAAGCTGGTCCAGGGCTTCATGCCCCACTTCTTCAGGCTGTTCCGGAGCACGGTCAAGCAAGTGGACTTTTCA
GAGGTGGAGAGAGCCAGATTATCATCAATGACTGGGTGAAGACACACAAAAGGTATGATCAGCAACTTGCTT
GGGAAAGGAGCCGTGGACCAGCTGACACGGCTGGTGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAGACT
CCCTTCCCCGACTCCAGCACCACCGCCGCCCTCTTCCACAAATCAGACGGCAGCACTGTCTCTGTGCCCATGATG
GCTCAGACCAACAAGTTCAACTATACTGAGTTCACCACGCCCCGATGGCCATTACTACGACATCCTGGAAGTGCCC
TACCACGGGGACACCCCTCAGCATGTTCAATTGCTGCCCTTATGAAAAAGAGGTGCCTCTCTCTGCCCTCACCAAC
ATTCTGAGTGCCAGCTCATCAGCCACTGGAAAGGCAACATGACCAGGCTGCCCCGCTCCTGGTTCTGCCCAAG
TTCTCCCTGGAGACTGAAGTCGACCTCAGGAAGCCCCTAGAGAACCTGGGAATGACCGACATGTTTCAGACAGTTT
CAGGCTGACTTCACGAGTCTTTCAGACCAAGAGCCTCTCCACGTCGCGCAGGCGCTGCAGAAAGTGAAGATCGAG
GTGAACGAGAGTGGCACGGTGGCCTCCTCATCCACAGCTGTCTAGTCTCAGCCCGCATGGCCCCCGAGGAGATC
ATCATGGACAGACCCTTCCTCTTGTGGTCCGGCACAACCCACAGGAACAGTCTTTTTCATGGGCAAGTGATG
GAACCCTGACCCTGGGGAAAGACGCCTTCATCTGGGACAAAACCTGGAGATGCATCGGGAAAGAAGAAACTCCGAA
GAAAAGAATTTTAGTGTTAATGACTCTTCTGAAGGAAGAGAAGACATTTGCCTTTTGTAAAAGATGGTAAACC
AGATCTGTCTCCAAGACCTTGGCCTCTCCTTGGAGGACCTTTAGGTCAAACCTCCTAGTCTCCACCTGAGACCCT
GGGAGAGAAGTTTGAAGCACAACCTCCCTTAAGGTCTCCAAACCAGACGGTGACGCCTGCGGGACCATCTGGGGCA
CCTGCTTCCACCCGTCTCTCTGCCACTCGGGTCTGCAGACCTGGTTCCCACTGAGGCCCTTTGCAGGATGGAAC
TACGGGGCTTACAGGAGCTTTTGTGTGCCTGGTAGAACTATTTCTGTTCCAGTCACATTGCCATCACTCTTGTA
CTGCCTGCCACCGCGGAGGAGGCTGGTGACAGGCCAAAGGCCAGTGGAAGAAACACCCTTTCATCTCAGAGTCCA
CTGTGGCACTGGCCACCCCTCCCCAGTACAGGGGTGCTGCAGGTGGCAGAGTGAATGTCCCCCATCATGTGGCCC
AACTCTCCTGGCCTGGCCATCTCCCTCCCCAGAAACAGTGTGCATGGGTTATTTTGGAGTGTAGGTGACTTGTTT
ACTCATTGAAGCAGATTTCTGCTTCCTTTTATTTTATAGGAATAGAGGAAGAAATGTCAGATGCGTGCCAGCT
CTTACCCCCCAATCTCTTGGTGGGGAGGGGTGTACCTAAATATTTATCATATCCTTGCCCTTGAGTGCTTGTTA
GAGAGAAAGAGAACTACTAAGGAAAATAATATTATTTAACTCGCTCCTAGTGTTCCTTTGTGGTCTGTGTCACC
GTATCTCAGGAAGTCCAGCCACTTGACTGGCACACACCCCTCCGGACATCCAGCGTGACGGAGCCCACACTGCCA
CCTTGTGGCCGCCTGAGACCCTCGCGCCCCCGCGCCCCCGCGCCCCCTCTTTTCCCCCTTGATGGAAATTGACC
ATACAATTTTCATCCTCCTTCAGGGGATCAAAAGGACGGAGTGGGGGGACAGAGACTCAGATGAGGACAGAGTGGT
TTCCAATGTGTTCAATAGATTTAGGAGCAGAAATGCAAGGGGCTGCATGACCTACCAGGACAGAACCTTTCCCCAA
TTACAGGGTGACTCACAGCCGCATTGGTGACTCACTTCAATGTGTCAATTCGGGCTGCTGTGTGTGAGCAGTGGA
CACGTGAGGGGGGGGTGGGTGAGAGAGACAGGCAGCTCGGATTCAACTACCTTAGATAATATTTCTGAAAACCTA
CCAGCCAGAGGGTAGGGCACAAGATGGATGTAATGCACTTTGGGAGGCCAAGGCGGGAGGATTGCTTGAGCCCA
GGAGTTCAAGACCAGCCTGGGCAACATACCAAGACCCCGTCTCTTTAAAAATATATATATTTTAAATATACTTA
AATATATATTTCTAATATCTTTAAATATATATATATATTTTAAAGACCAATTTATGGGAGAATTGCACACAGATG
TGAAATGAATGTAATCTAATAGAAGC

2570/6881
FIGURE 2362

MQMSPALTCLVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPYGVASVLAMLQLTTGG
ETQQQIQAAAMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAIFVQRDLKLVQGFMPPHFFRLFRSTVKQVDFS
EVERARFIINDWVKTHTKGMISNLLGKGAVDQLTRLVLVNALYFNGQWKTPFPDSSTHRRLFHKSDGSTVSVPM
AQTNKFNYTEFTTPDGHYDILELPYHGDLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPK
FSLETEVDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVASSSTAVIVSARMAPEEI
IMDRPFLFVVRHNPTGTVLFMGQVMEP

2571/6881
FIGURE 2363

GTGGGACGCGCCGAGCCGGAGGCTGCAGGATGATGCGGTTTCATGCTATTATTCAGCCGGCAGGGAAAACCTGCGGC
TGCAAAAATGGTACCTGGCCACTTCGGACAAGGAACGGAAGAAGATGGTGCGCGAGCTCATGCAGGTTGTCCTGG
CTCGAAAGCCCAAGATGTGCAGCTTCCTGGAGTGGAGGGACCTCAAAGTTGTCTATAAGAGATATGCCAGCCTCT
ACTTCTGCTGCGCCATCGAGGGCCAAGACAATGAGCTCATCACACTGGAGCTGATCCACCGATACGTGGAGCTCT
TAGACAAATACTTTGGCAGTGTGTGCGAGCTGGACATCATCTTCAACTTTGAGAAGGCCTACTTCATCCTGGATG
AGTTTTTGATGGGGGGGGATGTCCAGGACACCTCCACTTTCCCCTTTTCCCACTTGAAGGTTTTAGAAGCTAGGAG
GCAGGAAAATGTGACCCAGATGGGGGTGCTATTTGGCTTTTATTCCCTGCCTTTGCAGAACTGATGTCACCCAG
ATGTCCTTCCCTCCCTAATAACTGTAAATATATAAATATGTCAGGTTAAAGGGAAAAGGTGTTTCAGGGCACTTCT
TGTCTCTCTGTCCCATAACTACCTCCACCCTCCCCCTAGCCAGCCAGGCAGCTTCTCTGCCTGGGAGGGGAGC
CTGGACCCCCCTCTTTCTCCTTGGCTGCAGTGGGGCCTTTATCCAGTGCCAGGGAGGAACAACATAGTTAATTTT
TTTCTAACCTTGCCACTTTGAGGGAAGGAAGGGTTGGGGGAAGGGCAAGCTTTATGGGACCCTGGTCTGGCCCT
GGCCTTTCACTCCAGTTCTGGGTGAGGCAGGAGCTGGGAGGGGTGGGGAGGGGGAGGGGGAAGTGTCTGCCTTTA
TGTCTTTCTTCTGAAATAAAAGGAAAAGCATTTCTGGAIAAAAAAAAAAAAAAAAAAAAAA

2572/6881
FIGURE 2364

MMRFMLLFSRQGKLRLOKWYLATSDKERKKMVRELMQVVLARKPKMCSFLEWRDLKVVKRYASLYFCCAIEGQD
NELITLELIHRYVELLDKYFGSVCELDIIFNFEKAYFILDEFLMGGDVQDTSTFFFSH

2573/6881
FIGURE 2365

GTGGGACGCGCCGAGCCGGAGGCTGCAGGATGATGCGGTTTCATGCTATTATTCAGCCGGCAGGGAAAACCTGCGGC
TGCAAAAATGGTACCTGGCCACTTCGGACAAGGAACGGAAGAAGATGGTGCGCGAGCTCATGCAGGTTGTCCTGG
CTCGAAAGCCCAAGATGTGCAGCTTCCTGGAGTGGAGGGACCTCAAAGTTGTCTATAAGAGATATGCCAGCCTCT
ACTTCTGCTGCGCCATCGAGGGCCAAGACAATGAGCTCATCACACTGGAGCTGATCCACCGATACGTGGAGCTCT
TAGACAAATACTTTGGCAGTGTGTGCGAGCTGGACATCATCTTCAACTTTGAGAAGGCCTACTTCATCCTGGATG
AGTTTTTGATGGGGGGGGATGTCCAGGACACCTCCAAGAAGAGTGTGCTGAAAGCCATCGAGCAGGCTGACCTAC
TGCAAGAGGAGGATGAGTCGCCACGGAGTGTGCTGGAGGAGATGGGTTTGGCATAGCCCCCTGCTGGGCCGGGGTG
TGGCGATGGGGTCCTGGCAGCGTGGCGGGAACGGCTGCTTCTCCTCTGCCCAGGGCCCTGTTCTTGGTGGGACTC
GGCTGCCCCCTCCTC

2574/6881
FIGURE 2366

MMRFMLLFSRQGKLRLOKWYLATSDKERKKMVRELMQVVLARKPKMCSFLEWRDLKVVKRYASLYFCCAIEGQD
NELITLELIHRYVELLDKYFGSVCELDIIFNFEKAYFILDEFMLGGDVQDTSKKSVLKAIEQADLLQEEDESPRS
VLEEMGLA

2575/6881
FIGURE 2367

CCAGCGTGCTGAAGCCGGAGCGAGCTAGCCGCCCCGAGCCGCGCCGACCCAGCTGAGCCCAGCCCACGGGACGCC
AGACCTCGACCGTCGCTCCTACCCCGGCCACCGCTCGGAGCCGAGGCGGACGCGTCCCGATCTTCCCCTGTCCCC
ACCCTGCCCCGACCCCTCCTCTCCACCTCTCGCGTCGTGACACCAGCGTCTCCGGCAGCCTCTTGGTC**ATG**AAAGC
CCTCAGATTGTGGCTTCCGCCCTCTTCTGCCTTCTGCTGATCAACGGGTTAGGGGCAGCACCCCTGGTCGCCC
TGAGGCGCAGCCTCCTCCTCTCAGCTCTGAGCATAAAGAGCCGGTAGCCGGGGACGCAGTGCCCCGGGCCAAAGGA
TGGCAGCGCCCCAGAGGTCCGAGGCGCTCGGAATTCGAGCCGCAGGACGAGGGAGAGCTTTTCCAGGGCGTGGA
TCCCCGGGCGCTGGCCGCGGTGCTGCTGCAGGCACTCGACCGTCCCGCCTCACCCCGGCACCAAGCGGCTCCCA
GCAGGGGCCGGAGGAAGAAGCAGCTGAAGCTCTGCTGACCGAGACCGTGCGCAGCCAGACCCACAGCCTCCCCGC
GCCGGAGAGCCCCGAGCCCCGCGGCTCCGCCTCGCCCTCAGACTCCGGAGAATGGGCCCCGAGGCGAGCGATCCCTC
CGAGGAGCTCGAGGCGCTAGCGTCCCTGCTCCAGGAACTGCGAGATTTTCACTCCAAGTAGCGCCAAGCGCCAGCA
GGAGACGGCGGCAGCAGAGACGGAACCCGCACGCACACGCTGACCCGAGTGAATCTGGAGAGCCCCGGGGCCAGA
GCGCGTATGGCGCGCTTCCTGGGGAGAGTTCCAGGCGCGTGTCCCGGAGCGCGCGCCCCCTGCCGCCCCCGGCCCC
CTCTCAATTCCAGGCGCGTATGCCCGACAGCGGGCCCCCTTCCCGAAACCCACAAGTTCCGGGAAGGAGTGTCTCTC
CCCCAAAACACACCTAGGCGAGGCATTGGCACCCCTGTCCAAGGCGTACCAAGGCGTGCCCGCCCCGTTCCCCAA
GGCGCGCCGGCCGGAGAGCGCACTCCTGGGCGGCTCCGAGGCGGGCGAGCGCCTTCTCCAGCAAGGGCTGGCGCA
GGTGGAGGCCGGGCGGCGGCGAGGCGGAGGCCACGCGGCAGGCCGCGGCGCAGGAAGAGCGGCTGGCCGACCTCGC
CTCGGACCTGCTGCTCCAGTATTTGCTGCAGGGCGGGGCCCGGCAGCGCGGCTCGGGGTGGGGGCTGCAGGA
GGCGGCGGAGGAGCGAGAGAGTGAAGGAGGAGGAGGAGGCGGAGCAGGAGAGACGCGGCGGGGAGGAGAGGGT
GGGGGAAGAGGATGAGGAGGCGGCCGAGGCGGAGGCGAGGCGGAGGAGGCGGAGAGGGCGGCGGAGAACGCGCT
CCTGTTCGCGGAGGAGGAGGACGGGGAAGCCGGCGCCGAGGACAAGCGCTCCCAGGAGGAGACGCCGGGCCACCG
GCGGAAGGAGGCCGAGGGGACAGAGGAGGGCGGGGAGGAGGAGGACGACGAGGAGATGGATCCGCAGACGATCGA
CAGCCTCATTGAGCTGTCCACCAAATCCACCTGCCAGCGGACGACGTGGTCAGCATCATCGAGGAGGTGGAGGA
GAAGCGGAAGCGGAAGAAGAAGCGCCCTCCCGAGCCCGTGCCGCCCCCGTGCCGCCCCCGCCCCACCCACGT
CCGCTCCCCCGAGCCCCCGCCCCCGCCCCCGCTCCCGCACGAGACGAGCTGCCGGACTGGAACGAGGTGCTCCC
GCCCTGGGATCGGGAGGAGGACGAGGTGTACCCGCCAGGGCCGTACCACCCCTTCCCCAACTACATCCGGCCGCG
GACACTGCAGCCGCCCTCGGCCCTTGCGCCGCCGCACTACCACACGCTTGCCGCCCTTCGCGCCACTATCCGGG
CCGGGAGGCCAGGCGCGGCGCGCAGGAGGAGGCGGAGGCGGAGGAGCGCCGGCTGCAGGAGCAGGAGGAGCT
GGAGAATTACATCGAGCACGTGCTGCTCCGGCGCCCG**TGA**CTGCCCTTCCCGGTCCCGCCCCGCGCGCCCCCGC
CGCGCGCGCGCGCCGGCGCCCCCTCCGTGTTGCCGCTCCCCCTCGGTGTTTGCATGCGCCCCGGCCCTGCCCC
TTGGCCCTGCCCCCTGTCCCCGGGTGCGTCGGGACCTGCCAGACCCCCCTCCCGGTCTGAGCCCGAACTCCCA
GAGCTACCCGCGGGTGACCGGGGGCCAGCCAGGAGGGCGGGTGTTTGTGCGAGTTCCCTTGCCACGCGGGGC
CCCGGCCCATCAAGTCCCTCTGGGGACGTCCCGTCGGAACCGGAAAAAGCAGTTCCAGTTAATTGTGTGAAG
TGTGTCTGTCTCCAGCCCTTCGGGCTCCACGAGCCCTCCAGCCTCTCCAAGTCGCTGTGAATTGACCCCTTC
TTTCCTTTCTCTGTTGTAAATACCCCTCACGGAGGAAATAGTTTTGCTAAGAAATAAAAGTGAATTTTT

2576/6881
FIGURE 2368

MKALRLSASALFCLLLINGLGAAPPGRPEAQPPPLSSEHKPEVAGDAVPGPKDGSAPFVRGARNSEPQDEGELFQ
GVDPRALAAVLLQALDRPASPPAPSGSQQGPEEEAAEALLTETVRSQTHSLPAPESPEPAAPPRPQTPENGPEAS
DPSEEEALASLLQELRDFSPSSAKRQQETAAAETETRTHTLTRVNLESPGPERVWRASWGEFQARVPERAPLPP
PAPSQFQARMPDSGPLPETHKFGEVSSPKTHLGEALAPLSKAYQGVAAPFPKARRPESALLGGSEAGERLLQQG
LAQVEAGRQAEATRQAAAQEERLADLASDLLLQYLLQGGARQRGLGGRGLQEAAEERESAREEEEEAEQERRGGE
ERVGEEDDEAAEAAEAAEAAERARQNALLFAEEEDGEAGAEDKRSQEETPGHRRKEAEGTEEGGEEEDDEEMDPQ
TIDSLIELSTKLHLPADDVVSIIIEVEEKRRKKKNAPPEPVPPPRAAPAPTHVRSPQPPPPAPAPARDELDPWNE
VLPPWDREEDDEVYPPGPYHPPFNYIRPTLQPPSALRRRRHYHHALPPSRHYPGREAQARRAQEEAAEERRLQE
EELNYIEHVLLRRP

2577/6881
FIGURE 2369

GGCACGAGGGCTTCCACATGTGTCAAGCGGCTGGCTCAGCCCAGAGTCCCTGTCTCCCGCCCCGCCGCCGAGCC
GCCGCCCCCTCCCCCGCCTCCCGTGCGCCCGGGACAATCCTCGCCTTGTCTGTGGCGCCGGCATCTGGAGCTTTCT
GTAGCCTCCGGATACGCCTTTTTTTCAGGGCGTAGCCCCAGCCAAGCTGCTCCCCGCGGCGGCCGCACAGCAGCC
CGAGCGCCCCCTTTCCGGAGCTCCCCCTCCGGAGCTGGGATCCAGGCGCGTAGCGGAGATCCCAGGATCCTGGGTG
CTGTCTGGGCCCCGCTCCCCACCATGACCTCCTCGGGGCCTGGACCCCGGTTCCCTGCTGCTGCTGCCGCTGCTGCT
GCCCCCTGCGGCCTCAGCCTCCGACCGGCCCGGGGCCGAGACCCGGTCAACCCAGAGAAGCTGCTGGTGATCAC
TGTGGCCACAGCTGAAACCGAGGGGTACCTGCGTTTTCTGCGCTCTGCGGAGTTCTTCAACTACACTGTGCGGAC
CCTGGGCCTGGGAGAGGAGTGGCGAGGGGGTGATGTGGCTCGAACAGTTGGTGGAGGACAGAAGGTCCGGTGGTT
AAAGAAGGAAATGGAGAAATACGCTGACCGGGAGGATATGATCATCATGTTTGTGGATAGCTACGACGTGATTCT
GGCCGGCAGCCCCACAGAGCTGCTGAAGAAGTTTCGTCCAGAGTGGCAGCCGCTGCTCTTCTCTGCAGAGAGCTT
CTGCTGGCCCCGAGTGGGGGCTGGCGGAGCAGTACCCTGAGGTGGGCACGGGGAAGCGCTTCTCAATTCTGGTGG
ATTATCGGTTTTTGCCACCACCATCCACCAAATCGTGCGCCAGTGGAAAGTACAAGGATGATGACGACGACCAGCT
GTTCTACACACGGCTCTACCTGGACCCAGGACTGAGGGAGAAACTCAGCCTTAATCTGGATCATAAGTCTCGGAT
CTTTTCAGAACCTCAACGGGGCTTTAGATGAAGTGGTTTTAAAGTTTGATCGGAACCGTGTGCGTATCCGGAACGT
GGCCTACGACACGCTCCCCATTGTGGTCCATGGAACGGTCCCCTAAGCTGCAGCTCAACTACCTGGGAAACTA
CGTCCCCAATGGCTGGACTCCTGAGGGAGGCTGTGGCTTCTGCAACCAGGACCGGAGGACACTCCCGGGGGGGCA
GCCTCCCCCCCCGGGTGTTTCTGGCCGTGTTTGTGGAACAGCCTACTCCGTTTCTGCCCCGCTTCTGACGCGGT
GCTACTCCTGGACTATCCCCCGACAGGGTCACCCTTTTCTGCAACAACAGAGGTCTTCCATGAACCCACAT
CGCTGACTCCTGGCCGACGCTCCAGGACCACTTCTCAGCTGTGAAGCTCGTGGGGCCGAGGAGGCTCTGAGCCC
AGGCGAGGCCAGGGACATGGCCATGGACCTGTGTGCGCAGGACCCCGAGTGTGAGTTCTACTTCAGCCTGGACGC
CGACGCTGTCTTACCAACCTGCAGACCCTGCGTATCCTCATTGAGGAGAACAGGAAGGTGATCGCCCCATGCT
GTCCCGCCACGGCAAGCTGTGGTCCAACCTTCTGGGGCGCCCTGAGCCCCGATGAGTACTACGCCCGCTCCGAGGA
CTACGTGGAGCTGGTGCAGCGGAAGCGAGTGGGTGTGTGGAATGTACCATACTCTCCAGGCCTATGTGATCCG
GGGTGATACCCTGCGGATGGAGCTGCCCCAGAGGGATGTGTTCTCGGGCAGTGACACAGACCCGGACATGGCCTT
CTGTAAGAGCTTTTCGAGACAAGGGCATCTTCTCCATCTGAGCAATCAGCATGAATTTGGCCGGCTCCTGGCCAC
TTCCAGATACGACACGGAGCACCTGCACCCCGACCTCTGGCAGATCTTCGACAACCCCGTCGACTGGAAGGAGCA
GTACATCCACGAGAACTACAGCCGGGGCCCTGGAAGGGGAAGGAATCGTGGAGCAGCCATGCCCGACGTGTACTG
GTTCCCACTGCTGTGAGAACAATGTGTGATGAGCTGGTGGCAGAGATGGAGCACTACGGCCAGTGGTCAGGCGG
CCGGCATGAGGATTCAAGGCTGGCTGGAGGCTACGAGAATGTGCCACCGTGGACATCCACATGAAGCAGGTGGG
GTACGAGGACCAGTGGCTGCAGCTGCTGCGGACGTATGTGGGCCCCATGACCGAGAGCCTGTTTCCCGGTTACCA
CACCAAGGCGCGGGCGGTGATGAACTTTGTGGTTTCGCTACCGGCCAGACGAGCAGCCGTCTCTGCGGCCACACCA
CGACTCATCCACCTTACCCCTCAACGTTGCCCTCAACCACAAGGGCCTGGACTATGAGGGAGGTGGCTGCCGCTT
CCTGCGCTACGACTGTGTGATCTCCTCCCCGAGGAAGGGCTGGGCACTCCTGCACCCCGGCCGCTCACCCACTA
CCACGAGGGGCTGCCAACGACCTGGGGCACACGCTACATCATGGTGTCTTTGTGACCCCTGACACTCAACCAC
TCTGCCAAACCTGCCCTGCCATTGTGCCTTTTTAGGGGGCCTGGCCCCCGTCTGGGAGTTGGGGGATGGGTCTC
TCTGTCTCCCCACTTCTGAGTTCATGTTCCGCGTGCCTGAACTGAATATGTCACCTTGCTCCCAAGACACGGCC
CTCTCAGGAAGCTCCCGGAGTCCCCGCTCTCTCCTCCGCCACAGGGGTTCGTGGGCACAGGGCTTCTGGGGAC
TCCCCGCGTGATAAATTATTAATGTTCCGCAGTCTCACTCTGAATAAAGGACAGTTTGTAACAAAAAAAAAAAAAA
AA

2578/6881
FIGURE 2370

MTSSGPGPRFLLLLLPLLLPPAASASDRPRGRDPVNPEKLLVITVATAETEGYLRFLRSAEFFNYTVRTLGLGEEW
RGGDVARTVGGGQKVRWLKKEMEKEYADREDMIIMFVDSYDVILAGSPTELLKKFVQSGSRLLFSAESFCWPEWGL
AEQYPEVGTGKRFLNSGGFIGFATTIHQIVRQWKYKDDDDQLFYTRLYLDPGLREKLSLNLDHKSRIQNLNGA
LDEVVLKFDRNRVRI RN VAYDTLP IVVHGNGPTKLQLNYLGNYVPNGWTPEGGCGFCNQDRRTLPGGQPPPRVFL
AVFVEQPTPFLPRFLQRLLLLDYPPDRVTFLHNNEVFHEPHIADSWPQLQDHFSAVKLVGPPEEALSPGEARDMA
MDLCRQDPECEFYFSLDADAVLTNLQTLRILIEENRKVIAPMLSRHGKLWSNFWGALSPDEYYARSEDYVELVQR
KRVGVWNVPIYSQAYVIRGDTLRMELPQRDVFSGSDTDPDMAFCKSF RDKGIFLHLSNQHEFGRL LATSRYDTEH
LHPDLWQIFDNFVDWKEQYIHENYSRALEGE GIVEQPCPDVYWFPLLSEQMCDELVAEMEHYGQWSGGRHEDSRL
AGGYENVPTVDIHMKQVGYEDQWLQLLR TYVGPMTESLFPGYHTKARAVMNFVVRYPDEQPSLRPHHDSSTFTL
NVALNHKGLDYEGGGCRFLRYDCVISSPRKGWALLHPGRLTHYHEGLPTTWGTRYIMVSFVDP

2579/6881
FIGURE 2371

GCAGTTTATTCCGACAGTTGTGTTGTGCCAATGGTGGAGAAGAAAACCTTCGGTTCGCTCCCAGGACCCCGGGCAG
CGGCGGGTGCTGGACCGGGCTGCCCAGGAGCGTCGCATCAACCGGCAGCTGGAGGCCCTGGAGAATGACAACTTC
CAGGATGACCCCCACGCGGGACTCCCTCAGCTCGGCAAGAGACTGCCTCAGTTTGATGACGATGCGGACACTGGA
AAGAAAAAGAAGAAAACCCGAGGTGATCATTTTAACTTCGCTTCCGAAAAAACTTTCAGGCCCTGTTGGAGGAG
CAGAACTTGAGTGTGGCCGAGGGCCCTAACTACCTGACGGCCTGTGCGGGACCCCCATCGCGGCCCCAGCGCCCC
TTCTGTGCTGTCTGTGGCTTCCCATCCCCCTACACCTGTGTCAGCTGCGGTGCCCCGGTACTGCACTGTGCGCTGT
CTGGGGACCCACCAGGAGACCAGGTGTCTGAAGTGGACTGTGTGAGCCTGGGCATTCCCAGAGAGGAAGGGCCGC
TGTGCACTGCCCCGGCCTTCAGAAAAGACAGAATTTTCATCACCCAATGCAGGGGGAGCTCTTCCTGGACCAAGGGAG
GAGCCGCTCATTCACCCAACAAAACCTGTGTCTTATCTGCCAGGAAAGACCAGCCTCACTCCTGGGAAGTGTCTGG
CAGGTAGGCTGGGCCCCCAGTGCTGTTAGAATAAAAAGCCTCGTGCCGG

2580/6881
FIGURE 2372

MVEKKTSVRSQDPGQRRVLDRAARQRRINRQLEALENDNFQDDPHAGLPQLGKRLPQFDDADTGKKKKKTRGDH
FKLRFRKNFQALLEEQNLSVAEGPNYLTACAGPPSRPQRPFCAVCGFPSPYTCVSCGARYCTVRCLGTHQETRCL
KWTV

2581/6881
FIGURE 2373

ATATACTTGC GCGCCGACGCCGCCGCTCGCTTGTGAAACTGGAAGGCTGCCATGGCTAGCCCAGCCGCCTCCTCG
GTGCGACCACCGAGGCCCAAGAAAGAGCCGCAGACGCTCGTCATCCCCAAGAATGCGGCGGAGGAGCAGAAGCTC
AAGCTGGAGCGGCTCATGAAGAACCCGGACAAAGCAGTTCCAATTCCAGAGAAAATGAGTGAATGGGCACCTCGA
CCTCCCCCAGAATTTGTCCGAGATGTCAIGGGTTCAAGTGCTGGGGCCGGCAGTGGAGAGTTCCACGTGTACAGA
CATCTGCGCCGGAGAGAATATCAGCGACAGGACTACATGGATGCCATGGCTGAGAAGCAAAAATTGGATGCAGAG
TTTCAGAAAAGACTGGAAGAATAAAATTGCTGCAGAGGAGCAGACCGCAAAGCGCCGGAAGAAGCGCCAGAAG
TTAAAAGAGAAGAAATTACTGGCAAAGAAGATGAACTTGAACAGAAGAAACAAGAAGGACCCGGTCAGCCCCAAG
GAGCAGGGGTCCAGCAGCTCTGCGGAGGCATCTGGAACAGAGGAGGAGGAGGAAGTGCCCAAGTTTACCATGGGG
CGATGACAATGTTTGCCACAGCCTCTGCCTGGAACCTGGCTCGTGCTGTGACCAGAAGGGAAAGGCGGCTGTTTG
GCTCTTTCTCCCCCGCAAGGACCCGCTGACCCGCTGGATGGAGAGCAAAGGAGACCCCTCCCGAGCCGCTCACAG
TCCTGTATTTTGGCAGGTTTGGGAGCCTGAGGGGCCATCTCCCTGACACTCAGAGGCACTGCCTTGCAGACACCAT
CCGTGCTCCTGGTAAAGGGGGACAGAGAGCCTCACCTTGCCACATATTTGAACAGTGATGAGTTTGGGGCTGGTT
TCTGGGAAGGGAACGTTTATTTAGTAAAGAGCAGAACACCCCTTGCGTTTTTGTGGGACATGTGGACCGTGAGTCG
CAAACACTCTGGAGAAGGCTGAGATGCCACCATTCCCACGGGGACTGAAGACACATTACGTGGACCTGGTCCAG
GCTCAGTGAGGAGATGGCCTCAGCTGTGGGGCTGGTCCATGTTGCCCCACTCACTCCAGTGGGAAGTGGGGACCAC
GCCATAGAGGGTCTGCTCCCACTGCAGCTCCCGGTGCTCTCGTGTCTGGGAAGGCCTGGGTGTGTGCACAAGGA
GGCCCGGGCCAGGGACTTCACCAGGGGCTGGGTACAAGGGCACAGGGTGTGTGGAAAGCGCTGTGGGGGAAGAG
CCGGTCACCGGAGAGTGAGCAGGCGGAGACTCCAAGCTGGGCTGAGCCAGAGCAGAAGGCGAGGGATTCCAGCC
GGACGGGGTTCTCTCACCAACAGCTGTGATTTTCATCCGAAGTGGAAGGGGTCTAAACAGAACAGGCTGAGAG
AGGCGGGACTGGGTCAAGTGGGTGGAGCTCCTCCTTGATGACTGCAACTGTGCGGGCTTTCCGCCGGCTCACAG
CAGTTGGGGCCAGCGGGGAGAAGAGAGGCGGAACCTGCTGTGTCTCCTACGTGGCGCAGCCTCAAACCTGGCATCCAG
GCACTGGGCCCCGTGCAGAGAAGGCACCTGCAGAGAGCAGGGCAGCCCGGCGCAGGGGCATGCGCCTAGAATCCCA
GCTACTCGGAAGGCCAAGGCAGGAGGACCGCTTGAGTCCAGGGATTCAAGGCCAACCTGGGCAATAGAGCGAGAC
CCTGTCTCTTAAAAAACGATGATGATGAACACAGAGGACGGGGCACTGTGCTGGGAGCCAGGGGGCCTGGGAGGA
GCCGAGACCAGCCTTTTACCTCGGGGTTTTGAGGCCAACAGGGACGACAGAGACAGTTTCTAGTTAGAGCCTTGG
CTCCATTTTTTGGATGATTTAGCCCCGAGTTCTTGAGTCTATTTTATGCCCCCTTACGTACTTTGATAGAACTAAGG
AAATAGTGGTTTTGAGTGAAGGGAAAGGAAACCCAGAAACATTTTACGTTGCTTTTACTTCTGTAGTGTAGATTG
CCCCGGCCCTCTCTGAGCCCTGTAGCATCTGTGATAGCTTCTGTCCCTTCATCGGTTTCATGTCACAGGGATTTT
CTTCCCAGGAAGCGGACACGGAGAGTCAGCCCTAATAAATGAGCACATGCCCTGGCTGTACATTTTGAAACCTG

2582/6881
FIGURE 2374

MASPAASSVRPPRPKKEPQTLVIPKNAAEEQKLKLERLMKNPDKAVPIPEKMSEWAPRPPPEFVRDVMGSSAGAG
SGEFHVYRHLRRREYQRQDYMDAMAEKQKLDAEFQKRLEKNKIAAEEQTAKRRKKRQKLKEKKLLAKKMKLEQKK
QEGPGQPKEQGSSSSAEASGTEEEEEEVPSFTMGR

2583/6881
FIGURE 2375

CGCTCGGCGCCCCGGCCGGGCCACTGGGCCACAGGCCACGCGGCCACGCAGTCCGAGCGGGAGCCGAGCCGGGGCG
GGGCGAGGGCAGCTCCGGAACGTCCCAGGGATGGAAGTGCTTGGATGCGGTGCTGCTGGCTGCGGATGTGCGCAA
GGAGATGGGATGGAGAGCCTGAGTTGGCATTTCGTATAAATGACCTGCCTGGCTCCCACCATGAGTGCTGAGCTTA
ACGTGCCTATCGACCCCTCTGCTCCTGCCTGCCCTGAGCCCGGCCATAAGGGCATGGATTACCGGGACTGGGTCC
GCCGCAGCTACCTGGAAGTGGTCACCTCTAACCACCACTCGGTACAGGCCCTGTCGTGGCGGAAGCTCTACCTGA
GCAGGGCCAAGCTGAAGGCCTCCAGCAGGACCTCCGCCCTCCTCTCCGGCTTTGCCATGGTGGCCATGGTGGAGG
TGCAGCTGGAGACGCAGTACCAGTACCCGCGGCCGCTGCTGATTGCCTTCAGCGCCTGCACCACGGTGTCTGGTGG
CCGTGCACCTGTTTCGCCCTCCTCATCAGCACCTGCATCCTGCCCAATGTGGAGGCCGTGAGCAACATCCACAACC
TGAATCCATCAGCGAGTCCCCGCATGAGCGCATGCACCCCTACATCGAGCTGGCCTGGGGCTTCTCCACCGTGC
TTGGCATCCTACTCTTCTGGCCGAGGTGGTGTCTGCTGCTGCTGATCAAGTTCTCCCGTGGATGCCCGGCCCGC
AGCCTGGCCCCCACCTGGCCCTGGGAGTCACACGGGCTGGCAGGCCGCCCTGGTGTCCACCATCATCATGGTGC
CCGTGGGCCTCATCTTCGTGGTCTTACCATCCACTTCTACCGCTCCCTGGTGCGCCACAAAACGGAGCGCCACA
ACCGCGAGATCGAGGAGCTCCACAAGCTCAAGGTCCAGCTGGACGGGCATGAGCGCAGCCTGCAGGTCTTGTGAG
GGGCCGAGGGCCGGGGCTGGGAGCGGCCCTGTGCCCGGGAGTCCGCAGAGGCGGGGATTTGTGAGATGCAGACAT
TTTGCAAGGCTGCCGGGTAGTTCAAGACCAAAGTTTTCTCTTGTCTTAATACCATAAGGACTGGATGACTTCTC
CTGAGATAGAACCGTTTGGTTCAATGAGGGACTGTGTTGCTAAGAGCGTTGGGGGCAAAGCCAGGCTGGTTCCCTT
GGCCTCGGGGTTTTCTGGGTGCGGGACACGGTGAAGAGGCTCCAGCGGGACCTGCCCATCAGTCTGGGCCAGGA
GGGGCTCCAAGCAGCACCCAGCGTCCGGGGGAGTCTCAGACCCGGCATGCGTGGCTGGCAGACCTGGGAGAGCC
AGGGCAGGGTTTTGCGTTCAGAGAAGGATTGCCCCAGAGACCCGTGGTGGACTTCATGGGTGCTGAGTGGCCCGT
GTGACAGTGATGACACGAAGGCTTCGGCGTTTGAAGTGGGTGCAGGTGCACGCCAGGGCTTGGTGTCTCCCTGCCT
GGCCCTGGAGGGAGCTGGGTGGCCTGGCTTCAGGGGAAGACAGGAGCCAGGACACACGTACAGCCAGCAGGTGTG
GGGGGTGCTGCAGCCCTCGGCAGTGGGGTCAGGCCCTGGGGGATGTTTCCAATGGTGGGCAGCCTGGCCAGGCCG
GAGAAGACATGTTACGGGCATCTATCAGATGCCCCCTTGAGGAGGCTGAGTTATTTGAGGGCTGCTGCAAAGTA
CGCTAGGCTCAAATTCTCTTTTCCCAGCCAGAGCCCTGGCCACACGGACTCAGAGGGGGCCACCGGGGTGGGGAAA
GGACCCCTCCCCCACCCCGCAGCCACTGGCCTCCAGCTCTCGGCCACAGAATGGCCTCTAAGGCTGACTCAGC
CACTCCCTTGGGCTGTGGCAGCAGGAGGCGGGGGCTCTGGCTCAGGCCCGGAGCCTGTGCAGCTTGCCCATGGC
CCTAGGCAGCGAGGGGACAGCCTGGGGGACTTCCTGCCTAGGCAAGGTCATTGGCCGGGCCTGGCCTGTGGATAG
TGGGGCCAGGGGCCGGCCAGGCCAAATGAGTGCCCTCCTTGTTATGACACCAAGTGAATAAAGGAGGCAAGA
CCCCTCCAGGCCTCTCAGCCGACACTGGGTCCCACACACAGTGACTGTGCCGTGCAGTGCAGGTTCTGGCCT
TTTCCTTGAAGGCATCTGGTAGACCCGAAGCCACGCTCTCGGGCCGCACATGCACGCCGACAGCACCAGCTGCCCT
GAGCTGCTTGTACAACCAAAACACCTTTCCCTCTTCTCCAGCTGTAACCTGGAGAGTCAGCCATGCCTTGTCTTT
TGTTCTCATAAATAGTCACTGGGGCCGGGCGCAGTGACTCACGCCTGTAATCCCAGCACTTTGGGAGGCCTAGGT
GGGCGGATCACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCCTGTCTCTACTAAAAAAAT
ACAGAAAATTAGCTGGGCGTGGTGGCGGGCGCCTGTAGCCCCAGCTACTTGGGAGGCTGAGGCGGGAGAATGGCA
ATGGCGTGAACCCGGGAGGCAGAGCTTGCAGTGAGCTGAGATGGCGCCACTGCACTCCAGCCTGGGCGACAGAGC
CAGACTCCATCTC

2584/6881
FIGURE 2376

CGGCGGTGGCGGACACTTGGGGTCTGGACGCAACGGCGGCGGGAGCATGAACGCCCCTCCAGCCTTCGAGTCGTT
CTTGCTCTTCGAGGGCGAGAAGATCACCATTAAACAAGGACACCAAGGTACCCAATGCCTGTTTATTACCATCAA
CAAAGAAGACCACACACTGGGAAACATCATTAAATCAGTGCCTGCTTCCCCTTCGCCTTCTGCCGTGATTGTCA
GTTTCCTGAGGCCTCCCCAGCCACGCTTCCTGTACAGCCTGCAGAACTCTGCCCCAGAGCACATCAGCTATGTGC
CCCAGCTCTCAAACGACACCTTGGCGGGGAGGCTCACCTGTCCACCTTCACGCTGGAGCAGCCTCTAGGCCAGT
TCAGCAGCCACAACATCTCTGA

2585/6881
FIGURE 2377

MNAPPAFESFLLFEGEKITINKDTKVPNACLF TINKEDHTLGNI IKS RACFPFAFCRDCQFPEAS PATLPVQPAE
LCPRAHQ LCAPALKRHLGGEAHPVHLHAGAASRPVQQPQHL

2586/6881
FIGURE 2378

CCATTGTGCTCTAAAGGGAAGGTGCTGTGTAATCATTAAAGGAGCGGAGGCTTTTGGAGCTGCTAAAATGCCGGAT
TACCTCGGTGCCGATCAGCGGAAGACCAAAGAGGATGAGAAGGACGACAAGCCCATCCGAGCTCTGGATGAGGGG
GATATTGCCTTGTTGAAAACCTTATGGTCAGAGCACTTACTCTAGGCAGATCAAGCAAGTTGAAGATGACATTGAG
CAACTTCTCAAGAAAATTAATGAGCTCACTGGTATTAAAGAATCTGACACTGGCCTGGCCCCACCAGCACTCTGG
GATTTGGCTGCAGATAAGCAGACACTCCAGAGTGAACAGCCTTTACAGGTTGCCAGGTGTACAAAGATAATCAAT
GCTGATTCCGAGGACCCAAAATACATTATCAACGTAAAGCAGTTTGCCAAGTTTGTGGTGGACCTTAGTGATCAG
GTGGCACCTACTGACATTGAAGAAGGGATGAGAGTGGGCGTGGATAGAAATAAAATATCAAATTCACATTCCATTG
CCTCCTAAGATTGACCCAACAGTTACCATGATGCAGGTGGAAGAGAAAACCTGATGTCACATACAGTGATGTTGGT
GGCTGTAAGGAACAGATTGAGAAAACCTGCGAGAAGTAGTTGAAACCCCATTACTTCATCCAGAGAGGTTTGTGAAC
CTTGGCATTGAGCCTCCCAAGGGCGTGCTGCTCTTTGGTCCACCCGGTACAGGCAAGACACTCTGTGCGCGGGCA
GTTGCTAATCGGACTGATGCGTGCTTCATTTCGAGTTATTGGATCTGAGCTTGTACAGAAAATACGTCGGTGAGGGG
GCTCGAATGGTTTCGTGAACTCTTTGAAATGGCCAGAACAAAAAAGCCTGCCTTATCTTCTTTGATGAAATTGAT
GCTATTGGAGGGGCTCGTTTTGATGATGGTGCTGGAGGTGACAATGAAGTGCAGAGAACAAATGTTGGAACCTGATC
AATCAGCTTGATGGTTTTGATCCTCGAGGCAATATTAAAGTGCTGATGGCCACTAACAGACCTGATACTTTGGAT
CCAGCACTGATGAGGCCAGGGAGATTGGATAGAAAAATTGAATTTAGCTTGCCCGATCTAGAGGGTCGGACCCAC
ATATTTAAGATTACGCTCGTTCAATGAGTGTGAAAGAGATATCAGATTTGAACTGTTAGCACGACTGTGTCCA
AATAGCACTGGTGCTGAGATTAGAAGCGTCTGCACAGAGGCTGGTATGTTTGCCATCAGAGCACGGCGAAAAATT
GCTACCGAGAAGGATTTCTTGGAAGCTGTAAATAAGGTCATTAAGTCTTATGCCAAATTCAGTGCTACTCCTCGT
TACATGACATACAACTGAACCCTGAAGGCTTTCAAGTGAAAACCTTTAAATTGGAATCCTAACCTTATATAGACTT
GTTAATAACCAATTCATAAACAAATAAATGGCTTCAACTTTAGAGCACAAATGG

2587/6881
FIGURE 2379

MPDYLGADQRKTKEDKDDKPIRALDEGDIALLKTYGQSTYSRQIKQVEDDIQQLKKINELTGIKESDTGLAPP
ALWDLAADKQTLQSEQPLQVARCTKIINADSEDPKYIINVKQFAKFVVDLSQVAPTDIEEGMRVGVDNRKYQIH
IPLPPKIDPTVTMMQVEEKPDVTYSDVGGCKEQIEKLREVVETPLLHPERFVNLGIEPPKGVLLFGPPGTGKTL
ARAVANRTDACFIRVIGSELVQKYVGEARMVRELFEMARTKKACLIFFDEIDAIGGARFDDGAGGDNEVQRTML
ELINQLDGFDPGRNIKVLMATNRPDTLDPALMRPGRDLRKIEFSLPDLEGRTHIFKIHARMSVERDIRFELLAR
LCPNSTGAEIRSVCTEAGMFAIRARRKIATEKDFLEAVNKVIKSYAKFSATPRYMTYN

2588/6881
FIGURE 2380

CTTCCCTCTGCCAACATGGCGGCCTCAGCAAAAAAGAAGAATAAGAAGGGGAAGACTATCTCCCTAACAGACTT
TCTGGCTGAGGATGGGGGTACTGGTGGAGGAAGCACCTATGTTTCCAAACCAGTCAGCTGGGCTGATGAAACGGA
TGACCTGGAAGGAGATGTTTCTACAACCTGGGCACAGTAACGATGACGATGTGTACAGGGCGCCTCCAATTGACCG
TTCCATCCTTCCCACTGCTCCACGGGCTGCTCGGGAACCCAATATCGACCGGAGCCGTCTTCCCAAATCGCCACC
CTACACTGCTTTTCTAGGAAACCTACCCCTATGATGTTACAGAAGAGTCAATTAAGGAATTCTTTCGAGGATTAAA
TATCAGTGCAGTGCGTTTACCACGTGAACCCAGCAATCCAGAGAGGCTGAAAGGTTTTGGTTATGCTGAATTTGA
GGACCTGGATTCCCTGCTCAGTGCCCTGAGTCTCAATGAAGAGTCTCTAAGTAACAGGAGAATTCGAGTGGACGT
TGCTGATCAAGCACTGGATAAAGAGTATCGAGATCGTTATGATTTCAGACCGGTATCGGGATGGGTATCGGGATGG
CCCACGCCGGGATATGGATCGATATGGTGGCCGGGATCGCTATGATGACCGAGGCAGCAGAGACTATGATAGAGG
CTATGATTCCCGGATAGGCAGTGGCAGAAGAGCATTGTCAGTGGGTATCGCAGGGATGATGACTACAGAGAAGG
CAGGGACTGCTATGAAGACCAATATGACAGACGGGATGATCGGTTCGTGGAGCTCCAGAGATGATTACTCTCGGGA
TGATTATAGGCGTGATGATAGAGGTCCCCCCCCCCCCAAAGACCCAACTGAATCTAAAGCCTCGGAGTACTCCT
AAGGAAGATGATTCTCTGCTAGTAACCTCCAGTCCACTCGAGCTGCTTCTATCTTTGGAGGGGCAAAGCCTGTT
G

2589/6881
FIGURE 2381

CCTAACAGACTTTCTGGCTGAGGATGGGGTACTGGTGGAGGAAGCACCTATGTTTCCAAACCAGTCAGCTGGGC
TGATGAAACGGATGACCTGGAAGGAGATGTTTCTACAACCTTGGCACAGTAACGATGACGATGTGTACAGGGCGCC
TCCAATTGACCGTTCCATCCTTCCCCTGCTCCACGGGCTGCTCGGGAGAGACACCCAAGCTGGCAAAGTGAAGA
AACTCAGGAACGGGAACGGTCGAGGACAGGAAGTGAGTCATCACAGACTGGGACCTCCACCACATCTGGCAGAAA
TGCATGAAGGAGAGAGAGTGAGAAGTCTCTAGAAAATGAAACACTCAATAAGGAGGAAGATTGCCACTCTCCAAC
TTCTAAACCTCCCAAACCTGATCAGCCCCTAAAGGTAATGCCAGCCCCTCCACCAAAGGAGAATGCTTGGGTGAA
GCGAAGTTCTAACCCTCCTGCTCGATCTCAGAGCTCAGACACAGAGCAGCAATCCCCTACAAGTGGTGGGGGAAA
AGTAGCTCCAGCTCAACCATCTGAGGAAGGACCAGGAAGGAAAAGATGAAAATAAAGTAGATGGGATGAATGTCCC
AAAAGGCCAAACTGGGAACCTAGCCGTGGTCCAGGAGACTGAGGGAACAGAGACCACTGGGAAGGAGTCAGATAG
GAAAGATGGCAAAAAGGATCAAGACTCCAGATCTGCACCTGAGCCAAAGAAACCTGAGGAAAATCCAGCTTCCAA
GTTTCAGTTCTGCAAGCAAGTATGCTGCTCTCTCTGTTGATGGTGAAGATGAAAATGAGGGAGAAGATTATGCCAA
ATAGACCTCTACATCCTGTGCTTTTCTCCTAGTTTCTCTCCACCCTGGAACATTCGAGAGCAAATCAAAACCTCT
ATCCAGACAAGACAAAATAAAACTCACCATCTCCTGAAGACCTTTCTTACCTTTTTTTTTTAAACAAAAAATGAAA
TTATTTTGCATGCTGCTGCAGCCTTTAAAGTATTGAAGTAACTGGAGAATTGCCAATACAGCCAGAGAGAAAGGG
ACTACAGCTTTTTAGAGAAGTTGTGGTGCCTTATGTCACCATGCAGTTGCCAGTGTGATTAGTGCCTAGGGGTCT
CCATTTAGCAGAAATGGTAATGACAGTGATATAACGCCTGGAACCTGGTTGGGCAGTAGGGGAGGGAGGTAGAAG
GAAAAGTGTGAGATTTCTACCTTTTAGTTTTTTCTATTTGTGGCATATATGAATTCTCAAACATTATCTGAATA
AATTTTCCATTCTTGGAAGGTAGATTTAGCCTCAAGTTGTTTTAGTCTCCAGGAGGCTGCCAGCCCCTCCTCTT
ATTTAATTCTGAGTTTGGGGGACAGCCTAGAGGGAATTCCTTTTTTTTTTTTTTTTACCCCCAAGGGGGTTAG
TTGGGAGTGAGACTATAGGCCATAAAGAATGGGACTCATTGGACCAAATAAATGGGAAAATCGTGGTTTGAAAG
GAAGCTTTTGGGAATTGATGAGTCATTTTGCACCAGGTAATAGGGGAAAATTGTGTGACCTCCAGCAAACACATG
AATGGTTATTTCTTGAGCCGGAAGCACTTGGGGGTGCTGGTAATTTCCAATGTTTTCTGTGCTAGTTTTACC
CTTTCTAAACACTGTCCTTTTTGAAAGTTTGAATATATCCACATTCTATTGAAACCTTGAAACTAAAAATTTAGA
CTCTTATCGTCATCTTAAGTTCTTCATGCTACTCTTAACCTCCCAAAAAGCAGTATCTAAGTCACATACATGATG
TCTTGGGCATTTTCTCTCTCAGCCATGGAGAACTCTGAAAGGAAGAATCGCTGCTTTTCTCAAGCAAATCGGTTT
CTTGATATCTTCTGGTTCTCACTCCTTGCTGCTGCTGATGCTTTGACCCCTTTTATTGATCAGAGTGCTCTAGA
ATAATGGATGGTCTTGATGGTGGATAAATAGGGACAGGGACAGTTAAATTGGGAGCCTTTCTTACAACCTTGAT
GGGTTTTTTTTCCCCCAAGTTTCTTCTCCACTGAAATGCCACACTAATGTTTGTGGATTGATGAGGTGGCCAG
ACCAATGTGTTTTGTTTTGTTTTTTTTTTTTTAAAGCTTCCCTTGAGAGAATAAACGGAAATGGAGAGAACTATTT
AACAAGGTCTGTTTTCTTGTCAACACAGTAGCTAAACTTGCTGCTTTTATATGCATTTTTGTAGGGATCAGC
TTGGTAGACAGTATTAGCAGAGAAACACCTTGATCTTGGTTTGCAAACCCTTCTGCCATCAGTCCTAGATTAGGC
CCTGTTTCAGCCATGCAGGGGTGTTGGTTTATGCGTGCTGCAGCAGTGGGCATAATGAATATAATTTACCCAGTGG
ACAAAGGTGTGTACCAAGTGAATTTAAATAATTGGTGTGGATTGGCCAGTAGCTAAGAAGTGGGCTTTTAAAGAG
TATTGAAGATTGAAAGGTGTTTTTTTTCTTTTTTAAAAAAGAAAAAAACTATTGATTGTAGATAATGAAAAGC
TAGGGTTTGCCCTCTTCATGTCTACTCTCCTTCCAAATAGTTATATCCAAACTGTTTTTCCCTGTCCCTACCT
TGTCCCCCATTAATAAGAAACAGGGATTGATTAATGTCCCGCTCCTGAATACATGTAAAATTTGTACAAAAA
TATCTTCTATGAAAATGATTTGTAATCTGTAGACTTATTACCTGGGAGATGTCTTGATGTAAAATCCCATCCTTT
GGGTTGTGGGTTTTTGTCTTCTCAATAAATCTGATCTTTAAAGTTC

2590/6881
FIGURE 2382

MAASAKKKNKKGKTISLTDFLAEDGGTGGGSTYVSKPVSWADETDDLEGDVSTTWHSNDDDVYRAPPIDRSILPT
APRAAREPNIDRSRLPKSPPYTAFLGNLPYDVTEESIKEFFRGLNISAVRLPREPSNPERLKGFYAEFEDLDSL
LSALSLNEESLGNRRIRVDVADQAQDKDRDDRSFGRDRNRDSDKTDTDWRRARPATDSFDDYPPRRGDDSFGDSYD
SRIGSGRRAFGSGYRRDDDYRGGGDYEDRYDRRDRSWSSRDDYSRDDYRRDDRGPPQRPKLNKPRSTPKEDD
SSASTSQSTRAASIFGGAKPVDTAAREREVEERLQKEQEKLRQLDEPKLERRPREHPSWRSEETQERERSRTG
SESSQTGTSTTSSRNARRRESEKSLNETLNKEEDCHSPTSKPPKPDQPLKVMPPAPPKAWVKRSSNPPARSQ
SSDTEQQSPTSGGGKVAPAPQPSSEGPGRKDENKVDGMNAPKGQTGNSSRGPGDGGNRDHWKESDRKDGKKDQDSR
SAPEPKPEENFASKFSSASKYAALSVDGEDENEGEDYAE

2591/6881
FIGURE 2383

GTAGCGGGAGCGGAGAGCGGACCCCGGAGAGCGGACCCCGAGAGAACCCTGAGCAGCCCCGCCGCTGCCGGCCTAG
TTACCGTCATACCACGGGAGGAGCCGCAGCTGCCGCAGCCGGCCCCAGTCTCCATCACCGCAACCAATGAGCAGC
AAGGCCGAGACCCAGCAGCCACCCGCCGCCCGCCGCTTTCCCCCACCGCCCCCTCCCGTCCCCCGCCGCCCC
CGCCCTCAGCGCCGCCGACACCAAGCCCGGCACTACGGGCAGCTGCGCAGGGAGCGGTGGTCCGGGCGGCCTCAC
ATCGGCGGCGCCTGCCAGCGTGGACAAGAAGGTCATCGCAGTGAAGGTTTTGGGAACAGTAAAATGGTTCAATGT
AAGGAACGGATATGGTTTCATCAACAGGAATGACACCAAGGAAGATGTATTTGTACACCAGACTGCCATAAAGAA
TAACCCAGGAAGTACCTTCGCAGTGTAGGAGATGAAGAGACTGTGGAGTTTGATGTTGTTGAAGGAGAAGAGGG
TGCGGAGGCAGCAAAATGTTACAGATCCTGGTGGTGTTCGAGTTCAAGGCGGTAAATATGCAGCAGATCGTAACCA
TTATAGACGCTATCCACGTCATAGGGGTCTCCACGCAATTACCAGCAAAATTACCAGAACAGTGAGAGTGGGGA
AAAGACCGAGGGATCGGAGAATGCTCCCGAAGGCCAGGCCCAACAATGCCGGCCCTACCGCAGGCCAAAGGTTCCC
ACCTTACTACATGCGGAGACCCTATGGGTGTGACACAGTATTCAGCCCTCCTGTGCAGGGAGAAGTGATGGA
GGGTGCTGACAACCAGGGTGCAGGAGAACAAGGTAGACCAGTGAGGCAGAATATGTATCGGGGATATAGACCACG
ATTCCGCAGGGGGCCCTCCTTGCCAAAGACAGCCTAGAGAGTACGGCAATGAAGAAGATAAAATCAAGGAGATGAG
ACCCAGGGTCAGCAGCCACCTCAACGTCGGTACCGCAGCAACTTCAATTACCAACGCAGATGCCAGAAAACCCT
AAATCACAAGATGGCAAAGAGACAAAATCAGCCAATCCACCAGCTGAGAATTCGTCTGCTCCCGAGGCTGAGCAG
GGCGGGGCTGAGTAAATGCCGGCTTACCATCTCTACCATCATCCGTTTTAGTCATCCAACAAGAAGAAATATGAA
ATTCCAGCAATTAAGAAATGAACAAAAGATTGGAGCTGAAGACCTTAAGTGCTTGCTTTTTGCCCCTTGACCAGAT
AAATAGAACTATCTGCATTATCTATGCAGCATGGGGTTTTTATTATTTTTTACCTAAATATGTCTCTTTTTTGTTAA
TAACAAACGTGTTTTTTTTTAAAAAGCCTTGTTTTTCTCAATACGCCTTTAAAGG

2592/6881
FIGURE 2384

MRRPYGCRPQYSSPPVQGEVMEGADNQGAGEQGRPVRQNMRYRGYRPRFRRGPPCQRQPREYGNEDKIKEMRPRV
SSHLNVGTAATSITNADAQKTLNHHMAKRQNQPIHQLRIRLLPRLSRAGLSKCRLTISTIIIRFSHPTRRNMKFQQ

2593/6881
FIGURE 2385A

GGGACCTGGAAGCGCCCCAGCCCCGAGCGATCGCAGATTTCGGCTTTCAAACAAAAGAGGCGCCCCGGGGGGTGG
GACCGGGACCTCACCCGGTCTCGCAGAGTTGCGGCCGCCGCCCTTCAGCCCCGGCTCTCCGTATGCGCATGA
GCAGAGGCGCCTCCCTCTGTTCTCCCAAGGCTAAACTTTCTAATTCCTTCTTTGGGCTCGGGGGCTCCCGGAG
CAGGGCGAGAGCTCGCGTCGCCGAAAGGAAGACGGGAAGAAAGGGCAGGCGGCTCGGCGGGCGTCTTCTCCACT
CCTCTGCCGCGTCCCCGTGGCTGCAGGGAGCCGGCATGGGGCTTCTCCAGTTGCTAGCTTTTCACTTTCTTAGCCC
TGTGCAGAGCCCCGAGTGC GCGCTCAGGAACCCGAGTTTCACTACGGCTGCGCAGAAGGCAGCTGCTATCCCGCCA
CGGGCGACCTTCTCATCGGCCGAGCACAGAAAGCTTTTGGTGACCTCGACGTGCGGGCTGCACAAGCCCGAACCC
TACTGTATCGTCAGCCACTTGCAGGAGGACAAAAATGCTTCATATGCAATTCCTAAGATCCTTATCATGAGACC
CTGAATCCTGACAGCCATCTCATTGAAAATGTGGTCACTACATTTGCTCCAAACCGCTTAAGATTTGGTGGCAA
TCTGAAAATGGTGTGGAAAATGTAATATCCAATGGATTTGGAAAGCAGAATTCATTTTACTCATCTCATAATG
ACTTTCAAGACATTCCGTCCAGCTGCTATGCTGATAGAACGATCGTCCGACTTTGGGAAAACCTGGGGTGTGTAT
AGATACTTCGCCTATGACTGTGAGGCCTCGTTTTCCAGGCATTTCAACTGGCCCCATGAAAAAAGTCGATGACATA
ATTTGTGATTCTCGATATTCTGACATTGAACCTCAACTGAAGGAGAGGTGATATTTTCGTGCTTTAGATCCTGCT
TTCAAATAGAAAGATCCTTATAGCCCAAGGATACAGAATTTATTAAAAATTACCAACTTGAGAATCAAGTTTGTG
AAACTGCATACTTTGGGAGATAACCTTCTGGATTCCAGGATGGAAATCAGAGAAAAGTATTATTATGCAGTTTAT
GATATGGTGGTTCGAGGAAATTGCTTCTGCTATGGTCATGCCAGCGAATGTGCCCTGTGGATGGATTCAATGAA
GAAGTGAAGGAATGGTTCACGGACACTGCATGTGCAGGCATAACACCAAGGGCTTAAACTGTGAAGTCTGCATG
GATTTCTACCATGATTTACCTTGGAGACCTGCTGAAGGCCGAAACAGCAACGCCTGTAAAAAATGTAAGTCAAT
GAACATTCCATCTCTTGTCACTTTGACATGGCTGTTTACCTGGCCACGGGGAACGTGAGCGGAGGCGTGTGTGAT
GACTGTGAGCACAACACCATGGGGCGCAACTGTGAGCAGTGCAAGCCGTTTTACTACCAGCACCCAGAGAGGGAC
ATCCGAGATCCTAATTTCTGTGAACGTATGTACGTGTGACCCAGCTGGCTCTCAAATGAGGGAATTTGTGACAG
CTATACTGATTTTTCTACTGGTCTCATTGCTGGCCAGTGTGCGGTGTAATTAATGTGGAAGGAGAATTTGTGA
TGTTTGCAAAGAAGGCTTCTATGATTTAAGCAGTGAAGATCCATTTGGTTGTAAATCTTGTGCTTGCAATCCTCT
GGGAACAATTCCTGGAGGGAATCCTTGTGATTCCGAGACAGGTCACTGCTACTGCAAGCGTCTGGTGACAGGACA
GCATTGTGACCAGTGCCTGCCAGAGCACTGGGGCTTAAGCAATGATTTGGATGGATGTGACCATGTGACTGTGA
CCTTGGGGGAGCCTTAAACAACAGTTGCTTTGCGGAGTCAGGCCAGTGTCTCATGCCGCCCTCACATGATTGGACG
TCAGTGCAACGAAGTGGAACCTGGTTACTACTTTGCCACCCTGGATCACTACCTCTATGAAGCGGAGGAAGCCAA
CTTGGGGCCTGGGGTTAGCATAGTGAGCGGCAATATATCCAGGACCGGATTCCTCCTGGACTGGAGCCGGCTT
CGTCCGAGTGCCTGAAGGGGCTTATTTGGAGTTTTTTCATTGACAACATACCATATTCCATGGAGTACGACATCCT
AATTCGCTACGAGCCACAGCTACCCGACCCTGGGAAAAAGCTGTCAACAGTGCAGCGACCTGGAAGGATTCC
AACCAGCAGCCGATGTGGTAATACCATCCCCGATGATGACAACAGGTGGTGTGATTATACCAGGCTCAAGATA
TGTCGTCTTCTCGGCCGGTGTGCTTTGAGAAGGGAACAACTACACGGTGAGGTTGGAGCTGCCTCAGTACAC
CTCCTCTGATAGCGACGTGGAGAGCCCCCTACACGCTGATCGATTCTCTTGTCTCATGCCATACTGTAAATCACT
GGACATCTTACCGTGGGAGGTTTCAAGAGATGGGGTGGTACCAACAGTGCCTGGGAAACCTTTTCAAGATACCG
ATGTCTAGAGAACAGCAGAAGCGTTGTGAAAACACCGATGACAGATGTTTGCAGAAACATCATCTTTAGCATTTT
TGCCCTGTTACACCAGACAGGCCTGGCTTGTGAATGCGACCCTCAGGGTTCGTTAAGTTCCGTGTGTGATCCCAA
CGGAGGCCAGTGCCAGTGCCGGCCCAACGTGGTTGGAAGAACCTGCAACAGATGTGCACCTGGAACTTTTGGCTT
TGGCCCCAGTGGATGCAAACCTTGTGAGTGCCATCTGCAAGGATCTGTCAATGCCTTCTGCAATCCCGTCACTGG
CCAGTGCCACTGTTTCCAGGGAGTGTATGCTCGGCAGTGTGATCGGTGCTTACCTGGGCACTGGGGCTTTCCAAG
TTGCCAGCCCTGCCAGTGCAATGGCCACGCCGATGACTGCGACCCAGTGAAGTGGGAGTGCTTGAAGTCCAGGA
CTACACCATGGGTGATAACTGTGAAAGGTGCTTGGCTGGTTACTATGGCGACCCCATCATTGGGTGAGGAGATCA
CTGCCGCCCTTGCCCTTGCCAGATGGTCCGACAGTGGACGCCAGTTTGCAGGAGCTGCTACCAAGATCCTGT
TACTTTACAGCTTGCTGTGTTGTGATCCTGGATACATTGGTTCCAGATGTGACGACTGTGCTCAGGATACTT
TGGCAATCCATCAGAAGTTGGGGGGTCTGTGTCAGCCTTGCCAGTGTGACAACAACATTGACACGACAGACCCAGA
AGCCTGTGACAAGGAGACTGGGAGGTGTCTCAAGTGCCTGTACCACACGGAAGGGGAACACTGTCAGTTCTGCCG
GTTTGGATACTATGGTGTATGCCCTCCAGCAGGACTGTGCAAGTGTGTCTGTAATTACCTGGGCACCGTGCAAGA
GCACTGTAACGGCTCTGACTGCCAGTGGCAGAAAGCCACTGGTCAGTGTCTGTGCTTCTTAATGTGATCGGGCA
GAACTGTGACCGCTGTGCGCCCAATACCTGGCAGCTGGCCAGTGGCACTGGCTGTGACCCATGCAACTGCAATGC

2594/6881
FIGURE 2385B

TGCTCATTCTTCGGGCCATCTTGCAATGAGTTCACGGGGCAGTGCCAGTGCATGCCTGGGTTTGGAGGCCGCAC
CTGCAGCGAGTGCCAGGAACTCTTCTGGGGAGACCCCGACGTGGAGTGCCGAGCCTGTGACTGTGACCCCAAGGGG
CATTGAGACGCCACAGTGTGACCAGTCCACGGGGCAGTGTGTCTGCGTTGAGGGTGTGAGGGTCCACGCTGTGA
CAAGTGCACGCGAGGGTACTCGGGGGTCTTCCCTGACTGCACACCCTGCCACCAGTGCTTTGCTCTCTGGGATGT
GATCATTGCCGAGCTGACCAACAGGACACACAGATTCTTGGAGAAAAGCCAAGGCCTTGAAGATCAGTGGTGTGAT
CGGGCCTTACCGTGAGACTGTGGAAGTGGAGAGGAAAGTCAGCGAGATAAAAAGACATCCTGGCGCAGAGCCC
CGCAGCAGAGCCACTGAAAAACATTGGGAATCTCTTTGAGGAAGCAGAGAACTGATTAAAGATGTTACAGAAAT
GATGGCTCAAGTAGAAGTGAAATTATCTGACACAACCTTCCCAAAGCAACAGCACAGCCAAAGAACTGGATTCTCT
ACAGACAGAAGCCGAAAAGCCTAGACAACACTGTGAAAGAACTTGCTGAACAACTGGAATTTATCAAAAACCTCAGA
TATTCGGGGTGCCTTGGATAGCATTACCAAGTATTTCCAGATGTCTCTTGAGGCAGAGGAGAGGGTGAATGCCTC
CACCACAGAACCCAAACAGCACTGTGGAGCAGTCAGCCCTCATGAGAGACAGAGTAGAAGACGTGATGATGGAGCG
AGAATCCCAGTTCAAGGAAAAACAAGAGGAGCAGGCTCGCCTCCTTGATGAACTGGCAGGCAAGCTACAAAGCCT
AGACCTTTTCAGCCGCTGCCGAAATGACCTGTGGAACACCCCCAGGGGCCCTCCTGTTCCGAGACTGAATGTGGCGG
GCCAAACTGCAGAACTGACGAAGGAGAGAGGAAGTGTGGGGGGCCTGGCTGTGGTGGTCTGGTTACTGTTGCACA
CAACGCCTGGCAGAAAGCCATGGACTTGGACCAAGATGTCTGAGTGCCCTGGCTGAAGTGAACAGCTCTCCAA
GATGGTCTCTGAAGCAAACTGAGGGCAGATGAGGCAAAACAAAGTGCTGAAGACATTCTGTTGAAGACAAATGC
TACCAAAGAAAAAATGGACAAGAGCAATGAGGAGCTGAGAAATCTAATCAAGCAAATCAGAACTTTTTGACCCA
GGATAGTGCTGATTTGGACAGCATTGAAGCAGTTGCTAATGAAGTATTGAAAATGGAGATGCCTAGCACCCCA
GCAGTTACAGAACTTGACAGAAGATATACGTGAACGAGTTGAAAGCCTTTCTCAAGTAGAGGTTATTCTTCAGCA
TAGTGCTGCTGACATTGCCAGAGCTGAGATGTTGTTAGAAGAAGCTAAAAGAGCAAGCAAAAGTGCAACAGATGT
TAAAGTCACTGCAGATATGGTAAAGGAAGCTCTGGAAGAAGCAGAAAAGGCCCAGGTTCGAGCAGAGAAGGCAAT
TAAACAAGCAGATGAAGACATTCAAGGAACCCAGAACCTGTAACTTCGATTGAGTCTGAAACAGCAGCTTCTGA
GGAAACCTTGTTCAACGCGTCCCAGCGCATCAGCGAGTTAGAGAGGAATGTGGAAGAACTTAAGCGGAAAGCTGC
CCAAAACCTCCGGGGAGGCAGAAATATATTGAAAAAGTAGTATATACTGTGAAGCAAAGTGCAAGATGTTAAGAA
GACTTTAGATGGTGAACCTTGATGAAAAGTATAAAAAAGTAGAAAAATTTAATTGCCAAAAAACTGAAGAGTCAGC
TGATGCCAGAAGGAAAGCCGAAATGCTACAAAATGAAGCAAAAACCTTTTTAGCTCAAGCAAATAGCAAGCTGCA
ACTGCTCAAAGATTTAGAAAAGAAAATATGAAGACAATCAAAGATACTTAGAAGATAAAGCTCAAGAATTAGCAAG
ACTGGAAGGAGAAGTCCGTTCACTCCTAAAGGATATAAGCCAGAAAAGTTGCTGTGTATAGCACATGCTTGTAACA
GAGGAGAATAAAAAATGGCTGAGGTGAACAAGGTAAAACAACCTACATTTTAAAACTGACTTAATGCTCTTCAAA
ATAAAACATCACCTATTTAATGTTTTTAATCACATTTTGTATGGAGTTAAATAAAG

2595/6881
FIGURE 2386

CTCTTTTTCCGGCTGGAACCATGGTGGGTGTAGAAGAGAAGAAGAAGGTTTCCTGCTGTGCCAGAAACCCTTAAGA
AAAAGCGAAGGAATTTCTCAGAGCTGAAGATGAAGCGCCTGAGAAAGAAGTTTGCCCAAAGATGCTTCGAAAGG
CAAGGAGGAAGCTTATCTATGAAAAAGCAAAGCACTATCACAGGGAATATAGGCAGATGTACAGAACTGAAATTC
GAATGGCGAGGATGGCAAGAAAAGCTGGCAACTACTTTGTACCTGCAGAACCCAAACTGGCATTGTGCATCAGAA
TCAGAGGTATCAGTGGCGTGAGCCCAAAGGTCCGAAAGGTGTTGCAGCTTCTTCGCCTTCGTCAAATCTACAATG
GAACCTTTGTGAAGCTCAACAAGGCTTCGACTAACATGCTGAGGATTGTAGAGCCATATATTGCATGGGGGTACC
CCAATCTGAAGTCAGTAAATGAACTAATCTACAAGAGTGGTTATGGCAAAATCAATAAGAAGCGAATTGCTTTGA
CAGATAACGCTTTGATTGCTCGATCTCTTGGTAAATATGGCATCATCTGCATGGAGGATCTGATTTCATGAGATCT
ATACTGTTGGAAAACGCTTCAAAGAGGCAAATAACTTCCTGTGGCCCTTCAAATTGTCTTCTCCACGAGGTGGAA
TGAAGAAAAAGACCACCCATTTTGTAGAAGGTGGAGATGCTGGCAACAGGGAGGACCAGATCAACAGGCTTATTA
GAAGAATGAACTAAGGTGTCTACCATGACTATTTCTCTAAGCTGGTTGGTTAATAAACAGTACCTGCTCTCAAAT
TGG

2596/6881
FIGURE 2387

CTTCCTAGAAGGTAATGTACGAACTCGTCTCCAAAGGATACTTAGGTTGCACCAGTGTATTTGTAAAACAGGAGC ,
AAATTTGGACCTTGCCGGGCCAAAGTCGTGTCACGTGGAACCTCTTAATCTCAGCATCCGGAGCTCCAGGAAGGG
AAAATTTCAAGTCAGATAGAATTCTATATATAACATTTCTAGGAACCTTCAGCCCTCAAGATTCCAACATCATGA
CCTCAGTTTCAACACAGTTGTCCTTAGTCCTCATGTCACTGCTTTTGGTGCTGCCTGTTGTGGAAGCAGTAGAAG
CCGGTGATGCAATCGCCCTTTTGTAGGTGTGGTTCTCAGCATTACAGGCATTTGTGCCTGCTTGGGGGTATATG
CACGAAAAAGAAATGGACAGATGTGACTTTGAAAGGCTACTGAGTCAAACCTCACCTGAAAACCTTTGCGCTT
TAGAGGCTAAACCTGAGATTTGGTGTGTGAAAGGTTCCAAGAATCAGTAAATAAGGGAGTTTCACATTTTTTCATT
GTTTCCATGAAATGGCAACAAACATACATTTATAAATTGAAAAAAAAAATGTTTTCTTTACAACAAATAATGCACA
GAAAAATGCAGCCTATAATTTGCTAGTTAGGTAGTCAAGAAGTAAGATGGCTGAAATTTACATAAGTAATATTT
CATAATCTTAGAATTCTCTCAAAGCATGTGAAATAGGAAGAAGGAAGTTCTTGCCCGAATCTTAGGAAATCACC
ACTGTTTCGGTTATAATCACTGCCTCCTGAATCGTTGAGGAGTCTTTTAAATTAGATTTTTGTTTTGTTGTCTCCC
AAGTTAATATTATATTTAGATATCAGAGAGTCAGGCAAAAAGGAAAACTTTTATCTCTAGGGAAAAAACATTTAG
AAAAATGTATTCAGTGTATCTAATACTGAAATGCGGAAAAAAATTTAATGTTAAAAAAAACATATAGACATTGAC
ATGGAAGAGATTTAATGTTTTGAAAAAAACTTTATATTAAGTAACTGAGTAACATCCTCCTGATGAGAAGTACTAT
ATTAAATATAAACCCATTATGTTAT

2597/6881
FIGURE 2388

MYELVSKGYLGCTSVFVKQEQIWTLPGQSRVTWNLLISASGAPGRENFKSDRILYIPFLGTFSPQDSNIMTSVST
QLSLVLMSSLLLVLPVVEAVEAGDAIALLLGVVLSITGICACLGVIYARKRNGQM

2598/6881
FIGURE 2389

GAGTGGCTGTTGAGCGGCGCCGCGGGAGTTCCGCAGGTTTCCCGTGTTTCGCAGCGGAGCCGGAGGCCAGCTGAAC
CCGGCCGTGGGATCCCGGATAGGAGGAGGAGGGGACCCATAGGACGCGTTAACATGGACCTGGAAAACAAAGTGA
AGAAGATGGGCTTAGGTACAGAGCAAGGATTTGGAGCCCCTTGTTTAAAATGCAAAGAAAATGTGAAGGATTCTG
AACTGCACTTCTGGAGAAAAATATGTCGTAAGTGTGGCCAAGAAGAGCATGATGTCCTCTTGAGCAATG
AAGAGGATCGAAAAGTGGGAAAACCTTTTGAAGACACCAAGTATACCACTCTGATTGCAAACTAAAGTCAGATG
GAATTCCCATGTATAAACGCAATGTTATGATATTGACGAATCCAGTTGCTGCCAAGAAGAATGTCTCCATCAATA
CAGTTACCTATGAGTGGGCTCCTCCTGTCCAGAATCAAGCATTGGCCAGGCAGTACATGCAGATGCTACCCAAGG
AAAAGCAGCCAGTAGCAGGCTCAGAGGGGGCACAGTACCGGAAGAAGCAGCTGGCAAAGCAGCTCCCTGCACATG
ACCAGGACCCCTTCAAAGTGCCATGAGTTGTCTCCAGAGAGGTGAAGGAGATGGAGCAGTTTGTGAAGAAATATA
AGAGCGAAGCTCTGGGAGTAGGAGATGTCAAACCTCCCTGTGAGATGGATGCCAAGGCCCCAAACAAATGAACA
TTCCTGGAGGGGATAGAAGCACCCCAGCAGCAGTGGGGGCCATGGAGGACAAATCTGCTGAGCACAAAAGAAGCTC
AATATTCCTGCTATTGCTGCAAACCTGAGTATGAAAGAAGGTGACCCAGCCATCTATGCCGAAAGGGCTGGCTATG
ATAAACTGTGGCACCCAGCTTGTTTTGTCTGCAGCACCTGCCATGAACTCCTGGTTGACATGATTTATTTTTGGA
AGAATGAGAAGCTATACTGTGGCAGACATTACTGTGACAGCGAGAAACCCCGATGTGCTGGCTGTGACGAGCTGA
TATTCAGCAATGAGTATACCCAGGCAGAAAACAGAATTGGCACCTGAAACACTTCTGCTGCTTTGACTGTGATA
GCATTCTAGCTGGGGAGATATACGTGATGGTCAATGACAAGCCCGTGTGCAAGCCCTGCTATGTGAAGAATCACG
CTGTGGTGTGTCAAGGATGCCACAATGCCATCGACCCAGAAGTGCAGCGGGTGACCTATAACAATTTAGCTGGC
ATGCATCCACAGAGTGCTTTCTGTGCTCTTGCTGCAGCAAATGCCTCATTGGGCAGAAGTTCATGCCAGTAGAAG
GGATGGTTTTCTGTTCAGTGGAATGTAAGAAGAGGATGTCTTAGGAGGAGGGCACCCAGAAGTATCGAGCCATAG
CTATCCAAAGTGGTCTGCATTTCTACTGTAAAATGCAATTTGAAAAAATAAAACGCAAAAAAGAACTGTAAA
GGAAACCAAGAGATTTTGTTTAATTTTTTTGGCCATTTTTCTTCATCAATTTTTTTTCGGTCTCAACTTTTAAA
CTTGGTTTAAGCATTTGATTTGTAAAACAGTAAATAATTGTATCTTTCCATAGCTTTTCAAATGTGAAATCATTT
TTGGAAGCTTGGATCTCATTAAACTTCATGTCTCTATTCCATTTGTGCCACACACTTAAAAGTTAGTGTACTGAA
TGGAAGATGAGCATTCTAGTTCTACACTTCTTTTTTCCCCCTCATGTGTAAAATGAAAAGAAAAGTAAATTTG
CCCTAATACCAAGGCGCTACGTTTATTGCCTCGTCTTATTCACTGACCTTTGTAATGATACACAGTGAATTCCTT
TTGACAAAGAGAAATGCAGTGTAGTATGCAGAGCTGCTGTTTTAATGCCTATGCATTTACTCTTTTCTGATTTAG
GCAGAGGTGGCATTCTTTTATTGCATTTCTCTATTTTTTTAATGTACCCTACCTTCAGTATTCTCTTTGTAAAGT
TGGTGACTTGCACTGTGGCCTTGAATATTTTATTATCACATGTGGCATAACAGTATCCACACTTTTTTAGTTCTT
TATTTTTTTTTTTTTTATTTTGAAGCAATTCTCCTGCCTCAGCCTCCCAAATAGCTGGGATTACAGGTGCATGCCAC
CACACCCAGCTAATTTTTTGTATTTTTTAGTAGAGACAGGTTTTACCATGTTAGCCAGGCTGGTCTCAAACCTCTG
ACCTCAGATGATCCGCCTGCCTTGGCCTCCCAAAGTGCTGGGATTACAGGTGTGGGAGCCACCATGCCTGACCCA
CACACTTTTTTACTTGTATAGATGATTTTTTGGCTTGACATAAAAGCCAAGCCACCCATTTGCTTTTAAATCCAAAG
AACATGTATAGTTTTTGTACCCAGAGACTATGATTTATATTGATTGCACTTGCCCTGCCATGATTTAGATAAGATT
TTTTTTGCATGGTTTTTATTCTTTCCTAATGGATCCTGTTTTATAATACTTCCAAGCCTGTCCATGGATATATCA
AATGTCTTCACTTGTATATTTTCATGGCTAGGTATTTCTAATGTTTATTCTTCCCTGTGTACTTCTACACATAGC
TATGCACTATGAAAATTAAATGGAATGAATGATATGTATATTACTCAAATAAAGTTTCTTTCACCTT

2599/6881
FIGURE 2390

MDLENKVKKMGLGHEQGFGAPCLKCKEKCCEGFELHFWRKICRNCKCGQEEHDVLLSNEEDRKVGKLFEDTKYTTL
IAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWAPPVQNQALARQYMQLPKEKQPVAGSEGAQYRKKQL
AKQLPAHDQDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQGPKQMNIPGGDRSTPAAVGAMEDK
SAEHKRTQYSCYCCKLSMKEGDPAIYAERAGYDKLWHPACFVCSTCHELLVDMIFYWKNEKLYCGRHYCDSEKPR
CAGCDELIFSNEYTQAEQNWNHLKHFFCCFDCDSILAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRV
TYNNFSWHASTEFCFLSCCSKCLIGQKMPVEGMVFCVSVECKKRMS

2600/6881
FIGURE 2391

GGGAGAAACGTTCTCACTCGCTCTCTGCTCGCTGCGGGCGCTCCCCGCCCTCTGCTGCCAGAACCTTGGGGATGT
GCCTAGACCCGGGCGCAGCACACGTCCGGGCCAACCGCGAGCAGAACAAACCTTTGGCGGGCGGCCAGGAGGCTCC
CTCCCAGCCACCGCCCCCTCCAGCGCCTTTTTTTTCCCCCATACAATAACAAGATCTTCCTTCCTCAGTTCCCTT
AAAGCACAGCCCAGGGAAACCTCCTCACAGTTTTTCATCCAGCCACGGGCCAGC**ATGT**CTGGGGGCAAATACGTAG
ACTCGGAGGGACATCTCTACACCGTTCCCATCCGGGAACAGGGCAACATCTACAAGCCCAACAACAAGGCCATGG
CAGACGAGCTGAGCGGAGAAGCAAGTGTACGACGCGCACACCAAGGAGATCGACCTGGTCAACCGCGACCCATAAC
ACCTCAACGATGACGTGGTCAAGATTGACTTTGAAGATGTGATTGCAGAACCAGAAGGGACACACAGTTTTGA^oCG
GCATTTTGAAGGCCAGCTTCACCACCTTCACTGTGACGAAATACTGGTTTTACCGCTTGCTGTCTGCCCTCTTTG
GCATCCCGATGGCACTCATCTGGGGCATTTACTTCGCCATTCTCTCTTTCTGCACATCTGGGCAGTTGTACCAT
GCATTAAGAGCTTCCTGATTGAGATTCACTGTCATCAGCCGTGTCTATTCCATCTACGTCCACACCGTCTGTGACC
CACTCTTTGAAGCTGTTGGGAAAATATTAGCAATGTCCGCATCAACTTGCAGAAAGAAATAT**TAAAT**GACATTTT
AAGGATAGAAGTATACCTGATTTTTTTTTTCTTTTAATTTTCTGGTGCCAATTTCAAGTTCCAAGTTGCTAATAC
AGCAACAATTTATGAATTGAATTATCTTGGTTGAAAATAAAAAGATCACTTTCTCAGTTTTTCATAAGTATTATGT
CTCTTCTGAGCTATTTTCATCTATTTTTTGGCAGTCTGAATTTTTTAAACCCTTTTAAATTTTTTCTTACCTTTT
TATTTGCATGTGGATCAACCATCGCTTTATTGGCTGAGATATGAACATATTGTTGAAAGGTAATTTGAGAGAAAT
ATGAAGAACTGAGGAGGAAAAAAAAAAAAAAAAAGAAAAGAACCAACAACCTCAACTGCCTACTCCAAAATGTTGGTC
ATTTTATGTTAAGGGAAGAATTCAGGGTATGGCCATGGAGTGACAAGTATGTGGGCAGATTTTCAGCAAACCTC
TTTTCCCACTGTTTAAGGAGTTAGTGGATTACTGCCATTCACTTCATAATCCAGTAGGATCCAGTGATCCTTACA
AGTTAGAAAACATAATCTTCTGCCTTCTCATGATCCAATAATGCCTTACTCTTCTTGAAATTTTAACTATGAT
ATTTTCTGTGCCTGAATATTTGTTATGTAGATAACAAGACCTCAGTGCCTTCCTGTTTTTTCATTTTTCTTTT
AAATAGGGTCTAACTCAGCAACTCGCTTTAGGTCAGCAGCCTCCCTGAAGACCAAATTAGAATATCCATGACCT
AGTTTTCCATGCGTGTCTGACTCTGAGCTACAGAGTCTGGTGAAGCTCACTTCTGGGCTTCATCTGGCAACAT
CTTTATCCGTAGTGGGTATGGTTGACACTAGCCCAATGAAATGAATTAAAGTGGACCAATAGGGCTGAGCTCTCT
GTGGGCTGGCAGTCCTGGAAGCCAGCTTTCCCTGCCTCTCATCAACTGAATGAGGTCAGCATGTCTATTCACTT
CGTTTTATTTTCAAGAATAATCACGCTTTTCTGAATCCAACTAATCCATCACCGGGGTGGTTTAGTGGCTCAACA
TTGTGTTCCCATTTTCACTGATCAGTGGGCCTCCAAGGAGGGGCTGTAAAATGGAGGCCATTGTGTGAGCCTATC
AGAGTTGCTGCAAACTGACCCCTGCTCAGTAAAGCACTTGCAACCGTCTGTTATGCTGTGACACATGGCCCCCTC
CCCCTGCCAGGAGCTTTGGACCTAATCCAAGCATCCCTTTGCCAGAAAGAAGATGGGGGAGGAGGCAGTAATAA
AAAGATTGAAGTATTTTGTGGAATAAGTTCAAATCTTCTGAACTCAAACCTGAGGAATTTACCTGTAAACCTG
AGTCGTACAGAAAGCTGCCTGGTATATCCAAAGCTTTTTTATTCTCTGCTCATATTGTGATTCTGCCTTTGGG
GACTTTTCTTAAACCTTCAGTTATGATTTTTTTTTTTCATACACTTATTGGAACCTCTGCTTGATTTTTTGCCTCTTCC
AGTCTTCTGACACTTTAATTACCAACCTGTTACCTACTTTGACTTTTTTGCAATTTAAACAGACACTGGCATGGA
TATAGTTTTACTTTTAACTGTGTACATAACTGAAAATGTGCTATACTGCATACTTTTTAAATGTAAAGATATTT
TTATCTTTATATGAAGAAAATCACTTAGGAAATGGCTTTGTGATTCAATCTGTAACTGTGTATTCCAAGACATG
TCTGTTCTACATAGATGCTTAGTCCCTCATGCAAATCAATTACTGGTCCAAAGATTGCTGAAATTTTATATGCT
TACTGATATATTTTACAATTTTTTATCATGCATGTCCTGTAAAGGTTACAAGCCTGCACAATAAAAAATGTTTAA
GGTT

2601/6881
FIGURE 2392

MSGGKYVDSEGHLYTVP IREQGNIYKPNNKAMADELSEKQVYDAHTKEIDLVNRPKHLNDDVVKIDFEDVIAEP
EGTHSFDGIWKASFTTFTVTKYWFYRLLSALFGIPMALIWGIYFAILSFLHIWAVVPCIKSFLIEIQCISRVYSI
YVHTVCDPLFEAVGKIFSNVRINLQKEI

2602/6881
FIGURE 2393

TTTGTGCCAGAAGGAAGATGGCGGATCTGGAGGAGCAGTTGTCTGATGAAGAGAAGGTGCGTATAGCAGCAAAA
TTCATCATTCATGCCCCCTCCTGGAGAATTTAATGAGGTTTTCAATGATGTTTCGGTTACTGCTTAATAATGACAAT
CTTCTCAGGGAAGGAGCAGCCCATGCATTTGCACAGTATAACTTGGACCAGTTTACTCCAGTAAAAATGAAGGT
TATGAAGATCAGGTATTGATAACAGAACATGGCGACTTGGGAAATGGAAAGTTTTTGGATCCAAAGAACAGAATC
TGTTTTAAATTTGATCACTTAAGGAAGGAGGCAACTGATCCAAGACCCTGTGAAGTAGAAAATGCAGTTGAATCA
TGGAGAACTTCAGTAGAACTGCTCTGAGAGCTTACGTAAAAGAACATTACCCGAATGGAGTCTGCACTGTGTAT
GGCAAAAAAATAGATGGACAGCAAACCATTATTGCATGCATAGAAAGCCATCAGTTCCAAGCAAAAAATTTTGG
AATGGTCGTTGGAGGTCAGAATGGAAGTTTACAATCACTCCTTCAACCACTCAAGTGGTTGGCATCTTGAAAATT
CAGGTTTATTATTATGAAGATGGTAATGTTTCAGCTAGTGAGTCATAAAGATATACAAGATTCCCTAACAGTGTCT
AATGAAGTGCAAAACAGCAAAAGAATTTATAAAGATTGTAGAAGCTGCAGAAAATGAATACCAGACTGCCATCAGT
GAGAATTATCAGACAATGTCGGACACTACTTTCAAAGCCTTACGTCGACAGTTGCCAGTTACACGCACTAAGATT
GATTGGAACAAGATCCTTAGCTACAAGATTGGCAAAGAGATGCAGAATGCATTAAGATGAACATTGCATGACCGGA
TCATTTTAGTGTCTTTGC

2603/6881
FIGURE 2394

MADLEEQLSDEEKVRIAAKFIIHAPPGEFNEVFNDVRLLLNNDNLLREGAAHAFQYNLDQFTPVKIEGYEDQVL
ITEHGDLDGNGKFLDPKNRICFKFDHLRKEATDPRPCEVENAVESWRTSVETALRAYVKEHYPNGVCTVYGKKIDG
QQTIIACIESHQFQAKNFWNGRWRSEWKFTITPSTTQVVGILKIQVHYEDGNVQLVSHKDIQDSLTVSNEVQTA
KEFIKIVEAAENEYQTAISENYQTMSDTTFKALRRQLPVTRTKIDWNKILSYKIGKEMQNA

2604/6881
FIGURE 2395

CTCTCCGGTCCGTGCCTCCAAGATGACAAAGAAAAGAAGGAACAATGGTCGTGCCAAAAAGGGCCGCGGCCACGT
GCAACCTGTTTCGCTGTACTAACTGTGCCCCGATGCGTGCCCAAGGACAAGGCCATTAAGAAATTCGTCATTGAAA
CATAGTGGAGGCCGTAGCAGTCAGGGACATTTCTGAAGCAAGCGTCTTCGATGCCTATGTGCTTCCCAAGCTGTA
TGTGAAGCTACATTACTGTGTGAGTTGTGCAATTCACAGCAAAGTAGTCAGGAATCGATCTCGTGAAGCCCGCAA
GGACCGAACACCCCCACCCAGATTTAGACCTGCGGGTGCTGCCCCACGTCCCCACCAAAGCCCATGTAAGGAGC
TGAGTTCTTAAAGACTGAAGACAGGTTATTCTCTGGAGAAAAATAAAATGGAAATTGTA

2605/6881
FIGURE 2396

TGGAGCTAAGCTGTTTCCAGGGTGACAGAGTGGCGACCTCGGTGGTCGATTGAGCAGGTCTGAGAATTGTTCCCA
AAGGGTTGTGCGTCACCGAGTCGTTGGCGCTGTC**ATCG**CGGGTGTGCTGAAGAAGACCACTGGCCTTGTGGGATT
GGCTGTGTGCAATACTCCTCACGAGAGGCTAAGAATATTGTACACAAAGATTCTTGATGTTCTTGAGGAAATCCC
TAAAAATGCAGCATATAGAAAGTATACAGAACAGATTACAAATGAGAAGCTGGCTATGGTTAAAGCGGAACCAGA
TGTTAAAAAATTAGAAGACCAACTTCAAGGCGGTCAATTAGAAGAGGTGATTCTTCAGGCTGAACATGAACTAAA
TCTGGCAAGAAAAATGAGGGAATGGAACTATGGGAGCCATTAGTGGAAGAGCCTCCTGCCGATCAGTGGAATG
GCCAAT**TAA**ATTATTAAGTGACTTTGGTGTGTTTCATGGGAACTGATGTAATTAAATATTCTGTTATATTAAGAG
CGTGTTCCTTATTACTGACATTTTGTAAATCAAGAAAAGTGATATAGAAAATATGTAGGAGACTGTTAAAAATTGGTG
ATTATGGTAATATGGTCATGTGAATCAATTTTTGATTTATAAAAGTACTCACACAAGTTGTTTCAAAGATGATATT
TCTGTGAACAGAGAGGCCATGGGAAGATTTGAAAATTATTAAAGAAAAATTTCCTACAGATTTTCAATGCAGAGAC
CATAATCAAAAAGTAAACTTTCTTTAGTAGTATGTTCAATACATCATTTAATTTTTTAAAGTTATCCTGAAGAAGG
AAAGGTCCTTAATTATTATAGTCTAAACAAATTTATAGATTACTGTTTGAAGTAAATAATACGAGTGAATATTTT
CAAATGTGATAAAATAGCACAAAGTGGCTGGTGATAAAATTTGAAATTATGGTTAACCTCAGCTGTGATCTTATGT
ATGTAAAGTGAAATTTAAATAGATAATTATAGGTTGATTACAAATCCATAGTGTCAATTTATTTTAGTCATTAT
TGAATTATACCATTTACTCTGTTTTCTTATAGTCTTAATTTTATTATATTTTGTGTTACTGTATTATATTTGAA
AACCTTCAAATTAGAATACATTGTACAGTTAAAGAAATTGACTTGGTACTTAAAGAAAGATTTCCCATTCGATA
CAGGTTATTGGAGAAATTTTCCTTTTGTTCATTTGTGGAAGTTAGTTTCTGGCCCGTGGCCTTTAATTTTCTT
AATCAACCTAATTACATCAGGATAGAGGTAGAGTTTCTGTAAAAGAAGAGACATTAAGAGTTCCTGAAATTTATA
TCTGGCATACCGATAGGCTTATATTCAAACATCTTAGTCATACGACCATAAATTAAAAGTGGAGTCACTAAATA
GTTTGCAGTACGTTTCTAATATAAGTGTAGGTGGGTATCAAAACAAGACAAATGCTGTTTCAGGGAAAGAAGTTGG
CAAGCTTAAGGTTAAACAAAAATAAAATTACATGTGTTTTCGCCTTCCTA

2606/6881
FIGURE 2397

MAGVLKKT TGLVGLAVCNTPHERLRILYTKILDVLEEIPKNAAYRKYTEQITNEKLAMVKAEPDVKKLEDQLQGG
QLEEVILQAEHELNLARKMREWKLWEPLVEEPPADQWKWPI

2607/6881
FIGURE 2398

CCGCGTCGGTGCCCGCGCCCCCTCCCCGGGCCCCGCCATGGGCCTCACCGTGTCCGCGCTCTTTTCGCGGATCTTC
GGGAAGAAGCAGATGCGGATTCTCATGGTTGGCTTGGATGCGGCTGGCAAGACCACAATCCTGTACAAACTGAAG
TTGGGGGAGATTGTCACCACCATCCCAACCATAGGCTTCAATGTAGAAACAGTGGAATATAAGAACATCTGTTTC
ACAGTCTGGGACGTGGGAGGCCAGGACAAGATTTCGGCCTCTGTGGCGGCACTACTTCCAGAACACTCAGGGCCCTC
ATCTTTGTGGTGGACAGTAATGACCGGGAGCGGGTCCAAGAATCTGCTGATGAACTCCAGAAGATGCTGCAGGAG
GACGAGCTGCGGGATGCAGTGCTGCTGGTATTTGCCAACAAGCAGGACATGCCCAACGCCATGCCCCGTGAGCGAG
CTGACTGACAAGCTGGGGCTACAGCACTTACGCAGCCGCACGTGGTATGTCCAGGCCACCTGTGCCACCCAAGGC
ACAGGTCTGTACGATGGTCTGGACTGGCTGTCCACGAGCTGTCAAAGCGCTTAACCAGCCAGGGGCAGGCCCCTG
ATGCCCGGAAGCTCCTGCGTGCTATCCCCGGGATGACCAGACTCCCGGACTCCTCAGGCAGTGCCCTTTCTCCCA
CTTTTCCTCCCCCATAGCCACAGGCCTCTGCTCCTGCTCCTGCCTGCATGTTCTCTCTGTTGTTGGAGCCTGGAG
CCTTGCTCTCTGGGACACAGAGGGGTCCACTCTCCTGCCTGCTGGGACCTATGGAAGGGGCTTCTTGCCAAGGCC
CCCTCTTCCAGAGGAGGAGCAGGGATCTGGGTTTCCTTTTTTTTTTCTGTTTTGGGTGTACTCTAGGGGCCAGGT
TGGGAGGGGAAGGTGAGGGCTTCGGGTGGTGCTATAATGTGGCACTGGATCTTGAGTAATAAATTTGCTGTGGT
TTG

2608/6881
FIGURE 2399

MGLTVSALFSRIFGKKQMRILMVGLDAAGKTTILYKLKLGEIVTTIPTIGFNVETVEYKNICFTVWDVGGQDKIR
PLWRHYFQNTQGLIFVVDSDNREERVQESADELQKMLQEDEL RDAVLLVFANKQDMPNAMPVSELTDKLG LQH LRS
RTWYVQATCATQGTGLYDGLDWLSHEL SKR

2609/6881
FIGURE 2400

GCGAGTAGAACGTGTGGCGGCGGCGGAGATCGCGTCTCTTTTCGCTCCGTGTCCCGCTGCTGCTCCTGTGAGCGCC
CGGCGAGTCCGTCCCGTCCACCGTCCGCAGCTGGTAGCCAGCCTGCCCCCTCGCCTCGACTCCCTTTACCAACAC
CGACACCCACATTGACACCTCCAGTCCGGCCAGCCGCTCCACTCGTTGCCTTTGCATCTCCACACATGGCGTCCT
CCGCGCAGAGCGGCGGCTCCTCCGGGGGACCCGCGGTCCCCACCGTGCAGCGGGGCATCATCAAGATGGTCCTCT
CAGGGTGCGCCATCATTGTCCGAGGTACAGCCTCGTGGTGGGCCTCCTCCTGAGCGGCAGATCAACCTCAGCAACA
TTCGTGCTGGAAATCTTGCTCGCCGGGCAGCCGCCACACAACCTGATGCAAAGGATAACCCCTGATGAGCCCTGGG
CATTTCCAGCTCGAGAGTTCTTTCGAAAGAAGCTGATTGGGAAGGAAGTCTGTTTCACGATAGAAAAACAAGACTC
CCCAGGGGCGAGAGTATGGCATGATCTACCTTGAAAAAGATAACCAATGGGGAAAAACATTGCAGAATCACTGGTTG
CAGAGGGCTTAGCCACCCGAGAGAAGGCATGAGAGCTAATAATCCTGAGCAGAACCGGCTTTTCAGAAATGTGAAG
AACAAGCAAAGGCAGCCAAGAAAGGGATGTGGAGTGAGGGGAACGGTTCACATACTATCCGGGATCTCAAGTATA
CCATTGAAAAACCAAGGCACCTTTGTGGACTCACACCACCAGAAGCCTGTTAATGCTATCATCGAGCATGTGCGGG
ACGGCAGTGTGGTCAGGGCCCTGCTCCTCCCAGATTACTACCTGGTTACAGTCATGCTGTGAGGCATCAAGTGCC
CAACTTTTTCGACGGGAAGCAGATGGCAGTGAAACTCCAGAGCCTTTTGTGTCAGAAGCCAAATTTTTCACTGAGT
CGCGACTGCTTCAGAGAGATGTTTCAGATCATTCTGGAGAGCTGCCACAACCAGAACATTCTGGGTACCATCCTTC
ATCCAAATGGCAACATCACAGAGCTCCTCCTGAAGGAAGTTTCGCACGCTGTGTGGACTGGTCGATTGCAGTTT
ACACCCGGGGCGCAGAAAAGCTGAGGGCGGCAGAGAGGTTTGCCAAAGAGCGCAGGCTGAGAATATGGAGAGACT
ATGTGGCTCCACAGCTAATTTGGACCAAAAGGACAAGCAGTTTGTGCAAGGTGATGCAGGTTCTGAATGCTG
ATGCCATTGTTGTGAAGCTGAAGTCAAGTCAAGGCGATTACACCTGTCCAGCATCCGACCACCGAGGCTGG
AGGGGGAGAACACCCAGGATAAGAACAAGAACTGCGTCCCCTGTATGACATTCTTACATGTTTGAGGCCCGGG
AATTTCTTCGAAAAAAGCTTATTGGGAAGAAGGTCAATGTGACGGTGGACTACATTAGACCAGCCAGCCCAGCCA
CAGAGACAGTGCCTGCCTTTTCAGAGCGTACCTGTGCCACTGTCACCATTGGAGGAATAAACATTGCTGAGGCTC
TTGTTCAGCAAAGGTCTAGCCACAGTGATCAGATACCGGCAGGATGATGACCAGAGATCATCACACTACGATGAAC
TGCTTGCTGCAGAGGCCAGAGCTATTAAGAATGGCAAAGGATTGCATAGCAAGAAGGAAGTGCCTATCCACCGTG
TTGCAGATATATCTGGGGATACCCAAAAAGCAAAGCAGTTCTTGCCTTTTCTTCAGCGGGCAGGTGCTTCTGAAG
CTGTGGTGGAATACGTCTTCAGTGGTTCTCGTCTCAAACCTCTATTTGCCAAAGGAACTTGCTTATCACCTTCT
TGCTTGAGGCATTGAATGCCCCAGAGGAGCCCGAAACCTCCCAGGCTTGGTGCAGGAAGGAGAGCCCTTCAGCG
AGGAAGCTACACTTTTACCAAGGAAGTGGTGTGTCAGCGAGAGGTGGAGGTGGAGGTGGAGAGCATGGACAAGG
CCGGCAACTTTATCGGCTGGCTGCACATCGACGGTGCCAACCTGTCCGTCTGCTGGTGGAGCACGCGCTCTCCA
AGGTCCACTTCACCGCCGAACGCAGCTCCTACTACAAGTCCCTGCTGTCTGCCGAGGAGGCCGCAAAGCAGAAGA
AAGAGAAGGTCTGGGCCACTATGAGGAGCAGCCCGTGGAGGAGGTGATGCCAGTGCTGGAGGAGAAGGAGCGAT
CTGCTAGCTACAAGCCCGTGTGTTGTGACTGAGATCACTGATGACCTGCACTTCTACGTGCAGGATGTGGAGACCG
GCACCCAGTTGGAGAAGCTGATGGAGAATGCGCAATGACATTGCCAGTCACCCCCCTGTAGAGGGCTCCTATG
CCCCCGCAGGGGAGAGTTCTGCATTGCCAAATTTGTAGATGGAGAATGGTACCGTGCCCGAGTAGAGAAAGTCG
AGTCTCCTGCCAAAATACATGTCTTCTACATTGACTACGGCAACAGAGAGGTCTGCCATCCACCCGCTGGGTGTA
CCCTATCACCTGCCTTCAGCACTCGGGTGCTGCCAGCTCAAGCCACGGAGTATGCCTTCGCCTTCATCCAGGTGC
CCCAAGATGATGATGCCCCGACGGACGCCGTGGACAGCGTAGTTCGGGATATCCAGAACACTCAGTGCCTGCTCA
ACGTGGAACACCTGAGTGCCGGCTGCCCCATGTACCCCTGCAGTTTGCAGATTCCAAGGGCGATGTGGGGCTGG
GCTTGGTGAAGGAAGGGCTGGTCATGGTGGAGGTGCGCAAGGAGAAACAGTTCCAGAAAGTGATCACAGAATACC
TGAATGCCCAAGAGTCAGCCAAGAGCGCCAGGCTGAACCTGTGGCGCTATGGAGACTTTCGAGCTGATGATGCAG
ACTGCCCTCGTCCCAGCTCTCTGTCCAAGTGTGATTATGTGATTTTCTGATACGTCCATTCTCAAATGCCAGT
GTGTTACATCTTCGCTCTGGCCAGCCATTCTGTATTTAAAGCTTTTGAGGCCCAATAAAATAGTACGTGCTGT
C

2610/6881
FIGURE 2401

MASSAQSGSSGGPAVPTVQRGI IKMVLSGCAI IVRGQPRGGPPPERQINLSNIRAGNLARRAAATQPDAKDTPD
EPWAFPAREFLRKKLIGKEVCFTIENKTPQGREYGMIIYLGKDTNGENIAESLVAEGLATRREGMRANNPEQNRLS
ECEEQAKAAKKGMWSEGNGSHTIRDLKYTIENPRHFVDSHHQKPVNAIIEHVRDGSVVRALLLPDYLLVTVMVLSG
IKCPTFRREADGSETPEPFAAEAKFFTESRLLQRDVQI ILESCHNQNILGTILHPNGNITELLKKEGFARCV DWS
IAVYTRGAEKLRAAERFAKERRLRIRWDYVAPTANLDQKDKQFVAKVMQVLNADAI VVKLNSGDYKTIHLSSIRP
PRLEGENTQDKNKKLRPLYDIPYMFAREFLRKKLIGKKVNVTVDYIRPASPATETVPAFSERTCATVTIGGINI
AEALVSKGLATVIRYRQDDQRRSSHYDELLAAEARA IKNGKGLHSKKEVPIHRVADISGDTQKAKQFLPFLQ RAG
RSEAVVEYVFGSRLKLYLPKETCLITFLLAGIECPRGARNLPGLVQEGEPFSEEATLFTKELVLQREVEVEVES
MDKAGNFIGWLHIDGANLSVLLVEHALSKVHFTAERSSYYKSLLSAEEAAKQKKEKVWAHYEEQPVEEVMPVLEE
KERSASYKPVFVTEITDDLHFYVQDVETGTQLEKLMENMRNDIASHPPVEGSYAPRRGEFCIAKFVDGEWYRARV
EKVESPAKIHVFYIDYGNREVL PSTRLGTLSPAFSTRVLPAQATEYAFAFIQVPQDDDARTDAVD SVVRDIQNTQ
CLLNVEHLSAGCPHVTLQFADSKGDVGLGLVKEGLVMVEVRKEKQFQKVITEYLN AQESAKSARLNLWRYGDFRA
DDADCPRPSSLSNC

2611/6881
FIGURE 2402

TCGGAAGGGGCCAGGAGACACTGGAAGGTCCGGACGGCAGGGAAGGGGACGGGGTTCTTTCCAGTCCCACCCGTG
TAGGGACACCTCTCCCCCTCATCCCCGATGTACCCTCGCTGAATCTGGGATGGGAGAGACGAACCGAGTCTAGG
CATCTGCGTAGCAGCGCCGGGGAGAGCGGGGAGCCCAGGGCGGAGCCAGTCGACTCCCGGATTCCCCTGCCCGG
CCCCCGGCACGAGGCCCGCCCGGGCGGCCCGCCCTCCTCGGGACTCGACCGGGCTGCGCTCACTGCCCAGCC
GGGGCCCCGGGAGCCTCCAGGCTCCCGCCCGCCCTGAGCTGCGGCCTCCGCATGGAGGGGGCCACTCACTCCACCA
CCGCTGCAGGGAGGCGGAGCCGCCGCTGTTCCGGAGCCCGGAGCCCGGCAACACCCGGGACACGAGACGGCGGCG
CAGCGGTACAGCGCCCCGACTGCTGCAGGCCGGCTACGAGCCCGAGAGCCCTAGATTGGACCTCGCTACACACCCG
ACGACACCCCCGTTTCAAGACTATCTTCAGTGGTCTTACTGGCAGGTGTTGGTGTCCAGATGGATCGCCTTCGCAGG
GCTAGCATGGCGGACTACCTGATCAGCGGCGGCACCGGCTACGTGCCCGAGGATGGGCTCACCGCGCAGCAGCTC
TTCGCCAGCGCCGACGGCCTCACCTACAACGACTTCCTGATTCTCCCAGGATTCATAGACTTCATAGCTGATGAG
GTGGACCTGACCTCAGCCCTGACCCGGAAGATCACGCTGAAGACGCCACTGATCTCCTCCCCCATGGACACTGTG
ACAGAGGCTGACATGGCCATTGCCATGGCTCTGATGGGAGGTATTGGTTTCATTACCCACAACCTGCACCCAGAG
TTCCAGGCCAACGAGGTGCGGAAGGTCAAGAAGTTTGAACAGGGCTTCATCACGGACCCTGTGGTGCTGAGCCCC
TCGCACACTGTGGGCGATGTGCTGGAGGCCAAGATGCGGCATGGCTTCTCTGGCATCCCCATCACTGAGACGGGC
ACCATGGGCAGCAAGCTGGTGGGCATCGTCACCTCCCGAGACATCGACTTTCTTGCTGAGAAGGACCACACCACC
CTCCTCAGTGAGGTGATGACGCCAAGGATTGAACCTGGTGGTGGCTCCAGCAGGTGTGACGTTGAAAGAGGCAAAT
GAGATCCTGCAGCGTAGCAAGAAAGGGAAGCTGCCTATCGTCAATGATTGCGATGAGCTGGTGGCCATCATCGCC
CGCACCGACCTGAAGAAGAACCGAGACTACCCTCTGGCCTCCAAGGATTCCCAGAAGCAGCTGCTCTGTGGGGCA
GCTGTGGGCACCCGTGAGGATGACAAATACCGTCTGGACCTGCTCACCCAGGCGGGCGTCGACGTCATAGTCTTG
GACTCGTCCCCAAGGGAATTTCGGTGTATCAGATCGCCATGGTGCATTACATCAAACAGAAGTACCCCCACCTCCAG
GTGATTGGGGGGAACGTGGTGACAGCAGCCCAGGCCAAGAACCTGATTGATGCTGGTGTGGACGGGCTGCGCGTG
GGCATGGGCTGCGGCTCCATCTGCATCACCCAGGAAGTGATGGCCTGTGGTGGCCCCAGGGCACTGCTGTGTAC
AAGGTGGCTGAGTATGCCCGGCGCTTTGGTGTGCCCATCATAGCCGATGGCGGCATCCAGACCGTGGGACACGTG
GTCAAGGCCCTGGCCCTTGGAGCCTCCACAGTGATGATGGGCTCCCTGCTGGCCGCCACTACGGAGGCCCTGGC
GAGTACTTCTTCTCAGACGGGGTGCGGCTCAAGAAGTACCGGGGCATGGGCTCACTGGATGCCATGGAGAAGAGC
AGCAGCAGCCAGAAAACGATACTTCAGCGAGGGGGATAAAGTGAAAGATCGCGCAGGGTGTCTCGGGCTCCATCCAG
GACAAAGGATCCATTCAAGATTTCGTGCCCTACCTCATAGCAGGCATCCAACACGGCTGCCAGGATATCGGGGCC
CGCAGCCTGTCTGTCTTCGGTCCATGATGTACTCAGGAGAGCTCAAGTTTGAGAAGCGGACCATGTGCGGCCAG
ATTGAGGGTGGTGTCCATGGCCTGCACTCTTACGAAAAGCGGCTGTACTGAGGACAGCGGTGGAGGCCGAGGTGG
TGGAGGGGATGCACCCAGTGTCCACTTTTGGGCACAGCCTCCCTCCATAACTGAGTGGTCCACAGATTTGCACT
ACGGGTTTCTCCAGCTCCTTTCCAGGCAGAGAGGAGGGGAGGTCTTGAGGGGACTGCTGCCCCCTCACTCGGCATCC
CCTGCAGAGTCAGGACTGCTCCCGGGGCCAGGCTGCCCTGGGAGCCCCCTCCGAGCCAGCCAGCCAGGCTCTC
AGGCCCTGCGCCTGCCCTCAGGTCTTTCTTGCTGCAGCCTGCTCCAGCCTGGCCCCCAGCCAGGGGCAGGCGGCC
CCTCCTGGCTTCTCCTGTAGGGCACCTCCCTGCCCCTAGCCTCCAGGAAATGGTGCTCTCCTGGCCCTGCCCTCT
GGCCCTTCCCGGGCCGCTGCCCTCAGCCATGTGGCACTTCTGAGCTCCTGACCTAGGCCAAGGGGAGGTCTCTG
CCCCCTTCCCGGGCCCTGGGCTACCCTTGGGTCTGCTCCTCAGGCCGCTCCCTGTCCCTGGCCATGGGTAGGA
GACTGCCCTGGTCAATGGCCGCTGCCCTGTCATTCTGACTCACCAACCGTCCCCAGGTGAACCATTCCTCCCTTCT
CCTCAGCTGCAGTCGAAGGCTTTAACTTTGCACACTTGGGATCACAGTTGCGTCATTGTGTATTAAATACTTGA
ATAAATCAAGCAGGT

2612/6881
FIGURE 2403

TTTCCAGCCCCAGCCCCGGACCCTGCAGCCGCAGAGATGTTGACGCCTAAGAAGAACCGGATTGCCATTTATGAA
CTCCTTTTTTAAGGAGGATGGTCATGGTGGCCAAGAAGGATGTCCACATGCCTAAGCACCCAGAGCTGGCAGACAA
GAATGTGCCCCAACCTTCATGTTCATGAAGGCCATGCAGTCTCTCAAGTCCCGAGGCTACGTGAAGGAACACTTTGC
CTGGAGACATTTCTACTGGTACCTTACCAATGAGGGTATCCAGTATCTCCGTGATTACCTTCATCTGCCCCCGGA
GATTGTGCCTGCCACCCTACCCCGTAGCCGTCCAGAGACTGGCAGACCTTGGCCTAAAGGTCTGTATGTGAGGAG
TGCTGTGCTACCTGGTGCCGACAAGAAAGCCGAGGCTGGGGCTGGGTCAGCAACCGAATTCTAGTTTAGAGGCGG
ATTTGGTCGTGGACGTGGTCAGCCACCTCAGTAAACTGGAGAGGATTCTTTTGCATTGAATAAACTTACAGCCA
AAAAA

2613/6881
FIGURE 2404

TGGGATTACAGGTAAGTGCCACCACACCCAGCTGATTTTTGTGTTTTTTGTAGAGACGAGGTTTCGCCATGTTTC
CCAGACTGTTCTCAAACCTCCTGAGCTCAAAGCAGTCCACCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGTG
TGAGCCACCTTGCTCATTCTAGTTTAAACTTTGGAGTGGTTTGTGTCTCCTGATTGGACTCCTGCAAATACAGAA
TTGATGCTAGGAAGGGTACCAGGAGATAGACGCACACAGATGGGATTGGAATAGGTTTGGTTATCCAAGGAGC
AGTGCTGAGCTCCTTGCTAATGGGATATGGGATGCTGGTGATTTCAGTAAGTGACCTCAAAATTA CT CAGGCTA
CCAATACTGTTGATTGTGATGAAATGCCAGTTGAAGCACCTGTCCTGCGAGCTTAGGGGTGCTACAAGTTGACC
ACTGCAGCAGTAAAGATGACTCTGAAGAATGGCATGGGATGGATCCTTTTCAATGCACTTGAGCAGCGGTCTCCA
ACACAGGGCCACAGAGCTGGAGCTGGATCTACCATGAAAGACCTCTGAATCCAGGAAGAGAGACTGACTGAGCA
ACATGTTATT CAGGTGGGACCATCCAGTTGCAGGAAAACAAGCTTAAGACGCCCACTGATTCTACATTATGCTCC
TACCTCCCGGCAGCCTCTCCAGGCCCAGA ACTTTCTCCAATCAGCCTCTACAGACCAAGCTCATGACTCACAATG
GCCTATTTAGGCCCATAACCTACGTACGGCAGTCTCCGCGAGATGAGCCTACTGCCCCACAACAGCCTCCACAGG
CACAGCTCCATCGTTACAATGGCCTCTTTAGACCCAGCTCCTGCCTCCAGCCTTCTCTCCAGGCCCCTGAAC TTT
CTCAAGTCGACCTCACCAGGCCCAGCTCATGCTTCTTTGCAGCCTCTCCAGGCCCAGCTCCTGCATCTTGGTGCC
CCCTCCAGGCCCAGCCTCTGCCTCCCGTCGGCCTCTACAGTCCCAACATCTGCCTCACAGCAGATTCTTCAGGCC
CAGCATCTGCCTCACTGTGGACCCCCCAAGCCAAGCTCCCAACCTTTCAGCAGCTTCTACACACCCAGCTCCTGC
CACCCAGTGGCCTCTTTAGGCCAAGCTCATGCTTACAAGGGCCTTTCAGGCCCCA ACTTTTGTCTCATGGCAAC
CTTCCCTGGCCAGATTCTGCTGTCTCCAGCAGCCTAGACAGGCCCAGGGCCTCTCTACATGCAGCTTATGCC
TCACGGTGGCCTCTCCAGGCCCCA ACTCCTGTCCAGGACGTCATCTCCGGGCCCAAACTTACTCAAGTCAGACT
CTGTAGTCCCAACTGCTGCCTCCTGGTGGCCTATGAAGGCCCAAAATCTCCTCAAGTTGACCTTTCAGGCCCAG
CTCCTGCCTCCTGTGACGCTCTACAGGCCCCA ACTCTACGTCATGGGGGCTTCTCCAGGCCCACCTCTTCTCTT
GGCTGGGTCTACAGGCACA ACTGCTGCCTCACAACAGCCTTTTTTGGCCCAGTTCCTGTCCAGCTCATGGCGGCC
AATGTAGGCCCAAACTTCTCAAGTCAA ACTCTCCAGGCCCCA ACTTCTGCTTCCCAGTGGCATGAACAGGCCCA
GCTTTGACTTGAGAACAGCCTCTGCAGGCCCTGCTCTTGCTCCAGGGGCTTTTTTCCAGGCCCAGCTCTTGCT
CATGGCAGCTGCCCCAGGCCAAATTTCTGCCTGCCTGCCAGCAGCCTCAACAGGCATAGCTCCTCCCTCACAGTG
GCCATTTAGGCCCA ACTCATGACTGTCGGGCCATTTCCAGGCCTAGTGCCTGCCTCGTGGCTGACTCTTGAAGC
CCAAA ACTTCTCAAATCAGCCTTTTGGCCAACTTCTGTCTACTGTGGACTCTACAGGCCAGCCTCTGCCTCAC
AGTGGACCCTCCAGACCCAGATGGTGTCTCACTGTGGCATCCTCAGTCGAAGCTCCTGCCTTTGGGCAGCCTCTC
CAGGCCCAGCTCCTCCTGCCTCCAGTGGCCTCTTTCCGGCCCAGC

2614/6881
FIGURE 2405

MLLPPGSLSRPRTFSNQPLQTKLMTHNGLFRPIPYVTAVSADEPTAPQQPPQAQLHRYNGLFRPSSCLPAFSPGP
ELSQVDLTRPSSCFFAASPGPAPASWWPLQAQPLPPVGLYSPNICLTADSSRPASASLWTPQAKLPTFQQLLHTQ
LLPPSGLFRPSSCFTRAFFGPTFVSWQPSLARFLPVSQQPRQAQGLSTCSLCLTVASPGPTPVFGRHLRAQNLLK
SDSVVPTAASWWPMKAQNLLKLTFFGPAPASCQRLQAQPLRHGGFSRPTSSSWLGLQAQLLPHNSLFWPSSCPAH
GGQCRPKTSSSQTLQAHLLLPSGMNRPSFDLRTASAGPALASQGLFPGPALASWQLPQAKFLPACQQPQQA

2615/6881
FIGURE 2406

TCTAATACCTATTGATCTGTCACTTTCTCCCATCACGCTCAGGTGGGACCATCCAGTTGCAGGAAAACAAGCTTA
AGACGCCCAGTGAATTCTACATTATGGTGAGTTCTATAATTATTTATTATATATTACAGTGTAATAATGGAAATA
AAGTGCCTAATAAAATGCAAATGTGCTTACATCTTTTGGCCCAGCTCCTACCTCCCGGCAGCCTCTCCAGGCCCAG
AACTTTCTCCAATCAGCCTCTACAGACCAAGCTCATGACTCACAATGGCCTATTTAGGCCCATAACCTACGTCAC
GGCAGTCTCCGCAGATGAGCCTACTGCCCCACAACAGCCTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTT
TAGACCCAGCTCCTGCCTCCCAGCCTTCTCTCCAGGCCCTGAACTTTCTCAAGTCGACCTCACCAGGCCCAGCTC
ATGCTTCTTTGCAGCCTCTCCAGGCCAGCTCCTGCATCTTGGTGGCCCCCTCCAGGCCAGCCTCTGCCTCCCGT
CGGCCTCTACAGTCCCAACATCTGCCTCACAGCAGATTCTTCACGCCCAGCATCTGCCTCACTTGGACCCCTCCAG
ACCCAGATGGTGTCTCACTGTGGCATCCTCAGTCGAAGCTCCTGCCTTTCGGCAGCCTCTCCAGGCCAGCTCCT
CCTGCCTCCCAGTGGCCTCTTTCGGCCCAGCCCAGCTCATGCCTCCCGCGGCCTTCCCAAGCCCCGCTTTTGAC
TTTCGGTGGCCTCTGCAGGCCTCGACAAGGCCAGCCTCCTGCCTCCCGAAGGCCTGCACAGGCCAGCCTCTGC
CTCACAGCGGACTCTC

2616/6881
FIGURE 2407A

AGCCCAAACCGCGGCCCTAGCCCCGGCCGCACCCCCAGCCCGGCCAGCATGATGAACAACAGCGGCTACTCAGA
CGCCGGCCTCGGCCTGGGCGATGAGACAGACGAGATGCCGTCCACGGAGAAGGACCTGGCGGAGGACGCGCCGTG
GAAGAAGATCCAGCAGAACACATTCACGCGCTGGTGAATGAGCACCTCAAGTGCGTGGGCAAGCGCCTGACCGA
CCTGCAGCGCGACCTCAGCGACGGGCTCCGGCTCATCGCGCTGCTCGAGGTGCTCAGCCAGAAGCGCATGTACCG
CAAGTTCATCCGCGCCCCAACTTCCGCCAAATGAAGCTGGAGAACGTGTCCGTGGCCCTCGAGTTCCTCGAGCG
CGAGCACATCAAGCTCGTGTCCATAGACAGCAAGGCCATCGTGGATGGGAACCTGAAGCTGATCCTGGGCCTGAT
CTGGACGCTGATCCTGCACTACTCCATCTCCATGCCCATGTGGGAGGATGAAGATGATGAGGATGCCCCGAAACA
GACGCCCAAGCAGCGGCTGCTTGGCTGGATCCAGAACAAGGTGCCCCAGCTGCCCATCACCAACTTCAACCGTGA
CTGGCAGGACGGCAAAGCTCTGGGCGCCCTGGTGGACAACCTGCGCCCCCGTCTCTGCCCCGACTGGGAGGCCTG
GGACCCCAACCAGCCCCGTGGAGAACGCCCGGGAGGCCATGCAGCAGGCCGACGACTGGCTTGGGGTGCCCCAGGT
CATTGCCCTGAGGAGATTGTGGACCCCAACGTGGATGAGCATTCTGTTATGACCTACCTGTCCAGTTCCCCAA
GGCCAAGCTCAAACCTGGTGGCCCTGTTTCATCCAAGCAGCTGAACCCCAAGAAAGCCATCGCCTATGGGCCTGG
CATCGAGCCACAGGGCAACACCGTGCTGCAGCCTGCCACTTCACCGTGACAGCGGTGGACGCGGGCGTGGGCGA
GGTGCTGGTCTACATCGAGGACCCTGAAGGCCACACCGAGGAGGCTAAGGTGGTTCCCAACAATGACAAGGATCG
CACCTATGCTGTCTCTATGTGCCCAAGGTGCTGGGTACACAAGGTGACCGTGCTCTTTGCTGGCCAGAACAT
TGAACGCAGTCCCTTTGAGGTGAACGTGGGCATGGCCCTGGGAGATGCCAACAAGGTGTCAGCCCGTGGCCCTGG
CCTGGAACCTGTGGGCAATGTGGCCAACAACCCACCTACTTTGACATCTACACTGCGGGGGCCGGCACTGGCGA
TGTGCTGTGGTGATCGTGGACCCACAGGGCCGGCGGGACACAGTGAGGTGGCCCTGGAGGACAAGGGTGACAG
CACGTTCCGCTGCACATACAGACCTGCCATGGAGGGGCCACATAACCGTGATGTGGCCTTTGCGGGTGCCCCAT
CACCCGAGTCCCTTCCCTGTCCATGTGTGCGAAGCCTGTAAACCCCAACGCCTGCCGCGCCTCTGGGCGAGGCCT
GCAGCCCAAGGGTGTTTCGCGTGAAAGAGGTGGCTGACTTCAAGGTGTTTACCAAGGGTGCCGGCAGCGGGGAGCT
CAAGGTACGGTCAAGGGGCCAAAGGGCACAGAGGAGCCAGTGAAGGTGCGGGAGGCTGGGGATGGTGTGTTGCA
GTGCGAGTACTACCCGGTGGTGCCCTGGGAAGTATGTGGTGACCATCACGTGGGGCGGCTACGCCATCCCTCGCAG
CCCCTTTGAGGTACAGGTGAGCCAGAGGCAGGAGTGCAAAAGGTCCGGGCCCTGGGGTCTGGTTTGGAGACTGG
CCAGGTGGGCAAGTCAGCCGATTTTGTGGTGGAAGCCATTGGCACCGAGGTGGGGACACTGGGCTTCTCCATCGA
GGGGCCCTCACAAGCCAAGATCGAATGTGACGACAAGGGGGATGGCTCCTGCGATGTGCGGTACTGGCCACGGA
GCCTGGGGAGTACGCTGTGCACGTCTCTGTGACGATGAGGACATCCGAGACTCACCCCTTATTGCCACATCCT
GCCCGCCCCACCTGACTGCTTCCCAGATAAGGTGAAGGCCTTTGGGCCTGGCCTGGAGCCTACCGGCTGCATCGT
GGACAAGCCCGCTGAGTTACCATTTGATGCTCGTGACGTGGCAAGGGAGACCTGAAGCTCTATGCCCAGGACGC
CGACGGCTGTCCATCGACATCAAGGTGATCCCCAACGGCGACGGCACCTTCCGCTGCTCCTACGTGCCACCAA
GCCATTAAGCACACCATCATCATCTCCTGGGGAGGCGTAAACGTGCCCAAGAGCCCCCTTCCGGGTGAACGTGGG
CGAGGGCAGCCACCCCGAGCGGTAAAGGTGTACGGCCCCGAGTGAGAGAACAGGCCTCAAGGCCAATGAGCC
CACCTACTTCACGGTGGACTGCAGCGAGGCGGGGCAAGGCGACGTGAGCATCGGCATCAAGTGCGCCCCAGGCGT
GGTGGGCCCTGCAGAGGCTGACATTGACTTCGACATCATCAAGAATGACAACGACACCTTCACCGTCAAGTACAC
GCCACCAGGGGCGGGCCGCTACACCATCATGGTGCTGTTTGCCAACCAGGAGATCCCCGCCAGCCCCCTTCCACAT
CAAGGTGGACCCATCCACGATGCCAGCAAAGTCAAGGCCGAGGGCCCTGGGCTGAATCGCACAGGTGTGGAAGT
CGGGAAGCCCACCCACTTCACGGTGCTGACCAAGGGAGCCGGCAAGGCCAAGCTGGATGTGCAGTTTGCAGGGAC
AGCCAAGGGCGAGGTTGTGCGGGACTTTGAGATCATAGACAACCATGACTACTCCTACACTGTCAAGTACACCGC
TGTCAGCAGGGCAACATGGCAGTGACAGTGACTTATGGCGGGGACCCTGTCCCCAAGAGCCCCCTTTGTGGTGAA
TGTGGCACCCCGCTGGACCTCAGCAAAATCAAAGTTCAGGGCCTTAATAGCAAGGTGGCTGTGGGACAGGAACA
AGCATTTCTGTGAACACACGAGGGGCTGGCGGTGAGGGCCAACTGGATGTGCGGATGACTTCGCCCTCTCGCCG
GCCATCCCCCTGCAAGCTGGAGCCAGGCGGTGGAGCGGAAGCCAGGCTGTGCGCTACATGCCCCCGGAGGAGGG
GCCCTACAAGGTGGATATCACCTACGATGGTACCCGGTGCTGGCAGCCCCGTTGCTGTGGAGGGTGTCTGCGC
CCCTGATCCCTCCAAGGTCTGTGCTTATGGCCCGGGTCTCAAGGGTGGACTGGTAGGCACCCCGCGCCATTCTC
CATCGACACCAAGGGGGCTGGCACAGGTGGCCTGGGGCTGACCGTAGAGGGCCCCCTGCGAGGCCAAGATCGAGTG
CCAGGACAATGGTGATGGCTCATGTGCTGTGAGCTACCTGCCCACGGAGCCTGGCGAGTACACCATCAACATCCT
GTTTGTGAGGGCCACATCCCTGGCTCGCCCTTCAAAGCCACCATTCGGCCTGTGTTTGACCCGAGCAAGGTGCG
GGCAGTGAGCCGGGCCTGGAGCGCGCAAGGTGCGGTGAGGCAGCCACCTTCACTGTGGACTGCTCAGAGGCAGG

2617/6881
FIGURE 2407B

CGAGGCGGAGCTGACCATTGAGATCCTGTICGGATGCCGGGGTCAAGGCCGAGGTGCTGATCCACAACAACGCGGA
TGGCACCTACCACATCACCTACAGCCCTGCCTTCCCTGGCACCTACACCATTACCATCAAGTATGGCGGGCATCC
CGTGCCCAAATTCCCCACCCGTGTCCATGTGCAGCCTGCGGTGCGATACCAGTGGCGTCAAGGTCTCAGGGCCTGG
TGTTGAGCCACACGGTGTCTGTGCTCAACCCCTCGGGGGCCAAGACAGACACCTATGTGACAGACAATGGGGA
CGGCAACCACGTGACGGCTCGTGTGCTCAACCCCTCGGGGGCCAAGACAGACACCTATGTGACAGACAATGGGGA
CGGCACCTACCGAGTGCAGTACACCGCCTACGAGGAGGGCGTGCATCTGGTGGAGGTCCTGTATGATGAGGTGCG
TGTGCCCAAGAGCCCTTCCGAGTGGGCGTGACCGAGGGCTGTGATCCCACCCGCGTCCGAGCCTTCGGGGCCAGG
CCTGGAGGGTGGCTTGGTCAACAAGGCCAACCATTACTGTGGAGACCAGGGGAGCGGGCACCGGGGGCCTTGG
CCTAGCCATCGAGGGTCCCTCGGAAGCCAAGATGTCTTGCAAGGACAACAAGGATGGTAGCTGCACCGTGGAGTA
CATCCCCTTCACTCCTGGAGACTATGACGTCAACATCACCTTCGGGGGGCGGCCATCCCAGGGAGCCCGTTCCG
CGTGCCAGTGAAGGATGTGGTGGACCCTGGGAAGGTGAAGTGCTCAGGGCCAGGGCTGGGGGCTGGTGTGAGGGC
CCGGGTTCCCTCAGACCTTCACAGTGGATTGCAGTCAAGCTGGCCGGGCGCCCTGCAGGTGGCTGTGCTGGGCCC
CACAGGTGTGGCCGAGCCTGTGGAGGTGCGGGACAATGGAGATGGCACCCACACTGTCCACTACACCCAGCCAC
TGACGGGCCCTACACGGTAGCCGTCAAGTATGCTGACCAGGAGGTGCCACGCAGCCCTTCAAGATCAAGGTCTCT
CCCAGCTCATGATGCCAGCAAGGTGCGGGCCAGCGGCCAGGCCTCAACGCCTCTGGCATCCCTGCCAGCCTGCC
TGTGGAGTTACCATCGACGCACGGGACGCGGGCGAGGGGTTGCTCACTGTCCAGATCTTGGACCCGAGGGTAA
GCCAAGAAGGCCAACATCCGGGACAATGGGGATGGCACGTACACTGTGTCTTACCTGCCGGACATGAGTGGCCG
GTACACCATCACCATCAAGTATGGCGGTGATGAGATCCCCTACTCGCCCTTCCGCATCCATGCTCTGCCCACTGG
GGATGCCAGCAAGTGCCTCGTCACAGTGTCCATTGGAGGCCATGGCCTGGGTGCCTGCCTGGGGCCCTCGAATCCA
GATTGGGCAGGAGACGGTGTACCGTGGATGCCAAGGCAGCCGGTGAGGGGAAGGTGACATGCACGGTGTCCAC
GCCGGATGGGGCAGAGCTCGATGTGGATGTGGTTGAGAACCATGACGGTACCTTTGACATCTACTACACAGCGCC
CGAGCCGGGCAAGTACGTATCACCATCCGCTTCGGGGGTGAGCACATCCCCAACAGCCCTTCCACGTGCTGGC
GTGTGACCCCTGCGGCACGAGGAGGAGCCCTCTGAAGTGCCACAGCTGCGCCAGCCCTACGCTCTCCCCGGCC
CGGCGCCCCGCCACACACTGGGCCACAGAGGAGCCAGTGGTGCCTGTGGAGCCAATGGAGTCCATGCTGAGGCC
CTTCAACCTGGTCATCCCCTTCGCGGTGCAGAAAGGGGAGCTCACAGGAGAGGTGCGGATGCCCTCGGGGAAGAC
GGCACGGCCCAACATCACCGACAACAAGGACGGCACCATCACGGTGAGGTATGCACCCACTGAGAAAGGCCTGCA
CCAGATGGGGATCAAGTATGACGGCAACCACATCCCTGGGAGCCCTTACAGTTCTATGTGGATGCCATCAACAG
CCGCCATGTGAGTGCTATGGGCCAGGCCTGAGCCATGGCATGGTCAACAAGCCAGCCACCTTCACTATTGTAC
CAAAGATGCTGGAGAAGGGGGTCTGTCACTGGCCGTGGAGGGCCCATCCAAGGCAGAGATCACTGTAAAGGACAA
CAAGGATGGCACCTGCACCGTGTCTTATCTGCCGACTGCGCCTGGAGACTACAGCATCATCGTGCCTTCGATGA
CAAGCACATCCCGGGGAGCCCTTACAGCCAAGATCACAGGTGATGACTCCATGAGGACCTCACAGCTGAATGT
GGGCACCTCCACGGACGTGTCACTGAAGATCACCGAGAGTGATCTGAGCCAGCTGACCGCCAGCATCCGTGCCCC
CTCGGGCAACGAGGAGCCCTGCCTGTGAAGCGCTGCCAACCAGGCACATTGGGATCTCCTTACCCCCAAGGA
GGTCGGGGAGCAGTGGTGAGCGTGCGCAAGAGTGGCAAGCATGTACCAACAGCCCTTCAAGATCCTGGTGGG
GCCATCTGAGATCGGGGACGCCAGCAAGGTGCGGGTCTGGGGCAAGGGGCTTCCGAGGGACACACATTCCAGGT
GGCAGAGTTTATCGTGACACTCGCAATGCAGGTTATGGGGGCTTGGGGCTGAGTATTGAAGGCCCAAGCAAGGT
GGACATCAACTGTGAGGACATGGAGGACGGGACATGCAAAGTCACTACTGCCCCACCGAGCCCGGCACCTACAT
CATCAACATCAAGTTTGTGACAAGCACGTGCCTGGAAGCCCTTCACTGTGAAGGTGACCGGCGAGGGCCGCAT
GAAGGAGAGCATCACCCGGCGGAGACAGGCACCTTCCATCGCCACCATCGGCAGCACCTGTGACCTCAACCTCAA
GATCCCAGGAACTGGTTCCAGATGGTGTCTGCCAGGAGCGCCTGACACGCACCTTACACGCAGCAGCCACAC
CTACACCCGCACGGAGCGCACGGAGATCAGCAAGACGCGGGGCGGGGAGACAAAGCGCGAGGTGCGGGTGGAGGA
GTCCACCCAGGTGCGCGGGGACCCCTTCCCTGCTGTGTTTGGGGACTTCTGGGCCGGGAGCGCCTGGGATCCTT
CGGCAGCATCACCCGGCAGCAGGAGGGTGAGGCCAGCTCTCAGGACATGACTGCACAGGTGACCAGCCCATCGGG
CAAGGTGGAAGCCGAGAGATCGTCGAGGGCGAGGACAGCGCCTACAGCGTGCCTTTGTGCCCCAGGAAATGGG
GCCCCATACGGTCGCTGTCAAGTACCGTGGCCAGCACGTGCCCGGCAGCCCTTTCAGTTCACTGTGGGGCCGCT
GGGTGAAGGTGGTGGCCACAAGGTGCGGGCCGGAGGCACAGGGCTGGAGCGAGGTGTGGCCGGCGTGCCAGCCGA
GTTTACGATCTGGACCCGGGAGGCTGGCGCTGGGGGCTGTCCATTGCTGTGGAGGGTCTTAGCAAAGCGGAGAT
TGCATTTGAGGATCGCAAAGATGGCTCCTGCGGCGTCTCCTATGTGCTCCAGGAACCAGGTGACTATGAGGTCTC

2618/6881
FIGURE 2407C

CATCAAGTTCAATGATGAGCACATCCCAGACAGCCCCCTTTGTGGTGCCTGTGGCCTCCCTCTCGGATGACGCTCG
CCGTCTCACTGTCACCAGCCTCCAGGAGACGGGGCTCAAGGTGAACCAGCCAGCGTCCTTTGCCGTGCAGCTGAA
CGGTGCCCCGGGGCGTGATTGATGCCCCGGGTGCACACACCCTCGGGGGCTGTGGAGGAGTGCTACGTCTCTGAGCT
GGACAGTGACAAGCACACCATCCGCTTCATCCCCACGAGAATGGCGTCCACTCCATCGATGTCAAGTTCAACGG
TGCCACATCCCTGGAAGTCCCTTCAAGATCCGCGTTGGGGAGCAGAGCCAGGCTGGGGACCCAGGCTTGGTGTCTC
AGCCTACGGTCCCTGGGCTCGAGGGAGGCACTACCGGTGTGTCTATCAGAGTTCATCGTGAACACCCTGAATGCCGG
CTCGGGGGCCTTGTCTGTCTACCATGATGGCCCCCTCCAAGGTGCAGCTGGACTGTCTGGGAGTGTCTTGAGGGCCA
TGTGGTCACTTATACTCCCATGGCCCCCTGGCAACTACCTCATTGCCATCAAGTACGGTGGCCCCCAGCACATCGT
GGGCAGCCCCCTTCAAGGCCAAGGTCACTGGTCCGAGGCTGTCCGGAGGCCACAGCCTTCACGAAACATCCACGGT
TCTGGTGGAGACTGTGACCAAGTCTCCTCAAGCCGGGGCTCCAGCTACAGCTCCATCCCCAAGTTCTCCTCAGA
TGCCAGCAAAGGTGGTGACTCGGGGCCCTGGGCTGTCCAGGCCCTTCGTGGGCCAGAAGAACTCCTTCACCGTGGA
CTGCAGCAAAGCAGGCACCAACATGATGATGGTGGGCGTGCACGGCCCCAAGACCCCTGTGAGGAGGTGTACGT
GAAGCACATGGGGAACCGGGTGTACAATGTCACCTACACTGTCAAGGAGAAAGGGGACTACATCCTCATTGTCAA
GTGGGGTGACGAAAGTGTCCCTGGAAGCCCCTTCAAAGTCAAGGTCCCTTGAATCCCAAAGTGCTCCCCAGCC
TCAGCCCCCACCTCCAGCCACACACACATTACACACACACACACACACACAAATGTGCCACACCCAGACACGC
ACAGAATCAGACACTACAAACACCTGCCTTGGGGGTGAAGTGAAGGCCCAGCCTCCCCACCCACCGCGCCCCAG
GGGTGGAGGACCTTGTCTGTGTCTCAGGACAGTGTCCCTCCCTGGGAATGTGACATGAGGGCCGACTGGGGCCAGG
CTCAGGGGCAGAGGCTGGGACACAAGGGGCTGGCGAGGGCTGCGAGGCCAGGGAAGCCCTGAGTTTCTGGCGGGG
CTGAGCAGTGGGGGAGCATTGTGTTGTGGGTGTCTGTGTGTGAGGTCACCCTCAAAGTGCACCGCCGGCCAGATA
CCCTCCTGACCCCGAGGACTTGGTCTGGTCTCTCTGGTGGCTACAACCCAGAGTTTTTAAGGACTTGGAAGGAA
AGCACAATCAGAGAAGAAAACAGCCCCGAACCAGCAGGAGTGGCCTGGCACATGGACCGGCCTGAGCGATGTGC
ACTCCACCCAAGCCAGGCTCCAGGGGGCCTGATTTCTCTCTCACTGTCTCTTTTTTTAAATGGTTGCACGGCT
CTGCCCCATGGGGGGCCTTTTTTACACACTGCGAGGCCAGCTTTCTAGGGGACTTTTGCACATGTCATGCAGCT
CAGCTGGGAGCTGCTTAGGTGGAAAAC TCAAATAAAGTGC GGCTGTCTCG

2619/6881
FIGURE 2408

MAPGNYLIAIKYGGPQHIVGSPFKAKVTGPRLSGGHS LHETSTVLVETVTKSSSSRGSSYNSIPKFSSDASKVVT
RGPGLSQAFVGQKNSFTVDCSKAGTNMMMVGVHGPKTPCEEVYVKHMGNRVYNVTYTVKEGTTSLSSSGVTKVS
LEAPSKSRSLSESQKCLPSLSPHLQPNTHYIHTHTHTNVPHPDHTQNQTLQTPALGVK

2620/6881
FIGURE 2409A

GGAGGCGGGGCGGACCAAGAGCAGGAGCTGGAGTCTGAGCCGGTGGTTGCAGCGGAGGCGGTG**ATGT**CGGTGCAG
GTTGTGTACCCGCGGCTGCCGCCAAGGTGCCTGAGGTGGAGCTGAAGGACCTGAGCCCCCTCCGAGGCGGAGTCCG
CAACTAGGACTGAGCACGGCCGCCGTGGGCGCCATGGCCCCCGGCGGGCGGTGGAGACCCTGAGGCTCCAGCT
CCCGCCGCGGAGCGGCCCCCGGTCCCCGGCCCGGGCTCGGGGCCCCGCCGCCGCTCTCAGCCCCGCCCGGGGAAG
GTGCCTCAGGCGTCGGCCATGAAGCGGAGCGACCCACATCACCAGCACCAGCGGCACCGCGACGGCGGCGAGGCC
CTGGTCAGCCCCGACGGCACCGTCACCGAGGCGCCGCGCACAGTCAAGAAGCAGATCCAGTTTGCTGACCAGAAG
CAAGAATTCAACAAACGTCCCACCAAAATTGGACGTCGCTCTTTGTCTCGTTCCATTTCTCAGTCATCTACTGAC
AGCTACAGCTCAGCGGCTTCATATACAGATAGCTCTGATGATGAGACATCGCCCAGGGACAAGCAGCAAAAAGAAC
TCTAAGGGAAGCAGTGACTTCTGTGTTAAGAACATCAAACAGGCAGAGTTTGGACGAAGAGAAATTGAAATTGCT
GAACAAGAAATGCCTGCATTGATGGCTTTGAGGAAGAGAGCTCAAGGAGAAAAGCCTTTGGCTGGAGCCAAAATC
GTGGGTTGCACACACATCACTGCTCAGACTGCTGTGCTTATGGAACCTCTGGGTGCTCTGGGGGCCCCAGTGCCGA
TGGGCTGCCTGCAACATCTATTCCACTCTCAATGAAGTGGCTGCTGCTCTAGCAGAAAGTGGATTTCTGTTTTT
GCCTGGAAGGGAGAGTCAGAAGATGACTTTTGGTGGTGTATCGATAGATGTGTGAATGTGGAGGGCTGGCAGCCA
AACATGATCTTGGATGATGGAGGGGATCTTACCCACTGGATTTATAAAAAGTATCCCAACATGTTTAAGAAAATC
AAGGGCATAGTAGAGGAGAGTGTTACTGGAGTTTACAGGCTGTACCAACTGTCCAAAGCTGGGAAGCTGTGTGTT
CCAGCCATGAATGTCAATGACTCAGTCACCAACAGAAATTTGACAACCTCTACTGTTGCCGTGAATCAATTCTT
GATGGACTTAAAAGGACAACAGACATGATGTTTGGTGGAAAGCAAGTGGTAGTCTGTGGCTATGGAGAGGTGGGG
AAAGGTGCTGTGCTGCCCTGAAAGCCATGGGCTCCATTGTGTATGTAAGTGAATTTGACCCCATCTGTGCCCTG
CAAGCCTGTATGGATGGATTTGACTGGTGAATTAATGAGGTATCCGACAAGTGGACATTGTTATTACCTGT
ACAGGTAACAAGAATGTGGTAACCAGAGAGCACTTGGACCGTATGAAGAATAGCTGCATCGTTTGTAAACATGGGA
CATTCCAACACAGAGATTGACGTGGCGAGTCTGCGGACACCAGAAGTACCTGGGAGCGAGTGAGATCTCAAGTT
GACCATGTGATATGGCCTGATGGCAAGAGGATAGTACTGCTGGCAGAGGGCCGCCCTGCTGAACCTTAGCTGCTCC
ACAGTGCCTACATTTGTGCTCTCAATCACTGCTACTACTCAGGCTCTTGCCCTTGATAGAGCTTTACAATGCTCCT
GAGGGTCGCTATAAGCAGGATGTCTACCTGTTGCCCAAGAAGATGGATGAGTATGTGGCCAGCCTACACCTGCCT
ACCTTTGATGCCCACTTGACAGAGCTGACAGATGAACAGGCCAAGTATCTGGGACTCAACAAGAATGGGCCCTTC
AAGCCTAATTACTACAGGTAT**TAA**GTTCCTGTAAGTCAAAACCAGAATTTTAAAGGAATAGAAGTCAAGCCTTTT
CTCCACTACTATAACAAGAAAGAATTCAGCAAGCTGCTTCTCCAATCAAAGCTGCCTGCCGTGCTCACCCCTGTGTG
TTAGGTTATTTATTTATTTAAATCAAGAATCCTGTGCCTGTAGTGTGGCCAGAGTGTGGTTACTGCCCTGAGG
GCCATGAAAGCCACAGAGGATGGGCTGAGGAAGGAAAGAAATGGGGTTACTGCTCCAGTGCATCATTTGCATCA
TTCCCCATTGACTGAATCCTCAGCAGTGGCCGTTTTTCTCTTGTCCAGGCTCACGAGTTAGTCCAGGGATTCCA
TACTCCCTATTCCCTGGAGTTTTCTGGAATAAATTTTACGACCTGCTTTTCTCAGCTTGGCCCTTCCCCGGGTG
AGGCCGTTTGAATTAACATGGCCAGTGTTCACACAAGATTGGGTTCCCAATCTTGACCATCACTATCACTGCC
TTCTTTATATAAAGGCTAATAAGGAAGGAGTGTATTTATGGCTTTGCCAAGCTACATCAAGAAGTCAAGTGTGC
TGTGCCATACCAGGGGTCTCCTTTCTTACCCAGGACTCCTTTCTCTCCTTGAATATTTATGTCCATTTTAACACT
TCCTGGTTGCAAGAGGGATGTGCCCTCATTATTTCTCCACAGTTTTGGTATTTGTGACACATTTGTTCTGCTGT
CTTTCTAATCCAGCCAACGTCTGCTCAGGAAGTGGGGCCAGCTCCACTGGGACCCATAGTTTTACTTCCTTGTC
TTTGATTGGATAGTTTCCAAGGAAGCCCCCTCAGATTGGCACTATCTCAGAAAAGGAGAGCTTGTGTGAAACAC
TGCTTCCTGAAACTTCCTGCTATTGCCTAAAGCTACGTCTGAAACTGAGTAGGGAAGGCATACTTTTCCAGGGA
CTTAGGGGGATAGGCTTTGGAATGGGACAGGCTTTTCAGACTCACAGCTTGATACCCTAACAAAGCAGAGTATA
TTTATTTGTTTCCCAGGAAGGCCATTGCAGTTTGACTGGCTGAGGGATACAGAGATGAAATTGTAAACTGTATCC
AGATTATCAAAGCTAATTTGACTAGTTTGAACCTCGTCAGACATTCATTCTTTGGCCATTGCCATGGATGAAAC
CGAGATCTGCAGTCTGATCTGTGGACTTCTCTGCTGGCATATCTTTATGATTAACTCTTCCATTTGATGATT
CTGTATTTCAGAGTCAGTTTCTTGAGTAACTCCAGTGCTACAAAAAGAAATAGTAATGTGGTGTGGGCAGCGTGA
CATTTTATGTCCACCCAAAAATGGATTCTTTTGGAGACTGATCTGTTGGTCTCAGGCATTTTCATTAGGACCA
GATTGGTTCTAAGAGTTAGTCTGGACTGGCCCTAGGAAACTTGAATTAATAAGCCTCTTCCCTTACCGATCCT
TTTTAACACTCTCAGGTTTGTGTTTCCCACTTTTTTCTATGCTGGTCTGCCTCAAAGTCTCAAGACCAAGGT
GACTCAAGATAACACCAGACCACGCATGATCACCAAAACCTTCCCATCCTGATTCTCTTCTTCTACCTCTACCTT
CTCCAACCTCTCCTGGTCTTACATATACTCTCAAAGCTAGTCTGAAAGTGACCTTACTTTCCGAAGTAGGGAAG

2621/6881
FIGURE 2409B

TGGAAC TTTGGTAAATGACTGTTTGCCTCATTTAATAGTATACAGGCTCAGCCCATAGACTACAGTTCTTCAGAG
GCCATATGTCTCAGCAAGTACTGGTTATATTCTTTTTTTGTAAAGGAAGATCATAAATGCTAAAAATTCCACTAAG
CCATT CAGTTCTTCCTTTTGCCTACCTAGTCCTGATTTTTGTATTAATTGGTTCCCTTTAGCAAGGGATT CAGAT
CTTTGTACCTTATCTTATATCCAGAGCAGATTCCATTTGGCAGATAGATGGTCTCTAGCCTATTGTATTCTTAGA
CCAAAAATCATAACCTGCTGTTTCTCAGCAAAGCCTTGCTCTCTGGAGCTTACTATGTGCTGGTACTTAAAGAGT
ACATTCTGCCTTGCTGTAAGAGACCCACTCCAAATAAAAAAGGGGCCACACGGGGCTTCTAAGTTAGGTTG
CCAGTGTTGCTGCCCATGATGAGTTATTTGCCTCTGAGTTTCAGATGACCTCTCTGTAGGGACACTGTGTTATCA
ACCATTAAGAAGAAAGAACCAAGCCTCCCAAGTATTTGGGTTCTATCTTAGGGTTGAAATCTGGTCATTATTC
CCTCTACCCTTGGAATCAGAGCAATGTGTCTTCTTTCCCTCCAACCTCTTACCTTAGATGCATCCTGGTTATCTGG
AAGCATGGGAAAGAAGGCTACTTATCTCTTTGTATGTGGCTCCAGTCTGTGAGGATACATAACATTTTCTCTACA
ATGAATCTGTGCTAATATTTTGCCTTCTTTCTTTCTTTTCTTTTACCCTTAGAGACAGGGTTTCACTATGTTGC
CCAGGCTGGTCTCAAACCTCCTGGGCTCAAGCAATCCTCCTGCCTCAGCTTCCTGAGTAGCTGGAACCACAGGTGT
GTGCTACCGTGCCTGGCACTTTTTTGCCTTCTTAATGGAGATATTCAGTTTTCTTTTTTTTCATTTAAACAAAGAA
AAAAAATGTATCTACTCTACCTTCCCTCTGCTCTCCTCCCTCCCTATCCTACTTGCCCATATGAGCACGGCTCCC
CATGGCCACATACTCCTGCAAAGCTTTTATGCTGCTTCGCTTTTCTCTAAACAGATCTGATATTGCTGCTCCTGT
GGTTTTCTCAAAATTAAC TTTGCCGTGGTTTTTAAAAAGGAATCAAAATGCATTGTTGCATTAAGCTTTTTCAAT
AAAGGAAAATTACGGAAGGAAAATAGGCAACACCAGCAAATTATATGTGGACAGGTTCTAAACTCTATATATACA
TATATATATATATATCTATATATCTATATACGTAATCATCTAGTTCTGTCATCTTACTGAAAGGAATAACACTTC
TAAAGATCACCATTTCTGAGAAGTTCTTGGAATCTTTATGTCTAAGTGATTGTATTAGATCAGCAATAATGACT
ATGTAATCTCAAAAAACAAATAAAATATTCTTAACATGG

2622/6881
FIGURE 2410

MSVQVVSAAAAAKVPEVELKDLSPSEAESQLGLSTAAVGAMAPPAGGGDPEAPAPAAERPPVPGPGSGPAAALSP
AAGKVPQASAMKRSDPHHQHRHRDGGEALVSPDGTVEAPRTVKKQIQFADQKQEFNKRPTKIGRRSLRSISQ
SSTDYSSAASYTDSSDDETSRDKQQKNSKGSSDFCVKNIKQAEFGRRREIEIAEQEMPALMALRKRAQGEKPLA
GAKIVGCTHITAQTAVLMETLGALGAQCRWAACNIYSTLNEVAAALAESGFPVFAWKGESEDDFWWCIDRCVNVE
GWQPNMILDDGGDLTHWIYKKYPNMFKKIKGIVEESVTGVHRLYQLSKAGKLCVPAMNVNDSVTKQKFDNLYCCR
ESILDGLKRTTDMMFGGKQVVVCGYGEVGKGCCAALKAMGSIVYVTEIDPICALQACMDGFRLVKLNEVIRQVDI
VITCTGNKNVVTREHLDRMKNSCIVCNMGHSNTEIDVASLRTPELTWERVRSQVDHVIWPDGKRIVLLAEGRLLN
LSCSTVPTFVLSITATTQALALIELYNAPEGRYKQDVYLLPKKMDEYVASLHLPTFDAHLTELTDQAKYLGLNK
NGPFKPNYYRY

2623/6881
FIGURE 2411

AGTTCCTGGTCCAGAACTTTACACAGAAAAGGTGCTCAAAGGATATTTGTTTAAATGAATGTGGTATGCTGACATT
TAAACAGGACAAAACCTTGTAGAACTTCATGGAGGAACACGGAGTGACCCAAACCGAACATATGGCTACCATAGAA
GCACATGCAGTGGCCCAGCAAGTGCAGCAGGTCCATGTGGCTACTTACACCGAGCATAGTATGCTGAGTGTCTGAT
GAAGACTCGCCTTCTTCTCCCGAGGACACCTCTTACGATGACTCAGATATACTCAACTCCACAGCAGCTGATGAG
GTGACAGCTCATCTGGCAGCTGCAGGTCTGTGGGAATGGCCGCTGCTGCTGCTGTGGCAACAGGAAAGAAACGG
AAACGGCCTCATGTATTTGAGTCTAATCCATCTATCCGGAAGAGGCAACAAACACGTTTGCTTCGGAAACTTCGA
GCCACGTTAGATGAATATACTACTCGTGTGGGACAGCAAGCTATTGTCTCTGTATCTCACCTCCAAACCTAAC
CCTGTCTTTAAAGTGTTTGGTGCAGCACCTTTGGAGAATGTGGTGCCTAAGTACAAGAGCATGATCCTGGAAGAC
CTGGAGTCTGCTCTGGCAGAACACGCCCCCTGCGCCACAGGAGGTTAACTCAGAAGTCCCGCCTCTCACCATCGAC
GGAATTCAGTCTCTGTGGACAAAATGACCCAGGCCCAGCTTCGGGCATTTATCCCAGAGATGCTCAAGTACTCT
ACAGGTTCGGGGAAAACAGGCTGGGGGAAAGAAAGCTGCAAGCCCATCTGGTGGCCTGAAGATATCCCCTGGGCA
AATGTCCGGAGTGATGTCCGCACAGAAGAGCAAAAGCAGAGGGTTTCATGGACCCAGGCACTACGGACCATAGTT
AAAAACTGTTATAAACAGCATGGGCGGGAAGACCTTTTGTATGCCTTTGAAGATCAGCAAACGCAAACACAGGCC
ACAGCCACACATAGTATAGCTCATCTTGTACCATCACAGACTGTAGTCCAGACTTTTAGTAACCTGATGGCACT
GTCTCACTTATCCAGGTTGGTACGGGGCAACAGTAGCCACATTGGCTGATGCTTCAGAATTGCCAACCACGGTC
ACCGTTGCCCAAGTGAATTATCTGCCGTGGCTGATGGAGAGGTGGAACAAAATTGGGCCACGTTACAGGGAGGT
GAGATGACCATCCAGACGACGCAAGCATCAGAGGCCACCCAGGCGGTGGCATCGTTGGCAGAGGCCGCACTGGCA
GCTTCTCAGGAGATGCAGCAGGGAGCTACAGTCACTATGGCGCTTAACAGCGAAGCTGCCGCCCATGCTGTGCGC
ACCCTGGCTGAGGCCACCTTACAAGGTGGGGGACAGATCGTCTTGTCTGGGGAAACCGCAGCAGCCGTCGGAGCA
CTTACTGGAGTCCAAGATGCTAATGGCCTCTTTATGGCAGATCGTGCAGGTCGCAAGTGGATCCTGACTGACAAA
GCCACAGGCCTGGTCCAGATCCCTGTGAGCATGTACCAGACTGTGGTGACCAGCCTCGCCAGGGCAACGGACCA
GTGCAGGTGGCCATGGCCCCCTGTGACCACCAGGATATCAGACAGCGCAGTCACCATGGACGGCCAAGCTGTGGAG
GTGGTGACATTGGAACAGTGACATACAGCCATATTATGGCATCGTTTTCTAGTCTACTTCAAATTTTTTACACG
TTTGAGAGGTGCAATCAAATGGAATTAAGTCTCTCGACTTTGGAAGGAAAGTTTTGTTAACCTTTTTTTTTTTA
AAAGGAAGAAAGCGGATTTTGGAAATGCATTTTTTAAAGCACCCTCTTGATTTTCTGGGATTGGTGAAGAACT
GCATTGTCAATTTCACTGTCCCAAAAAGCCAAATTGTGGCAGGACTTCTTCTGCGGAAATGTGTGTGTATACT
TATGTGTGTGTATGTGTGAGTGTGAATATATGTATATGTGTACATATGGACATACACATTTACATATATATAAG
TATATATATACATATATATATATATATATATGTATGAAACCCGCATGGAATTATCTGTATGAAATCAAGGTGCGCTG
TGGAACAATAATTCACCCAGTTTAGTGGGTGGTAGGGTACGTGGCCAGACACAGTCACCCAGTTTTTGTTCATA
CCAGGGTCATGCGTTGAGCTACTGACAACTCAGGCGGAGGTGACCATGCCCTTCACCAAAGCTGCCTCCAGTG
GCCACACAGAATCTCCCTGCTGGACTCACCTGAGGAAAGAGGCTCCAGCATGGGGTGGGTGAGAGATGTGCTTG
CAAGGTCCAGGGACTGCGTGGTCTGCCAGCTGAGATGCTCCTCGGGCTGGCCCAGGTGCTGACCTTGCCACAGGC
AGATGAATGTCTTGAAAGCTCCCGGGCCTCAGCCTCCCATCTCCTCTCCTTCCCAGGAATCCTTGATCTCATGAC
TATTAATAATGTTGCTCTGGTTTTAAGGTCACTCCTGAATTGCTCGTATATATGAAGTGAAGGTAAACGAAGTATT
AGGGGTTTGAGGAGTGCCTGCGTGAAGTGTGCTTGTGTGTGTGCGTGCATGGTGGGGAGAGGATGGGAAGGGG
GCGGGGGCAGTGGAAGGGAAAGGAAGGAAAGAAAATCGTCCTAGACCAGGATACACCCGTGGGAGCAATTTTCT
CTACTGTCTGTAGCTTCACAGAGGAGGCGCTGGAATGAACAAGAAGAGACATCTGGTCTGTGGCCACAGCACCTT
GAACGCCCTGATCTTGTGTGATCTTGAAGCTAAGCTTGGTTGGGCCCGGTGAGTACGCGGAAGGGAAGAAGGG
ACACCTGGCCATAGAAAACAGCTGAGGGTGTGCTGTGTTCTGGATCAGGCCCTGCTTCAGAAGGGACTCCTG
GAGGCCCATGTTCTTGATGCAACCTCGTGGCCAGGCCGGGAGCAGCTTGCTCCTCAGAGGTGTTGACTATCT
GGGTGTTCTTGGTAAC

2624/6881
FIGURE 2412

MEEHGVQTQTEHMAITIEAHAVAQQVQQVHVATYTEHSMLSADEDSPPSSPEDTSYDDSDILNSTAADEVTAHLAAAG
PVGMAAAAAVATGKKRKRPHVFESNPSIRKRQOTRLLRKLRLATLDEYTTRVGQQAIVLCISPSKPNPVFKVFGAA
PLENVVRKYKSMILEDLESALAEHAPAPQEVNSELPLTIDGIPVSVDKMTQAQLRAFIPEMLKYSTGRGKPGWG
KESCKPIWWPEDIPWANVRSDVRTEEQKQRVSWTQALRTIVKNCYKQHGRELLYAFEDQQTQTQATATHSIAHL
VPSQTVVQTFSPNDGTVSLIQVGTGATVATLADASELPTTVTVAQVNYSADGEVEQNWATLQGGEMTIQTTQA
SEATQAVASLAEAAVAASQEMQQGATVTMALNSEAAAHAVATLAEATLQGGGQIVLSGETAAAVGALTGVQDANG
LVQIPVSMYQTVVTSLAQGNGPVQVAMAPVTTTRISDSAVTMDGQAVEVVTLEQ

2625/6881
FIGURE 2413

GCCTCAAGAGGCGGATATTAACCTCCCAGGACGGAAGTTCCGGAGCCTTCAAACCTCTCGGGGAAGCAACTCGGCA
GCGGACCAAGATGGCGGCGCCCTGTGAGGGACAAGCGTTTGCCGTAGGGGTTGAAAAGAATTGGGGTGACAGTAGT
TCGCTCCCCAGAAGGGACCCCCCAGAAAATCCGGCAGCTGATAGATGAGGGGATTGCCCCGGAAGAGGGAGGCGT
GGACGCGAAGGACACGTCCTGCCACATCCCAGTCAGTTAATGGATCACCCCAAGCGGAACAACCTTCATTGGAATC
TACAAGCAAAGAAGCCTTCTTTAGCAGAGTGGAACATTTTCTTCTTTGAAATGGGCAGGTAAGCCCTTTGAGCT
GTCTCCACTCGTCTGTGCAAAATATGGCTGGGTACAGTGGAATGTGATATGCTCAAGTGCTCTAGCTGTCAAGC
TTTTCTCTGTGCCAGTTTACAACCAGCTTTTGACTTTGACAGATATAAGCAACGATGTGCTGAGCTGAAGAAAGC
CTTGCTGTACTGCCCATGAGAAGTTCTGTTTCTGGCCAGACAGCCCATCCCCAGACCGATTTGGGATGTTGCCCT
GGATGAGCCTGCTATTCTTGTTAGTGAATTCCTAGATCGTTTTCAAAGCCTTTGTCACTTGGACCTCCAGCTTCC
TTCCCTAAGGCCCGAGGACTTGAAAACATATGTGCTTGACAGAAGACAAGATCAGTCTTCTCTACACTTGCTTGA
AGATGAACCTTGATCACCGAACTGATGAGAGAAAACTACAATCAAATTAGGCTCAGACATCCAAGTCCACGTCAC
TGCCTGTATTCTCTCTGTGTGTGGCTGGGCGTGTAGTTCTCTTTGGAATCCATGCAGCTCTCCCTGATAACATG
TTCGCAATGTATGAGGAAGGTGGGGCTCTGGGGCTTCCAGCAGATTGAATCGTCCATGACTGACCTGGATGCATC
CTTTGGCCTGACCAGCTCCCCAATCCCAGGCCTTGAGGGGCGACCAGAGCGCTTACCTCTGGTGCCTGAATCTCC
TCGGAGGATGATGACCCGGAGCCAGGATGCCACTTTCTCCCCAGGCTCAGAGCAGGCTGAAAAGAGCCCTGGTCC
CATTGTCTCTCGAACTCGGAGCTGGGACTCTTCCAGTCTGTGTGACCGTCCCTGAGCCAGAGGCTGCTAGCCCCAC
CACCAGAACTCGCCCAGTGACCCGAAGCATGGGAACAGGAGACACCCCTGGCCTGGAGGTACCATCTAGCCCTCT
GCGGAAAGCCAAGCGAGCTCGCCTCTGCTCCTCCAGCAGTTCCGGACACATCTTCCCGAAGCTTCTTTGATCCAC
CTCTCAGCATAGAGACTGGTGCCCTTGGGTGAATATCACACTTGGCAAAGAAAGCAGGGAGAATGGTGGAACCTGA
ACCAGATGCCAGCGCCCCAGCAGAGCCAGGCTGGAAGCAGTGCTGACCATCCTCTTGGCGCACAAACAGTCTAG
CCAGCCAGCTGAAACGGACTCCATGAGTCTCTCTGAGAAATCAAGGAAAGTATTCCGAATATTTGGCAGTGCGA
ATCTCTGTGCTCATGCTGAAGATACTCCAGCGCCTTCTGGAGATAGCTGGAATGAGAGTGACTTTTTGAAAAAT
TAAGGCTGAGTTCTTTTCGGTCAGCTGACACTAAGTTTTTCTGTTCTGGGTTAATCATAAGGAGCCCCCTGCCA
TAGCAAAGGCAGTGAGTGTCAACTATCTGCATCTGGCTGAGAGAGACCCGTTTCTTTTCAGGGATGTGGACAGGG
TAAGGGCAGCAAGCATGGTTCTGTAAAGGAGTGTGGGATTAACAGACTAGAAGGAAGACTAAGGACCTGACCAC
CCATTTTCAGCATCTTCAATGTGGAGCAGTGTTCTGAGGACTCTTCTATCCTAGGACTATGACAGTGTGTATTAAT
AAAAATTTTGCTAAGATTCTCA

2626/6881
FIGURE 2414

GGCGCTGACGCCTGGCAGGGAGAAGGCGGCAGCACATGCTGGGCTCGGGGGCGATGGGCTTGTGCGCGGACCTGG
CGACGCTCTAGCCCCGAGCCGCGTATTCGTGGCCGGGTCTCCCTGGGAACAGGGTGAAGGCCGAGAACCTCTGG
CCTCAGGAAGCGCATGCGCAACCGGTTCTCCGAAACATGGAGTCTGTAGGCAAGGTCTTACCTGAATCAGGATG

AGGGAGTGGTGGGTCCAGGTGGGGCTGCTGGCCGTGCCCCTGCTTGCTGCGTACCTGCACATCCCACCCCTCAG
CTCTCCCTGCCCTTCACTCATGGAAGTCTTCAGGCAAGTTTTTCACTTACAAGGACTGCGTATCTTCTACCAA
GACTCTGTGGGTGTGGTTGGAAGTCCAGAGATAGTTGTGCTTTTACACGGTTTTTCCAACATCCAGCTACGACTGG
TACAAGATTTGGGAAGGTCTGACCTTGAGGTTTCATCGGGTGATTGCCCTTGATTTCTTAGGCTTTGGCTTCAGT
GACAAACCGAGACCACATCACTATTCCATATTTGAGCAGGCCAGCATCGTGGAAGCGCTTTTGGCGCATCTGGGG
CTCCAGAACCGCAGGATCAACCTTCTTTCTCATGACTATGGAGATATTGTTGCTCAGGAGCTTCTCTACAGGTAC
AAGCAGAATCGATCTGGTCGGCTTACCATAAAGAGTCTCTGTCTGTCAAATGGAGGTATCTTTCCTGAGACTCAC
CGTCCACTCCTTCTCCAAAAGCTACTCAAAGATGGAGGTGTGCTGTCAACCCATCCTCACACGACTGATGAACCTC
TTTGTATTCTCTCGAGGTCTCACCCAGTCTTTGGGCCGTATACTCGGCCCTCTGAGAGTGAGCTGTGGGACATG
TGGGCAGGGATCCGCAACAATGACGGGAACCTTAGTCATTGACAGTCTCTTACAGTACATCAATCAGAGGAAGAAG
TTCAGAAGGCGCTGGGTGGGAGCTCTTGCCCTGTGTAACATATCCCCATTCATTTTATCTATGGGCCATTGGATCCT
GTAAATCCCTATCCAGAGTTTTTGGAGCTGTACAGGAAAACGCTGCCGCGGTCCACAGTGTGATTCTGGATGAC
CACATTAGCCACTATCCACAGCTAGAGGATCCCATGGGCTTCTTGAATGCATATATGGGCTTCATCAACTCCTTC
TGAGCTGGAAAGAGTAGCTTCCCTGTATTACCTCCCTACTCCCTTATGTGTTGTGTATTCCACTTAGGAAGAAA
TGCCCAAAGAGGTCTTGCCATCAAACATAATTCTCTCACAAAGTCCACTTTACTCAAATTGGTGAACAGTGTA
TAGGAAGAAGCCAGCAGGAGCTCTGACTAAGGTTGACATAATAGTCCACCTCCCATTACTTTGATATCTGATCAA
ATGTATAGACTTGGCTTTGTTTTTTGTGCTATTAGGAAATTCTGATGAGCATTACTATTCAGTATGCAGAAAGA
CGTTCTTTTGCATAAAAGACTTTTTTTTAACTTTGGACTTCTCTGAAATATTTAGAAGTGCTAATTTCTGGCC
CACCCCAACAGGAATTCTATAGTAAGGAGGAGGAGAAGGGGGCTCCTTCCCTCTCCTCGAATGACGTTATGGG
CACATGCCTTTTTAAAGTTCTTTAAGCAACACAGAGCTGAGTCTCTTTGTCATACCTTTGGATTTAGTGTTC
TCAGCTGTTTTTAGTTATAAACATTTTGTTAAAATAGATATTGGTTTAAATGATACAGTATTTTAGGTATGATTT
AAGACTATGATTTACCTATACATTATATATTTTATAAAGATACTAAACCAGCATACCCTTACTCTGCCAGAGT
AGTGAAGCTAATTAAACACATTTGGTTTCTGAATAAATTGAACTAAATCCAACTATTTTCTAAAATCACAGGAC
ATTAAGGACCAATAGCATCTGTGCCAGAGATGTACTGTTATTAGCTGGGAAGACCAATTCTAACAGCAAATAACA
GTCTGAGACTCCTCATACTCAGTGTTAGAAGCATGTCTCTCTTGAGCTACAGTAGAGGGGAAGGGATTGTTGT
GTAGTCAAGTCACCATGCTGAATGTACACTGATTCCTTTATGATGACTGCTTAACTCCCCACTGCCTGTCCCAGA
GAGGCTTTCCAATGTAGCTCAGTAATTCCTGTTACTTTACAGACAGGAAAAGTCCAGAACTTTAAGAACAACT
CTGAAAGACCTATGAGCAAATGGTGCTGAATACTTTTTTTTTAAAGCCACATTTTCATTGTCTTAGTCAAAGCAGG
ATTATTAAGTGATTATTTAAATTCGTTTTTTTTTAAATTAGCAACTTCAAGTATAACAACCTTTGAACTGGAATAA
GTGTTTATTTTCTATTAATAAAAAATGAATTGTGAC

2627/6881
FIGURE 2415

MREWWVQVGLLAVPLLAAYLHIPPPQLSPALHSWKSSGKFFTYKGLRIFYQDSVGVVGSPEIVVLLHGFP TSSYD
WYKIWEGLTLRFHRVIALDFLGFGFSDKPRPHHYSIFEQASIVEALLRHLGLQNRRLNLLSHDYGDIVAQELLYR
YKQNRSGRLTIKSLCLSNGGIFPETHRPLLLQKLLKDGGVLSPILTRLMNFFVFSRGLTPVFGPYTRPSESELWD
MWAGIRNNDGNLVIDSLLQYINQRKKFRRRWVGALASVTIPIHFIYGPLDPVNPYPEFLELYRKTLPRSTVSILD
DHISHYPQLEDPMGFLNAYMGFINSF

2628/6881
FIGURE 2416

TGCTTGTAACCTAGAAAGGGAGACGAGGAAACACACATGTAGCTGAGCAAACCTTAAACCAGTGCACCGCTGAAAACG
AGAGAAAAAGGATACAAACAGTCCAGAAACAATGTACTTTCCTAGCATCATAAGCTGAAGTCTGAAGCTCCACTG
ACCTGTAGAGAAGCTCCTGAGCAACAATATCTCCATAGTCATGAGAAAGAAGGTTGATCCTGCGGTTCTGGAGCC
CCAGATGCCGCAAAAGCGCTTCCACGATGCTGGCCTGCTCAAATATGGAATAGTGATGTGGTCTCTGAGGAAAGG
AAAGCCCACATACACAGGATGAAGTCATGAGGACAGCTCTCTCTGCCAGCCTGACCCTCATAGTCTGCGTCTGCC
CCCACACCCCATCACCAGCCCCACATAGGTGCTGCTTACCGGTTTGTCACTGAAGCCAAAGCCTAAGAAATCAAG
GGCAATCACCCGATGAAACCTCAAGGTCAGACCTTCCCAAATCTACAAGAAAGAAACGATGATTTGGGCTTTCTG
CTCCTGCCCCCTCCCTTTTACCAGACCTACAGTTGCACAGGAGCTTCAGCCCTATCTTGGCTTAACAGACTTCCAT
AAAGAGAAAACGCCATGAAACTACCACAGGTCCACAGATGATCCTCTTGGAATGCTTTATTCTGGTAATTA
ATCCCTGTTGAGGGAGGGTAACCTGGCAGTGATCCCTTCCAGAGTGCCAAGGAGTTGTTTATTCCCTTCAGTAAA
TAAGGAACAGTTCAACATTTAATGTTTTTTTTTAAAGCAATTCAAATGTGCAAGAGCCTTCTGGTGCTGACAACAA
AATCCTTGAGGTTTTTTAAATTTTTATTAAAAAAAATTTTTTTTTTGAGACAGACTCTCGCTCTGTACCTAGGC
TGAAGTGCAGTGGTGCAATCTCAGCTCACTGCAACCTCTGCCTCCCGGTTCAAGCGATTCTCCTGCCTCAGCCT
CCCAAGTAGCTGGGATTACAGGCTTGTGCCACCATGCCTGGCCAATTTTTTATACTTTTAGTAGAGATGGGGTTTT
GCCATGTTGGCCTGGCTGGTCTCAAACCTCCTGACCTCAGGTCATCCTCCACCTCAGCCTCCCAAAGTGCTAGGA
TTTGAGCCCCCGCGCCCGCCGAGATTTTTTAAAGACATAGTAGGACGTAGAAGTCTGACTTCATTACCTTGTACC
AGTCGTAGCTGGATGTTGGAACCGTGTAAGACACAACCTATCTCTGGACTTCCAACCACACCCACAGAGTCTA
GGAAGAAGGAAAGTACAATCAATTATGCCAAATCCCTATAAAAAATAACCTCGAAGATGTTAAATCTAAGTAATC
TGATACAAAGAACAAGCAACTGTGACCAAATTGACATTAAATGACACAATTATTTGTAAGTAAATGTAAGCTTAAC
GCGTTAGGTGAGAACAGGCCCTTTCTCCTTTCAATCTGTATATTAAACATTGTAAGTAAATCATGCTATGTAAAA
TACTTGAAGGCACCTTGTTTACTTTACCTAGGTGTTTTTAAACAGCATCTCCCCATTTCTCCTTTTGTCTGTAT
ATATGCAAATTTTTTTCAGTGAAAAGTAAATTTTCAGTTAAAGCATATGATCACAACACATAAACTACAAATTCT
TTGTACTTTATCATGAATGGCCTCACAGAAATTTCTCTAAGATACAGCAACTATTCCCAAGGAACACCTTTAGCTT
ATGCTGTTTGCTCAGCACTTTTTATTTCAGCAGGAGACCCAATCTAACATCAAAAACATAATAAACTATTACAAA
ATCCTGTCAACTATAAAAAAGGGCTTAATCAACATAAACATGAACCTTTTTTAATGCATATGACAATATGGAAGCAT
TCAGCATCATCTAAATTAGGTAAACATTTAGACAATATTAACCTTGCTAATAGTATGGGATTAGAACAGGTATAT
TCATATACTGCCAGTGACATGAAAATTTGGTAATAAGGTTTTCAAAAAATAATTTAGAAGCAGTTAAAAATTGTAT
ATACTTTAGCCTAAGAGTTTTTGTCTTGAGAATCTGTGCAAATAAAATCATTCCATTTATACAAGTAGTATAGTT
TGAAAATGTAAGGAAAAAATAAACTGTATGGACATGAAGCTTTTACTTCAACATTAGTTTTCTAAAACAGTAAAA
CTGGAAGTAACCCAAGCCAACATAATAAAAAATTGTATACTTACTTAATTGAATATAGCAAATGAGAGGAGGTCAG
GAGCAATAATGAAAAACGGTTTTATGACAAACATTTTTTCGTTATTGCTCTTGACCCCCGCTCAAAACAAATCATT
CCAATCTGTTTCTCAGTTTCTTCACCTATAAAATGAGGTTAATGGCACCTATCTCCAAATGCTGTTGTAAAGATT
AAACAATGAAGGCTGAAAACATAACTCAGTGCCTGGCATATGGTAATTACTTGATAAGTAGTGGTCATAATAATC
ATCATCACTAGCAAATTAATTTATATAATGGTATCAAGACTTAAATCACAGTTACACTACAAATAATCTACAGAA
AAAATGAAATCAGGGATGGTAAGGAGAGAGAACCAATGGTGTTATATCTATTAATATTTTATATATTACCTGAC
AGGTTGCTC

2629/6881
FIGURE 2417

TTTCCAGCCCCGGCCCCGGACCCTGCAGCTGCAGAGATGTTGATGCCTAAGAAGAAGCTGGATTGCCATTTATGAA
CTCCTTTTTTAAGGAGGGAGTCATGGTGGCCAAGAAGGATGTCCACATGCCTAAGCACCCGGAGCTGGCAGACAAG
AATGTGCCCAACCTTCATGTCATGAAGGCCATGCAGTCTCTCAAGTGCCGAGGCTACGTGAAAGAACAACCTTTGCC
TGGAGACATTTCTACTGGTACCTTACCAATGAGTGTATCCAGTATCTCCGTGATTACCTTCATCTGCCCCCGGAG
ATTGTGCCTGCCACCCTACGCCGTAGCCGTCCAGAGACTGGCAGGCCTCGGCCTAAAGGTCTGTATATGAGGAGT
GCTGTGCTACCTGGTGCCGACAAGAAAGCCGAGGCTGGGGCTGGGTCAGCAACCGAATTCTAGTTTAGAGGCGGA
TTTGGTTGTGGACGTGGTCAGCCACCTCAGTAAAACTGGAGAGGATTCTTTTGCATTGAATAAAATTTACAGCCAA
AAAA

2630/6881
FIGURE 2418

CTCTTTCTGCTGCTCCCCAGCTCTCGGATACAGCCGACACCATGGGTTTTCGGAGACCTGAAAAGCCCCACCGGCC
TCCAGGTGCTCAACGATTACCTGGCGGACAAGAGCTACATCAAGGGGTATGGTGCCATCACAAGCAGATGTGGCA
GTATTTGAAGCCGTGTCCGGCCCCACCACCTGCCGACTTGTGTCATGCCCTACGTTGGTATAATCACATCAAGTCT
TACGAAAAGGAAAAGGCCGGCCTGCCAGGAGTGAAGAAAGCTTTGAGCAAGTATGGTCCTGCCGATGTGGAAGAC
ACTACAGGAAGTGGAGCTACAGACAGTAAAGATGATGATGACATTGATCTCTTTGGATCCGATTATGAGGAGGAA
AGTGAAGAAGCAAAGAGGCTAAGGGAAGAACATCTTGACACAATATGAATCAAAGAAAGCCAATGATGAGACAGAT
ATGGCGAAATTAGAGGAGTGTGTCAGAAGCATTCAAGCAGACGGCTTAGTCTGGGGCTCATCTAAACTAGTTCCA
GTGGGATACGGAATTAAGAACTTCAAATACAGTGTGTAGTTGAAGATGATAAAGTTGGAACAGATATGCTGGAG
GAGCAGATCACTGCTTTTGGAGACTATGTGCAGTCCATGGATGTGGCTGCTTTCAACAAGATCTAAAAAATCCATC
CTGGATCATG

2631/6881
FIGURE 2419

MVPSQADVAVFEAVSGPPPADLCHALRWYNHIKSYEKEKAGLPGVKKALSKYGPADVEDTTGSGATDSKDDDDID
LFGSDYEEEESEEAKRLREEHLAQYESKKANDETDMAKLEECVRSIQADGLVWGSSKLVPVGYGIKKLQIQCVVED
DKVGTDMLEEQITAFEDYVQSMDVAAFNKI

2632/6881
FIGURE 2420

CTTTCCTTTCGCGAATCACCATGGCGGGCTGGGACCCTGTACACGTATCCTGAAAACCTGGAGGGCCTTCAAGGCTCT
CATCGCTGCTCAGTACAGCGGGGCTCAGATCCGCGTGCTCTCCGCACCACCCCACTTCCATTTTGGCCAAACCAA
CCGCACCTCTGAATTTCTTCGCAAATTTCTTGCCGGCAAGGTCCCAGCATTGAGGGTGATGATGGATTCTGTGT
GTTTGAGAGCAACGCCATTGCCTACTATGTGAGCAATGAGGAGCTGCGGGGAAGTACTCCAGAGGCAGCAGCCCA
GGTGGTGCAGTGGGTGAGCTTTGCTGATTCCGATATAGTGCCCCCAGCCAGTACCTGGGTGTTCCCCACCTTGGG
CATCATGCACCACAACAAACAGGCCACTGAGAATGCAAAGGAGGAAGTGAGGCGAATTCTGGGGCTGCTGGATGC
TTACTTGAAGACGAGGACTTTTCTGGTGGGCGAACGAGTGACATTGGCTGACATCACAGTTGTCTGCACCCCTGTT
GTGGCTCTATAAGCAGGTTCTAGAGCCTTCTTTCCGCGGGGCCCTTTCGCAATACCAACCGCTGGTTCCCTCACCTG
CATTAAACCAGCCCCAGTTCCGGGCTGTCTTGGGGGAAGTGAACCTGTGTGAGAAGATGGCCCAGTTTGATGCTAA
AAAGTTTGCAGAGACCCAGCCTAAAAAGGACACACCACGGAAAGAGAAGGGTTACGGGAAGAGAAGCAGAAGCC
CCAGGCTGAGCGGAAGGAGGAGAAAAAGGCGGCTGCCCTGCTCCTGAGGAGGAGATGGATGAATGTGAGCAGGC
GCTGGCTGCTGAGCCCCAAGCCAAGGACCCCTTCGCTCACCTGCCAAGAGTACCTTTGTGTTGGATGAATTTAA
GCGCAAGTACTCCAATGAGGACACACTCTCTGTGGCACTGCCATATTTCTGGGAGCACTTTGATAAGGACGGCTG
GTCCCTGTGGTACTCAGAGTATCGCTTCCCTGAAGAACTCACTCAGACCTTCATGAGCTGCAATCTCATCACTGG
AATGTTCCAGCGACTGGACAAGCTGAGGAAGAATGCCTTCGCCAGTGTCATCCTTTTTGGAACCAACAATAGCAG
CTCCATTTCTGGAGTCTGGGTCTTCCGAGGCCAGGAGCTTGCCCTTCCGCTGAGTCCAGATTGGCAGGTGGACTA
CGAGTCATACACATGGCGGAACTGGATCCTGGCAGAGAGGAGACCCAGACGCTGGTTCGAGAGTACTTTTCCTG
GGAGGGGGCCTTCCAGCATGTGGGCAAAGCCTTCAATCACGGCAAGATCTTCAAGTGAACATCTCTTGCCATCAC
CTAGCTGCCTGCACCTGCCCTTCAGGGAGATGGGGGTCATTAAAGGAACTGAACATTG

2633/6881
FIGURE 2421

MAAGTLYTYPENWRAFKALIAAQYSGAQIRVLSAPPHFHFQGQTNRTSEFLRKFPAGKVPAFEGDDGFCVFESNAI
AYYVSNEELRGSTPEAAAQVVQWVSFADSDIVPPASTWVFPTLGIMHHNKQATENAKEEVRILGLLDAYLKTRT
FLVGERVTLADITVVCTLLWLYKQVLEPSFRRAFRNTNRWFLTCINQPQFRAVLGELKLCEKMAQFDAKKFAETQ
PKKDTPRKEKGSREEKQKPQAERKEEKAAAAPAPEEEMDECEQALAAEPKAKDPFAHLPKSTFVLDEFKRKYSNE
DTLSVALPYFWEHFDKDGWSLWYSEYRFPEELTQTFMSCNLITGMFQRLDKLRKNAFASVILFGTNNSSSISGVW
VFRGQELAFPLSPDWQVDYESYTWKLDPGREETQTLVREYFSWEGAFQHVKGAFNHGKIFK

2634/6881
FIGURE 2422

ATCACCATGGCGGCTGGGACCCTGTACACGTATCCTGAAAACCTGGAGGGCCTTCAAGGCTCTCATCGCTGCTCAG
TACAGCGGGGCTCAGATCCGCGTGCTCTCCGCACCACCCCACTTCCATTTTGGCCAAACCAACCGCACCTCTGAA
TTTCTTCGCAAATTCCTGCCGGCAAGGTCCCAGCATTTGAGGGTGATGATGGATTCTGTGTGTTTGAGAGCAAC
GCCATTGCCTACTATGTGAGCAATGAGGAGCTGCGGGGAAGTACTCCAGAGGCAGCAGCCCAGGTGGTGCAGTGG
GTGAGCTTTGCTGATTCCGATATAGTGCCCCAGCCAGTACCTGGGTGTTAGCCCAAGGCCAAGGACCCCTTCGC
TCACCTGCCCCAAGAGTACCTTTGTGTTGGATGAATTTAAGCGCAAGTACTCCAATGAGGACACACTCTCTGTGGC
ACTGCCATATTTCTGGGAGCACTTTGATAAGGACGGCTGGTCCCTGTGGTACTCAGAGTATCGCTTCCCTGAAGA
ACTCACTCAGACCTTCATGAGCTGCAATCTCATCACTGGAATGTTCCAGCGACTGGACAAGCTGAGGAAGAATGC
CTTCGCCAGTGTCATCCTTTT

2635/6881
FIGURE 2423

GAAGGCCGCACCGTACTGGGCGGGGGTCTGGGGAGCGCAGCAGCCATGGCAAGCCGTCTCCTGCTCAACAACGGC
GCCAAGATGCCCATCCTGGGGTTGGGTACCTGGAAGTCCCCTCCAGGGCAGGTGACTGAGGCCGTGAAGGTGGCC
ATTGACGTCGGGTACCGCCACATCGACTGTGCCCATGTGTACCAGAATGAGAATGAGGTGGGGGTGGCCATTGAG
GAGAAGCTCAGGGAGCAGGTGGTGAAGCGTGAGGAGCTCTTCATCGTCAGCAAGCTGTGGTGCACGTACCATGAG
AAGGGCCTGGTGAAAGGAGCCTGCCAGAAGACACTCAGCGACCTGAAGCTGGACTACCTGGACCTCTACCTTATT
CACTGGCCGACTGGCTTTAAGCCTGGGAAGGAATTTTTCCCATTGGATGAGTCGGGCAATGTGGTTCCCAGTGAC
ACCAACATTCTGGACACGTGGGCGGCCATGGAAGAGCTGGTGGATGAAGGGCTGGTGAAAGCTATTGGCATCTCC
AACTTCAACCATCTCCAGGTGGAGATGATCTTAAACAAACCTGGCTTGAAGTATAAGCCTGCAGTTAACCAGATT
GAGTGCCACCCATATCTCACTCAGGAGAAGTTAATCCAGTACTGCCAGTCCAAAGGCATCGTGGTGACCGCCTAC
AGCCCCCTCGGCTCTCCTGACAGGCCCTGGGCCAAGCCCCGAGGACCCCTTCTCTCCTGGAGGATCCCAGGATCAAG
GCGATCGCAGCCAAGCACAATAAACTACAGCCCAGGTCTTGATCCGGTTCCCCTATGCAGAGGAACCTGGTGGTG
ATCCCCAAGTCTGTGACACCAGAACGCATTGCTGAGAACTTTAAGGTCTTTGACTTTGAACTGAGCAGCCAGGAT
ATGACCACCTTACTCAGCTACAACAGGAACCTGGAGGGTCTGTGCCTTGTTGAGCTGTACCTCCCACAAGGATTAC
CCCTTCCATGAAGAGTTTTTGAAGCTGTGGTTGCCTGCTCGTCCCCAAGTGACCTATACCTGTGTTTCTTGCCCTCA
TTTTTTTTCCCTTGCAAATGTAGTATGGCCTGTGTCACTCAGCAGTGGGACAGCAACCTGTAGAGTGGCCAGCGAGG
GCGTGTCTAGCTTGATGTTGGATCTCAAGAGCCCTGTCAGTAGAGTAGAAGTCTCTTCCAGTTTGCTTTGCCCTT
CTTTCTACCCTGCTGGGGAAAGTACAACCTGAATACCCTTTTCTGACCAAAGAGAAGCAAAATCTACCAGGTCAA
AATAGTGCCACTAACGGTTGAGTTTTGACTGCTTGGAACCTGGAATCCTTTCAGCAAGACTTCTCTTTGCCTCAAA
TAAAAAGTGCTTTTGTG

2636/6881
FIGURE 2424

MASRLLLNNGAKMPILGLGTWKSPPGQVTEAVKVAIDVGYRHIDCAHVIQNENEVGVAIQEKLREQVVKREELFI
VSKLWCTYHEKGLVKGACQKTLSDLKLDYLDLYLIHWPTGFKPGKEFFPLDESGNVVPSDTNILD TWAAMEELVD
EGLVKAIGISNFNHLQVEMILNKPGLKYKPAVNQIECHPYLTQEKL IQYCQSKGIVVTAYSPLGSPDRPWAKPED
PSLLEDPRIKAIAAKHNKTTAQVLRFPMQRNLVVIPKSVTPERIAENFKVDFELSSQDMTLLSYNRNWRVCA
LLSCTSHKDYPFHEEF

2637/6881
FIGURE 2425

GGCACGAGGCCTGAGCTCAGGAGTTTGAGACCAGCCTGTCTCTACTAACAATATAAAAATTAGCTGGGAGTCACG
GTGGGCGCCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATTGCTTGAACCCAGGAGACAGAGGTTGTA
GTGAGCTGAGATCGCAACCACTGCACTCTAGCCTTGGCAACAGTGCAAGACTGTCTCAAAAACAGCAACAGAGAGC
AGGACGTGAGACTTCTACCTGCTCACTCAGAATCATTCTGACCAACCAATGGCCACGTTTGTGGAGCTCAGTAC
CAAAGCCAAGATGCCCATTGTGGGCCTGGGCACTTGGAAGTCTCCTCTTGGCAAAGTGAAAGAAGCAGTGAAGGT
GGCCATTGATGCAGGATATCGGCACATTGACTGTGCCTATGTCTATCAGAATGAACATGAAGTGGGGGAAGCCAT
CCAAGAGAAGATCCAAGAGAAGGCTGTGAAGCGGGAGGACCTGTTTCATCGTCAGCAAGTTGTGGCCCACTTTCTT
TGAGAGACCCCTTGTGAGGAAAGCCTTTGAGAAGACCCTCAAGGACCTGAAGCTGAGCTATCTGGACGTCTATCT
TATTCAGTGGCCACAGGGATTCAAGTCTGGGGATGACCTTTTCCCAAAGATGATAAAGGTAATGCCATCGGTGG
AAAAGCAACGTTCTTGGATGCCTGGGAGGCCATGGAGGAGCTGGTGGATGAGGGGCTGGTGAAAGCCCTTGGGGT
CTCCAATTTTCAGCCACTTCCAGATCGAGAAGCTCTTGAACAAACCTGGACTGAAATATAAACCAGTGACTAACCA
GGTTGAGTGTCACCCATACTCACACAGGAGAACTGATCCAGTACTGCCACTCCAAGGGCATCACCGTTACGGC
CTACAGCCCCCTGGGCTCTCCGGATAGACCTTGGGCCAAGCCAGAAGACCCTTCCCTGCTGGAGGATCCCAAGAT
TAAGGAGATTGCTGCAAAGCACAAAAAACCGCAGCCAGGTTCTGATCCGTTTCCATATCCAGAGGAATGTGAT
TGTCATCCCCAAGTCTGTGACACCAGCACGCATTGTTGAGAACATTCAGGTCTTTGACTTTAAATTGAGTGATGA
GGAGATGGCAACCATACTCAGCTTCAACAGAACTGGAGGGCCTGTAACGTGTTGCAATCCTCTCATTTGGAAGA
CTATCCCTTCGATGCAGAATATTGAGGTTGAATCTCCTGGTGAGATTATACAGGAGATTCTCTTTCTTCGCTGAA
GTGTGACTACCTCCACTCATGTCCCATTTTAGCCAAGCTTATTTAAGATCACAGTGAACCTAGTCCTGTTATAGA
CGAGAATCGAGGTGCTGTTTTAGACATTTATTTCTGTATGTTCAACTAGGATCAGAATATCACAGAAAAGCATGG
CTTGAATAAGGAAATGACAATTTTTTCCACTTATCTGATCAGAACAAATGTTTATTAAGCATCAGAACTCTGCC
AACACTGAGGATGTAAAGATCAATAAAAAAATAATAATCATAAAAAAAAAAAAAAAAAAAAAA

2638/6881
FIGURE 2426

MATFVELSTKAKMPIVGLGTWKSPLGKVKEAVKVAIDAGYRHIDCAYVYQNEHEVGEAIOEKIOEKAVKREDLFI
VSKLWPTFFERPLVRKAFEKTLKDLKLSYLDVYLIHWPQGFKSGDDLFPKDDKGNAIGGKATFLDAWEAMEELVD
EGLVKALGVSNFSHFQIEKLLNKPGLKYKPVTNQVECHPYLTQEKLIQYCHSKGITVTAYSPLGSPDRPWAKPED
PSLLEDPKIKEIAAKHKKTAQAQLIRFHIQRNVIVIPKSVTPARIVENIQVDFKLSDEEMATILSFNRNWRACN
VLQSSHLEDYPFDAEY

2639/6881
FIGURE 2427

CAGAGTTTGGGCGCCAGGCGAGACGGCAGGGCTTAAAGTTCCGGGAATCAAAGATCAACTCCCCTGAGGACAAA
TGGACCTGTAATTCGGGTGTGACGAGAGAACGAGATTTACCTTCCTGAATTAAAAACAGGTCATTAAGCTTGG
GCCCTGACTTTTCTTTGTGAGAAGGTACAGAGATGGAAACCTTACAATCCGAGACTAAAACGAGGGTCCCTCCCT
CATGGCTGACAGCCCAGGTGGCTACAAAGAATGTGGCACCATGAAGGCCCCCAAGAGGATGAGAATGGCAGCAG
TGCCAGTGGCAGCAGCAAGACTCCCTGCGACAAGGACTGTGTACTGCATGAATGAGGCTGAGATAGTTGATGTTG
CTCTGGGAATCCTGATTGAGAGCCGCAAACAGGAAAAGGCCTGCGAGCAGCCGGCCCTGGCGGGGGCTGATAACC
CAGAGCACTCCCCCTCCCTGCTCCGTGTGCGCTCACACAAGTTCTGGGAGCAGCAGTGAGGAAGAGGACAGTGGGA
AACAGGCACTGGCTCCAGGCCTCAGCCCTTCCCAGAGGCCGGGGGGTTCCAGCTCTGCCTGTAGCAGGAGCCCTG
AGGAGGAGGAGGAAGAGGATGTGCTGAAATACGTCCGGGAGATCTTTTTCAGCTTAGGGCATAAACTGTGCACTGA
ACTGTCTGCCGAGAGCAGCTGGAGGACAGCTGAGCTTCCACTGGTGCTGCTGGGCCGCCCGCCTGTGGGAATGGG
GCTCTCTGTGCTCCTACCTTTGTGCTTCTTGGGCCTGGCAGATTCACCTCAGGCCAGAAGCCCCCTGGACACTCC
GGGCCTTGGGGCTGCCGTTCTGAGTGTGCGGAAGGCAGGACTCAAAATGAGATCCCATTGTACTCCCTCTGTATG
TACTGTGCCCTCTCCTGGCTCTTGAGGCTCTGGAGTCCCAATTGTCTGTGTTAGTCAGTGACCAGGTTCCAGGGA
AAATGATGTGATGTGGTGGTCCAACCTTACTGGAACCAAGAGACAGTACTTTGCAAAGAAAAGGATCACTGCCAG
GTGCACTGGAATTGCTACAGTTTAGTCCGCATGATCTCTCCTGAAGGAGGAAGCCTGTTTCAAAAATAGTTTCCA
TCATGAGTCTATCAATGAGCTCCACCTCTCCAGCCAGCCTAGAAAGCAAACGAGCTGCCCACAGTTCTCTGCCC
TGTCTGGGAGGTTGAGGCCACAGTGTATAGACTGGTAAGCCAGACAGGCCTCCTCCCGCAAGCTGCTACCTTGCT
TTCACCTGTACCTTGGTCCCCGGGCAGCTAGCTATAAAGCAAGAGGGACAGGAGCCCAGAAGAGACACTGAGGAC
AAGAGATCACACCAGAGTACATGTCTCTGCCTCTGTTTTAGTGTGGCTTTGGACAGGAATATATGAATAAATCA
CTGCCATACAGGTTTCCAATACACAAGTGCTAGAAAATACACACAATTCCCCAATGAAAAAAAAAAAAAAAAA

2640/6881
FIGURE 2428

MKAPKRMRAAVPVAAARLPATRTVYCMNEAIVDVALGILIESRKQEKACEQPALAGADNPEHSPPCSVSPHTS
SGSSSEEDSGKQALAPGLSPSQRPGGSSACSRSPEEEEEDVLKYVREIFFS

2641/6881
FIGURE 2429

GAGGTAGGCTCGGACCGGCCCGCGGAGCTGCTGCAGTCCTTCGCGCCCTCCTCGCCCTCCCCACCGACATCATGC
TCCAGTTCCTGATACCAAACCTGGCTAAAAAACTTGAAGAAATTAAAAAGGACTTGGATGCCAAGAAGAAACCCC
CTAGTGCAATGAGACTGCCTCCAGCACTGCCTTCAGGATATACTGATTCTACTGCTCTTGAGGGCCTCGTTTACTA
TCTGAACCAAAAGCTTTTGTTCGTCTCCAGCCTCAGCACTTCTCTTCTTTGCTAGACCTGTGTTTTTTGCTT
TAAAGCAAGCAAAATGGGGCCCCAATTTGAGAACTACCCGACATTTCCAACATACTCACCTCTTCCATAATCCC
TTTCCAACATGCATGGGAGGTTCTAAGACTGGAATTATGGTGCTAGATTAGTAAACATGACTTTTAATGAGTAGTG
TCTTCTTTATCGTTTGGGATTTTACTACCTTTTTTCAAAGAAAAATTGATGAGTTTTGTATAGCTGGTCAGAT
ACAAATAATAGTGACTTCACAGTTTAGTAATTATAATGGGTACTTGTTAAACATTTGGTACTAAATTATGTTGCT
GCAAAGTAATTAAAATTAGTATCTAGAGCTAGTTTCTGGTGAATTATTCATTTATTTTGTACTGTTGTTAGGCAG
CTCTGTAGTTGCTAATTTAAACCAATAAGTCAATTTGCTATTTCATGAAGAAACGATTCTGAGAATCCTGTCAGGAA
TTGGGGAATGAAAAAATACACAAAAATAATGGTCTTTGTCCCAGTAGAGTTTCATAGTCTATTTAGTGTGCATGTTT
TTCCTTAATGATGTATTTGATCTGACTTTTTTCTTCTCAAAGAAATCATACTTGGGATTACAGGTACATTTGAT
GTTATATGATGGATAAGTGAAAAGTTTTTAAAGGAGATTTTATACCTTTTACATTAAAAAAGGTATTTATATTA
TTACTTTGTAGTGATTGCTCTTAAGAAAAAATATAGCCCAAATGTATAGTAAATCAGCAGCTCAAGAAGAATTTT
TGCTTCTCTTTGTAGTTGATGCTTTGTTTTTCTGTCAGTCAGAAATTCCTTGTAATTTGTCAAATGTATAATCAG
CTTGATTTGTTTTTAAATTAAAAAAATTTGAATAATTAACCTTTTGCCATGGGACAAGATACAAAAGTAATTTCA
TATAAAGGGCCTCTCCACCCCTGTTCTCTGGCTCCTGGCTCCTGTTTGACAAGTTACTGTTACCACTTCGCCTT
ATACTTTTGAGAAAGAGTCTGTGCCTAAACAAACACGTGTAACACAAATAGTAACATACATGGAGGTCTAGCCC
TCACCTTTTTTTTTCTTTTTTTCTTTTTTAATGGAGATCATTCTATACCAGCATGTAAGTAGCAAGGAACCTCA
TTCTTTTTTTGGCTGCCTAAAATTTTTTTGAATAGATATAACATAATTGATTTAATCTGCTACTGGTGAATGCTT
AGGTTGTTCTTTTGCTATTACAGTGATAACTTCAATCCTAATGTTATTAAGCATATCGATTACAGGTATAGCTAT
AAGATGAAGTCCTAAAAGTATAATTTAGACTAAATACAAATACCCATTTTCGCTAGCTGTTTTGTTTCAGAGGACT
TGTTGAGCAGCTTCACTAATAATGCCATTTTTGAAGACATGGCAGGTTTCAAGTCAATAAACTGGAAGAATTGTT
CAGAGCATCTTTTTTCAGACAGTGATGACATTGATTCTGTATATGATAAAGTGATTCTGCTTCTCTTTGACAACT
TGCATCTCTCCTACATGGAAGTAAGTTTTATTCTGTCAATGTTGTCTTTGTGTGTGACAGATTAGGATTAAATT
ATGGTTTGACTTTTCTAGCAGCGTGATCATGGGCAAGTGGCTTATTTTTTTTTTTTTTTTTTTGAGACAGAGTCTC
ACTCTGCTGCCAGGCTGGAGTGCACTGGCACAGTCTGGCTCACTGCAACTCCTGCCTCCCGGTCCAAGTGATT
CTCGTGCTGCAGCTTCTCAAGTAGCTGGCATCACCACCACACCTGGCTAATTTTTGTATTTTTTAGTAACGACGAG
GTTTCACCATGTTGGCAAAGCTGGTCTCAAATTCCTGGCCTCAAGTGATCTGCCCCTTCAGCCTCCCAAAGTGT
TGGGATTACAGGCGTGAGCCACTGCGCCCGGCTTTTTTAACTTTTAGATTCAATTAATAGGTAAATTGCATGTC
ACGGGTTTGTAGCTTATTTCTTTTCAAGAACTCTTGCAATTATCTGTAGACGTGGACGTAAATATCCACCTCATAGGG
TTTTCATAAAAAATAATTGAGATAATGTATGTAATGTTTCACAGTGCTTTGCAGACTATCTAATAAATAGTAGCT
ATTAGTACAAA

2642/6881
FIGURE 2430

CGCGGAGGAGAAGAGGAAGAGGAAGTTGGGGGAGGGTCTAGCGGGGAGTGAACCGGAAGTGTAAGGTTCTCTGC
CTCTCCTCGGCCAGGCGGAACCTCTCTGCTGGGCCCCGGTGGCCGCAAAAGAACTTTCTTTCTCCCGCCGAACGG
TCGCCGCGGCCAACTGCCTCGCCCGCCTGGCAGCCTAACCTCCTTCTTCTTCTCCTCTCCGGCTTCGCGCGG
CCCTGCCTCCCTCTCGCCCGCGGCATCCGCTTGCTGCTGCCACCGCCTCCTCATCTTCTGCCCGGCCAACCGGC
CTGCCCCGCTGCAGT**GATG**TGCGACAAGGAGTTTCATGTGGGCCCTGAAAAACGGAGACTTGGATGAGGTGAAAGA
CTATGTGGCCAAGGGAGAAGATGTCAACCGGACACTAGAAGGTGGAAGGAAACCTCTTCATTATGCAGCAGATTG
TGGGCAGCTTGAAATCCTGGAATTTCTGCTGCTGAAAGGAGCAGATATTAATGCTCCAGATAAACATCATATTAC
TCCTCTTCTGTCTGCTGTCTATGAGGGTCAIGTTTTCTGTGTGAAATTGCTTCTGTCAAAGGGTGCTGATAAGAC
TGTGAAAGGCCCAGATGGACTGACCGCCTTTGAAGCCACTGACAACCAGGCAATCAAAGCTCTTCTCCAG**TGATG**
GATGGATGGACTGATAACTCCGGAAGAATGACTCTCCTGTGGCCTCACACTGCTGCCTGTCTGTCTGTCACTCTC
TATCTGCCAGCTTCTTCAGCTAAATACTTTAAGAGGGGTGAGGGGAGAGAGAAATTCATAACAAATCCGACTACC
AGAAAAAATAATTGTTTTGGAGGAGGGGCAAAAGGAACCATGATCAGGCTTTTACTGGGATTCTGATCAAGTA
AGCCTCTTCCCTTTCTAATAAAATATACACCTTATACCCAAGGGAGAGCAAAGACAAAATACACCAGTAACATTT
GACCTTTTCAGCTCCCTAGCTAATTTATTAGATTGTGTTGAAGGTCTGATTCTACAAAGGCCAACTCTACATATT
TGGTAGCCCTAACTGTCTGAGCAGTAGTGGCTGCTGTGATGTAACTTAGGGTGCTGAGATAAGCAATTAGCTCT
AGCCTTCTGCCTTAAGAATGCACTCTACTGGGGATTTCTTGGCATAAGTTAAGAGCGCTGCCTATAAGGTTGGTGA
CCAAATCTTTCTCGGTGACTTTAAGCTTTATGTGAAAGCTTAGTTAAGGTGAGGAGGGGCACACTCCTAAATTG
CTGGATGACTGAACTTTGGATTTTCTCTCCCTTTTACATGGATTTTCATGTCTCTTTAGATAAACTGACTAGTT
TTATTTATAAAATCTTAAGTTTTGGAAGTCTAAAGGAGAAACCATTCCAGTATGCATATTTTTTTCTCCTCTAGA
TTCATACATTTATATAGCATTGAAACACTTTCAAACCTCTGCTGGTAGTAAAAGGGGATTTAAAAATAGAATCAT
AGCCATAAGCCTGTTAGTATCATATGAAGAGAGAACAGTTATCTTAGTACCTATGGATTTTCTTTATTTGCTGTT
TGAATGGATTGACCTTGGTTATGTGTTGAGAATTAAGGAACATTCTTGAAATGCCTCTCTCAGACCCATCTTGG
AGGCTGATTACTTACTGCACCAAAGCTATCACTGGGGTGAGATTTACTGTTTGGACAAATTTAGCCCCATCCCTT
CAAAAATACACTTGTAACCAGGTTTCCAGAGTTGTTGATAGGCTTCTGCTGAACATATGCCAACCCACCTGCAT
AATATATTTTTGTTGCTTTTATAAATCATGCATTACATAAAGTGTGACAACCTCAAATGTATTCTCTGTTCTTG
GAATACAGTGCCCTAAATGGTGTTCCTATGACCTGCAGAAAATATTTACACATAAATAAGCAATTGCAGTGTTT
TGCATGCAAAATATAAAAAATTTAAATTGTCCTGATTCTATTTTGTAAATGGAGAAACAATCATATCTTTCTAAG
CGGTAATGGAGGAAGACTAGTGCTTTGTGCATTTTGATATATTTGAGTTCATTTTTTCCACAATGTCATACTTTT
GACGCAGTTGGGTTTCTCATAAGTATCCTAGTTCATGTACATCCGAATGCTAAATAATACTGTGTTTTAAGTTTT
GTGTTGCAAGAACAAATGGAATAAAGTTGAATTGTGCT

2643/6881
FIGURE 2431

MCDKEFMWALKNGDLDEVKDYVAKGEDVNRTLEGGRKPLHYAADCGQLEILEFLLLKGADINAPDKHHITPLLSA
VYEGHVSCVKLLLSKGADKTVKGPDGLTAFEATDNQAIKALLQ

2644/6881
FIGURE 2432

ATGAGGCGGTTTTTCAGTAGTACAGAGGGTACTTTGCATATTAGACCTTTTCTGGCTCTTTTAACAAGGACGCTG
TTGCTTATTCCTAATAACAATGTCGTTCTCTGGCAGATTCATAGTCCACCAGTCCAGCTCTGGCCCAAGATCTCCT
CTCACCATGATCCCAAGTTATTCTTTCCGGATATCATTAGGAAAGGACAGCGAATCATCCCTTTTCATCCTCTTC
CCATATGCCAACCCCTCACTCCCTCTTTTCTTATTTGCAATCAGAGAGGGAAGAATGCAGATCTGCCAAGTGCGT
TATAAATACTGTGAAACAAAAGGGACGCTCTGGGGCAGCGCAGGAGGGGTACAGTCCTACAAGGTGTCCACCTCT
GGCCCTGGGCCTTCAGCAGCCGCTCCTGCACGAGTGGGCCCTGTGCCC GCATGAGCTCCTCGAGCTTCTCCCGA
GTGGACAGCAGCAGCTTTCGGGGTGGCCTGGGCAGCGGCTATGAGGTGAACCCCAACATCCAGGCCGTGCGCATC
CAGGGGAAGGAGCAGATCAAGACCCTCAACAAGAAGTTTGCCTCCTTCATAGACAAGGTACGGTTTCTGGAGCAG
CAGAACAAAGATGCTGGAGACCAAGTGGAGCCTCCTGCAGCAGCAGACGACGACTCGGAGCAACATGGACAACATG
TTCGAGAGCTACATCAACAACCTTAGGCGGCAGCTGAAGCACTCTTCTTTTAAAAGTTTCTGA

2645/6881
FIGURE 2433

CTCTTTCCCATCTTGCAAGATGGCGGGTGAAAAAGTTGAGAAGCCAGATACTAAAGAGAAGAAACCTGAAGCCAA
GAAGGCTGATGCTGGTGGCAAGGTGAAAAAGGTAACTCAAGGCTAAAAAGCCCAAGAAGGGGAAGCCCCATTG
CAGCCGCAACCTGTCAATTGTCAGAGGAATTGGCAGGTATTCCCGATCTGCTATGTATTCCAGAAAGGCCATGTA
CAAGAGGAAGTACTCAGCCGCTAAATCCAAGTTGAAAAGAAAAAGAAGGAGAAGGTTCTTGCAACTGTTACAAA
ACCAAGTTGGTGGTGACAAGAACGGCAGTACCCGGGTGGTTAACTTCGCAAAATGCCTAGATATTATCCTACTGA
AGATGTGCCTCGAAAGCTGTTGAGCCACAGCAAAAAACCTTCAGTCAGCACGTGAGAAAACCTGCGAGCCAGCAT
TACCCCGGGACCATTTCTGATCATCCTCACTGGACGCCACAGGGGCAAGAGGGTGGTTTTCTGAAGCAGCTGGC
TAGTGGCTTGTTACTTGTGACTGGACCTCTGGTCCTCAATCGAGTTTCTCTACGAAGAACACACCAGAAATTTGT
CATTGCCACCTCAACCAAAAATCGATATCAGCAATGTAAAAATCCCAAAACATCTTACTGATGCTTACTTCAAGAA
GAAGAAGCTGCGGAAGCCCAGACACCAGGAAGGTGAGATCTTCGACACAGAAAAAGAGAAATATGAGATTACGGA
GCAGTGCAAGATTGAGCAGAAAGCTGTGGACTCACAAATTTTACCAAAAAATCAAAGCTATTCTCAGCTCCAGGG
CTACCTGTGATCTGTGGTTGCCCTGACGAATGGAATTTATCCTCACAAATTGGTGTCTAAATGTCTTAAGAACT
TAATTAAATAGTTGACTAC

2646/6881
FIGURE 2434

CAGGGCCCCTGAGATCATCCTTGGTTTACCATTTTGTGAGGCAATTGACATGTGGTCCCTGGGCTGTGTTATTGC
AGAATTGTTCCCTGGGTGGCCGTTATATCCAGGAGCTTCGGAGTATGATCAGATTCCGTATATTTACAAACACA
GGGTTTGCCTGCTGAATATTTATTAAGCGCCGGGACAAAGACAACCTAGGTTTTTCAACCGTGACACGGACTCACC
ATATCCTTTGTGGAGACTGAAGACACCAGATGACCATGAAGCAGAGACAGGGATTAAGTCAAAAGAAGCAAGAAA
GTACATTTTCAACTGTTTAGATGATATGGCCAGGTGAACATGACGACAGATTGGAAGGGAGCGACATGTTGGT
AGAAAAGGCTGACCGGCGGGAGTTCATTGACCTGTTGAAGAAGATGCTGACCATTGATGCTGACAAGAGAATCAC
TCCAATCGAAACCTGAACCATCCCTTTGTACCATGACACACTTACTCGATTTTCCCCACAGCACACACGTCAA
ATCATGTTTCCAGAACATGGAGATCTGCAAGCGTCGGGTGAATATGTATGACACGGTGAACCAGAGCAAAACCCC
TTTCATCACGCACGTGGCCCCCAGCACGTCCACCAACCTGACCATGACCTTTAACAACCAGCTGACCAGTGTCCA
CAACCAGGCTCCCTCCTCTACCAGTGCCACTATTTCCCTTAGCCAAATCCCGAAGTCTCCATACTAAACTACCCATC
TACACTCTACCAGCCCTCAGCGGCATCCATGGCTGCAGTGGCCAGCGGAGCATGCCCCCTGCAGACAGGAACAGC
CCAGATTTGTGCCCCGGCTGACCCGTTCCAGCAAGCTCTCATCGTGTGTCCCCCGGCTTCCAAGGCTTGCAGGC
CTCTCCCTCTAAGCACGCTGGCTACTCGGTGCGAATGGAAAATGCAGTTCCCATCGTCACTCAAGCCCCAGGAGC
TCAGCCTCTTCAGATCCAACCAGGTCTGCTTGCCAGCAGGCTTGGCCAAGTGGGACCCAGCAGATCCTGCTTCC
CCCAGCATGGCAGCAACTGACTGGAGTGGCCACCCACACATCAGTGCAGCATGCCACCGTGATTCCCGAGACCAT
GGCAGGCACCCAGCAGCTGGCGGACTGGAGAAATACGCATGCTCACGGAAGCCATTATAATCCCATCATGCAGCA
GCCTGCACTATTGACCGGTCATGTGACCCTTCCAGCAGCACAGCCCTTAAATGTGGGTGTGGCCACGTGATGCG
GCAGCAGCCAACCAGCACCACCTCCTCCCGGAAGAGTAAGCAGCACCAGTCATCTGTGAGAAATGTCTCCACCTG
TGAGGTGTCTCCTCTCAGGCCATCAGCTCCCCACAGCGATCCAAGCGTGTCAAGGAGAACACACCTCCCCGCTG
TGCCATGGTGCACAGTAGCCCGGCTGCAGCACCTCGGTACCTGTGGGTGGGGCGACGTGGCCTCCAGCACCAC
CCGGGAACGGCAGCGGCAGACAATTGTCAATCCCGACACTCCCAGCCCCACGGTCAGCGTCATCACCATCAGCAG
TGACACGGACGAGGAGGAGGAACAGAAACAGCCCCCACCAGCACTGTCTCCAAGCAAAGAAAAAACGTATCAG
CTGTGTACAGTCCACGACTCCCCCTACTCCGACTCCTCCAGCAACACCAGCCCCCTACTCCGTGCAGCAGCGTGC
TGGGCACAACAATGCCAATGCCTTTGACACCAAGGGGAGCCTGGAGAATCACTGCACGGGGAACCCCCGAACCAT
CATCGTGCCACCCCTGAAAACCCAGGCCAGCGAAGTATTGGTGGAGTGTGATAGCCTGGTGCCAGTCAACACCAG
TCACCACTCGTCCTCCTACAAGTCCAAGTCTCCAGCAACGTGACCTCCACCAGCGGTCACTCTTCAGGGAGCTC
ATCTGGAGCCATCACCTACCGGCAGCAGCGGCCGGGCCCCCACTTCCAGCAGCAGCAGCCACTCAATCTCAGCCA
GGCTCAGCAGCACATCACCACGGACCGCACTGGGAGCCACCGAAGGCAGCAGGCCTACATCACTCCCACCATGGC
CCAGGCTCCGTACTCCTTCCCGCACAAACAGCCCCAGCCACGGCACTGTGCACCCGCATCTGGCTGCAGCCGCTGC
CGCTGCCCACCTCCCCACCCAGCCCCACCTCTACACCTACACTGCGCCGGCGGCCCTGGGCTCCACCGGCACCGT
GGCCACCTGGTGGCCTCGCAAGGCTCTGCGCGCCACACCGTGCAGCACACTGCCTACCCAGCCAGCATCGTCCA
CCAGGTCCCCGTGAGCATGGGCCCCCGGGTCTGCCCCTCGCCACCATCCACCCGAGTCAGTATCCAGCCCAATT
TGCCACACAGACCTACATCAGCGCTCGCCAGCCTCCACCGTCTACACTGGATACCCACTGAGCCCCGCCAAGGT
CAACCAGTACCCTTACATATAAACACTGGAGGGGAGGGAGGGAGGGAGGGAGGAGAGAATGGCCCCGAGGGAGGA
GGGAGAGAAGGAGGGAGGCGCTCCTGGGACCGTGGGCGCTGGCCTTTTATACTGAAGATGCCGCACACAAACAAT
GCAAACGGGGCAGGGGCGGGGGGGGGGGGGGGCAGAGGGCAGGGGGACGGGTGGGACACCAGTGAAACTTGA
ACCGGGAAGTGGGAGGACGTAGAGCAGAGAAGAGAACATTTTAAAGGAAGGGATTAAAGAGGGTGGGAAATCT
ATGGTTTTTATTTTAAAAAA

2647/6881
FIGURE 2435

CCTGCGTGGCTGGGCTGCTCGGGTTAGATCGTCAGGAAAAGCCTAAAGATTAGACTGTAAGAAAAGAAAATAGAA
GCCATGTTTTCGAAGACCTGTATTACAGGTACTTCGTCAGTTTGTAAGACATGAGTCCGAAACAACCTACCAGTTTG
GTTCTTGAAAGATCCCTGAATCGTGTGCACTTACTTGGGCGAGTGGGTCAGGACCCTGTCTTGAGACAGGTGGAA
GGAAAAATCCAGTCACAATATTTTCTCTAGCAACTAATGAGATGTGGCGATCAGGGGATAGTGAAGTTTACCAA
CTGGGTGATGTCAGTCAAAAAGACAACATGGCACAGAATATCAGTATTCCGGCCAGGCCTCAGAGACGTGGCATAT
CAATATGTGAAAAAGGGGTCTCGAATTTATTTGGAAGGGAAAAATAGACTATGGTGAATACATGGATAAAAAATAAT
GTGAGGCGACAAGCAACAACAATCATAGCTGATAATATTATATTTCTGAGTGACCAGACGAAAGAGAAGGAGTAG

AAAGGATGATTCTTCTTTGGCCATCATTIGGTACAGTCTCATTTCCAAGTCATGTATAATCTTTATGGCTTCCAA
GGACAAGAATTAAAATACTCTTTTACGT

2648/6881
FIGURE 2436

MFRRPVLQVLRQFVRHESETTTSLVLERSLNRVHLLGRVGQDPVLRQVEGKNPVTIFSLATNEMWRS
GDSEVYQL
GDVSQKTTWHRISVFRPGLRDVAYQYVKKGSRIYLEGKIDYGEYMDKNNVRRQATTIIADNII
FLSDQTKEKE

2649/6881
FIGURE 2437

GACCAGCCGTGCAAATCTCTAGAAGATGACGGTGTTCCTTTAAAAACGCTTCGAAATCACTGGAAGAAAACTACAGC
TGGGCTCTGCCTGCTGACCTGGGGAGGCCATTGGCTCTATGGAAAACACTGTGATAACCTCCTAAGGAGAGCAGC
CTGTCAAGAAGCTCAGGTGTTTGGCAATCAACTCATTCTCCCAATGCACAAGTGAAGAAGGCCACTGTTTTTCT
CAATCCTGCAGCTTGCAAAGGAAAAGCTAGGACTCTATTTGAAAAAATGCTGCCCCGATTTTACATTTATCTGG
CATGGATGTGACTATTGTTAAGACAGATTATGAGGGACAAGCCAAGAACTCCTGGAACCTGATGGAAAAACACGGA
TGTGATCATTGTTGCAGGAGGAGATGGGACACTGCAGGAGGTTGTTACTGGTGTCTTCGACGAACAGATGAGGC
TACCTTCAGTAAGATTCCCATTGGATTTATCCCACTGGGAGAGACCAGTAGTTTGAGTCATACCTCTTTGCCGA
AAGTGGAAACAAAGTCCAACATATTACTGATGCCACACTTGCCATTGTGAAAGGAGAGACAGTTCCACTTGATGT
CTTGAGATCAAGGGTGAAAAGGAACAGCCTGTATTTGCAATGACCGGCCCTTCGATGGGGATCTTTTCAGAGATGC
TGGCGTCAAAGTTAGCAAGTACTGGTATCTTGGGCCTCTAAAAATCAAAGCAGCCCACTTTTTTCAGCACTCTTAA
GGAGTGGCCTCAGACTCATCAAGCCTCTATCTCATACACGGGACCTACAGAGAGACCTCCCAATGAACCAGAGGA
GACCCCTGTACAAAGGCCTTCTTTGTACAGGAGAATATTACGAAGGCTTGCCTCCTACTGGGCACAACCACAGGA
TGCCCTTTCCCAAGAGGTGAGCCCGGAGGTCTGGAAAGATGTGCAGCTGTCCACCATTGAACCTGACACCATCAGCAA
ACGGAATAATCAGCTTGACCCGACAAGCAAAGAAGATTTTCTGAATATCTGCATTGAACCTGACACCATCAGCAA
AGGAGACTTTATAACTATAGGAAGTCGAAAGGTGAGAAACCCCAAGCTGCACGTGGAGGGGCACGGAGTGTCTCCA
AGCCAGCCAGTGCACCTTTGCTTATCCCGAGGGAGCAGGGGGCTCTTTTAGCATTGACAGTGAGGAGTATGAAGC
GATGCCTGTGGAGGTGAAACTGCTCCCCAGGAAGCTGCAGTCTTCTGTGATCCTAGGAAGAGAGAACAGATGCT
CACAAGCCCCACCCAGTGGAGCAGCAGAAGACAAGCACTCTGAGACCACACTTTAGGCCACCGGTGGGACCAAAAG
GGAACAGGTGCCTCAGCCATCCCAACAGTGTCTGTCAGAGGGTCCCCAGGGCATTTCATGGCAAGTACCCCTCTG
CCCCCACTCCAGCAGTGTCTCCCAAAGTGTGCTCTGTCACTGCTTTGCAATCGGCTTCCATTAGCGCATGTTTT
ATTTTGGTGTGACGGTTGGCCCTCCTAAACACGGACTTTCTCAGGCTGGTTCAAGACGGAAGGACTTTCTTC
TGTTTTCTTCCAAAGTGCAACCACAGTGGAGAGCCACGGTGGGCTTAGCCTGCCTAGGCCCTTCCATTTCTCTT
CTTTGACCGTGCTAGGAATTCCAGGAAAGTGCATTCTGCCCCTGGTGACCTTTTCTATGTCTAGGCTCCTCCAC
AGGTGCTGCTATTTTGTGAGCTCCGGCCTCTGTTTAGCTTTTATTTTCAAGTCTAACCTCAGTCCAGAAACATATG
TGAGGTTGTTTCCCTCTTCAGCCACGGCTACAATACCGGAAAAATGCTAGTTTTTTATTTATTTTTTTAAGTAGTGC
TTCCTAAATGGTTTGCATGAGAGCCACCTGGGGTACATGTTGAAAACCTTATTTGGGGTCTACCCCAAACCTAATA
ACCCAAATTTGGGGATGGGGCCCAGGAATATGCATTTTTTAAAAAGTCATCTGCCCTTCCCAGGTGATTCTGTAAAG
TTGTCCCTCAACTGTACTTGGAGAAATCGTGTTTTTAAAGCAGTAGTCCACAAAGTATTCTGCTCATGTGCCCCCA
AAAGTATTTTGAATAATCATGTATACCTCACCCTACCCATCTAAGTTGATATCTAAAATTTTATCTAAGTTGGTATCTA
AAATTTTTTCATGGGAAGTTAAATAGTTGACAAAGTATGTATTTGCTGGTGTCTGTAAATATTGGTATTTTTAAAA
TAAAAACTGTTACATCACTATTTTTAAACATATCCAGTACAATTTAAATATCACAACAATTTGACACCTTCATT
ATTTATAAAAAATAAATGAGCTAGTTCTTTAGTAGTTAAACATTTCAAATTGGCTTTTCTCCTTCTGTATTTCCAT
ACCACTTTTCAGCCAAGAATCCTATCATAATGTAATCTATTATGCCCCACATCTTTTAATCATTACCCCCATTAC
TTCTTGTCAACAAAAAATATAAATGGAAATTTTTTTTTTAGCTCTTGCTTTAAGTGTGTTTGTGTTATCTCAGTC
CAGAACCAATATTATCGTAATTAATTATTGGTATATAATGAAAACGGTATTAATTCTTGGATGATTAAAAGTTTT
TTTATTAGAATGTTCTTTATCCTAATTAGTTTATTTATCCAAGAATACATGAATGTGATTTACAGCTGAGATGGG
GTTCAACCTCAGCTGTATTCCTTGTCTGTATAGATGTAAGCACATAAATTCGATGGAATAGAATTACGTTAAC
AATGAAAAAAAAAAAAAAAAA

2650/6881
FIGURE 2438

MTVFFKTLRNHWKKT TAGLCLLTWGGHWLYGKHCDNLLRRAACQEAQVFGNQLIPPNAQVKKATVFLNPAACKGK
ARTLFEKNAAPILHLSGMDVTIVKTDYEGQAKKLELEMENTDVII VAGGDGTLQEVVTGVLRRRTDEATFSKIPIG
FIPLGETSSLSHTLFAESGNKVQHITDAILAIVKGETVPLDVLQIKGEKEQPVFAMTGLRWGSFRDAGVKVSKYW
YLGPLKIKAAHFFSTLKEWPQTHQASISYTGPTERPPNEPEETPVQRPSLYRRILRRLASYWAQPQDALSQEVSP
EVWKDVQLSTIELSITTRNNQLDPTSKEDFLNICIEPDTISKGDFITIGSRKVRNPKLHVEGTECLQASQCTLLI
PEGAGGSFSIDSEYEAMPVEVKLLPRKLQFFCDPRKREQMLTSPTQ

2651/6881
FIGURE 2439

CGCCTCCCTTCCCCCTCCCCGCCGACAGCGGCCGCTCGGGCCCCGGCTCTCGGTTATAAGATGGCGGCGCTGAG
CGGTGGCGGTGGTGGCGGCGCGGAGCCGGGCCAGGCTCTGTTCAACGGGGACATGGAGCCCGAGGCCGGCGCCGG
CGCCGGCGCCGCGGCCTCTTCGGCTGCGGACCCTGCCATTCCGGAGGAGGTGTGGAATATCAAACAAATGATTAA
GTTGACACAGGAACATATAGAGGCCCTATTGGACAAATTTGGTGGGGAGCATAATCCACCATCAATATATCTGGA
GGCCTATGAAGAATACACCAGCAAGCTAGATGCACTCCAACAAAGAGAACAACAGTTATTGGAATCTCTGGGGAA
CGGAACTGATTTTTCTGTTTCTAGCTCTGCATCAATGGATACCGTTACATCTTCTTCTTCTTAGCCTTTCAGT
GCTACCTTCATCTCTTTCAGTTTTTCAAAAATCCACAGATGTGGCACGGAGCAACCCCCAAGTCACCACAAAAACC
TATCGTTAGAGTCTTCTGCCCCAACAAACAGAGGACAGTGGTACCTGCAAGGTGTGGAGTTACAGTCCGAGACAG
TCTAAAGAAAAGCACTGATGATGAGAGGTCTAATCCCAGAGTGTGTGCTGTTTACAGAATTCAGGATGGAGAGAA
GAAACCAATTGGTTGGGACACTGATATTTCTGGCTTACTGGAGAAGAATTGCATGTGGAAGTGTGGAGAATGT
TCCACTTACAACACACAACCTTTGTACGAAAAACGTTTTTCACCTTAGCATTTTGTGACTTTTGTGAAAGCTGCT
TTTCCAGGGTTTCCGCTGTCAAACATGTGGTTATAAATTTACCAGCGTTGTAGTACAGAAGTCCACTGATGTG
TGTTAATTATGACCAACTTGATTTGCTGTTTGTCTCCAAGTCTTTGAACACCACCCAATACCACAGGAAGAGGC
GTCCTTAGCAGAGACTGCCCTAACATCTGGATCATCCCCTTCGCGACCCGCTCGGACTCTATTGGGCCCCAAAT
TCTCACCAGTCCGTCTCCTTCAAATCCATTCCAATTCACAGCCCTTCGACCAGCAGATGAAGATCATCGAAA
TCAATTTGGGCAACGAGACCGATCCTCATCAGCTCCCAATGTGCATATAAACACAATAGAACCTGTCAATATTGA
TGACTTGATTAGAGACCAAGGATTTCTGTTGATGGAGGATCAACCACAGGTTTGTCTGCTACCCCCCTGCCTC
ATTACCTGGCTCACTAATAAGTGAAGCCTTACAGAAATCTCCAGGACCTCAGCGAGAAAGGAAGTCATCTTC
ATCCTCAGAAGACAGGAATCGAATGAAAACACTTGGTAGACGGGACTCGAGTGATGATTGGGAGATTCTGTATGG
GCAGATTACAGTGGGACAAAGAATTGGATCTGGATCATTTGGAACAGTCTACAAGGGAAAGTGGCATGGTGTATGT
GGCAGTGAAAATGTTGAATGTGACAGCACCTACACCTCAGCAGTTACAAGCCTTCAAAAATGAAGTAGGAGTACT
CAGGAAAACACGACATGTGAATATCCTACTCTTCATGGGCTATTCCACAAAGCCACAACCTGGCTATTGTTACCCA
GTGGTGTGAGGGCTCCAGCTTGTATCACCATCTCCATATCATTGAGACCAAAATTTGAGATGATCAAACTTATAGA
TATTGCACGACAGACTGCACAGGGCATGGATTACTTACACGCCAAGTCAATCATCCACAGAGACCTCAAGAGTAA
TAATATATTTCTTCATGAAGACCTCACAGTAAAAATAGGTGATTTTGGTCTAGCTACAGTGAAAATCTCGATGGAG
TGGGTCCCATCAGTTTGAACAGTTGTCTGGATCCATTTTGTGGATGGCACCAGAAAGTCATCAGAATGCAAGATAA
AAATCCATACAGCTTTCAGTCAGATGTATATGCATTTGGAATTGTTCTGTATGAATTGATGACTGGACAGTTACC
TTATTCAAACATCAACAACAGGGACCAGATAATTTTTATGGTGGGACGAGGATACCTGTCTCCAGATCTCAGTAA
GGTACGGAGTAACGTCCAAAAGCCATGAAGAGATTAATGGCAGAGTGCCTCAAAAAGAAAAGAGATGAGAGACC
ACTCTTTCCCCAAATTTCTCGCCTCTATTGAGCTGCTGGCCCGCTCATTGCCAAAAATTCACCGCAGTGCATCAGA
ACCCTCCTTGAATCGGGCTGGTTTCAAACAGAGGATTTTAGTCTATATGCTTGTGCTTCTCCAAAAACACCCAT
CCAGGCAGGGGGATATGGTGCCTTCTGTCCACTGAAACAAATGAGTGAGAGAGTTTCAAGAGAGTAGCAACAAA
AGGAAAATAAATGAACATATGTTTGCTTATATGTTAAATTGAATAAAATACTCTCTTTTTTTTTTAAGGTG

2652/6881
FIGURE 2440

GGCACGAGGGTGTCCCTCCCCGCCCGGCTGGAGGCTGCTCCGGACCGGGACGCAGAGTCTGCGGACCCGGCGCCG
AGGCGGCCACCCGAGACGCGGCGCGCACGCTCCGGCCTGCGCAGCCCGGCCCGGCC**ATG**GCGGCCCCCGCCCGT
CTCCCGCGATCTCCGTTTTCGGTCTCGGCTCCGGCTTTTTACGCCCCGCAGAAGAAGTTCGGCCCTGTGGTGGCC
CAAAGCCCCAAAGTGAATCCCTTCCGGCCCCGGGACAGCGAGCCTCCCCCGGCACCCGGGGCCCAGCGCGCACAGA
TGGGCCGGGTGGGCGAGATTCCCCCGCCGCCCCCGGAAGACTTTCCCTGCTCCACCTCCCTTGCTGGGGATG
GCGACGATGCAGAGGGTGCTCTGGGAGGTGCCTTCCCGCCGCCCCCTCCCCGATCGAGGAATCATTTCCTCCCTG
CGCTCTGGAGGAGGAGATCTTCCCTTCCCGCCGCTCCTCCGGAGGAGGAGGGAGGGCCTGAGGCCCCCATAC
CGCCCCACACAGCCAGGGAGAAGGTGAGCAGTATTGATTGGAGATCGACTCTCTGTCTCTACTGCTGGATG
ACATGACCAAGAATGATCCTTTCAAAGCCCGGTGTATCTGGATATGTGCCCCACCAAGTGGCCACTCCATTCA
GTTCCAAGTCCAGTACCAAGCCTGCAGCCGGGGGCACAGCACCCCTGCCTCCTTGGAAGTCCCTTCCAGCTCCC
AGCCTCTGCCCCAGGTTCCGGCTCCGGCTCAGAGCCAGACACAGTTCCATGTTTCAGCCCCAGCCCCAGCCCAAGC
CTCAGGTCCAACCTCCATGTCCAGTCCCAGACCCAGCCTGTGTCTTTGGCTAACACCCAGCCCCGAGGGCCCCAG
CCTCATCTCCGGCTCCAGCCCCTAAGTTTTCTCCAGTGACTCCTAAGTTTACTCCTGTGGCTTCCAAGTTCAGTC
CTGGAGCCCCAGGTGGATCTGGGTCAACAACAAATCAAAAATTGGGGCACCCCGAAGCTCTTTCTGCTGGCACAG
GCTCCCCTCAACCTCCAGCTTCACCTATGCCAGCAGAGGGAGAAGCCCCGAGTGCAGGAGAAGCAGCACCCCCG
TGCCCCACCGGCTCAGAACCAAAACAGGTGCGCTCCCCTGGGGCCCCAGGGCCCCCTGACTCTGAAGGAGGTGG
AGGAGCTGGAGCAGCTGACCCAGCAGCTAATGCAGGACATGGAGCATCCTCAGAGGCAGAATGTGGCTGTCAACG
AACTCTGCGGCCGATGCCATCAACCCCTGGCCCGGGCGCAGCCAGCCGTCCGCGCTCTAGGGCAGCTGTTCCACA
TCGCCTGCTTACCTGCCACCAAGTGTGCGCAGCAGCTCCAGGGCCAGCAGTTCTACAGTCTGGAGGGGGCGCCGT
ACTGCGAGGGCTGTTACACTGACACCCTGGAGAAGTGTAACACCTGCGGGGAGCCCATCACTGACCGCATGCTGA
GGGCCACGGGCAAGGCCTATCACCCGCACTGCTTACCTGTGTGGTCTGCGCCCGCCCCCTGGAGGGCACCTCCT
TCATCGTGGACCAGGCCAACCGGCCCCACTGTGTCCCGACTACCACAAGCAGTACGCCCCGAGGTGCTCCGTCT
GCTCTGAGCCCATCATGCCTGAGCCTGGCCGAGATGAGACTGTGCGAGTGGTGCCTTGGACAAGAAGTTCACACA
TGAAGTGTTACAAGTGTGAGGACTGCGGGAAGCCCCTGTGATTGAGGCAGATGACAATGGCTGCTTCCCCCTGG
ACGGTCACGTGCTCTGTGCGAAGTGCCACACTGCTAGAGCCAGACCT**TGAG**TGAGGACAGGCCCTCTTCAGACCG
CAGTCCATGCCCCATTGTGGACCACCCACACTGAGACCACCTGCCCCCACCTCAGTTATTGTTTTGATGTCTAGC
CCCTCCCATTTCCAACCCCTCCCTAGCATCCAGGTGCCCTGACCCAGGACCCAACATGGTCTAGGGATGCAGGA
TCCCCGCCCTGGGGTCTGGTCTCGCCATCCTGCAGGGATTGCCACCGTCTTCCAGACACCCACCTGAGGGG
GGCACCAGGTTTAGTGCTGCTGCTTTCACTGCTGCACCCGCGCCCTCGGCCGGCCCCCGAGCAGCCTTTGTACT
CTGCTTGCGGAGGGCTGGGAGACCCTCCAGGACATTCCACCCCTCCCCATGCTGCCAAGTTGTAGCTATAGCTA
CAAATAAAAAAAAAACCTTGTTTTCCAGAAAAAAAAAAAAAAAAAAAAA

2653/6881
FIGURE 2441

MAAPRPSPAISVSVSAPAFYAPQKKFGPVVAPKPKVNPFRPGDSEPPPAFPAQRAQMGRVGEIPPPPPEDFFPLPP
PPLAGDGDDAEGALGGAFFFFPPPIEESFPPAPLEEEIFPSPPPPPEEEGGPEAPIPPPPQPREKVSSIDLEIDS
LSSLLDDMTKNDFKARVSSGYVPPPVATPFSSKSSTKPAAGGTAPLPPWKSPSSSQPLPQVPAPAQSQTFHVQ
PQPQPKPQVQLHVQSQTQFVSLANTQPRGPPASSPAPAPKFSVTPKFSTPVASKFSPGAPGGSGSQPNQKLGHPE
ALSAGTGSPQPPSFTYAQQREKPRVQEKQHPVPPPAQNQNQVRSPGAPGPLTLKEVEELEQLTQQLMQDMEHPQR
QNVAVNELCGRCHQPLARAQPAVRALGQLFHIACTCHQCAQQLQGQQFYSLGAPYCEGCYTDLEKCNCTGEP
ITDRMLRATGKAYHPHCFTCVVCARPLEGTSFIVDQANRPHCVDPYHKQYAPRCSVCSEPIMPEPGRDETVRVVA
LDKNFHMCKYKCEDCGKPLSIEADDNGCFPLDGHVLCRKCHTARAQT

2654/6881
FIGURE 2442

GGCACGAGGGGCGGCGGAGCCGACTCGTCGCGGCCGAGGCGCACGCGGTCCGCGCCGGCGTCAGTCTGGGATTGG
CCGGCCCCGCGACTTCCCTCCGCCCCCTGCCAATCGCCGGGGACGACTTCCGTGGGTTTTTCCGGCTCTCCCGCGTC
GCTAAGGAGCGACGGGCTGTGCGGCCAGACCCCGAGTTCTCGGTGCGCTCAGCGGCCGCCGACGCTAGGAGGCCGC
GCTCCGCCCCCGCTACCA**ATG**AGGCCCCGGAAAGCCTTCTGCTCCTGCTGCTCTTGGGGCTGGTGCAGCTGCTGG
CCGTGGCGGGTGCCGAGGGCCCCGACGAGGATTCTTCTAACAGAGAAAAATGCCATTGAGGATGAAGAGGAGGAGG
AGGAGGAAGATGATGATGAGGAAGAAGACGACTTGGAAGTTAAGGAAGAAAAATGGAGTCTTGGTCTAAATGATG
CAAACCTTTGATAATTTTGTGGCTGACAAAGACACAGTGCTGCTGGAGTTTTATGCTCCATGGTGTGGACATTGCA
AGCAGTTTGCTCCGGAATATGAAAAATTGCCAACATATTAAAGGATAAAAGATCCTCCCATTCCTGTTGCCAAGA
TCGATGCAACCTCAGCGTCTGTGCTGGCCAGCAGGTTTGATGTGAGTGGCTACCCACCATCAAGATCCTTAAGA
AGGGGCGAGGCTGTAGACTACGAGGGCTCCAGAACCAGGAAGAAATTGTTGCCAAGGTCAGAGAAGTCTCCACAGC
CCGACTGGACGCCTCCACCAGAAGTCACGCTTGTGTTGACCAAAGAGAACTTTGATGAAGTTGTGAATGATGCAG
ATATCATTCTGGTGGAGTTTTATGCCCATGGTGTGGACACTGCAAGAACTTGCCCCGAGTATGAGAAGGCCG
CCAAGGAGCTCAGCAAGCGTTCTCCTCCAATTCCCCTGGCAAAGGTCGACGCCACCGCAGAAACAGACCTGGCCA
AGAGGTTTGATGTCTCTGGCTATCCACCCCTGAAAATTTCCGCAAAGGAAGGCCTTATGACTACAACGGCCCCAC
GAGAAAAATATGGAATCGTTGATTACATGATCGAGCAGTCCGGGCCTCCTCCAAGGAGATTCTGACCCTGAAGC
AGGTCCAGGAGTTCTGAAGGATGGAGACGATGTCATCATCATCGGGTCTTTAAGGGGGAGAGTGACCCAGCCT
ACCAGCAATACCAGGATGCCGCTAACACCTGAGAGAAGATTACAAATTTACCACACTTTACGACAGAAATA**G**
CAAAGTTCTTGAAAGTCTCCAGGGGCAGTTGGTTGTAATGCAGCCTGAGAAATTCAGTCCAAGTATGAGCCCC
GGAGCCACATGATGGACGTCCAGGGCTCCACCCAGGACTCGGCCATCAAGGACTTCGTGCTGAAGTACGCCCTGC
CCCTGGTTGGCCACCGCAAGGTGTCAAACGATGCTAAGCGCTACACCAGGCGCCCCCTGGTGGTCTGCTACTACA
GTGTGGACTTCAGCTTTGATTACAGAGCTGCAACTCAGTTTTGGCGGAGCAAAGTCCTAGAGGTGGCCAAGGACT
TCCCTGAGTACACCTTTGCCATTGCGGACGAAGAGGACTATGCTGGGGAGGTGAAGGACCTGGGGCTCAGCGAGA
GTGGGGAGGATGTCAATGCCGCCATCCTGGACGAGAGTGGAAGAAGTTCGCCATGGAGCCAGAGGAGTTTGACT
CTGACACCCTCCGCGAGTTTGTCACTGCTTTCAAAAAAGGAAAACTGAAGCCAGTCATCAAATCCCAGCCAGTGC
CCAAGAACAACAAGGGACCCGTCAAGGTGCTGGTGGGAAAGACCTTTGACTCCATTGTGATGGACCCCAAGAAGG
ACGTCCTCATCGAGTTCTACGCACCATGGTGCGGGCACTGCAAGCAGCTAGAGCCCGTGTACAACAGCCTGGCCA
AGAAGTACAAGGGCCAAAAAGGGCCTGGTCAATCGCCAAGATGGACGCCACTGCCAACGACGTCCCCAGCGACCGCT
ATAAGGTGGAGGGCTTCCCCACCATCTACTTCGCCCCCAGTGGGGACAAAAAGAACCAGTTAAATTTGAGGGTG
GAGACAGAGATCTGGAGCATTGAGCAAGTTTATAGAAGAACATGCCACAAAAGTGAAGCAGGACCAAGGAAGAGC
TT**TGA**AGGCCTGAGGTCTGCGGAAGGTGGGAGGAGGCAGACACCCCTGCGTGGCCCATGGTTCGGGGCGTCCACGCC
GAGGCCGGCAACAAACGACAGTATCTCGGATTCTTTTTTTTTTTTTTTTTTAAATTTTTTATACTTTGGTGTTCAC
TTCATGCTCTGAATACTGAATAACCATGAATGACTGAATAGTTTAGTCCAGATTTTTACAGAGGATACATCTATT
TTTATCATTATTTGGGGTTTGAAAAATTTTTTTTTTACACCTTCTAATTTCTTTATTTCTCAAAGCAGATAATTCT
TCTGTGTGAAAATGTTTTCTTTTTTTAATTTAAGGTTTAAATTCCTTTGCCAAATCATGTTGATTTTGCTCTTT
GCTTTTTCGTTGTCTGAGAAATTGTTGGCGTAGATTTGGCTTCTGGTATGTGTTTCTGATTGCTTCCTGTTGAGC
ACAAAGTGAGAGCTGCCACTGAGCAGCCCTGCCAGGGGTGCTGTTTCAGGCTGGGCATCGCCAGGCGGCCTCCCT
GCAAACCAAGGGCTGGGGGCAAAGGGGCATGATCCAGGGTCCCCAGGGTGGGCTCAGCTCCAGGGAGAGGCCAC
CCAGTGGCAGCCCCACCTCTTGAGAGCCCCAGTGCCGGAGCAGAAAGGACCCTGGACCCAGAGGCAGATACTG
CGGGGTGGTAGAAAAGGTAGAGTAGGCTGTGGCAATGGAATAAAACACGATTAAAAACGTTAAAAAAAAAAAAA
AAAAA

2655/6881
FIGURE 2443

MRPRKAFLLLLLLGLVQLLAVAGAEGPDEDSSNRENAIEDEEEEEEEDDDEEEDDLEVKEENGVLVLNDANFDNF
VADKDTVLLLEFYAPWCGHCKQFAPEYEKIANILKDKDPPIPVAKIDATSASVLA SRFDVSGYPTIKILKKGQAVD
YEGSRTQEEIVAKVREVSQPDWTPPEVTLVLTKENFDEVVNDADIILVEFYAPWCGHCKKLAPEYEKAAKELSK
RSPPIPLAKVDATAETDLAKRFDVSGYPTLKIFRKGRPYDYNPREKYGIVDYMIEQSGPPSKEILTLKQVQEFL
KDGDDVIIIGVFKGESDPAYQQYQDAANNLREDYKFHHTFSTEIAKFLKVSQGQLVVMQPEKFQSKYEPRSHMMD
VQGSTQDSAIKDFVLKYALPLVGHRKVSNDKRYTRRPLVVVYYSVDFSF DYRAATQFWR SKVLEVAKDFPEYTF
AIADEEDYAGEVKDLGLSESGEDVNAAILDESGKKFAMEPEEFDSDLREFVTAFKKGKLKPVIKSQPVPKNNKG
PVKVVVGKTFDSIVMDPKKDV LIEFYAPWCGHCKQLEPVYNSLAKKYKGQKGLVI AKMDATANDVP SDRYKVEGF
PTIYFAPSGDKKNPVKFEGGDRDLEHLSKFIEEHATKLSRTKEEL

2656/6881
FIGURE 2444A

GCCGCCGAAGGGGACTGTTTGCTCCTACGGGCTGTAGATGGAGCTGTCCGGCCCCGGAGAGGGGGAAGGCGCCTG
GAAAACGTTCTTCTTCTCCCTGGCCGACCCGAGCGGGGAACAGCACTCCCAGGATGCAGTTTGTGTCAACACGGC
CGCAGCCTCAGCAGCTGGGCATCCAGGGCCTGGGGCTGGACAGCGGGAGCTGGAGCTGGGCCCAGGCTCTGCCCC
CGGAGGAGGTCTGCCACCAGGAGCCGGCGCTGCGCGGGGAAATGGCCGAGGGAATGCCGCCCATGCAGGCTCAAG
AATGGGACATGGACGCCCCGGCGGCCAATGCCTTTTCAGTTCCCACCCTTTCAGATAGGGCACCTGTCTTCCCCG
ACCGCATGATGCGAGAGCCCCAGTTGCCACAGCAGAGATCTCACTCTGGACTGTGGTGGCTGCCATTTCAGGCTG
TGGAGAGGAAGGTGGATGCCCAGGCCAGCCAGCTGCTGAACCTGGAGGGGCGCACGGGGACAGCCGAGAAGAAGC
TGGCCGACTGTGAAAAGACGGCCGTGGAATTTGGGAACCACATGGAGAGCAAGTGGGCCGTGCTGGGGACCCTGC
TGCAGGAGTACGGGCTGCTGCAGAGGCGGCTGGAGAACTTGGAGAACTTGTGCGCAACAGGAACCTTCTGGGTCC
TGCGGCTGCCCCCGGGCAGCAAGGGGGAGGCCCCCAAGGTTCCAGTGACTTTTGTGACATTGCTGTGTACTTCT
CCGAAGACGAGTGGAAGAACTTGGACGAATGGCAGAAGGAGCTTTATAACAACCTTGTTAAGGAGAACTACAAAA
CCCTCATGTCCCTGGACGCGGAGGGCTCAGTCCCCAAGCCAGATGCTCCAGTCCAGGCTGAGCCCAGGGAAGAAC
CTTGTTGTGTTGGGAGCAGCGCCACCCCGAAGAGAGAGAAATCCCAATGGATCCCGAAGCAGGAGCAGAGCCCCCTGG
TGCTTGCAGAGATGCGTCTTCCAGGTGAAGCGTGAGGACACCCTGTGTGTCCGGGGTCAGCGGGGCCTGGAGG
AAAGAGCCATCCCTACGGAATCCATTACCGACTCCCCAATTTCTGCCCAGGACCTCTTGTCCCGGATTAAACAGG
AGGAGCATCAGTGCGTGTGGGATCAGCAGGATTTGGCAGACAGAGATATTTCCACGGATCCCAATTCAGAGTCTC
TCATCTCAGCACATGACATTTTGTATGGATCAAGCAGGAGGAGCAGCCATACCCATGGGGACCACGCGACTCAA
TGGACGGAGAGCTTGGATTAGACTCTGGCCCTAGTGACAGCCTGCTGATGGTGAAGAACCACCCCCGGCCCCGC
CACAGCCCCAGCCCCAGCCCCAGCCACCGCAGCCGAGCTGCAGTCGCAGCCCCAGCCCCAGAGCCTGCCCCCA
TCGCGGTGGCCGAGAACC CGGGCGGCCCCCCGAGCCGAGGGCTGCTGGACGACGTTTCCAGGTGCTGCCCCGGG
AGCGTGGCTCCGGCGAGGCGCCGCCGGGTGGGGACCGCAGCACCGGGGCGGCGGGGGCGATGGGGGCGGTGGGG
GCGGCGGCGCGGAGGCGGGGACGGGGGAGGCGGGCTGTGGCAGCTGCTGCCCTGGCGGGCTGCGGCGGAGCC
TCCTCTGACAGGCGCCCGCAGCAAGCCCTACTCGTGCCCCGAGTGCGGCAAGAGCTTCGGCGTGCGCAAGAGCC
TCATCATCCACCACCGCAGCCACACCAAGGAGCGGCCCTACGAGTGCGTGAGTGCGAGAAGAGCTTCAACTGCC
ACTCGGGCCTCATCCGCCACCAGATGACGCACCGCGGCGAGCGGCCCTACAAGTGCTCGGAGTGCGAGAAGACCT
ACAGCCGTAAGGAGCACCTGCAGAACCACAGCGGCTGCACACGGGCGAGCGGCCTTTCCAATGTGCACTGTGCG
GCAAGAGCTTCATCCGCAAGCAGAACCTGCTCAAGCACAGCGCATCCACACGGGCGAGCGCCCCTACACGTGCG
GCGAGTGCGGCAAGAGCTTCCGCTACAAGGAGTCGCTCAAGGACCACCTGCGCTGCACAGCGGCGGCCCGGGCC
CCGGCGCCCCACGGCAGCTCCCGCCGCCTCTGAGCGAGACTAGGGCTGGGCTGGGGGAGGGCAGGGCCGGACGG
AGTGGATCGGGGGCGGCTGAGCACCAACCACCTTGCCGGGTGTCTCTAGCCACCCTCTGGAAATCGGCAACAGG
CATTGCACTCCGTTTGGGGGTCCCCAGGGTGGGGCAGGGATCCCCAGATCTGTCTGGTCTGAATGGACGCCCCAG
CTCATCTAGGGTGGACCCAGCTGCTGGGGAAGAGCCAGGGGGACCGCGAGGAGCCGAGCGTCTCGGGCACCGCC
CTCACACCTCCTCGAGTGCCCTGGGACCCTGGGCCACAGATGGTCATCAGGGGAAGCCACCAGGGAGTCCCCGAA
GCCCTTCTGAGATCAGGAAATCAGGTCCCAAGGTTAGGAGACGCCCTGAAAAAAGCGAAGGCCGAGGGATGTGC
TAAGGGTAACACCTTCATGATGACAACACTGCCTCGCGTTTTCAATAGCGCTTTATACTTTTTTAAGTGTTTTCTA
TCCGTTATCCATTTACCCCTTGGCCTATCCCTCTCAGATAGGTGGGGTAGGATTTTCTGGTGACCGAGTAAAGT
GAGAGGCAGGTGAGACGGTTACCCCAATCACACGGGAAGGGGCGCGCGCTGCCCAACGCGCTCTCCGCTACCT
CCGCTGCTCGGGAAGCTGCTGGCCTGGCCCTCCTGGTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
TCACCCACGGATAAAACCAGAAGCGACAGGAGGCCAGCTCCTGGGGTTCTTGGAGCCGGGAACAGATTGGCTAC
GGAACGCCCCAGGTTGTACATTTCAGAGGGCTCTTTCTCCATGGGAGCTCCTGGTGCCGCTCGGCCCCAGCCTGT
CCCCAGCCCTCAATCTGGTGCAGCAGCATTTGTCTACTGCACAACAGTGGCCTGGTCCCCACAGGCAGTTAGG
GCCCCAGGTACAGCCTACCATGATGATTTGTTCCAGTTCTCCCAGGGCAGAGGGGCGAGGGAGAGGCTTTTGCT
GTGAGAGTAGCCGTACGTGTCTCTTCCAGCAGCGCCGGGCAAGTGGGTGCTAGAGTCTGAGCCTCAGGCTCTC
CTGCCCTGGGCCTCCCAATTGGTGCTATCTGTTACTGCCCGTGCTCACGGACATGGATACAGACCCTGCTGTGCT
CCACACCCTGCAGGCGCCTCGGGAAGCGCCCAAAGGATTCCTTTCACGTTGGTGCACCTGCTCCATAGCTCCGG
GCGCTGCGTCCCGAGGGGGCCACAGTCTCCATTTTCAGCGTCTTGATGGCCTGGCACCGGGTGGGGTGGTATGCC
CAGGACCCTTGTTTTGTGTCAAAAATGACTTTCCCTGCCCTTGCCGTGGGTCCGGCGTTCTTCCAGCCGGGATCA
CAGTGGGCAGCCGGCACCCGGCACCACTTTGGCGAGCGTCTGCTTCCGCCCTCGCCCTCATCTACGCTGCTCCG

2657/6881
FIGURE 2444B

CTTTCCTCAGACCCCTTTTGGCCGTGCAAAGGGAATTCTTGACATTAAATAAAAGGTATCCAGATTGCAGACTGC
ATGTTACAGAGCTGGGGGTCTCCAGCTTGCCTACAGTAAAGCCTCAATGAACTGG

2658/6881
FIGURE 2445

MQFVSTRPQPQQLGIQGLGLDSGSWSWAQALPPEEVCHQEPALRGEMAEGMPPMQAQEWDMDARRPMPFQFPFPF
DRAPVFPDRMMREPQLPTAEISLWTVVAAIQAVERKVDAQASQLLNLEGRGTAEKKLADCEKTAVEFGNHMESK
WAVLGTLLQEYGLLQRRLENLENLLRNRNFWVLRLPPGSKGEAPKVPVTFVDIAVYFSEDEWKNLDEWQKELYNN
LVKENYKTLMSLDAEGSVPKPDAPVQAEPREPCVWEQRHPEEREIPMDPEAGAEPLVPAQDASSQVKREDTLCV
RGQRGLEERAIPTESITDSPISAQDLLSRIKQEEHQCVWDQQDLADRDIPDTPNSESLSAHDILSWIKQEEQPY
PWGPRDSMDGELGLDSGPSDSLMLVKNPPPAPPQPQPQPQPQPQLQSQPQPQSLPPIAVAENPGGPPSRGLLDD
GFQVLPGERGSGEAPPGGDRSTGGGGGDGGGGGGGAEAGTGAGGGCGSCCPGGLRRSLLLHGARSKPYSCPECGK
SFGVRKSLIIHHRSHTKERPYECAECEKSFNCHSGLIRHQMTHRGERPYKCSECEKTYSRKEHLQNHQRLHTGER
PFQCALCGKSFIRKQNLKQRIHTGERPYTCGECGKSFRYKESLKDHLRVHSGGPGPGAPRQLPPPPPERD

2659/6881
FIGURE 2446

TCTTGTCCTCCGGATTAAACAGGAGGAGCATCAGTGCGTGTGGGATCAGCAGGATTTGGCAGACAGAGATATTCCCA
CGGATCCCTCGGGAAGCGCCCAAAGGATTCCCCTTCACGTGGGTGCACCTGCTCCATAGCTCCGGGCGCTGCGTC
CCGAGGGGGCCACAGTCTCCATTTACGCGTCTTGCAATGGCCTGGCACCAGGTGGGGTGGTATGCCCCAGGACCCTT
GTTTGTGTCAAAAATGACTTTCCCTGCCCTTGCCGTGGGTCCGGCGTTCTCCCAGCCGGGATCACAGTGGGCAG
CCGGCACCCGGCACCCTTTGGCGAGCGTCCTGCTTCCGCCCTCGCCCTCATCTACGCTGCTCCGCTTTCCCTCAG
ACCCCTTTTGGCGTGCAAAGGAATTCTTGACATTAAATAAAAGGTATCCAGATTGCAGACTGCATGTTACAG
AGCTGGGGGTCTCCAGCTTGCTACAGTAAAGCCTCAATGAAGTGG

2660/6881
FIGURE 2447

AGTGCCTGCGCTTCTTCCAGCAGCGCAAGAGCCTGCTGCTGCACCAGCGCCTGCACACCGGCAATGGCCAGGGCT
GGCCCGCCTGCCCCTACTGCGGCAAGGCCTTCCGCCGGCCCTCGGACCTCTTCCGGCACCAGCGCATCCACACCG
GTGAGCGGCCCTACCAGTGCCCCCAGTGTTGGCCGGACCTTCAACCGCAACCACCACCTGGCCGTGCACATGCAGA
CCCACGCCCCGAGGCCAGGTGGGCCCCACACTTCCCTGCCGCCCCCGCCGCCACGGGAGCCTGCCCTGCCCTGGC
CCAGCCGAAGGAGGAGGGCTGACCTGGCAGGAGCCCACAGAGGACCCCTGGCGGGGTCTCTCCCTGTGCCTGA

CGCAGGTTCTTCCTTTTCTGGGATGGAGAGAGGTTTGTGTTTTTACCCATTCAAATGGGAAGCTAGCTGCCCT
TCTGGTGACATTGTGTGTGACCGGGTGCTTTCTGTTTTCTGTTTGCACTCTTCGCTGCCTTTTCTGCATTCTCTGA
CTTCTAAAAGATGCCTTAAGGCTTAAGGGATGCCATATTTTTGATAAGGCCTCTGGTAGGTACCACAGCCAAGAG
GACCAGAGATCATGGCCCTTCCAGTATGGGGGCGATAGAGACATCGGGGACCTGGGATTTTTGTTTTGTGCAGAG
ATCTCCTGCCTGCTGTCAACCATGAGAAACAGTGGAGTGGAGTGGATGGATGGCCTGACTTGAAGAAAGGGCCCTG
GAAAGTTTTCTACTTTGCTATTTTTGAAATTTTTTCCCTTCTTATAGAGACTTTGAAATACTTTTGAAATGTGT
GTAGTTGTTAATGGAACCTTTGCCTTTTGCAAAGTGGAAAGAGTCGGCTTTTCCATGTGAGGCTCGCAGAGCTGA
AAGGGGAGCTACGTCCACCAGCCTGTGGGTCTTTTGGTTTTTTTTTGTGTTGTTGTTGTTTTTTAAGATGGA
GTTTCACTCTTGTGCCCAGGCTGGAGTGAATGGTACAATCTCCGCTCACTGCAACCTCCGCTCTCGGGTTCA
GGTGATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCGCCACCACCTCCCGCTAATTTTTGTGA
TTTTTAGTAGAGACAGGGTTTCATCATGTTGTCCAGACTGGTCTCGAACTCCTGATGTTAGGTGACCCGCACACC
TCGGCCTCCTGAAGTGCTGGGATTACAGGCGTGAGCCACCCTCTGGCCCAGCCTGTGGGTTTTGATGGGGATG
TCTTGGCTGCTGTCTTGGAGGCACAGTGTCTCCCATGTGTGTGTTTCTTGGCCCAGAGTGACTCCAGTATTCC
TAGTCTTCCCCACAGGATAGTCACATCCATTATTTACTTTTGTGTGCTAGCTGGGAGGGGAACTGAAGCCTGGA
CACGTCTCCCCAAGGGCTCAGTGTTTCATGGGTGTGTAAGATCCATTGACTGGACCCAGAAAGCACCCCTGAGGGG
CAGTGCAGAGAGAGCCAGGAAGCCCCCTCCACTAGAGGAGGCCCTTGGTCTGGCTGAGGACCACGTCCACCCTGG
GCCTCCAGGCCTGCTTTTACATTAAAGGCGGGCAGTCTCCTCTCAAAGGAGTTCTCCCTTGAGCACTTTGGGC
TCTGGGGCAGAGTTGGGCTAGGAGATCTGGGTGAATCCTTTAGTCACAGCTAGTCTCATGTTCTCTTCTGTCAA
AGGGGTCTAGGCCCCAGTGTGTCTACCTCAGAGTTGTGAGGGTCAAAGTAACAGGCCTGGGACAAATATGAAG
CCTAGCTTTGTGCTTCTTTCAAATTCAGGGCCTCCTTTCTACTCCATTCCAGCCTTTTTTTCTGTGAGAATCC
CTCAGGAAGGACCTTTATCTTCTGGAGTGAGTGGCAGTTCCACTGGGTTCAGTGAAAGAGTCGCCCATGGGGCTC
TGTTCCCCAGGAGTCTTTGTATTTTGGTGAACAAATTCTTACCAAAGCATGAGATTCCGACTGTAGAAGTTCAG
ACTGCCTCAGTTCAGACTGCCTCATGGGGCAGTCTGGAGGTGAGTGGCTTCTGGTGTCTCTCATCACACCCTG
CGGACGCTGTCTGTAGAGCAGCCTTGGTGTGGGTGACTCTGAAGCTGGAGTGATGGGACCCAGCTATCCTTGTT
TTTTACCGCCTTGTCTGGCACTGTGACCACGCTTCAGGGCTGCTTCTGGGGGTCTTGGTCCCTGGATGTGCCATT
TCCTTGCCCTTCTGACCTCACACTTCTTCCAAAGTCTTGAGCAGAGTTGGGGGCAATGGTAGCATTGCTGTCA
TCTCTGGGAGGAGAGTGAGTATACAAGTCAGTGACAGTTCAGCCAGGCTCCCTTGGGTTTTGGGAAGAGGCACTGC
CCTTCTGTGCTGTGGATCCTGCTTGTCTGCTCTGGAGTCCCCCACCCTTGCCAGGAGCTTCACAAACCAGAGAC
GGGCTGTCAGCAAGAGCTCAGACAGGATGTGGTGCAAGTGCAGGTGCACGAGTTTAACCCTCAGCTGCAGGAGCT
AGTCTCAGGTGTTCTGGGGATGCCTCAGGCTAAGAATTTTGGCGACTTTCTGGGCTTGGTTGGCTAATGCCAAAT
GCCCCTGCTTAAATATCACAAGGTGCTGATTCTCCTTTTTTCTTTTTTTCATACCAATGTGCTCAAACCTTTGAGC
TAGGTCTTGTGAGTTTGCCTAGCACTCAGACCTGTTTAAGTAACGTTCTTTACATTGAAACAAGTCAACCGAAGC
TTTGTGGTGCAGGAGCTGAGGGTGCCCCAGACTCAGTGGGAGCCCTGGTTGGGCCCCAACTCTCCAGCAGGGT
CCTCGGTTTTCTCATTTGTGAAATAAATGAGTGGGCCACGAGTTAATAAGCCCAAGAGAACTGTGAAGGTGGTA
GTCCCTTGCCCTAATTGGTGCTCAATAAAGTTGTTGGCAT

2661/6881
FIGURE 2448

MARAGPPAPTAARPSAGPRTSSGTSASTPVSGPTSAPSVAGPSTATTTWPECTCRPTPEARWAHTSLPPPPATGAC
PCPGPAGRRRADLAGAHRGFLAGSLPCA

2662/6881
FIGURE 2449

GCACGAGGCCAGCTTGGCCAGTGGCTCCGCAGGCTGCCGGCTCCACCCCTCAGGGACTGGCTGGCTTCGAGCAGG
GCATCGGAACCAGGCCTCCTGGCACTGGCCTGGGTAGAGCCAGGGCGAGCACCAGCTGACCCCCAGTGGAACCCCT
GTGACAGTCCTGCCAGGGCCCAGGCCATCCCAACCGACTTCCATCTCATGGACCCTCCAGCGGAGAAGCCGGGAG
AGGCTGGCGGACTGCAGATCACACCCCAGCTGCTGAAGTCACGCACAGGCGAGTTCTCCCTGGAGTCCATCCTGC
TACTGAAGCTGCGTGGCTTGGGACTGGCTGACCTGGGCTGCCTGGGAGAGTGCCTGGGCCTGGAGTGGCTGGACC
TATCAGGCAACGCGCTCACCCACCTGGGCCCGCTGGCCTCCTTGCGCCAGCTAGCTGTGCTCAATGTCTCCAACA
ATCGGCTGACGGGCCTGGAGCCACTGGCCACCTGTGAGAACTTGACAGAGTCTCAATGCCGCAGGCAACCTACTGG
CCACCCCGGGCCAGCTGCAGTGTCTGGCTGGGCTACCGTGCTGGAGTACCTGCGGCTCCGAGACCCCTTTGGCCC
GGCTCAGCAACCCGCTCTGTGCCAACCCCTCCTACTGGGCTGCAGTCCGGGAGCTGCTGCCTGGCCTGAAAGTCA
TCGACGGTGAGCGTGTGATTGGGCGTGGTAGTGAGTTCTACCAGCTGTGCCGAGACCTGGACAGCTCCTTGCGTC
CCAGCTCCAGTCCAGGCCCCAGAGCCACCGAGGCCAGCCCTGGGTGGAGCCAGGCTACTGGGAGTCCCTGGCCCCA
GCCGGAGCAGCTCCATCCTGGAGGAGGCCTGCCGGCAGTTCCAGGACACACTGCAGGAGTGTGGGACCTGGACC
GCCAGGCCAGCGACAGCCTGGCCCAGGCGGAGCAGGTACTCAGCTCTGCGGGCCCCACCTCTTCCTTCGTCTTCT
GAACGTGGCCTATGGCCCAGGACAGCCTGGCAGGTGGCCTCGCTGCCCCCAGTTCCCCTCTCTGCCCCCACACTC
GTCTTAGTTGCTTCACACTGGTCACTGGCCCTGCACACTGGGCTATTGCTTTATCCCTATCCTGAGAGCAGCCCC
TCCCCACCATCCCTCCACATGCTGCAAGGACAGACTGAAGGGCTGTGAGCAGGTGTAAGGGCTCCCACATCCGTG
AGCCTGTGTCCGCAGCTGCTGCCACTCTGGGCTGCTCCAGCCTGCAACTTAGTGGAAGGAATTACTTCCTCCTGA
GGCTACAGGCGAGAAAGGTAGGGATGGGCCAGCCTCCCGTCTCAGCTGTTGGGAGACAGTAGGCAGGCTGAGTGG
CCCAGAGCACTCCTGGAAGTGGGACTCCCCTGCCTTGCAAATGTGCCTCTCCAGACTGCTCCTGCACTTACCCCC
TCCCCGCAGCACCTTCTCTGCCCGTTCTTGTCCACACATCTATTAAATGCTTCTGTTTTCAAAAAAAAAAAAAA
AAAAA

2663/6881
FIGURE 2450

MDPPAEKPG EAGGLQITPQLLKSRTGEFSLESILLKLRGLGLADLGCLGECLGLEWLDLSGNALTHLGPLASLR
QLAVLNVSNNRLTGLEPLATCENLQSLNAAGNLLATPGQLQCLAGLPCLEYLRRLRDPLARLSNPLCANPSYWAAV
RELLPGLKVIDGERVIGRGSEFYQLCRDL DSSLRPSSSPGPRATEAQPWVEPGYWESWPSRSSSILEEACRQFQD
TLQECWDLDRQASDSLAEQVLSSAGPTSSFVF

2664/6881
FIGURE 2451

GGCAGGCACCAGCTGGGGAAGGCTGGTGTTCCTTGTGCGCCACATTCTGGAGCCCGGCAGACAGCCTCAGCAAG
CTCCTGTAGCCCTTCCAG**ATGG**TGGTCCGCGAGGCGAGTGCGGCACAGGCCTCTCTGAGCCAGGTGCTGCCCCAG
CTGCGCTACCTGCACATCTTCCTGGAGCAGGTTACACACACTTTTCAGGAGCAGAGTGTGCGGGAGAGGGGCGCA
GCCATCCAGCTGGCTGAGGGGTTGGCCCGGCAGCTCTGCACCGACTGTCAGCTCAACAAGCTCTTCTACCGCGAG
GAGTTTGTGCTGGCCACCTTGCTGGACCCTTGCTTCAAGGGGAAGATTGAGGCCATCCTGCCATGGGGGCCGACC
GACATTGACCACTGGAAGCAAGTCCTCGTGTACAAGGTGAAGGAGATTAGAGTGTCTGAATACTCTTTGAACCTC
CCAAGTCCCCTGCAAAGCCCCAGGGGTCTGTGCGTGGACCCACCAGGGTAGCCAAGAGCTCCGGGGTGGAGGGG
AGAAGCCAGGGGGAGCCTCTGCAGAGCAGCAGCCACTCTGGGGCCTTCTGCTGGCCCAGAGGGAGAAGGGCTTG
CTGGAGAGCATGGGGCTGCTGGCCTCTGAGAGAAGCGGGGGCTCGCTGTCCACCAAGAGCCACTGGGCCAGCATC
ATTGTCAAGAAGTATCTGTGGGAGAATGAGACCGTTGGAGCCCAGGATGACCCCTGGCTTACTGGGAGAAGAAG
CGAGAAGCCTGGCCACCATCTATCTGTCTTACCCCCACAGGAGCCTTCTCT**TGA**AAGCATCTTTGCCTCCCTGAA
CAGCCCCACCCCTTGTAAGCAAACTCTTCTCTCAAGGTGGAAGCCATTGAGCATCTCCTCTTCTTGAAGGCCAA
CCTGGAGCAGTTCCCCAACTACACCCCGCCTCCCTCATCTGCTCTAGTGGTGACCTGGCCAAGGGGATACAGAC
CCTGCAGTCCGCTCAGGGTGGGATGGCAGACATGGCAGGTGCCGGTGTCTACCCCTGCCCGTGAACCTCCTAGAGAG
CCCCTGCCTGTAATAGGTCAAAGCAGAGAGCTGGGTGTTGCATCCTGGGCGCCACATGCTCATGGCCAGAATCTT
AAACCTATTTGGTAGGAAAGGGTCAGTTTCTCACTTGACAGATTGCCATATTTTTTTTTTCTGGGAGATGTCATTT
TCCATCTCCCGATTACTTCTTTACGTCTAGCAGTATGTGCCGAGAAGAGGCTTACTCTCTTCGTAGGTGACTGT
GAATTTTGTACTACGTGGCTTTGTACATGTGATGCTCTGTTAAACATAAGTGGGTATGAAGGTCTTGCATACA
CCTTGTCTGTGTGGATAAGTGGACACATGCCCTTAAGAGGCTTGCTTTCTCAAAAAGTGGCCAAGGATGTGGAGT
GGGCATGTGCTGGCAGGTGGGATATGTCTCAGCCTTTGGGGGCCTGGATAAGCTATTGCAGCACTTTCTGAGGC
TTTCACTGTAGGGAGAAGGAAACCCCAAGGGTAGAATAGCCATTTCCAGAGGGAAGTACACACATACCCCCACAC
ACCAGTCTTTTTGGGGGTTTCAGAGTGGCCGGAGAAACCGACTGAAGGGACTGACCAGCTAGCTAGGAGAGCTGA
GACGCCAGTCCCTCAAATGGCGTTCTTACCAATAGTCTATTTCCAGACTACTGGAAACGTTGGGGTTTCTTCTCC
AGTGACAGCAGCCTCAGTAGCTTTCCTGGGCTCCAGGCGGCTGGCTGCACACCCTGCCTGCCATCACCCCTTGCCC
CTGCTTGTCTCTGGACCACTTTTAAAGGGGAAGTCCCTTATTTGGAAGAGAGAAAGGATGTGTGTAGCACACACTC
ATCATGGATTGCTCAGAGTTCCTTTAGGGCAGAGCTGAGGGCCTGGGATCCAGGAACAGTGGGATTGGATGGGA
GAAGAAGGAAGGGGGTGGCCCGTCACCCCGCAAGACTTGATCCAGGTAGCCTAAGGACTCCTGGTCACTGGGT
AGGGTGGCTGCTGAGATGCAGGTGGAAGAGGCAGGGGAAGGCTCCAGGCCTAACTGGAGCATGTCACTGGCCA
TGGGGGTGAGGGGACAGACTCTGCTCTCACTGGCTGGCAGCCCCAGGAGCCTGTTCCCTTGCTCTCTCTGGATGG
GTTGTGAGCCCTGTGTTTCACTGTGACCAATTCAATTATAACATTTGGATATTACTGAAAATGTAAGGAAGCAGGA
AAAATTAATACTTTTCACTCAGAGATAGCCTCTATCAATAGTTTGGACATTTTTCCCTCTTTTACATTGAGATCAT
ACCCTAGGTACTGTTTAGTATGCAATATTTTCATTTTCGCAGTATAATAATTGCACCTGTTAAATAAAGTTTTGT
AAACATTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

2665/6881
FIGURE 2452

MVREASAAQASLSQVLPQLRYLHIFLEQVHTHFQEQSVGERGAAIQLAEGLARQLCTDCQLNKLFYREEFVLAT
LLDPCFKGKIEAILPWGPTDIDHWKQVLVYKVKEIRVSEYSLNSPSPLOSPRGLCVDPTRVAKSSGVEGRSQGEP
LQSSSHSGAFLLAQREKGLLESMGLLASERSGGSLSTKSHWASIIVKKYLWENETVGAQDDPLAYWEKKREAWPP
SICLTPHRSL

2666/6881
FIGURE 2453

CTTGAAATGTTATCTAAAAACCCAAGATTGAAATAATACATACCACACAAGGAAACAGGAGAGTAGTCTAGCTCC
ATGTCGCGGGGCTCTAGGGGTTTCATAGATGGCAGCTCCTGTCCGGGGCTGAGGTTGGGAGGGGAGAAACAGGGGCA
GAGTGAGTTGGTCTCTGGAGTGACTGTGCTTTTCCACCCTCAGCAGAGGAAGAACCAGATGCTGGAACGTGCTTGC
AGGGGCCCCCTGGCCATGGGCTGGCCAGCCCCGACTCCTTTCTGGGCCCTCCCAGGAGTCACCCAGACCCTG
GGGAAGGAGTCCCGCGGGCTGAGGCAACAAGGCACGTGAGTGGCCAGTCTGGTGCCCAAGCCCCAGGCAGGGCC
CATCGCTGTGCCCACTGTGCAAGGCACTTCCCTGGCTGGGTGGCTCTGTGGCTTCACACCCGCCGGTGCCAGGCC
CGGCTGCCCTTGCCCTGCCCTGAGTGTGGCCGTGCTTTTCGCCATGCCCCCTTCTTAGCACTGCACCGCCAGGTC
CATGCTGCTGCCACCCAGACCTGGGCTTTGCCTGCCACCTCTGTGGGCAGAGCTTCCGAGGCTGGGTGGCCCTG
GTTCTGCATCTGCGGGCCCAATTCAGCTGCAAAGCGGGCCATCGCTTGTCCCAAATGCGAGAGACGCTTCTGGCGA
CGAAAGCAGCTTCGAGCTCATCTGCGGCGGTGCCACCCTCCCGCCCCGAGGCCCGGCCCTTCATATGCGGCAAC
TGTGGCCCGAGCTTTGCCAGTGGGACCAGCTAGTTGCCACAAGCGGGTGACGTAGCTGAGGCCCTGGAGGAG
GCCGCAGCCAAGGCTCTGGGGCCCCGGCCAGGGGCCGCCCCGCGGTGACCGCCCCCGGCCCGGTGGAGATGCC
GTCGACCGCCCCCTTCCAGTGTGCCTGTTGTGGCAAGCGCTTCCGGCACAAGCCCAACTTGATCGCTCACCGCCGC
GTGCACACGGGCGAGCGGCCCCACAGTGGCCCGAGTGGCGGAAGCGCTTTACCAATAAGCCCTATCTGACTTCG
CACCGGCGCATCCACACCGGCGAGAAGCCCTACCGTGCAAAGAGTGGCGCCGCCGCTTCCGGCACAACCCCAAC
CTGCTGTCTCACAGCAAGATTACAAAGCGATCCGAGGGGTGGGCCAGGCCGCCCCGGCCCCGGGGAGCCCCCAG
CTGCCAGCCGGCCCCCAGGAGTCCGCGGCCGAGCCACCCCGCGGTACCTCTGAAACCGGCCAGGAGCCGCCG
CCAGGGGCCCCGCCAGAGCACCGCGCAGGACCCGATCGAAGCCCCCCCCCTCCCTCTACAGCTGCGACGACTGCGGC
AGGAGCTTCCGGCTGGAGCGCTTCTGCGGGCCACCAGCGGCAGCACACCGGGGAGCGGCCCTTACCTGCGCC
GAGTGGCGGAAGAACTTCGGCAAGAAGACGCACCTGGTGGCGCACTCGCGCGTGCACTCCGGCGAGCGGCCCTTC
GCCTGCGAGGAGTGGCGCCGCCGCTTCTCCAGGGCAGCCATCTGGCGGCGCATCGGCGCGACCACGCCCCCGAT
CGGCCCTTCGTGTGTCCCGACTGCGGCAAGGCCTTCCGCCACAAACCCTACCTGGCGGCGCACCGGCGCATCCAC
ACCGGCGAGAAGCCCTACGTCTGCCCGACTGCGGCAAGCCTTCAGCCAGAAGTCCAACCTGGTGTGCGACCGG
CGCATCCACACGGGCGAGCGGCCCTACGCCTGTCCCGACTGCGACCGCAGCTTCAGCCAGAAGTCCAACCTCATC
ACCCACCGCAAGAGCCACATCCGGGACGGCGCCTTCTGCGTGCCATCTGTGGCCAGACCTTCGACGACGAGGAG
AGACTCCTGGCCACCAGAAAGAAGCACGATGTCTGAGACGGTGGGCGGGGCCGTGTTGGCTGAGAGAGGGCTGGG
GTCCTTCGTGGTGGGAGTCGCAGTGGGCTGGGGGTGCCTGCCTAGTGCTGGAGTAGGGGACAATGGGAATCCTAG
AGGGGATGGAAGACGCGGGGAGTGAGCTGGGTGGGCCCTGCTAGCGAGAGAGGTCAACCCCGGTGGCCAGGGAAC
CCACTTCCAAGCGCAGGGACGCCGGCCTCCAGCTGGTGTGTGCTAAGGCTCCGTCTCTGACTGCCCTGTGCCCTGG
AAAAGCAGCAATAGCATCCGCCCTTAGAGCCCTCTGGCTAGAGGAGCCACCAGTGGAAGGAAGACCCTCCATC
CTCTGGTATTAACGCCCTTAATGCCCTGTCTTTTACTGTAAGTTACTTAAGATCATTTTTTGAAGCAGGCGTGGT
AGAGTCCTGTAAATGAATGCTCTGGGCTAGATACAGCTTGGAGAACCTGCTGGCCTTGTTAGACAGCACTTGGGC
CTTTGCCAGCAGCAAGAGGTGAAGCGAAGCCACTCTTACCTCTCCCTTCCCTCCACCTGCCCCCTGCGTAGGC
ACCCAGACTTGGAGAGACCCGTCTGCTGTTAATACTTCCATCCTCTTCTTCCCAAAGAGCAGATCCCAAGGCAT
TTACTCCTTGGTCTGTCTCGCTTTATCTGTGCCCCCTCCAGCGCTGAGAGCCTCCCTGGCTGTCAGCAGCACT
GTGTCCAGGCTCTTGTCTGAACACCGCAGCCCCCTCCTTCGCTCCTTCCAGAGCTCAGCATGTCACGGCAAGGACT
GCCGCATTGGTGATGGAGGGCCAGCTGAGGGGAAGTTGCTGGTGAGTTTCTTTTCTCCATTTCTAGCATATGGA
CACCTGGCCTCTGCTTGAGCACTTAGGTGACAGGAACCTCCGCACCTCTGAGGCCCTGGATGATTCTAATTGTT
AGAAATTTCTAATTGTTAGAAATCCTTCTTATAATGAATGAATTCTGCTTCTCTATAATTTCTACCTATTGGGCC
TTGTTCTGTTCTCTGGAATAAACAGAACCACTTTACCCCTCCTTTTCAAAGTAGAGAATAAAGATTGGTTT
TAG

2667/6881
FIGURE 2454A

GGGGAGCCGGGAGCCGAGCGAGGACCCGGCGCCCGCAGTCCAGTCTTGCCCGCGCCCGTGCTCGGCTTGCCCGCG
GGGTGCGGGGACCACGGCCCGGCCGGGCCACCCGAAGCCTAGTGCTGGGCCGGGCGGGCGGGGTGGGTGGGGG
CCCGCCCGGCCCGCCCATGGGCTCAGGATGCCGGTGCGGAGGGGCCACGTGCGCGCCGAGAACACCTTCTTGAC
ACCATCATCCGCAAGTTTGGAGGGCCAGAGCCGTAAGTTTCATCATCGCCAACGCTCGGGTGAGAACTGCGCCGTC
ATCTACTGCAACGACGGCTTCTGCGAGCTGTGCGGCTACTCGCGGGCCGAGGTGATGCAGCGACCTGACCTGC
GACTTCCTGCACGGGCCGCGCACGCAGCGCCGCGCTGCCGCGCAGATCGCGCAGGCACTGCTGGGCGCCGAGGAG
CGCAAAGTGGAATCGCCTTCTACCGGAAAGATGGGAGCTGCTTCCTATGTCTGGTGGATGTGGTGCCCGTGAAAG
AACGAGGATGGGGCTGTCATCATGTTTCATCTCAATTTGAGAGTGGTGATGGAGAAGGACATGGTGGGGTCCCCG
GCTCATGACACCAACCACCGGGGCCCCCCCCACCAGCTGGCTGGCCCCAGGCCGCGCCAAGACCTTCCGCTGAAAG
CTGCCCCGCGCTGCTGGCGCTGACGGCCCGGAGTGCCTGGTGCGGTGCGGCGGCGCGGGCGGGCGGGCGCCCCG
GGGGCCGTGGTGGTGGACGTGGACCTGACGCCCGCGGCACCCAGCAGCGAGTGCCTGGCCCTGGACGAAGTGACA
GCCATGGACAACCACGTGGCAGGGCTCGGGCCCGCGGAGGAGCGGCGTGCGCTGGTGGGTCCCGGCTCTCCGCC
CGCAGCGCGCCCGGCCAGCTCCCATCGCCCCGGGCGCACAGCCTCAACCCCGACGCCTCGGGCTCCAGCTGCAGC
CTGGCCCGGACGCGCTCCCGAGAAAGCTGCGCCAGCGTGCGCCGCGCTCGTGGCCGACGACATCGAGGCCATG
CGCGCCGGGGTGCTGCCCCCGCCACCGCGCCACGCCAGCACCCGGGGCCATGCACCCACTGCGCAGCGGCTTGCTC
AACTCCACCTCGGACTCCGACCTCGTGCGCTACCGCACCATTAGCAAGATTCCCCAAATCACCTCAACTTTGTG
GACCTCAAGGGCGACCCCTTCTTGCTTCGCCACCCAGTGACCGTGAGATCATAGCACCTAAGATAAAGGAGCGA
ACCCACAATGTCACTGAGAAGGTACCCAGGTCTGTCCCTGGGCGCCGACGTGCTGCCTGAGTACAAGCTGCAG
GCACCGCGCATCCACCGCTGGACCATCCTGCATTACAGCCCCCTCAAGGCCGTGTGGGACTGGCTCATCTGCTG
CTGGTCACTTACACGGCTGTCTTACACCCCTACTCGGCTGCCTTCTGCTGAAGGAGACGGAAGAAGGCCCGCT
GCTACCGAGTGTGGCTACGCTGCCAGCGCTGGCTGTGGTGGACCTCATCGTGGACATCATGTTTATTGTGGAC
ATCCTCATCAACTTCCGCACCACCTACGTCAATGCCAACGAGGAGGTGGTCAGCCACCCCGGCCGCATCGCCGTC
CACTACTTCAAGGGCTGGTTCTCATCGACATGGTGGCCGCCATCCCCCTCGACCTGCTCATCTTCGGCTCTGGC
TCTGAGGAGCTGATCGGGCTGTGAAGACTGCGCGGCTGCTGCGGCTGGTGCGCGTGGCGCGGAAGCTGGATCGC
TACTCAGAGTACGGCGCGGCCGTGCTGTTCTTGCTCATGTGCACCTTTGCGCTCATCGCGCACTGGCTAGCCTGC
ATCTGGTACGCCATCGGCAACATGGAGCAGCCACACATGGACTCACGCATCGGCTGGCTGCACAACCTGGGCGAC
CAGATAGGCAAACCTACAACAGCAGCGGCCCTGGGCGGCCCTCCATCAAGGACAAGTATGTGACGGCGCTCTAC
TTCACCTTCAGCAGCCTACCAAGTGTGGGCTTCGGCAACGTCTCTCCCAACACCAACTCAGAGAAGATCTTCTCC
ATCTGCGTCATGCTCATTGGCTCCCTCATGTATGCTAGCATCTTCGGCAACGTGTCGGCCATCATCCAGCGGCTG
TACTCGGGCACAGCCCGCTACCACACACAGATGCTGCGGGTGGGGAGTTTCATCCGCTTCCACCAGATCCCCAAT
CCCCTGCGCCAGCGCCTCGAGGAGTACTTCCAGCACGCCTGGTCTTACACCAACGGCATCGACATGAACGCGGTG
CTGAAGGGCTTCCCTGAGTGCTGCGAGGCTGACATCTGCCTGCACCTGAACCGCTCACTGCTGCAGCACTGCAAA
CCCTTCCGAGGGGCCACCAAGGGCTGCCTTCGGGCCCCGCGCATGAAGTTCAAGACCACACATGCACCGCCAGGG
GACACACTGGTGCATGCTGGGGACCTGCTCACCGCCCTGTACTTCATCTCCCGGGGCTCCATCGAGATCCTGCGG
GGCGACGTGCTGCTGGCCATCCTGGGGAAGAAATGACATCTTTGGGGAGCCTCTGAACCTGTATGCAAGGCCTGGC
AAGTCGAACGGGGATGTGCGGGCCCTCACCTACTGTGACCTACACAAGATCCATCGGGACGACCTGCTGGAGGTG
CTGGACATGTACCCTGAGTTCTCCGACCACTTCTGGTCCAGCCTGGAGATCACCTTCAACCTGCGAGATACCAAC
ATGATCCCGGGCTCCCCCGGCAGTACGGAGTTAGAGGGTGGCTTCAGTCGGCAACGCAAGCGCAAGTTGTCCTTC
CGCAGGCGCACGGACAAGGACACGGAGCAGCCAGGGGAGGTGTCGGCCTTGGGGCCGGGCGGGCGGGGCGAGG
CCGAGTAGCCGGGGCCGGCCGGGGGGCCGTGGGGGGAGAGCCCGTCCAGTGGCCCTCCAGCCCTGAGAGCAGT
GAGGATGAGGGCCCAGGCCGAGCTCCAGCCCCCTCCGCTGGTGCCTTCTCCAGCCCCAGGCCCCCGGAGAG
CCGCCGGGTGGGGAGCCCCCTGATGGAGGACTGCGAGAAGAGCAGCGACACTTGCAACCCCTGTCAGGCGCCTTC
TCAGGAGTGTTCAACATTTTCAGCTTCTGGGGGACAGTCGGGGCCGCCAGTACCAGGAGCTCCCTCGATGCCCC
GCCCCACCCCCAGCCTCCTCAACATCCCCCTCTCCAGCCCGGGTGGCGGGCCCCGGGGCGACGTGGAGAGCAGG
CTGGATGCCCTCCAGCGCCAGCTCAACAGGCTGGAGACCCGGCTGAGTGCAGACATGGCCACTGTCTGACGCTG
CTACAGAGGCAGATGACGCTGGTCCCGCCCGCCTACAGTGCTGTGACCACCCCGGGGCTGGCCCCACTTCCACA
TCCCCGCTGTTGCCCCGTAGCCCCCTCCCCACCTCACCTTGGACTCGCTTTCTCAGGTTTCCAGTTTCATGGCG
TGTGAGGAGCTGCCCCGGGGGCCCCAGAGCTTCCCCAAGAAGGCCCCACACGACGCCTCTCCCTACCGGGCCAG

2668/6881
FIGURE 2454B

CTGGGGGCCCTCACCTCCCAGCCCCCTGCACAGACACGGCTCGGACCCGGGCAGTTAGTGGGGCTGCCCAGTGTGG
ACACGTGGCTCACCCAGGGATCAAGGCGCTGCTGGGCCGCTCCCCCTTGGAGGCCCTGCTCAGGAGGCCCTGACCG
TGGAAGGGGAGAGGAACTCGAAAGCACAGCTCCTCCCCAGCCCTTGGGACCATCTTCTCCTGCAGTCCCCCTGGG
CCCCAGTGAGAGGGGCAGGGGCAGGGCCGGCAGTAGGTGGGGCCTGTGGTCCCCCACTGCCCTGAGGGCATTAG
CTGGTCTAACTGCCCGGAGGCACCCGGCCCTGGGCCTTAGGCACCTCAAGGACTTTTCTGCTATTTACTGCTCTT
ATTGTTAAGGATAATAATTAAGGATCATATGAATAATTAATGAAGATGCTGATGACTATGAATAATAATAATTA
TCCTGAGGAGA

2669/6881
FIGURE 2455A

AGTCCAGAGCGAGCGGGTTATGCCTCCGCCTCGTTGCCCTGAAAGCCGCAGCGACAGCGAAAAGGGCTAAGATTCC
GGCCATGAGCAGCGCCCCCTCGGCGCCCCGCCAAGGGCGCAGATTCTTTCTGTACGCCAGAGCCAGAGAGCTTGGG
CCCTGGGACGCTGGGTTCCCCGAGCAGGAGGAAGACGAACTTCACCGCACCCCTGGGCGTGGAGCGGTTTGAGGA
GATCCTACAGGAGGCGGGTCTCGTGGAGGGGAGGAGCCAGGCCGCAGCTATGGGGAGGAAGACTTTGAGTACCA
CCGCCAGTCTCCACCACATCCATCACCCACTGTCCACCCACCTGCCCTCCGGATGCACGCCGCCGCAAGACACC
CCAGGGCCCAGGACGGAAGCCTCGAAGGCGCCCGGGAGCCTCCCCGACTGGAGAAACCCCGACCATTGAGGAGGG
GGAGGAAGATGAGGATGAGGCCAGCGAGGCTGAGGGGGCCCCGGGCTCTCACTCAGCCGTCCCCTGTCTCCACACC
CTCCTCGGTGCAGTTCTTTCTCCAAGAGGATGACAGTGCTGACCGGAAGGCAGAGAGGACCAGTCCATCTTCCCC
TGCACCACTGCCCCACCAGGAGGCGACTCCTCGGGCCTCCAAAGGGGCCAGGCTGGAACCCAGGTGGAGGAGGC
GGAGGCGGAGGCGGTGGCGGTGGCCAGTGGCACTGCAGGGGGTGACGACGGGGGTGCCCTCGGGGCGCCCCCTGCC
CAAAGCCCAGCCTGGGACCCGCAGCTACAACCTTCAGGAGAGGAGGCGCATCGGGAGCATGACTGGGGCTGAGCA
GGCACTGCTGCCCCGGGTCCCCACGGATGAGATTGAGGCCAGACGCTGGCCACGGCCGACCTAGACCTCATGAA
GAGTCAACGGTTTGAGGACGTTTCTGGGGTGC GGCGGC ACTTGGTGCGGAAGAATGCCAAAGGTTCCACACAGAG
TGGCCGAGAAGGGCGGGAGCCTGGCCCCACACCTCGGGCCCCGACCCCGGGCCCCCACAAGCCCCATGAGGTGTT
TGTGGAGCTGAATGAGTTGCTCCTGGACAAAAACCAGGAGCCCCAGTGGCGGGAGACAGCTCGCTGGATCAAATT
TGAAGAGGACGTGGAGGAGGAGACTGAGCGCTGGGGGAAGCCCCACGTGGCCTCCCTCTCCTTCCGCGAGTCTCCT
GGAGCTCCGCAGGACCCTGGCCCATGGGGCTGTGCTCTTGATCTGGACCAGCAGACCCTGCCCGGAGTGGCCCA
CCAGGTGGTGGAGCAGATGGTCATCTTGACCAGATCAAGGCCGAGGACAGGGCCAACGTGCTGCGGGCTCTGCT
GTTGAAACACAGCCACCCAAGTGATGAGAAGGACTTCTCCTTCCCCGCAACATCTCAGCTGGCTCCCTGGGCTC
CCTGCTGGGGCATCACCATGGTCAGGGGGCTGAGAGTGACCCCCACGTACCGAGCCTCTCATGGGAGGTGTTCC
TGAGACCCGGCTGGAGGTGGAGCGAGAGCGTGAGCTGCCGCCTCCAGCACCACCAGCTGGCATCACCCGCTCCAA
GTCCAAGCACGAGCTGAAACTGCTGGAGAAGATTCTGAGAATGCCGAGGCCACGGTGGTCTTGTGGGCTGCGT
GGAGTTCTCTCCCGCCCCACCATGGCCTTTGTGCGGCTCCGGGAGGCTGTGGAGTTGGACGCAGTGTTGGAGGT
GCCGGTGCCTGTGCGTTTCTCTTCTGCTGCTGGGCCCCAGTAGTGCCAACATGGACTACCACGAGATCGGCCG
CTCCATCTCCACCCTCATGTCAGACAAGCAATTCCACGAGGCAGCCTACCTGGCTGACGAGCGGGAGGACCTGCT
GACGGCCATCAACGCCTTCTGGACTGCAGCGTGGTGCTGCCGCCTTCAGAAGTGACGGGCGAGGAGCTGCTGCG
CTCTGTGGCCCACTTCCAGCGCCAGATGCTCAAGAAGCGAGAGGAGCAGGGCCGGCTGCTACCTACAGGGGCTGG
GCTGGAGCCCAAATCTGCCCAAGATAAGGCGCTCCTGCAGATGGTAGAGGCGGCAGGGGCAGCTGAAGATGATCC
CCTTCGGCGGACGGGGCGGCCCTTTGGGGGGCTGATCCGAGATGTGCGGCGCCGCTATCCCCACTACCTGAGTGA
CTTCCGAGATGCACTTGACCCTCAGTGCCCTGGCCGCGAGTCATCTTCTACTTTGCCGCCCTGTCTCCTGCCAT
CACCTTTGGGGGGCTGCTGGGAGAGAAGACGCAGGACCTGATAGGGGTGTGCGAGCTGATTATGTCCACAGCGCT
CCAGGGCGTGGTCTTCTGCTGCTGGGTGCCAGCCCCTGTTGGTGATCGGCTTCTCAGGGCCCCTGCTGGTCTT
TGAGGAGGCCTTCTTCTCGTTCTGTAGCAGCAACCACCTGGAGTACCTGGTGGGCCGTGTGTGGATCGGCTTCTG
GCTGGTGTTCCTGGCCCTGCTCATGGTGGCCCTGGAGGGGAGCTTCTGGTCCGCTTCGTCTCCCGCTTACCCA
GGAGATCTTCGCCTTCTTGATCTCACTCATCTTCTATGAGACCTTCTACAAGCTGGTGAAGATCTTCCAGGA
GCACCCCTGCATGGCTGCTCAGCCTCCAACAGCTCAGAGGTGGACGGCGGTGAGAACATGACATGGGCCGGGGC
AAGACCCACGCTGGGGCCGGGCAACAGGAGCTTGGCTGGGCAGTCTGGGCAGGGGAAGCCCCGGGGCCAGCCAA
CACGGCCCTGCTGTGCTGGTGCTCATGGCCGGCACCTTCTTCATCGCCTTCTTCTGCGCAAATTCAGAACAG
CCGTTCTTTCTGGCCGGATCCGCGGGTGATTGGGGACTTTGGGGTGCCCATCGCCATCCTCATCATGGTGCT
TGTGGATTACAGTATTGAGGACACCTATACCCAGAAGCTGAGCGTTCCAGTGGAATCTCGGTGACTGCCCCAGA
AAAGAGGGGGCTGGGTATCAACCCCTGGGAGAGAAGAGCCCTTCCCTGTGTGGATGATGGTTGCCAGCCTGCT
GCCCGCCATCCTGGTCTTCATTCTCATCTTCTATGGAGACACAGATCACACGCTCATCATCTCCAAGAAGGAGCG
CATGCTGCAGAAGGGCTCCGGCTTCCACCTGGACCTGCTGCTCATCGTGGCCATGGGCGGCATCTGTGCCCTCTT
TGGCCTGCCCTGGTTGGCTGCTGCCACTGTCCGCTCTGTCACTCACGCCAACGCGCTCACTGTATGAGCAAGGC
TGTGGCACCTGGGGACAAGCCCAAGATTCAGGAAGTCAAGGAGCAGCGGGTGACGGGGCTGCTGGTTGCCCTGCT
TGTGGGCTCTCCATAGTTATCGGGGATCTGCTCCGGCAGATCCCCCTGGCCGTGCTCTTTGGAATTTTCTGTGA
CATGGGAGTCACCTCCCTTAACGGGATCCAGTTCTATGAGCGGCTGCATCTGCTGCTCATGCCGCCAAACACCA
CCCAGATGTCACTTACGTCAAGAAGGTCCGGACCCTCCGTATGCACCTGTTACAGGCCCTGCAGCTGCTCTGCCT

2670/6881
FIGURE 2455B

GGCCCTGCTCTGGGCGTCATGTCCACAGCTGCCTCCCTGGCCTTCCCCTTCATCCTCATCCTCACAGTGCCGCT
CCGCATGGTGGTGCTCACCCGTATCTTCACCGACCGAGAGATGAAATGTCTGGATGCTAACGAGGCAGAGCCGGT
GTTTGATGAGCGGGAGGGTGTGGACGAGTACAATGAGATGCCCATGCCTGTGTAGCCGCCACCGAGGGACAGCCG
AGGGACCGATGGACGAGGGGACAGGCTGGTGGGATGGGGTTCCCCCTCCCATGCCCCCTCCCTCCTTTTTATTAA
GTGAATAATTTAAAGTCTTCTCCTCCCCACTGCCCTGCAGTAAAGTGCTTTGGCCCCCA

2671/6881
FIGURE 2456

GCGGCGGCGGGGAAGGAGGGGTGCTTCAGGTGCCTGCGACCTCCGCGCCTCCCGCCCGGAAGTGCCCGAGGGGCC
GCGATGGAGCTGGGGGAGCCGGGCGCTCGGTAGCGCGGCGGGCAAGGCAGGCGCCATGACCCTGATTGAAGGGGT
GGGTGATGAGGTGACCGTCCTTTTCTCGGTGCTTGCCTGCCTTCTGGTGCTGGCCCTTGCCCTGGGTCTCAACGCA
CACCGCTGAGGGCGGGGACCCACTGCCCCAGCCGTCAGGGACCCCAACGCCATCCCAGCCCAGCGCAGCCATGGC
AGCTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCCAGCCTGAGACACAGAGGTCAAGCTGCACA
GCCAGAGCCCAGCACGGGGTTACAGCAACACCGCCAGCCCCGGACTCCCCGCAGGAGCCCCCTCGTGCTACGGCT
GAAATTCTCTCAATGATTTCAGAGCAGGTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTTGAAAAGGACCCA
GTTTCCCGGCCGGGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCTGGG
CAGCCTTCACCTCCCTCCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCCCCAAATCCCCCCTG
CCCGCCGGGGTCCGAGCCCGGCCCTCCGGGCTGGAAATCGGCAGCCTGCTGCTGCCCTGCTGCTCCTGCTGTT
GCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGCCCTTCTTTCCCTGACCGCCACTCTGGGCCTGGCCGGCTT
CACCTGCTCCTCAGTCTCTTGCCATGTACCGCCCGTAGTGCCCTCCGCGGGCGCTTGGCAGCGTCGCC
GGCCCTCCGGACCTTGCTCCCCGCGCCGCGGCGGGAGCTGCTGCCTGCCAGGCCCGCCTCTCCGGCCTGCCTC
TTCCCGCCGCCCTGGAGCCCAGCCCTGCGCCGCAGAGGACTCCCGGGACTGGCGGAGGCCCGCCCTGCGACCGC
CGGGGCTCGGGGCCACCTCCCGGGGCTGCTGACCCTCAGCCCGCACTGGGAGTGGGCTCCTCGGGGTGCGGCATC
TGCTGTGCTGCCTCGGCCCCGGGCAGAGCCGGGCCGCCCGGGGGCCCGTCTTAGTGTTCTGCCGGAGGACCCA
GCCGCCTCCAATCCCTGACAGCTCCTTGGGCTGAGTTGGGGACGCCAGGTCGGTGGGAGGCTGGTGAAGGGGAGC
GGGGAGGGGCAGAGGAGTTCCCCGGAACCCGTGCAGATTAAAGTAACTGTGAAGTTTTCAAAAAAAAAAAAAA

2672/6881
FIGURE 2457

MTLIEGVGDEVTVLF SVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSMRGEAPGAETPSLR
HRGQAAQPEPSTGFTATPPAPDSPQEPLVLR LKFLNDSEQVARAWPHDTIGSLKRTQFPGREQQVRLIYQGQLLG
DDTQTLGSLHLPPNVCVLHCHVSTRVGPPNPPCPPGSEPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFFFPLTA
TLGLAGFTLLLSLLAFAMYRP

2673/6881
FIGURE 2458

CCCAGCTCCCTGAAACAACAGTAACCTACCCCTGTGGGTCAATCATCATCATGCCCCTCCGACCTGGCCAAGAAGAAGGC
AGCCAAAAAGAAGGAGGCTGCCAAAGCTCGACAGCGGCCAGAAAAGGACATGAAGAAAATGGAGATGTTGTCAC
AGAACCACAGGTGGCAGAGAAGAATGAGGCCAATGGCAGAGAGACCACAGAAGTAGATTTGCTGACCAAGGAGCT
AGAGGACTTTGAGATGAAGAAAGCTGCTGCTCGAGCTGTCACTGGCGTCCTGGCCTCTCACCCCAACAGTACTGA
TGTTACATCATCAACCTCTCACTCACCTTTTCATGGTCAAGAGCTGCTCAGTGACACCAAAGTGAATTAACTC
AGGCCGTCGTTATGGCCTCATTGGTTTAAATGGAATTGGAAAGTCCATGCTGCTCTCTGCTATTGGGAAGCGTGA
AGTGCCCATCCCTGAGCACATCGACATCTACCATCTGACTCGAGAGATGCCCCCTAGTGACAAGACACCCCTTGCA
TTGTGTGATGGAAGTCGACACAGAGCGGGCCATGCTGGAGAAAAGAGGCAGAGCGGCTGGCTCATGAGGATGCGGA
GTGTGAGAAGCTCATGGAGCTCTACGAGCGCCTGGAGGAGCTGGATGCCGACAAGGCAGAGATGAGGGCCTCGCG
GATCTTGATGGACTGGGTTTACACCTGCCATGCAGCGCAAGAAGCTAAAAGACTTCAGTGGGGGCTGGAGGAT
GAGGGTTGCCCTTGCCAGAGCCCTCTTTATTTCGGCCCTTCATGCTGCTCCTGGATGAGCCTACCAACCACCTGGA
CCTAGATGCTTGCGTGTGGTTGGAAGAAGAACTAAAAACTTTTAAAGCGCATCTTGGTCCTCGTCTCCCATTTCCA
GGATTTTCTGAATGGTGTCTGTACCAATATCATTACATGCACAACAAGAACTGAAGTATTATACGGGTAATTA
TGATCAGTATGTGAAGACGCGGCTAGAGCTGGAGGAGAACCAGATGAAGAGGTTTCACTGGGAGCAAGATCAGAT
TGCACACATGAAGAACTACATTGCGAGGTTTGGTTCATGGCAGTGCCAAGCTGGCCCGGCAGGCCAGAGCAAGGA
GAAGACGCTACAGAAAATGATGGCATCAGGACTGACAGAGAGGGTCGTGAGCGATAAGACACTGTCATTTTATTT
CCCACCATGTGGCAAGATCCCTCCACCTGTCATTATGGTGCAAAATGTGAGCTTCAAGTATACAAAAGATGGGCC
TTGCATCTACAATAATCTAGAATTTGGAATTGACCTTGACACACGAGTGGCTCTGGTAGGGCCCAATGGAGCAGG
GAAGTCAACTCTTCTGAAGCTGCTAACTGGAGAGCTACTACCCACAGATGGCATGATCCGAAAACACTCTCATGT
CAAGATAGGGCGTTACCATCAGCATTTACAAGAGCAGCTGGACTTAGATCTCTCACCTTTGGAGTACATGATGAA
GTGCTACCCAGAGATCAAGGAGAAGGAAGAAATGAGGAAGATCATTGGGCGATACGGTCTCACTGGGAAACAACA
GGTGAGCCCAATCCGGAACCTTGTGACAGCGGCAGAAAGTGCCGAGTGTGTCTGGCCTGGCTGGCCTGGCAGAACCC
CCACATGCTCTTCTGGATGAACCCACCAATCACCTGGATATCGAGACCATCGACGCCCTGGCAGATGCCATCAA
TGAGTTTGAGGGTGGTATGATGCTGGTCAGCCATGACTTCAGACTCATTAGCAGGTTGCACAGGAAATTTGGGT
CTGTGAGAAGCAGACAATCACCAAGTGGCCTGGAGACATCCTGGCTTACAAGGAGCACCTCAAGTCCAAGCTGGT
GGATGAGGAGCCCCAGCTCACCAAGAGGACCCACAACGTGTGCACCCTGACATTGGCATCTCTGCCAAGGCCATG
AGCATCATGAACTCGTTTGTAAACGACGTGTTTGTAGCAGCTGGCGTGTGAGGCTGCCCGGCTGGCCAGTACTCG
GGCCGACCAACCTGACATCCCGAGAAGTCCAGACGGCTGTGCGTCTGCTGCTGCCTGGGGAGCTGGCCAAGCAC
GCTGTGTCTGAGGGCACCAAGGCTGTACCAAGTACACCAGCTCCAAGTGACCCAGGGCCTGACAAAAATAAAGG
GTGAAGTGTAAAAA

2674/6881
FIGURE 2459

MPSDLAKKKAACKKEAAKARQRPRKGHEENGDVVTEPQVAEKNEANGRETTEVDLLTKELEDFEMKKAAARAVTG
VLASHPNSTDVHIINLSLTFHGQELLSDTKLELNSGRRYGLIGLNGIGKSMLLSAIGKREVP IPEHIDIYHLTRE
MPPSDKTPLHCVMEVDTERAMLEKEAERLAHEDAECCKLMELYERLEELDADKAEMRASRILHGLGFTPAMQRKK
LKDFSGGWRMRVALARALFIRPFMLLLDEPTNHLDLDACVWLEELKTFKRILVLVSHSQDFLNGVCTNIIHMHN
KKLKYYTGNYDQYVKTRLELEENQMKRFHWEQDQIAHMKNYIARFGHGSAKLARQAQSKEKTLQKMMASGLTERV
VSDKTLSFYFPPCGKIPPPVIMVQNVSFKYTKDGPCIYNNLEFGIDLDRVALVGPNGAGKSTLLKLLTGELLPT
DGMIRKSHSVKIGRYHQHLQEQLDLDSPLYMMKCYPEIKEKEEMRKIIGRYGLTGKQQVSPIRNLSDGQKCRV
CLAWLAWQNPMLFLDEPTNHLDIETIDALADAINFEFGMMLVSHDFRLIQQVAQEIWVCEKQTITKWPGDILA
YKEHLKSKLVDEEPQLTKRTHNVCTLTTLASLPRP

2675/6881
FIGURE 2460

GCCTAATTAAAAGGCGGCGGAAGAAGGTGGGAGGGTCATGACGCAGCGAGTTTCAGTCGTGACTTTTCTGGGGGC
ATCGCGGCGTCCCCTTTTTTTTGCCTTTAAAGTAAAACGTCGCCCCGACGCACCCCCGCGTATTTGCGGGGGGCG
GAGGCGGCGGGCCACGGCGCGAAGAGGGGCGGTGCTGACGCCGGCCGGTCACGTGGGCGTGTTGTGGGGGGGAGG
GGCGCCGCCGCGCGGTTCGGTTCCGGGCGGTGGGAGCGCGCGAGCTAGCGAGCGAGAGGCAGCCGCGCCCCGCCGCG
CGCCCCGTGCTCTGTATGCCGCTCTCTCCCGGCGCGGCCGCCGCCGATCACAGCAGCAGGAGCCACCGCCGCCGCG
GTTGATGTGGTTGGGCGGGGCTGAGGAGGCCGCCAAGATCGCGCAGTCCAAGTCCCGGAAGATCGCGATCCTGG
GCTACCGGTCTGTGGGAAATCCTCATTGACGATTCAATTTGTTGAAGGCCAATTTGTGGACTCCTACGATCCAA
CCATAGAAAACACTTTTACAAAGTTGATCACAGTAAATGGACAAGAATATCATCTTCAACTTGTAGACACAGCCG
GGCAAGATGAATATTCTATCTTTCTCAGACATACTCCATAGATATTAATGGCTATATTCTTGTGTATTCTGTTA
CATCAATCAAAAAGTTTTGAAGTGATTAAAGTTATCCATGGCAAATTTGTTGGATATGGTGGGGAAAGTACAAATAC
CTATTATGTTGGTTGGGAATAAGAAAGACCTGCATATGGAAAGGGTGATCAGTTATGAAGAAGGGAAAGCTTTGG
CAGAATCTTGGAAATGCAGCTTTTTTGAATCTTCTGCTAAAGAAAATCAGACTGCTGTGGATGTTTTTCGAAGGA
TAATTTTGGAGGCAGAAAAAATGGACGGGGCAGCTTCACAAGGCAAGTCTTCATGCTCGGTGATGTGATCTCTGCT
GCAAAGCCTGAGGACACTGGGAATATATTCTACCTGAAGAAGCAAACCTGCCCGTTCTCCTTGAAGATAAACTATG
CTTCTTTTTTCTTCTGTTAACCTGAAAGATATCATTTGGGTCAGAGCTCCCCTCCCTTCAGATTATGTTAACTCT
GAGTCTGTCAAATGAGTTCACTTCATTTTCAAATTTTAAGCAATCATATTTTCAATTTATATATTGTATTCT
TAATATTATGACCAAGAATTTTATCGGCATTAATTTTTCAGTGTAGTTTGTGTTTAAATAATGTAATCATCAA
AATGATGCATATTGTTACACTACTATTAAGTCTTCAGTATATCAGTGTATTATTTTCATTGTGTTAAATGTATA
CTTGTAATAAAATAGCTGCAAACCTCAAAAAAAAAAAAAAAAAAAAA

2676/6881
FIGURE 2461

MPQSKSRKIAILGYRSVGKSSLTIQFVEGQFVDSYDPTIENTFTKLITVNGQEYHLQLVDTAGQDEYSIFPQTYS
IDINGYILVYSVTISIKSFEVIKVIHGKLLDMVGKVQIPIMLVGNKKDLHMERVISYEEGKALAESWNAAFLESSA
KENQTAVDVFRRILEAEKMDGAASQGKSSCSVM

2677/6881
FIGURE 2462A

GATTTACTTGGAGAAGATTGCTATCTGGCAAAAAGAATCAGTCGGATTGTCAGATGAAGAGCTAAATGATGAT
CTTTTGCAGAGTGATAATGAAGATGAAGAAAATTCAGTTCTCAGGGTGTTACAATTAGTCTGAATGCTACATCT
GGCATGGTTACATCATTTGAACTCTCTGACAACACTAACGACCAATCTGGAGAACAGGAATCTGAGTATGAACAA
GAACAAGGAGAGGATGAAGTGGTTTATCACAAATCTGATGGATCAGAATTGTATACTCAAGAGTACCCAGAAGAA
GGACAGTATGAAGGCCACGAAGCTGAGTTGACAGAAGACCAAATAGAATATGTGGAAGAGCCAGAGGAGGAGCAG
CTTTTACACTGATGAAGTGTAGACATCGAGATCAATGAACCTTTAGATGAATTTACAGGAGGTATGGAAAACATTG
GAACTTCAAAAGGACATCAAAGAAGAATCAGATGAAGAAGAAGAAGATGATGAAGAATCTGGACGATTACGTTTC
AAAACCTGAAAGGAAAGAAGGAACAATTATTAGGCTCTCAGATGTAAGTAGAGAGAGAAGGAACATTCCAGAACT
TTGGAGCTTTTCAGCAGAGGCCAAGGCAGCATTGCTTGAATTTGAAGAAAGGGAGCGACAGCATAAAACAAGGACGC
TACAGCTCCAGGCGGGGAGGACGGCGAGGAGGTCCGCTGATGTGTCGTGGTGTGGGGGACCAGAGGAGAGAGAGC
ACCGAGAGGGGACAGGATGAAGGACCACAGACCTGCGCTGCTTCCCTACACAGCCTCCTGTCTGTATACTTCCAGAG
GAGGAATTAATGAGCGACCTGATGCCCTAAGATGACATAAGCTGTTGGACCTTGCTACCTAAAGCCTCTAGAGAG
CCCCAGGCTCCCCCTCCACCGCTCCGCGCCTCAGCAGCAGCCGATCAGAAGCCTGTTCCAGCCGAGCCGCTG
CAGCCGCTGCTTCCGGTGCAGCACCCGCACACCCATCCCCGCTCAGGGAATGCACATGCCTCCCCAGCTAGAG
ACCCCAAGGATGATGATGACCCCGCCACCCGTGACTCCACAGCAGCCCAAGAACATACACATCAACCCGCACTTC
AAAGGGACGGTGGTTCACGCTGTTCAAGTGCCCTTGCTACCAGTTCCGAGCCAGCCGAGACCTGCCGTGGGACCC
CAGAGATTCCAGGCCCTCCAGAATTTCCACAGCATAACCTGGACCTGTTCCCAACAGTTTCAGCCAGCCCCCA
CGACTCCCTCTCCAGGACCAGTGGAGAGCCCCACCCCGCCTCAGGATCGAGACCCTTTCTTCTTAGGAGTTTCA
GGTGAACCAAGATTCCCGAGCCATCTTTTTCTGGAACAGCGAAGTCCCCCTCCACCACCACCGCCTCCTACCCTT
CTTAACAGTAGCCATCCTGTTCTTACTCAGAGTCTCTACCATTCACTCAGCCAGGACCAGCATTTAATCAGCAA
GGACAGCAGCCAGTGTTCCTCAAGAGAGCGGCCCGTACGACCAGCCTTGCAGCCTCCAGGTCCGGTGGGGATTCTG
CACTTTAGCCAGCCTGGGTTCGGCAACCACACGGCCCTTCATTCTCTCTAGACAGCGTTCTTCCAGGCCCCAGGA
CAGCCGTTTCTGCCCCACACACACAGCCCAACCTGCAGGTAATGCATCCTGAGTGAACCTCCAGGGAAAAAATG
TGTAAGTTCAGGCTTTGTGTTCCATAAAGTTTCAGATTTTTATTTGAGCCTACTAATTTGTGGTTATTTAAAGA
ATAGAGTATTAGTCTCAAATGTACTGTTTGTAAAGACAACCTTTTTCAACAATGTTACTTATCTCAATACAAGA
AAAAAATGGGAAAATGTCATTTTTGGGAATTGAAAAATGCTACTTATTATAATTGTTTAAAGGGTATACTACTA
ATAAAATTAGGACATGTTTTGATAATACATTTGCTCATCTGTATAAAATTTTCATGAGAGGTTTACCAGTGGAAT
ACTTTGTCAAATTATATTCCTGCAGTAGACAGTTTTGAAAAGAGTCTTTCATGGAGGGAAGAAGATGTTGCTGT
TCACTGGTTATTTGAAGGCCTTGAGTGCCCTCTGCCGACCGGCTTCTGCTTCATGGGTTTTCTACTGGTTATTTGA
AGGCCTTGAGTGCCCTCTGCCCATCGGCTTCTGCTTCATGGGTTGACATGCGTCTGTAACATCTTCTTACCAAG
TGTATATTTCTTCTTGTATTGTAGGGTTACTATTAAATACATAGCGATGGTAAACTTGAATCAACTATTTAAAA
ATACGTGGAATACGTATCTAAGCCAAAAACGGAAAATGAATATTATCTAGGGTGTAAAGGAAGATAAAATGTTT
TTAAGAATTTTTCTTTTTATTAAAAAAATGCAATTAATACATCCCCATTGCAGAAAATTTCAAGTATATATAAGA
AAGGAAATTAATACTCTCGTTACCTAGAAAACAATTCAGGAGCTTTTTTTTTTGTCTTTTTTTAAATGCACATCT
TCTCGCCACCTGCTTTTTCCCTCCAGTGTACATATCATTTGATCTTTTCATGTCAGCGAGTTGGTTTTGATGCC
ATCGTTTGAGAGTGCTGTATGCGGTTCCCTTTTCATGCTGCTGCTGTTGATGTGTGTATACTGGTTTTAGTA
CTTTAGTATCATAGTGCTACAGGGAACATGCTTTAGAGTTATGAGTTTGTCTGCATACCTAGTTTTCTTAGGAC
AATTCAATCCTAGAATTACTGGATTAAATATAAAATTTAAGGTAATAGCTTCTGGCTTATTACTGCATTTTAGAT
AGTATTACCTTCATCAGCAAGTCTAAAATGAAGTTTGGTATCGCTGAAAGTTCCTTTCTTGTGTTGAGGTTTTT
TAGGAAATGATTGAAGTGATTATGCCCGGTGTAACCATTTATGAACTGTTGTTTCTCTTTCTTTGGAATGGAAG
GGGCGCTTGCATCCTCCATTGCCCCCTCCGCATCAGCCTCAGCCTCAGCAACCTCAGCAACAGCCCCCGCCACAG
CACCAGCCTCCGCACCAGCCCCCGCACCAGCCCCCGCCCGCAGCACCAGCCCCACCCAGCACCACACAGCAC
CCGCCGACGACCAGCACCACCACCACCACCACCTGTCCGTCCCGCCCCCTCCTTTGATGCCGATGTCTCAG
CCACAGTTCCGGCCTCAGTACAGACCGCTCAGCCTCAGGCCAGCAGCAGCCGATGAGTGCCCCCAGCGCCAG
GGGCTCCGGCATAATACTTCTCAGAATGTAAGCAAGCGGCCATGCAGCAAATGCAGCCCACTGCGCCAAGG
AACAGCAATTTGCGTGAATTACCCATAGCGCGCTCACACGTGATAGAAATGAGCAGCAGCCGCTGCTCTGCCACG
CCCTCAGCACAAGTGAAACCTATCGTCAGCGCGCTCACCACCTCGCGGGCGGTGGCGGGTTCCAGAAGCTCACAG
GGAAAGACGGAAGTGAAAGTCAAGCCAGCTAGCCCTGTGGCTCAACCTAAAGAAGAGGCAAAAACAGAAACAGAG

2678/6881
FIGURE 2462B

TTTCCTGATGAAGATGAGGAAACAAGGTTATATCGCTTAAAGATAGAAGAACAGAAACGCCTAAGAGAAGAAATC
CTGAAACAGAAGGAGTTACGGCGGCAGCAGCAGGCTGGTGCCAGGAAGAAGGAGCTGCTGGAGAGACTCGCGCAG
CAACAGCAGCAGCTGTACGCTCCCCACCCCCAGCAGAGCAGGAAGAGCAGGCACTGTCACCATCACCCACCAAC
GGTAACCCACTGTTGCCCTTTCCAGGTGCACAGGTCAGACAAAATGTGAAGAACAGACTTCTTGTTAAAAACCAG
GATGTCAGTATTTCAAACGTTTCAGCCCCAAAACATCCAATTTTGTACCATCCAGTGCCAACATGCAGTATCAAGGA
CAACAGATGAAAGCACTGAAACATTTGAGACAGACCAGAACAGTTCCTCAAAGTCAGACTCAGCCGCTGCATAAA
GTGCTCCCGATCAAACCTGCAGATGTGGAGGAGCCAGCTGTCCCCCAGACTCCTCGAGTGGCGTCCATCCAGGGC
CGGCCCCAGGACACAAAGCCTGGCGTGAAAAGGACTGTACGCACAGGACAAACAGTGGTGGTGGAGACGGGCCC
CACATCAGCTCCAAGGTCAGGGTGATTAAGCTGTACAGGTGGGGTAAAGTTGACAAGTTTTATGAGAGCCTCTTTGA
GTCTGTGTATCACATAGAATGTCCTCATTTCAGAGAAATGTTTTTGAAGAAAGAATTAAAAGTTACCTCTGTTAT
AGTCTTGTAaaaaaaaaaaaaaaaaaaaaaaaaa

2679/6881
FIGURE 2463

MIEVIMPGVTIYELLFLFLWKWKGPLHPPLPPPHQFPQFPQQPQQQPPPHQPPHQPPHQPPPHQPPPHQPPHPPQHPPQHPP
QHQHSHHHHHHLSVPPPLMPMSQPQFRPHVQTAQPQASSSRMQCPQRQGLRHNTTSQNVSKRPMQQMQPTAPRNS
NLRELPIAPSHVIEMSSSRCSATPSAQVKPIVSASPPSRAVAGSRSSQGKTEVKVKPASPVAPKEEAKTETETFP
DEDEETRLYRLKIEEQKRLREEILKQKELRRQQQAGARKKELLERLAQQQQQLYAPPPPAEQEEQALSPSPTNGN
PLLFPFGAQVRQNVKNRLLVKNQDVSI SNVQPKTSNFVPSSANMQYQGQMKALKHLRQTRTVFPQSQTQPLHKVL
PIKPADVEEPAVEPQTTPRVASIQGRPQDTKPGVKRTVTHRTNSGGGDGPHISSKVRVIKLSGGVS

2680/6881
FIGURE 2464

GCCGGTGTCTGTTGGTCGCGGTACCTGTTCCAACACGGCTCGCGGGCCCGTGCCGGCTCCGGTCCCCGGCGCGGGCTG
TCCGAGCCCCCTGCGGCGGGCGGACGATGGTGTGGCGGAGCACGCGGACGCGGGCGGCGCGGGCGGGCATGAAG
GAGG**ATG**GGAAGGGCAGGACGAGGTGTCGGCGCGGGAGCAGCACTTCCACAGCCAAGTGCGGGAGTCCACGATATG
TTTCTTTCTTTTTGCCATTCTCTACGTTGTTTCTTACTTTCATCATCACAAAGATACAAGAGAAAATCAGATGAACA
AGAAGATGAAGATGCCATCGTCAACAGGATTTGTTGTTTTTGAGCACGTTCACTCTCGCAGTGTGAGCTGGGGC
TGTTTTGCTTTTACCCTTCTCAATCATCAGCAATGAAATCCTGCTTTCTTTTCTCAGAACTACTATATTGAGTG
GCTAAATGGCTCCCTGATTCATGGTTTGTGGAATCTTGCTTCCCTTTTTTCCAACCTTTGTTTATTTGATTGAT
GCCCTTTGCCTTTTTCTTTCTGGAATCAGAAGGCTTTGCTGGCCTGAAAAAGGGAATCCGAGCCCGCATTTTAGA
GACTTTGGTTCATGCTTCTTCTTCTTGCGTTACTCATTCTTGGGATAGTGTGGGTAGCTTCAGCACTCATTGACAA
CGATGCCGCAAGCATGGAATCTTTATATGATCTCTGGGAGTTCTATCTACCCTATTTATATTCTGTATATCATT
GATGGGATGTTTGTACTTCTCTTGTGTACACCAGTTGGCCTTTCTCGTATGTTACAGTGATGGGTGAGTTGCT
AGTGAAGCCAACAATTCTTGAAGACCTGGATGAACAAATTTATATCATTACCTTAGAGGAAGAAGCACTCCAGAG
ACGACTAAATGGGCTGTCTTTCATCGGTGGAATACAACATAATGGAGTTGGAACAAGAAGCTTGAAAATGTAAAGAC
TCTTAAGACAAAATTAGAGAGGCGAAAAAAGGCTTCAGCATGGGAAAGAAATTTGGTGTATCCCGCTGTTATGGT
TCTCCTTCTTATTGAGACATCCATCTCGGTCTCTTGGTGGCTTGTAATATTCTTTGCCTATTGGTTGATGAAAC
AGCAATGCCAAAAGGAACAAGGGGGCCTGGAATAGGAAATGCCTCTCTTCTACGTTTGGTTTTGTGGGAGCTGC
GCTTGAAATCATTTTGTATTTCTATCTTATGGTGTCTCTGTTGTGCGCTTCTATAGCCTTCGATTTTTTGGAAA
CTTTACTCCCAAGAAAGATGACACAACATGACAAAGATCATTGGAATTTGTGTGTCCATCTTGGTTTTGAGCTC
TGCTCTGCCTGTGATGTGAGAACACTGGGAATCACTAGATTTGATCTACTTGGCGACTTTGGAAGGTTTAATTG
GCTGGGAAATTTCTATATTGTATTATCCTACAATTTGCTTTTTTGTATTGTGACAACATTGTGTCTGGTCCGAAA
ATTCACCTCTGCAGTTCGAGAAGAACTTTTCAAGGCCCTAGGGCTTCATAAACTTCACTTACCAAATACTTCAAG
GGATTGAGAAACAGCCAAGCCTTCTGTAAATGGGCATCAGAAAGCACTG**TGAG**ACGCACAGACGGCGTCTTCTGC
CACCAAGAGACCCGAGAACTCCAGATTCACGACATTCCTGTCCCATGTAGAAGCATTTCATTCAACCGTGGCCC
CTCTTCAGAACCTAGACCTATCAGTGCCATTTTTTTTTTTCATAATCTACGAAGAAGCTTGGCTATGGCTGATCTTTT
TTAAATTTAACTTTCTGATGGACCCTGTAGTTTCCAGTTAAGTGCAGATTCCTTACAGACATATAGAACAGCGCA
TTCTTCTGTAGACATTTGCTCATGTTGGTAAATACAATCACCCATATGAAAAAATTGTTTTACCTGATATGAAA
ATGTTAGAAAAGGCAAACTCCGGGACTTCTAAAGATTTACTTAAATCCCATTATGTACTTTATTGAGAATGTAGA
AGCTGACTTGAAAGGCATCCTTGGTACTAAGTGAAGCTTATTGAGAAAATGCATTTTTTCAAATGCAATGGCAACT
GCTTGTAGATATCATTTTTGCAGTGTATGTTGGAGCTGTAATGGTTGCAATTATGTTTCTTATTTCTTAAAGC
AAAAAGCGTAGTTTCTGATTTATGTTATAGAATGATACTGATTAGACTTTGAGCCAAGGGGAAAATACTAAATTC
TTTTAAACCTGGAGCCTTAGAGAGCCACAGGAATATCTTCTGTTGTACAGTCTAATAAGCTGTGGTAGGAAGTAT
CATGTAATCACAGTTTAAATGACAGTTTATGTATATATATAATTCAGTATTCCCTCTGATAACATAGTTGCCAGTG
TTTAATACACTTGTAACCTGGATTTTTTACCTTATAGGCTATATGTATACTCAGTTTTTTTAAAGCATTTTTTTTCAG
AGATCACTTAATTCCCCATGCTTCTGCAATGCATATAAAAACTATAAATGCCGAGTGGTAGAACTCCTCTTTCT
TCATAGTCCTCAGGCTTTGGTTACATTTGCATATGCCATTTGAAGCCTCCAGCTTTTACCAGTTTAACATCCAAA
GTTACAGCATCAGCATTGATGGTGAAGAACAGTTTTGAGTATAACACGATCTGATAATCATTGATTATTAA
ATTGTAAATAATTATTGGGATGGTTTCTTGGCTTTAAGTCCACTGAATAAAAACTATGAAATTGCAAAAAA
AAAAA

2681/6881
FIGURE 2465

MEGQDEVSAREQHFHSQVRESTICFLLFAILYVVSFYIITRYKRKSDEQEDEDIVNRISLFLSTFTLAVSAGAV
LLLPFSIISNEILLSFPQNYIIQWLNGSLIHGLWNLASLFSNLCLFVLMPPAFFFFLESEGFAGLKKGIRARILET
LVMLLLLALLILGIVWVASALIDNDAASMESLYDLWEFYLPYLYSCISLMGCLLLLLCTPVGLSRMFTVMGQLLV
KPTILEDLDEQIYIITLEEEALQRRNLGLSSSVEYNIMELEQELENVKTCLKLERKKASAWERNLVYPAVMVL
LLIETSISVLLVACNILCLLVDETAMPKGTRGPGIGNASLSTFGFVGAALEIILIFYLMVSSVVGFYSLRFFGNF
TPKKDDTTMTKIIGNCVSILVLSSALPVMSRTLGITRFDLLGDFGRFNWLGNFYIVLSYNLLFAIVTTTCLVRKF
TSAVREELFKALGLHKLHLPNTSRDSETAKPSVNGHQKAL

2682/6881
FIGURE 2466

TCTTTCCGTAACCGTAGCTTGAGGCACATTTCTAAATATGCAGCATGGAACGCTTGGCGGTTCTGAACGCGCAT
CTCGTGCTGCTCCTGTAGGGCGGTTAGGACGCGCTCCTCTGGCGAGGAAGGTGGCAGCCTCCACTGTGCACGGGT
CACAGGCGAGTGTGGTGTGGTGTGGTGTGGGTGGGGTGTGGACTGGATCTGCAGGCTTGTCCCTCTCTCGTGGA
GAGCTGTCTGGGGTCCAGGCAGTGTCTAGTGGTGAGAGCCACAGCACATTTGAAAGTCCACATGTGTTTGCCCCAC
TGTGGTCCAGGACATGTGTGAGCCACACTCAGTGGACTTGCACCTGTGACATGTTGGTCAGCGTGGCGGCCGTCA
GCTGGGTGTGGAATGCATCTGATTGGAGCCTGGCACCCGGCCTACCATGATTGTGATTCTCTGGGGCGAGTCTTG
AGTGTGGGCAGGGCCTCAGGCCCCAAGAGGGCTGTGAGCAGGCACCTTCTGTGAGGCACGATGCCACCATGTG
AAGTTGTGTGGGTCTTTGGAGAGTTCTGGCAGGTTGAGGGCCTGTGCGTGTGGGACCCAGGCTGCCCTGCCTGC
TGCCGGCCATGTTCCCTCTGCCCAGTCATGTTGACAATTGTGGCCAAATTCAACATCGGGCCTGTTTCTGCACC
CACGTTGGCACACACTGAGTTCAAGACAGTTTCTGCAGAAATGAATCCAGAGGTGTTTATTTCTGGCACGTTGGA
TCAGACGTTTCAGAGGGTGGGCGTCTTTCTCCATGCACTTCAGCTGGATCAGTCAGTGTGAGCCATTGACTTTAGC
AACAGGGAAATGAAAGACTTTTCTCAATAAGAAATGGGACTTTTCTCACGCTGGATGGCACAGAGCTGGCAAACAT
GAGGCCAGTCCACACCAAGGCTTTGCCTGCAGAAAGGCTGCACTGTGGCCAGCGGGGGAAGCGGAGGAGACACCT
GTGGACACCCTCCCCACAGGTGGGCACACCTTTGCGCAGGCCAGTGTGCGTTCCTGAAGGAGAGCCAGGGTGGG
GTTCCGGGACTGAGGTGCAGCCGTGTCCAGGGTGGGCTTCTAGCTCTGCCGCTGGGCGGAACTGGGGTAGGTCCC
AGGGTGGGGTTCCAGGACTGAGGTGCAGCCGTGCCAGGGTGGGCTTCTAGCTCTGCCGCTGGGCGAACTGGGG
TAGTCCCAGGGTGGGCTTTTAGCTCTGCCGCTGGGCGGAACTCGGGTAGGTGGGAGTCTCTACTTCTCTGCAGGG
TGGTGAAGCTCTCTGGGTAGTGTGAGCAGTTCTCAACGTGCACCTTGAAAGCGCCCGTTTTGAGGTTTAGCTGT
GGCCAAGATAGATGACTTCATTTTGTGTCTTTTGTCTTAAACATGGGGAGATATTTAGAAAACATGTTTGGCTC
TTGCTGGGGAAGCAGTGTCTTCCGTACAGTGTTTTACAAGCCGTGTTTCTTAGGATTGAAAGAAGGTGGCAAG
AGGAAGAAGCAGAAGCAGAGAGAGGAGTCAAGAAGAAGAAGTCGACCAAAGGCAATCACTAGACCGGACTTGAG
GCACGCGGTGCACCCCCAGACGCTGGCGCTCCACCGTGCTCGGCATGCGGTGCTGCACACGCGCTAGGTAGCAGC
GTCGGTCAGGACTGTCTCGAGGCCACACTCGCTCGGCAGGATTATGCGATCACGGATCAGTCAGAGCAGGGTCAG
GAGACGGGGCTGACGGCACGGGTGGCGGGGACAGACGTTTGGGACTTGGCCGCGACTCTCTGCTTCTCTCCAGCT
CTCAATCTGCTGCATTTTCTCTAGTGCTTCCGGATCCTCTTCATTCTTTTCGGCTACTCAACCACTCCGCATGC
TGCTGGAATATTTCTGGCTTTAGAAAGTACAGGAGGGCGCAGATGGCTAACTGAGTAACATTCATGAAATGAGGCT
TTCTGTGGCGGCGTAGTGTGTTGGAATTAGAAGGTAATTCAGTAGAGTGTAACCTTAGAGAATATTGCAAGTGACAC
ATTGAATCCTGCCGCTCAGGGCACCTTTTCTCAGAGCAATCCGGCCACACGAATAGAAGGCTGTCGTGAATCAC
ATCAGATGTAAAATCATTCTCTGTTTACTCTTTTAAATTTTTCATCCTTTGCAGGTAGTGCAAATTCAACTTCAA
ATATGGTGTAGGTTTTGCTAGATTCCATATTTTTTTCTTGATTGTTTGTCTAATTATTTTTAGCAAAAAATTTTTG
CTCAGTGGCACTCTCCCTAGTGTCCATGGGTTAGGGCCATGCTGGGGAAAAACGGGCGGTTATTTACACACGCGCA
AAACACCCAGAGACGGCACAAAGGAGGTTGAACTCATGTTTTCAGTTTCGCGAACATTGACTCCTTACGAAAGTCACT
TCATTCTAACTAGATGCGCCCACTTCCGGTCATTATTTTCGTTTGCATGATGATTGCTTCTTCACGTTTTGTTTT
TATTGAGCACGGAGTAGAATTCCAGGGCTGCCTTGACTTCTTCCCTGCATGCTCCCTCCCAGTGACTTTCCTTCC
CTTTCACATGAGGATCTGCCGTTTCATGTTGCTTTCTCCTTTGTCTCTTGGACTTGAGGGCATTTGTGAAAAGCTT
TGCTGTGATTTAAAAATGCCAGCAATTTAATCTAGCAGTGTTGAAGCTGGGAATTTTTTGGCGCAATCCATGTA
GCAGTGACCCAGGCTTGGGAGCCAGAAACAAGTGTGACCTGGGATTTTATTTAACACAACGTGTGCCAAAGAGTT
GGCTTTGTTTTATTTGGTTTTGGCGGGGAGAGGAGTGGTATTTGATGCTTTCTGTGGACAATGTAACCCTAAACAC
ATCATGTATTTTAAATGCCACCTACATAAAATAAACATAAGCATATTGAATAC

2683/6881
FIGURE 2467

CTAAGACAGGTGCAGACGTATGTCGGCTTTGGCGTATCCATCAAGCTTTATATTGCTTTGATTATGATTTGGAGG
AAAGTGGAGAAATTAAAGATATGTTACTTGAGTGCTTCATAAATATTAATTATATCAAGAAAGAAGAGGGAAGAA
GATTTCTTAGTTGTCTCTTCAACTGGAATATCAACTTCATCAAAATGATCCACGGGACCATTAAAAACCAGTTAC
AGGGATTACAAAAGTCTTTGATGGTATACATTGCAGAAATTTATTTTCAGAGCTTGGAAGGCTTCAGGGAAAA
TACTGGAGGCGATTGAAAATGATTGCATCCAGGACTTCATGTTTCACGGGATACACCTTCCGAGGAGGTCTCCAG
TGCATTCCAAAGTGCAGGAGGTTCTGAGTTACTTTACCATCAAAAGAAAGTTCCGGCAGGAGTGGAAGAGATGC
TTTATAGATTATATAAGCCCATCCTTTGGAGAGGATTAAAGGCCAGAACTCTGAAGTTTCGATCAAAATGCTGCAT
TGTTGTTTGTGGAAGCATTTCCTATTAGGGATCCAAACCTTCATGCTATTGAAATGGATAGTGAAATCCAGAAAC
AGTTTGAAGAGCTCTATAGCCTTTTAGAAGATCCTTACCCGATGGTCCGTTCCACAGGGATCCTTGGTGTTTGTA
AAATAACTTCTAAGTACTGGGAAATGATGCCCCGACCATTCCTATTGACCTCCTGAAGAAGGTGACTGGGGAAC
TGGCATTGTGACACGAGCTCAGCTGATGTTCTGTTGTTCTGTCTTTAAGTGTCTGCCAATGATTTTGGACAACAAAC
TGAGCCACCCATTGTTAGAGCAGCTCCTTCCAGCTCTCAGATACAGTCTCCACGACAATTCGGAGAAAGTGAGGG
TAGCTTTTGTGGACATGCTGTTGAAGATCAAAGCTGTGAGGGCTGCTAAGTTTGGAAAATATGTCCCATGGAGC
ACATTCTGGTTCGTCTGGAACTGATTCTCGACCTGTGTCTCGGCGCTGGTGAGCCTCATCTTTAATTCTTTCC
TGCCTGTGAATCAGCCGGAGGAGGTCTGGTGCAGCGCTGTGTCAACCTGGTGAGATGAACCACGCCGCTGCCA
GGAGGTTCTATCAGTACGCCACGAACACACCGCCTGCACCAACATAGCAAAGCTGATTACGTTATTTCGTCAAT
GCTTAAATGCCTGTATCCAGAGGGCAGTGAGAGAGCCTCCAGAGGACGAGGAGGAAGAGGACGGAAGGGAGAAGG
AGAATGTGACTGTTCTGGACAAAACACTGTCAGTAAACGATGTTGCATGCATGGCAGGTTTACTAGAAATCATTG
TGATTCTCTGGAAGTATTGACAGAAGTATGGAATAATAAAGAGGCCAACTTTACACGATTAACAAGTTTG
CCTCTGTGCTTCCAGAGTATCTGAAAGTATTTAAGGATGATCGCTGCAAGATCCCTTTATTTCATGCTAATGTCCT
TTATGCCGGCCTCTGCTGTCCCCCATTACAGCTGTGGTGTGATTTCACGCTGAGAAGCCGGGAGGAGGGCGCTG
TGGACAAGAGCTACTGCACTTTGTTGGATTGCCTCTGCTCCTGGGGGCAAGTGGGGCACATTCTGGAGCTTGTG
ACAAGTGGCTGCCACAGAGCATGCCAGGCCAAGAGCAACACAGCTTCTAAAGGTAGGGTGAGATCCATGACA
CACGCCAGTCAAACCTGAATTGGCATTGGTCTACATTGAGTATCTGCTGACTCATCCAAAGAACCAGAGTGTCT
TGCTCTCTGCTCCTCGGAAGAACTTAACCATCTTTTGAAAGCCCTTGAAACGTCAAAGGCAGATCTGGAGTCAC
TTCTGCAGACACCGGGTGGGAAGCCTCGTGGCTTCAGTGAAGCAGCTGCCCGCGAGCCTTTGGTCTCCACTGTC
GCCTGAGCATCCATCTTCAGCACAAAGTTCTGCTCAGAAGGAAAGGTGTATTTGTCCATGTTGGAAGACACTGGCT
TTTGTTAGAAAGCAAAATTTTATCTTTTATTCAAGATCAAGAAGAAGACTACCTGAAGCTTCATAGGGTCATTT
ATCAGCAAATTATCCAGACCTACCTGACTGTGTGTAAAGATGTTGTTATGGTAGGCCTTGGTGACCATCAGTTTC
AGATGCAACTCTTACAGCGGAGTCTTGGAATCATGCAACAGTGAAGGGATTTTTTTATGTTTCATTACTTCTTG
ACATTCTGAAAGAGATAACTGGAAGTTCCTTGATTTCAGAAAACAGATTTCAGATGAAGAAGTTGCAATGCTGTTGG
ACACAGTCCAGAAAGTATTTTCAGAAAATGTTGGAATGTATTGCACGGAGCTTCAGGAAGCAGCCGGAAGAAGGCC
TGCGGCTGCTTTATTCTGTTTCAGAGGCCCTTCATGAGTTTCATTACTGCTGTTTCAGTCTCGGCACACAGACACC
CTGTGCACCGGGGTGTACTTTCTACTCTGATCGCTGGGCCTGTGGTTGAGATAAGTACCAGCTACGGAAGGTTT
CTGACGTAGAAGAGCTTACCCCTCCAGAGCATCTTTCTGATCTTCCACCATTTTCAAGGTGTTTAAATAGGAATAA
TAATAAAGTCTTCGAATGTGGTCAGGTCATTTTTGGATGAATTAAAGGCATGTGTGGCTTCTAATGATATTGAAG
GCATTGTGTGCCTCACGGCTGCTGTGCATATTATCCTGGTTATTAATGCAGGTAAACATAAAAGCTCAAAAGTGA
GGGAGGTTGCAGCCACTGTTACAGAAAACATAAGACATTTCATGGAATTAATTTGGAAGAGGATAGCATTGAAA
GATTTCTCTATGAATCATCATCAAGAACTCTGGGAGAACTTTTGAATTCAATCAAGCCAACATCTCCAGACAT
GTAAAAATAGGGAAAAGTGATTCAAATTGAAATGCCTGTGTATTTTCTATTGTTTTTAATGTTAATAACCCATA
TAATAGGGAAAGGGTGGGATTTTTTTGTGGGAATGTGGGAAGGTGGGGGTTATGGAGGAGATAACTCAAACTTC
TTCAATTTTGCCTAGTGCCTGCGTAAATAATATATTTAATAAAGGACTCCAGGTATAAATGGTGTAGAAATCC
ATGATTCCAAGAAAAAACACTTTTCTAGCAAACCTGGTTGTTTTTAAATGACTTTTATATATGTAATATTGCTT
GGAACTATGAGTAATAAAGCAATGACAACAAAAA

2684/6881
FIGURE 2468

MLLECFININYIKKEEGRRFLSCLFNWNINFIKMIHGTIKNQLQGLQKSLMVYIAEIIYFRAWKKASGKILEAIEN
DCIQDFMFHGIHLPRRSPVHSHKREVLSYFHHQKKVRQGVEEMLYRLYKPILWRGLKARNSEVRSNAALLFVEAF
PIRDPNLHAIEMDSEIQQFEELYSLLEDPYPMVVRSTGILGVCKITSKYWEMMPPTILIDLLKKVTGELAFDTSS
ADVRCVSVFKCLPMLDNKLSHPLLEQLLPALRYSLHDNSEKVRVAFVDMLLKIKAVRAAKFWKICPMEHILVRLE
TDSRPVSRRLVSLIFNSFLPVNQPEEVWCERCVTLVQMNHAAARRFYQYAHEHTACTNIAKLIHVIRHCLNACIQ
RAVREPPPEDEEEEDGREKENVTVLDKTLNVNDVACMAGLLEIIVILWKSIDRSMENNKEAKLYTINKFASVLPEY
LKVFKDDRCKIPLFMLMSFMPASAVPPFSCGVISTLRSREEGAVDKSYCTLLDCLCSWGQVGHILEIVDNWLPT
HAQAKSNTASKGRVQIHDTRPVKPELALVYIEYLLTHPKNRECLLSAPRKKLNHLLKALETSKADLESLLQTPGG
KPRGFSEAAAPRAFGHLCRLSIHLQHKFCSEGVYLSMLEDTGFWLESKILSFIQDQEEDYLLKLRVYQQIIQT
YLTVC KDVMVGLGDHGFQMQLLQRLGIMQTVKGFFVYVSLLLDILKEITGSSLIQKTDSDDEEVAMLLDTVQKVF
QKMLECIARSFRKQPEEGLRLLYSVQRPLHEFITAVQSRHTDTPVHRGVLSTLIAGPVVEISHQLRKVSDVEELT
PPEHLSDLPPFSRCLIGIIKSSNVVRSFLDELKACVASNDIEGIVCLTAAVHIILVINAGKHKSSKVREVAATV
HRKLKTFMEITLEEDSIERFLYESSRTLGEELLNS

2685/6881
FIGURE 2469

CGGGACGGAGGGGGCGGCCCCGCGCTCGGGGCGCTCGGCTACAGCTGCGGGGCCCCGAGGTCTCCGCGCACTCGC
TCCCGGCCCATGCTGGAGGCGGCGGAACCGCGGGGACCTAGGACGGAGGCGGCGGGCGCTGGGCGGCCCCCGGCA
CGCTGAGCTCGGGATGCGGACGCTGCTGCCTCCCGCGCTGCTGACCTGCTGGCTGCTCGCCCCCGTGAACAGCAT
TCACCCAGAATGCCGATTTTCATCTGGAATACAGGAGGAAGAAACAAAATGTGCAGAGCTTCTGAGGTCTCAAAC
AGAAAAACACAAAGCCTGCAGTGCGCTCTGGGACAACATCACGTGCTGGCGGCCTGCCAATGTGGGAGAGACCGT
CACGGTGCCCTGCCCCAAAAGTCTTCAGCAATTTTTACAGCAAAGCAGGAAAACATAAGCAAAAACCTGTACGAGTGA
CGGATGGTCAGAGACGTTCCAGATTTTCGTCGATGCCTGTGGCTACAGCGACCCGGAGGATGAGAGCAAGATCAC
GTTTTATATTCTGGTGAAGGCCATTTATACACTGGGCTACAGTGCTCTCTCTGATGTCTCTTGCAACAGGAAGCAT
AATTCTGTGCCTCTTCAGGAAGCTGCACCTGCACCAGGAATTACATCCACCTGAACCTGTTCTGTCTTTCATCCT
GAGAGCCATCTCAGTGCTGGTCAAGGACGACGTTCTCTACTCCAGCTCTGGCACGTTGCACTGCCCTGACCAGCC
ATCCTCCTGGGTGGGCTGCAAGCTGAGCCTGGTCTTCTGTCAGTACTGCATCATGGCCAACCTTCTTCTGGCTGCT
GGTGGAGGGGCTCTACCTCCACACCCTCCTGGTGGCCATGCTCCCCCTAGAAGGTGCTTCTTGGCCTACCTCCT
GATCGGATGGGGCTCCCCACCGTCTGCATCGGTGCATGGACTGCGGCCAGGCTCTACTTAGAAGACACCGGTTG
CTGGGATACAAACGACCACAGTGTGCCCTGGTGGGTACATACGAATACCGATTTTAATTTCCATCATCGTCAATTT
TGTCCTTTTCATTAGTATTATACGAATTTTGCTGCAGAAGTTAACATCCCAGATGTCGGCGGCAACGACCAGTC
TCAGTACAAGAGGCTGGCCAAGTCCACGCTCCTGCTTATCCCGCTGTTTCGGCGTCCACTACATGGTGTTTGCCGT
GTTTCCCATCAGCATCTCCTCCAAATACCAGATACTGTTTGAGCTGTGCCTCGGGTCGTTCCAGGGCCTGGTGGT
GGCCGTCTCTACTGTTTCTGAACAGTGAGGTGCAGTGCGAGCTGAAGCGAAAATGGCGAAGCCGGTGCCCGAC
CCCGTCCGCGAGCCGGGATTACAGGGTCTGCGGTTCTCCTTCTCCCGCAACGGCTCGGAGGGCGCCCTGCAGTT
CCACCGCGGCTCCCGCGCCCAGTCCTTCTTGCAAACGGAGACCTCGGTTCATCTAGCCCCACCCCTGCCTGTGCGGA
CGCGGCGGGAGGCCCCACGGTTCGGGGCTTCTGCGGGGCTGAGACGCGCGGCTTCCTCCTTCCAGATGCCCGAGCAC
CGTGTCGGGCAGGTCAGCGCGGTCCTGACTCCGTCAAGCTGGTTGTCCACTAAACCCCATACCTGG

2686/6881
FIGURE 2470A

GTGAACCGTG CATGTGAGGGATCTAGGTTGCGCTATCCTTATGAGAATCTAATACCTATTGATCTGTCACTTTCT
CCCATCACGCTCAGGTGGGACCATCCAGTTGCAGGAAAAACAAGCTTAACACGCCCCTGATTCTACATTATGCTC
CTACCTCCCAGCAGCCTCTCCAGGCCCAGAACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCACAAT
GGCCTATTTAGGCCCATACCTACCTCACGGCAGTCTCCGCAGATGAGCCTACTGCCTCACAACAGCCTCCACAG
GCACAGCTCCATCGTTACAATGGCCTCTTTAGACCCAGCTCCTGCCTCCCAGCCTTCTCTCCAGGCCCTGAACTT
TCTCAAGTCGACCTCACCAGGCCCAGCTCATGCTTCTTTGCAGCCTCTCCAGGCCCAGCTCCTGCATCTTGGTGG
CACCTCCAGGCCCAGCCTCTGCCTCCCGTCGGCCTCTACAAATCCCAACATCTGCCTCACAGCAGATTCTTCAGGC
CCAGCATCTGCCTCACTGTGGACCCCCCAAGCCAAGCTCCCAACCTTTTCAGCAGCTTCTACACACCCAACTCCTG
CCACCCAGTGGCCTCTTTAGGCCAAGCTCATGCTTCACAAGGGCCTTTCCAGGCTCAACTTTTGTCTCATGGCAA
CCTTTTCTGGCCAGATTCTGCCTGTCTCCCAGCAGCCTAGACAGGCCCAGGTCTTGCCTCACACTGGCCTCTCT
ACATCCAGCTCATGCCTCACGGTGGCCTCTCCAGGCCCAACTCCTGTCCCAGGACGTCATCTCCGGGCCCAAAC
TTACTCAAGTCAGACTCTCTAGTCCCAACTGCTGCCTCCTGGTGGCCTATGAAGGCCCAAAATCTCCTCAAGTGG
ACCTCTCCAGGCCCAGCTCCTGCCTCCTGTGAGCGTCTACAGGCCCAACCTCTGCCTCATGGGGCTTCTCCAGG
CCCACCTCTTCTCTTGGCTGGGTCTACAGGCACAACCTGCTGCCTCACAACAGCCTTTTTTGGCCAGTTCTCT
CCAGCTCATGGCGCCAATGTAGGCCCAAACTTCTCAAGTCAAACCTCTCCAGGCCACCTTCTGCTTCCCGGT
GGCATGAACAGGCCCAGCTTTGACTTGAGAACAGCCTCTGCAGGCCCTGCTCTTGCCTCCCAGGGGCTTTTTCCA
GACCCAGCTCCTGCCTCATGGCAGCTGCCCCAGGCCAAATTTCTGCCTGCCTGCCAGCAGCCTCAACAGGCACAG
CTCTCCCTCACAGTGGCCATTTAGGCCCAACTCATGACTGTGGGCCATTTCCAGGCCTAGTGCCTGCCTCGT
GGCTGACTCTTGAAGCCCAAACTTCTCAAATCAGCCTTTTGCCCAACTTCTGTCTACTGTGGACTCTACAGG
CCAGCCTCTGCCTCACAGTGGACCTCCAGACCCAGATGGTGTCTCACTGTGGCATCCTCAGGCGAAGCTCCTGC
CTTTCCGCAGCCTCTACAGGCCCAGCTCCTGCCTTGAGTGGCCTCTTTAGGCCAAGCTCATGCCCCATGGCGAC
TTTTCCAGGCACAGCTTTTGCCTTTTGCAGCCTGTCCAGGCCCAGAAATGTCCTTAACTCGGCATCTCCAGGATGA
GCTCATCTCTCCAGTGGCTCTACAGGCCCGTCTCCTGCCTCACAACAACCTCCTTTGGCCCAACTCCTGCTGAGC
TGCTGGCAGCCTCTGTAGGCCACAGAATTCTTAAGGTAAAGCTTTCCAGGCCACCTTTGGCCTCCCGGCAGGCT
CAGCAATCAAATAATCCCTCACTGCGGCCACCGAAAGCCAAGTTTCTCCTGCCTCACGGCATCTCTCCGAAAAC
TGAGCATTTGCCTCACGGTGGCCTCCCAGGCCATGAATCTGCCTGCCTCCCAGGCAGCTGCTGCCTCACAATGG
TCTCTTTAGGCCCAGCTCATGCTAAAAGATGGACTCTCCAGGCACAGCTCTTGCCTCCTGGCAGCCTCTGCAGGC
CCAAATTCTCCAAAAGTTGGCCTCTCCTAACTCAGCTCCTGCCTCATGTGGCCTACACAGGCCCAGACTCTTAC
CACACAGTAGACCTCCAGGCCCACTTGCCTGATCATAGCCTCCTAAGGCCAAGCTCCTGCCTTTCCGGCAGC
CTCTACAGGCCAAGCTCCTGCCTCGCAATTGCCTCTGTAGGCCAAGATCATGCCGTGAAGTGGCCTTCCCTAGCC
TAACTTTTTGCTTTTTGACGCATACTCCAGTCCCAAACTTCTCCAGTCAGCCGGTCCAGGCCAAGCTCTTCTC
CCAAAGGCTTCTGCAGGCCAAATCATCTGAAGTCACCTCTGCAGGCGCAGCTCCTGCCTCCAAGTGCTGTGT
AGGCCAAGCTAATGCCTCACAGCACACTTTCAGGCTGAGCATTTCTTTTTGTGCATCTCTCCAAGCCCTGAAC
TTACTCCAGTTGGCCTCTCCAGACCAAGCTCTCCCTCCAGTGGCCTCTACAGGCCAAATGTCTCAGGTCAG
CCTCTCCAGGCCCAACTCCTAGCTACCGGTGGCTTCTGCAGGCCAAAATCGACCTCAAGTCAGCCTCTTACACC
CAGCTCTTGCCTCTGAGTGGCCTCTCCAGGAGCAAACTTCTCAAGTCGGCCTCTCCAGGCCCAGCCTCCTGCT
TCCCGAGGGCATGTACAGGCCCAGCCTCTGCCTCACAGCAGACTCTTACACCCAGCTCTTCCCTGTCTGCGGCC
TCTCCAGTCCAAAGCTGCTCCTGCCTTTTGGCAGCTTGTACAGGCCCAGCTCCTCCTCACGGTGGCCTCTTTCG
GCCAACTCATGCCTCTTGCAACGTGCCCAAGTGTGAGCTCCTGCCTCACACTGGCCTGTTGAGGCCCAGCTCAT
GCCTCTCGTGGCCTCAACGGGCCCATCCCTGCCTGTGCGGGCCTCTACAGGCCCGGCCTCTACCTCACAGTGG
GCTCTCCAGGCCACCTCTTCTCACCGTGGCCTCCTGGGGCAATGCTCCTCCTCTCGGGAGCCTCTGTGGGCC
CAGCTCCTGCCTCCCAGTGGCCTCTGCTGGCCAAGCCCGTGCCTCAGGGCAGCCTTTCCAGGCCTAGCGTTTGTCT
GCTTTGCATCTCTCCAGGCCCTGGACTTCTCCAGTCGGCCTCTCCAGGCCCAGCTCTTCTCTCGGCGGCCTC
TGCAGGCCCAGACTGTCTGTCAGTCGGCCTGTCCAGGGCCAGCTCCTGCCTCCCGGGCGGCCTCTGCAGGCCCAAG
TCGTCTCAAGTTGGCCTCCCCAGGCCCAGCAACGGCCTCTCGGGCGGCCTTTCCGGGTGCAAAAGTTTCTCGAGT
CAGCCTCTCCAGGCCCAGCTCCTCCTGCCTCCCAGTGGCCTCTTTCCGGGCCAGGCCAGCTCATGCCTCCCGGCGG
CCTTCCAGGCCCTGCTTTTTGACTTTTGGTGGCCTCTGCAGGCCTCGACAAGGCCAGGCCTCCTGCCTCCCAAG
GCCTGCACAGGCCCAGCCTCTGCCTCACAGCAGACTCTCCACGCCCAGCTAGCTCTCGCCTCACTGCGGCTTCCC

2687/6881
FIGURE 2470B

GAGTCCAAAGCTCCTGCCTCTCAGCCGCTTCGGCAGGCCCAGCTCCCGCCTGCCAGTGGCCTCTTCAGGCCCCATG
GGGCTCATTTCCTCACAACGGCCTTTCAGGCCCAGTTTTCCCTTCCGGCGGCCTCTTGGCCTCTAATTTGTTTA
TCTTTTGGGTATAAATCCCAAAATATTGAATTTTGGAATATTTCCACCATT

2688/6881
FIGURE 2471

TCTAATACCTATTGATCTGTCACTTTCTCCCATCACGCTCAGGTGGGACCATCCAGTTGCAGGAAAACAAGCTTA
ACACGCCCCTGATTCTACATTATGGTGAGTTCTATAATTATTTATTATATATTACAGTGTAATAATGGAAATA
AAGTGCCTAATAAATGTAAATGTGCTTAAATCTTTTGGCCCAGCTCCTACCTCCCAGCAGCCTCTCCAGGCCAG
AACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCACAATGGCCTATTTAGGCCCATACCCTACCTCAC
GGCAGTCTCCGCAGATGAGCCTACTGCCTCACAACAGCCTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTT
TAGACCCAGCTCCTGCCTCCCAGCCTTCTCTCCAGGCCCTGAACTTTCTCAAGTCGACCTCACCAGGCCAGCTC
ATGCTTCTTTGCAGCCTCTCCAGGCCAGCTCCTGCATCTTGGTGGCACCTCCAGGCCAGCCTCTGCCTCCCGT
CGGCCTCTACAATCCCAACATCTGCCTCACAGCAGATTCTTCAGGCCAGCATCTGCCTCACTGTGGACCCCCCA
GACCCAGATGGTGTCTCACTGTGGCATCCTCAGGCGAAGCTCCTGCCTTTCCGCAGCCTCTCCAGGCCAGCTCC
TCCTGCCTCCCAGTGGCCTCTTTCGGCCCAGCCCAGCTCATGGCTCTCGGCGGCCTTCCCAGGCCCCGCTTTTGA
CTTTTGGCGGCCTCTTCAGGCC

2689/6881
FIGURE 2472

TCTAATACCTATTGATCTGTCACTTTCTCCCATCACGCTCAGGTGGGACCATCCAGTTGCAGGAAAACAAGCTTA
ACACGCCCCTGATTCTACATTATGGTGAGTTCTATAATTATTTTATTATATATTACAGTGTAAATGGAAATA
AAGTGCCTAATAAATGCAAATGTGCTTACATCTTTTGGCCCAGCTCCTACCTCCTGGCAGCCTCTCCAGGCCCAG
AACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCACAATGGCCTATTTAGGCCCATAACCCTACGTAC
GGCAGTCTCCGCAGATGAGGCTACTGCCTCACAACAGCCTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTT
TAGACCCAGCTCCTGCCTCCCAGCCTTCTCTCCAGGCCCTGAACTTTCTCAAGTCGACCTCACCAGGCCCAGCTC
ATGCTTCTTTGCAGCCTCTCCAGGCCCAGCTCCTGCATCTTGGTGGCCCCCTCCAGGCCCAGCCTCTGCCTCCCGT
CGGCCTCTACAGTCCCAACATCTGTCTCACAGCAGATTCTTCAGGCCCAGCATCTGCCTCACTTGGACCCTCCAG
ACCCAGATGGTGTCTCACTGTGGCATCCTCAGGTGAAGCTCCTGCCTTTTCGGCAGCCTCTCCAGGCCCAGCTCCT
CCTGCCTCCCAGTGGCCTCTTTTCGGCCCAGCCCAGCTCATGCCTCCCGGCGGCCTTCCCAAGCCCCGCTTTTGAC
TTTCCACCGAAAGTCCCAGCCTCCTGCCTCCCGAAGGCCTGCACAGGCCCA

2690/6881
FIGURE 2473

ATGTTGCCAATAACACAGATGAAGAGACTGGGGGATGGCACTATCACTGCTGCTGTACTGAAGGTTAGCAAAGGT
GCTAATCCAGTGGAAATCAAGAGAGGTGTGATGTTAGCTGTTGATGCTGTAATTGCTGAACTTAAAAAGCAGTCT
AAACCTGTGACCAAACCTGAAGAAATTGCACAGGTTGCTACAATTTCTGCAAATGGAGACAAAGAAATTGGTAAC
ATCATCTCTGATGCAATGAAAAAGTTTGAAGAAAGGGCATCATCACAAAAATTTCTAGTGTCCAGTCCATTGTA
ACTGCTCTTGAAATTGCCAATGCTTACTGTAAGCCTTTGGTCATAATTGCTGGAGACATTGATGGAGAAGCTCTA
ACTACACTCATCCTGAATAGGCTAAAGGTTGGTCTTCAGGTTGTGGCAGTCAAAGCTCCAGGGTTTGGTGACAAT
AGAAAGAACCAGCTTAAAGATACGGTTATTGCTACTGGTGGAGAAAGTTGGAGAGGTCAGTGTGATCAAAGATTAT
GCCATGCTCTTAAAAGGAAAAGGTAACAAGTCTCAAATTGAAAAATGTGTTCAAGAAATCATTGACCAGTCAGAT
GTCACAACTAGTGAATACGAAAAGGAAAACTGAGTGGAGAAACTTTCAGATGGAGTAGCTGTGCTGAAGCTAAT
GAAGATAAAATAATTGGTATAGAAATTATTTAAAAGAACACTCAAAATTCAGCAATGACAATTGCTAAGAATGCA
GGTGTTGATGGATTTTGTATAGTTGAGAAAATTATGTAA

2691/6881
FIGURE 2474

MLPITQMKRLGDGTITA AVLKVS KGANPVEIKRGV MLAVDAVIAELKKQSKPVT KPEEIAQVATISANGDKEIGN
IISDAMKKFGRKGIITKISSVQSIVTALEIANAYCKPLVIIAGDIDGEALTTLILNRLKVGLQVVAVKAPGF GDN
RKNQLKDTV IATGGEVGEVTVIKDYAMLLKGKGNKSQIEKCVQEIIDQSDVTTSEYEKEKLSGETFRWSSCAEAN
EDKIIGIEI IKRTLKIPAMTI AKNAGVDGFLIVEKIM

2692/6881
FIGURE 2475

ATGTACTGGGACATCGTGTCTTTGGAGACAGCTATAACCCACTTGTCCATTCTGCTGAGGCCCACAAATGCCATC
ACCCAGAAGCCCTTCACATCCACTGGGGCCACAGCAGGATACAGTCTGTTGCTGGTCCAGCAGCCTGATAAAATC
ATTGTCCTCTCCACCCTGATTCCTACAGGAGACTACTCACCCCATAACCTCAAAAACCTCTTCATGAGGATGGTG
ACCCAGCCATGAGGACCCTCGCCATCCTTGCTGCCATTCTCCTGGTGGCCCTGCAGGCCCAGGCTGAGCCACTC
CAGGCAAGAGCTGATGAGGTTGCTGCAGCCCCGGAGCAGATTGCAGCGGACATCCAGAAGTGGTTGTTTCCCTT
GCATGGGACGAAAGCTTGGCTCCAAAGCATCCAGGCTCAAGGAAAAACATGGACTGCTATTGCAGAATACCAGCG
TGCATTGCAGGAGAACGTCGCTATGGAACCTGCATCTACCAGGGAAGACTCTGGGCATTCTGCTGCTGA

2693/6881
FIGURE 2476

CTATAGAAGACCTGGGACAGAGGACTGCTGTCTGCCCTCTCTGGTCACCCCTGCCTAGCTAGAGGATCTGTGACCC
CAGCCATGAGGACCCTCGCCATCCTTGCTGCCATTCTCCTGGTGGCCCTGCAGGCCCAGGCTGAGCCACTCCAGG
CAAGAGCTGATGAGGTTGCTGCAGCCCCGGAGCAGATTGCAGCGGACATCCCAGAAGTGTTGTTTCCCTTGCA
GGGACGAAAGCTTGGCTCCAAAGCATCCAGGCTCAAGGAAAAACATGGCCTGCTATTGCAGAATACCAGCGTGCA
TTGCAGGAGAACGTCGCTATGGAACCTGCATCTACCAGGGAAGACTCTGGGCATTCTGCTGCTTGAGCTTGCAGAA
AAAGAAAAATGAGCTCAAAATTTGCTTTGAGAGCTACAGGGAATTGCTATTACTCCTGTACCTTCTGCTCAATTT
CCTTTCCTCATCCCAAATAAATGCCTTGGTACAAGAAAAG

2694/6881
FIGURE 2477

MRTLAILAAILLVALQAQAEPLQARADEVAAAPEQIAADIPEVVVSLAWDESLAPKHPGSRKNMACYCRIPACIA
GERRYGTCTIYQGRLWAFCC

2695/6881
FIGURE 2478

CCTTGCTATAGAAGACCTGGGACAGAGGACTGCTGTCTGCCCTCTCTGGTCACCCTGCCTAGCTAGAGGATCTGT
GACCCCAGCCATGAGGACCCCTCGCCATCCTTGCTGCCATTCTCCTGGTGGCCCTGCAGGCCCAGGCTGAGCCACT
CCAGGCAAGAGCTGATGAGGTTGCTGCAGCCCCGGAGCAGATTGCAGCGGACATCCCAGAAGTGGTTGTTTCCCT
TGCATGGGACGAAAGCTTGGCTCCAAAGCATCCAGGCTCAAGGAAAAACATGGACTGCTATTGCAGAATACCAGC
GTGCATTGCAGGAGAACGTCGCTATGGAACCTGCATCTACCAGGGAAGACTCTGGGCATTCTGCTGCTGAGCTTG
CAGAAAAAGAAAAATGAGCTCAAAATTTGCTTTGAGAGCTACAGGGAATTGCTATTACTCCTGTACCTTCTGCTC
AATTCCTTTCTCATCTCAAATAAATGCCTTGTTAC

2696/6881
FIGURE 2479

MRTLAILAAILLVALQAQAEPLQARADEVAAAFEQIAADIFEVVVSLAWDESLAPKHGSRKNMDCYCRIPACIA
GERRYGTCTIYQGRLWAFCC

2697/6881
FIGURE 2480

ATGCAGGTCTGCAACTGCAGGTGCCTCTCACCTGGTGACCTGCAGGAAGATGGAGGAGCATATTGGGCACAGTGC
TCGGTTTGGGGGGCGCACTTCGACCCGGAAGTTTACCTAGACAAGCTGCATAGAGTGTGCCCTCTGGCCCAGCTG
ATGGACAGTGAGACGGACATGGTGCGGCAGATCCGGGCTATAGACAGCGACATGCAGACCCTGGTCTATGAGAAC
TACGACAAGGAGACTATCGGGGTGCAACCTGGCTGGGGCGGGGAGGAGGTGCAGGGCCTGGCCAGAGCGGGCCTG
GCCACGGGCAAGGGACAGCGACCGCCTGGGCCAGGACAGGTGAGAGCGGCGCAGTCCCGGGCCCCGGCGTGTCGCG
GCTGCGCGGGAGAGGCCAGCAGAGGGCGCCAGAGAGCCAGGAGCGGCCCGCGGAGGAGCCCGCGCCAGCCGGATG
CCCAGCTCCGCGCCGCGCGGACCCAACGAGCCCGCGCTCAGACGCCCCAGCTCCGCCGAGAGGCCGCTCGCGCCG
GGCAGAGCCCCTGGAGCCATGGCCAGCCCTTCCGGCAGCTCCGAAGCCACTGGCAAGCCCCGAGGCAGGGATGGC
CGGCCCAGGAGGGAGGAGGACGACGTCCCTCCCGAAGAGAAGAGGCTACGGCTGTTGCTGGAGGGGGGAAGCGCA
CAGCCCAGGACTGCGAGGACGGGGAGGACGCGCTGCGGCCGGGCAGGGAGGAGACCGGCACCTAG

2698/6881
FIGURE 2481

MQVCNCRCLSPGDLQEDGGAYWAQCSVWGAHFDPEVYLDKLHRVCPLAQLMDSETDMVRQIRAIIDSDMQTLVYEN
YDKETIGVQPGWGGEEVQGLARAGLATGKGQRPPGPGQVRAAQSRARRVRAARERPAEGAREPGAARGGARASRM
PSSAPRGPNEPALRRPSSAERPLAPGRAPGAMASPSGSSEATGKPRGRDGRPRREEDDVPPEEKRLRLLEGGSA
QPEDCEDGEDALRPGREETGT

2699/6881
FIGURE 2482

GAGAGTCGCGCCCGGGAGTCCGCGCCTGCGCCAGGATGGAGTTCGTGAAATGCCTTGGCCACCCCGAAGAGTTC
TACAACCTGGTGCGCTTCCGGATCGGGGGCAAGCGGAAGGTGATGCCCAAGATGGACCAGGACTCGCTCAGCAGC
AGCCTGAAAACTTGCTACAAGTATCTCAATCAGACCAGTCGCAGTTTTCGCAGCTGTTATCCAGGCGCTGGATGGG
GAAATGCGCAACGCAGTGTGCATATTTTATCTGGTTCTCCGAGCTCTGGACACACTGGAAGATGACATGACCATC
AGTGTGGAAGAAGGTCCCGCTGTTACACAACTTTCACTCTTTCCTTTACCAACCAGACTGGCGGTTTCATGGAG
AGCAAGGAGAAGGATCGCCAGGTGCTGGAGGACTTCCCAACGATCTCCCTTGAGTTTAGAAATCTGGCTGAGAAA
TACCAAACAGTGATTGCCGACATTTGCCGGAGAATGGGCATTGGGATGGCAGAGTTTTTGGATAAGCATGTGACC
TCTGAACAGGAGTGGGACAAGTACTGCCACTATGTTGCTGGGCTGGTCGGAATTGGCCTTTCCCGTCTTTTCTCA
GCCTCAGAGTTTTGAAGACCCCTTAGTTGGTGAAGATACAGAACGTGCCAACTCTATGGGCCTGTTTTTGCAGAAA
ACAAACATCATCCGTGACTATCTGGAAGACCAGCAAGGAGGAAGAGAGTTCTGGCCTCAAGAGGTTTGGAGCAGG
TATGTTAAGAAGTTAGGGGATTTTGCTAAGCCGGAGAATATTGACTTGGCCGTGCAGTGCCTGAATGAAC TTATA
ACCAATGCACTGCACCACATCCCAGATGTCATCACCTACCTTTTCGAGACTCAGAAACCAGAGTGTGTTTAAC TTC
TGTGCTATTCCACAGGTGATGGCCATTGCCACTTTGGCTGCCTGTTATAATAACCAGCAGGTGTTCAAAGGGGCA
GTGAAGATTTCGGAAGGGCAAGCAGTGACCCTGATGATGGATGCCACCAATATGCCAGCTGTCAAAGCCATCATA
TATCAGTATATGGAAGAGATTTATCATAGAATCCCCGACTCAGACCCATCTTCTAGCAAAACAAGGCAGATCATC
TCCACCATCCGGACGCAGAATCTTCCCAACTGTCAGCTGATTTCCCGAAGCCACTACTCCCCATCTACCTGTCG
TTTGTGTCATGCTTTTGGCTGCCCTGAGCTGGCAGTACCTGACCACTCTCTCCCAGGTAACAGAAGACTATGTT CAG
ACTGGAGAACTGATCCCAAATTTGTCCATAGCTGAAGTCCACCATAAAGTGGATTTACTTTTTTTCTTTAAGG
ATGGATGTTGTGTTCTCTTTATTTTTTTTCTACTACTTTAATCCCTAAAAGAACGCTGTGTGGCTGGGACCTTTA
GGAAAGTGAAATGCAGGTGAGAAGAACCTAAACATGAAAGGAAAGGGTGCCTCATCCCAGCAACCTGTCTTGTG
GGTGATGATCACTGTGCTGCTTGIGGCTCATGGCAGAGCATT CAGTGCCACGTTTTAGGTGAAGTCGCTGCATAT
GTGACTGTGATGAGATCCTACTTAGTATGATCCTGGCTAGAATGATAATTAAAAGTATTTAATTTG

2700/6881
FIGURE 2483

TCCGGCAACGCCAACCGCTCCGCTGCGCGCAGGCTGGGCTGCAGGCTCTCGGCTGCAGCGCTGGGCTGGTGTGCA
GTGGTGCAGACCACGGCTCACGGCAGCCTCAGCCACCCAGATGTAAGCGATCTGGTTCCACCTCAGCCTCCCGAG
TAGTGGATCTAGGATCCGGCTTCCAAC**ATGT**GGCAGCTCTGGGCCTCCCTCTGCTGCCTGCTGGTGTGGCCAAT
GCCCCGAGCAGGCCCTCTTTCCATCCCCTGTCGGATGAGCTGGTCAACTATGTCAACAAACGGAATACCACGTGG
CAGGCCGGGCACAACCTTCTACAACGTGGACATGAGCTACTTGAAGAGGCTATGTGGTACCTTCCTGGGTGGGCCC
AAGCCACCCCAGAGAGTTATGTTTACCGAGGACCTGAAGCTGCCTGCAAGCTTCGATGCACGGGAACAATGGCCA
CAGTGTCCCAACCATCAAAGAGATCAGAGACCAGGGCTCCTGTGGCTCCTGCTGGGCCTTCGGGGCTGTGGAAGCC
ATCTCTGACCGGATCTGCATCCACACCAATGCGCACGTACAGCGTGAGGTGTCGGCGGAGGACCTGCTCACATGC
TGTGGCAGCATGTGTGGGGACGGCTGTAATGGTGGCTATCCTGCTGAAGCTTGGAACCTTCTGGACAAGAAAAGGC
CTGGTTTCTGGTGGCCTCTATGAATCCCATGTAGGGTGCAGACCGTACTCCATCCCTCCCTGTGAGCACCACGTC
AACGGCTCCCGGCCCCCATGCACGGGGGAGGGAGATACCCCCAAGTGTAGCAAGATCTGTGAGCCTGGCTACAGC
CCGACCTACAAACAGGACAAGCACTACGGATAACAATTCCTACAGCGTCTCCAATAGCGAGAAGGACATCATGGCC
GAGATCTACAAAAACGGCCCCGTGGAGGGAGCTTTCTCTGTGTATTTCGGACTTCCTGCTCTACAAGTCAGGAGTG
TACCAACACGTCACCGGAGAGATGATGGGTGGCCATGCCATCCGCATCCTGGGCTGGGGAGTGGAGAATGGCACA
CCCTACTGGCTGGTTGCCAACTCCTGGAACACTGACTGGGGTGACAATGGCTTCTTTAAAATACTCAGAGGACAG
GATCACTGTGGAATCGAATCAGAAGTGGTGGCTGGAATTCACGCACCGATCAGTACTGGGAAAAGATCT**TAAT**CT
GCCGTGGGCCTGTCGTGCCAGTCTGGGGGCGAGATCGGGGTAGAAATGCATTTTATTCTTTAAGTTACGTAAG
ATACAAGTTTCAGACAGGGTCTGAAGGACTGGATTGGCCAAACATCAGACCTGTCTTCCAAGGAGACCAAGTCCT
GGCTACATCCCAGCCTGTGGTTACAGTGCAGACAGGCCATGTGAGCCACCGCTGCCAGCACAGAGCGTCTTCCC
CCTGTAGACTAGTGCCGTAGGGAGTACCTGCTGCCCCAGCTGACTGTGGCCCCCTCCGTGATCCATCCATCTCCA
GGGAGCAAGACAGAGACGCAGGAATGGAAAGCGGAGTTCTTAACAGGATGAAAGTTCCCCCATCAGTTCCCCCAG
TACCTCCAAGCAAGTAGCTTTCCACATTTGTACAGAAATCAGAGGAGAGACGGTGTGGGAGCCCTTTGGAGAA
CGCCAGTCTCCCAGGCCCTTGCATCTATCGAGTTTGCAATGTCACAACCTCTCTGATCTTGTGCTCAGCATGAT
CTTTTAATAGAAGTTTTATTTTTTCGTGCACTCTGCTAATCATGTGGGTGAGCCAGTGGAAACAGCGGGAGACCTG
TGCTAGTTTTTACAGATTGCCTCCTTATGACGCGGCTCAAAAGGAAACCAAGTGGTCAGGAGTTGTTTCTGACCCA
CTGATCTCTACTACCACAAGGAAAATAGTTTAGGAGAAACCAGCTTTTACTGTTTTTGAAAAATTACAGCTTCAC
CCTGTCAAGTTAACAAGGAATGCCTGTGCCAATAAAAGTTTTCTCCAACCTGA

2701/6881
FIGURE 2484

MWQLWASLCCLLVLANARSRPSFHPLSDELVNYVNKRNTTWQAGHNFYNVDMSYLRKLCGTFLGGPKPPQRMFT
EDLKLPASFDAREQWPQCPTIKEIRDQGSCGSCWAFGAVEAISDRICIHTNAHVSVEVSAEDLLTCCGSMCGDGC
NGGYPAEAWNFWTRKGLVSGGLYESHVGC RPYSIPPCEHHVNGSRPPCTGEGDTPKCSKICEPGYSPTYKQDKHY
GYNSYSVSNSEKDIMAEIYKNGPVEGAFSVYSDFLLYKSGVYQHVTGEMMGHAI RILGWGVENGTPYWL VANSW
NTDWGDNGFFKILRGQDHCGIESEVVAGIPRTDQYWEKI

2702/6881
FIGURE 2485

CTGGGAAGCAGAGTGTCTGGATGGAACCTGAGCTGGGTCTCTGACTCACTTCTGACTTTAGTTTTTTCAAGGGGG
AACATGGCAAAGGTGTTTCAGTTTCATCCTTGTTACCACCGCTCTGATAATGGGCAGGGAATTCGXXXXXXXXX
XX
XX
XX
AAACCTCTCCAGAGCCTAGCAGAATTTCTGTTTATTGTGACATGTCCGATGGAGGAGGATGGACTGTAATTCAG
AGACGATCTGATGGCAGTGAAAACCTTTAACAGAGGATGGAAAGACTATGAAAATGGCTTTGGAAATTTTGTCCAA
AAACATGGTGAATATTGGCTGGGCAATAAAAATCTTCACTTCTTGACCACTCAAGAAGACTACACTTTAAAAATC
GACCTTGCAGATTTTGAAAAAAATAGCCGTTATGCACAATATAAGAATTTCAAAGTTGGAGATGAAAAGAATTTCT
TACGAGTTGAATATTGGGGAATATTCTGGAACAGCTGGAGATTCCCTTGCGGGGAATTTTCATCCTGAGGTGCAG
TGGTGGGCTAGTCACCAAAGAATGAAATTCAGCACGTGGGACAGAGATCATGACAACATATGAAGGGAACCTGCGCA
GAAGAAGATCAGTCTGGCTTGTGGTTTAACAGGTGTCACTCTGCAAACCTGAATGGTGTATACTACAGCGGCCCC
TACACGGCTAAAACAGACAATGGGATTGTCTGGTACACCTGGCATGGGTGGTGGTATTCTCTGAAATCTGTGGTT
ATGAAAATTAGGCCAAATGATTTTATTCCAAATGTAATTTTAATTGCTGCTGTTGGGCTTTCTGTTCTGCAATTCA
GCTTTGTTTAAAGTGATTTGAAAAATACTCATTCTGAACATATCCATGCGCAATCATGATAACTGTTGTGAGTAG
TGCTTTTCATTCTTCTCACTTGCCCTTGTTACTTAATGTGCTTTCAGTACAGCAGATATGCAATATTCACCAAAT
AAATGTAGACTGTGTT

2703/6881
FIGURE 2486

MAKVFSFILVTTALIMGREISXX
XXXXXXXXXXIFNDGYKLSGFYKIKPLQSLAEFSVYCDMSDGGGWTVIQRRSDGSENFNRGWKDYENGFGNFVQK
HGEYWLGNKNLHFLTQEDYTLKIDLADFEKNSRYAQYKNFKVGDEKNFYELNIGEYSGTAGDSLGNFHPFVQW
WASHQRMKFSTWDRDHDNYEGNCAEEDQSGLWFNRCHSANLNGVYYSGPYTAKTDNGIVWYTWHGWWYSLKSVVM
KIRPNDFIPNVI

2704/6881
FIGURE 2487

GGGACAGAGGAGACAAGATGGCGCTGCGGGCGATGCGGGGGATTGTCAACGGGGCCGCACCCGAGCTACCCGTGC
CCACCGGTGGGCCGGCGGTGGGAGCTCGGGAGCAGGCGCTGGCAGTCAGTCGGAACACCTCTCCCAGCCTCGCC
TCACATACAAGACAGTATCTGGAGTCAATGGTCCACTAGTGATCTTAGATCATGTAAAGTTTCCCAGGTATGCTG
AAATTGTCCATTTGACCTTACCGGATGGCACAAGAGAAGTGGGCAAGTTCTGGAAGTTAGTGGTTCCAAGGCAG
TAGTTCAGGTATTTGAAGGGACTTCAGGTATAGATGCTAAGAAAACGTCCTGTGAGTTTACTGGGGATATTCTCC
GAACACCGGTGTCTGAGGATATGCTTGGTCCGGTATTCAATGGATCGGGAAAACCCATTGACAGAGGTCTGTG
TACTGGCCGAAGACTTCCTTGATATCATGGGTGAGCCAATCAACCCCTCAATGTGCAATCTACCCAGAGGAAATGA
TTCAGACTGGCATTTCGGCCATCGATGGGATGAACAGTATTGCTAGGGGGCAGAAAATTCCTATCTTCTCTGCTG
CTGGGCTACCACACAATGAGATTGCAGCTCAGATCTGTGCGCAGGCTGGTTTGGTAAAGAAATCCAAAGATGTAG
TAGACTACAGTGAGGAAAATTTTGCAATTGTATTTGCTGCTATGGGTGTAAACATGGAAACTGCCCCGTTCTTCA
AATCTGACTTTGAAGAAAATGGCTCAATGGACAATGTCTGCCTCTTTTTGAACCTGGCTAATGACCCAAACCATTG
AGCGAATTATCACTCCTCGCCTGGCTCTAACCACAGCTGAATTTCTGGCGTACCAATGTGAGAAACATGTATTGG
TTATTCTAACAGACATGAGTTCTTATGCTGAAGCACTTCGAGAGGTTTCAGCAGCCAGGGAAGAGGTACCTGGTC
GACGAGGTTTTCCAGGTTACATGTATACAGATTTAGCCACGATATATGAACGCGCTGGGCGAGTGGAAGGGAGAA
ACGGCTCGATTACTCAAAATCCCTATTCTAACCATGCCTAATGATGATATCACTCACCCCATCCCAGACTTGACTG
GCTACATTACAGAGGGGCAGATCTATGTGGACAGACAGCTGCACAACAGACAGATTTATCCACCTATCAATGTGC
TGCCCTCACTATCACGGTTAATGAAGTCTGCTATTGGAGAAGGGATGACCAGGAAGGATCATGCCGATGTATCTA
ACCAGCTAGTATGCGTGCTATGCTATTGGAAGGATGTGCAAGCCATGAAAGCTGTCGTTGGAGAAGAAGCCCTT
ACCTCAGATGATCTTCTCTACTTGGAAATTTCTGCAGAAGTTTGAGAGGAACTTCATTGCTCAGGGTCTTACGAA
AATCGCACTGTCTTTGAGACTTTGGACATTGGCTGGCAGCTACTCCGAATCTTCCCCAAAGAAATGCTGAAGAGA
ATCCCTCAGAGCACCCCTCAGCGAATTTTACCCTCGAGACTCTGCAAAGCATTAGCTGCTGCTTCTGCATTGCTCC
GCGCTCTTGTGAAATACTGGTTCTGTTTTCTTTATTCCTTTTGCACTCTCGGTTCCACCTTTGTGTTGGAGTTT
ACCATGTTACCCTGTAATTA AAAACAAAGAATAGGTAACATATTGTGCCAGTGTTGCAACGTTTTAACTGCTAA
CAGACCTTAAAATATCCCCCTACCTGGGTCTCAGTGCTATGTTTAAAGTGCTGCAGGGATGGAGTGGCGTTTTCT
TTATTGCTGTATGTATTGTACATAGTGGAGTAGTTAGTTACCTGATAACAGTCTTGTTATTTGGGTCTCTTAGAC
CTTACCTCTCAACTCCCTCAAGAGTACCAGTCTCTGAAGTTATAATGCTTTGGTCTCTACATTAGGGGCAAGATC
CAGTCTGAGAGAAGTCTCCTTTGAGAAGGGCCAAGAGGCTCTTTCCTGAGTGTTTGCTTTCGGTTTGTTGGTATG
CCTGTATTGCTGGGCTGTGCTGCTGCTCGAAGCAGATGGTTTTGACTGTCTTTTTGCTCTTTCCTATATAATGAA
TAGATGAGTGAAAGGAGTTTTCTTTTTCTTTTAGTACTTACGTATTGGGATTCCTGTGTCTTACAGCTCTCCCT
CTCCAAATAATACACAGAATCCTGCAACTTTTTGCACAGCTGGTATCTGCTGGTAGCAGTGAGACCCCTTGCTCT
TGGTGATCCTTACTGGGTTTCCAAGCAGAGGAGTCACATGATTACAATTGCCAGTAGAGTTGTTGTTTGGGGTAC
AAGATGAGAAGAAAGAAAAACCTACAGCCTTTCTACATTCTGACATGCTAACAGTGTTTTAAGTTTCTAAAGTGT
TTACCAGATGCTGAAGGCAAGGGGAGGGAGCAGAAGCACTTATGTTTACGGATATTTTAACTCTGTTAGAGAGC
AGCCTTTGAAAATCCCCAATTTGGTTCTGCTTTTTGACCTCTCTCTACCTTTTCAGGGTAATCTTTGTGGCACAA
ACGATAGCATTTC AAGCTTTAGAGTTTTCTGAATTC

2705/6881
FIGURE 2488A

CTGGCCGGGAGGCTGGAGCCCAGCAGCAGCGCGGCGCGCGCGCTCGTCCCAACTTGCAGGCGCGGAGGGACCC
CTGACATTTCACTAAAATGAGCGTGCTCAGCAGGAAGAGATGTGTTCCCTCACGCTAGAAGCCACCCCGTCACATG
TAGTGGTGTCCCGTTTAAATGGATTCTGACATGGATTATGAAAGGCCAAACGTAGAGACCATCAAGTGCGTTGTGG
TGGGGGACAACGCCGTGGGTAAGACCAGGCTCATCTGTGCCCGCGCTTGCAATGCCACCCTCACCCAGTACCAGC
TGCTGGCCACGCATGTGCCCACAGTATGGGCCATCGACCAATATCGTGTGTGCCAGGAGGTGCTGGAAACGCTCCC
GAGACGTGGTAGATGATGTCAGCGTCTCTCTGCGCCTCTGGGACACCTTTGGAGACCACCACAAAGACCGTCTGCT
TTGCTTATGGGAGATCTGATGTGGTGGTTCTGTGCTTCTCCATTGCCAACCCCAATTCCCTCCACCATGTCAAGA
CCATGTGGTACCCAGAAATCAAGCACTTCTGCCCCGAGCACCTGTCATCTTGGTGGGCTGCCAGTTGGACCTGC
GCTACGCTGACCTGGAGGCTGTCAACAGGGCTAGGCGACCCCTTGGCTAGGCCCATCAAACCTAATGAAATCCTGC
CCCCAGAGAAGGGTCTGGGAGGTGGCCAAGGAGCTGGGCATCCCCTACTATGAGACCAGCGTGGTGGCCAGTTCTG
GCATCAAGGACGTCTTTGACAACGCCATCCGAGCTGCACTCATCTCCCGCCGCCACCTGCAGTTCTGGAAGTCCC
ACCTCCGCAATGTGCAGCGGCCTCTGCTGCAGGCACCCCTTCCTACCCCCCAAGCCACCGCCCCCGATCATCGTGG
TGCCCGACCCCTCCCTCCAGCAGCGAGGAGTGCCCCGCCACCTCCTGGAGGACCCGCTCTGCGCGGACGTCTATCC
TGGTGTCTGCAGGAGCGGGTGCATCTTTGCCCCACAAGATCTACCTCTCCACCTCCTCCTCCAAGTTCTATGACC
TGTTCCCTCATGGACCTGAGTGAGGGGGAGCTGGGGGGCCCCCTCGGAGCCAGGGGGCACCCACCCAGAGGACCACC
AGGGCCACTCTGATCAACACCACCACCATCACACCACCACCATGGGCGAGACTTCCTGCTCCGAGCAGCCAGCT
TTGACGTGTGCGAGAGCGTGGATGAGGCTGGGGGCTCCGGTCTGCTGGCCTCCGTGCTTCCACCAGCGACGGGA
TCTTACGGGGCAACGGAACAGGGTACCTACCGGGCAGGGGTCTGTGTGCTGTCTTCTGGAGCCGAGCTTTTGTGA
GCATCCAGGAAGAGATGGCAGAAGATCCTCTCACCTACAAATCCCGGCTGATGGTGGTGGTGAAGATGGACAGTT
CCATCCAGCCGGGGGCCCTTCCGGGCTGTCTCAAGTACCTGTACACGGGGGAGCTAGATGAGAACGAGCGTGACC
TCATGCACATTGCCACATTGCTGAGCTGCTCGAGGTCTTTGATCTGCGCATGATGGTGGCCAACATTCTCAACA
ATGAGGCCCTTCATGAACCAGGAGATCACCAAGGCCTTCCACGTCCGCCGACCAACCGGGTTAAGGAGTGCTTGG
CAAAAGGCACCTTCTCAGATGTGACCTTCATCTGGATGATGGCACCATCAGCGCCACAAGCCCCCTGTTGATTT
CCAGCTGTGACTGGATGGCTGCCATGTTTGGGGGGCCATTTGTGGAGAGCTCCACCCGGGAGGTGGTGTTCCT
ACACAAGCAAGAGCTGCATGCGGGCCGTGCTGGAATACCTCTACACCGGCATGTTACCTCCAGCCCCGACCTGG
ATGACATGAAGCTCATCATTTCTAGCCAACCGCCTCTGCCTGCCACACCTGGTTGCCCTCACAGAGCAGTACACAG
TGACCGGGCTGATGGAAGCGACCCAGATGATGGTGGACATCGATGGGGACGTCTTGTGTTTCTGGAACCTGGCTC
AGTTCCACTGTGCGTACCAGCTGGCCGACTGGTGTCTCCACCACATCTGCACCAACTACAACAACGTGTGCCGCA
AGTTCCCCCGAGACATGAAGGCCATGTCCCAGAAAACCAGGAGTATTTGAGAAGCATCGGTGGCCACCTGTGT
GGTACCTGAAGGAGGAAGATCATTACCAGCGGGCACGGAAGGAGCGTGAGAAGGAGGACTACCTCCACCTCAAGC
GGCAGCCCCAAACGGCGTTGGCTCTTCTGGAACAGTCCATCTCCCGCTTCTCCTCGGCAGCCTCCTCCTCATCCC
CATCTTCTCCTCGGCTGTGGTCTGAGATGCTGCCACCCTCTTCTGACCCTGCTGCTGTTGTCCCCATCCGCCTT
CACCCCTCTGCTCTTCCGCATCACCCATCCACCTTACAGGGACCAGGGGGCCACGTAACCAGGACCCAGAGGG
TGGAGCTCTTCTTACCAGCCACCCTGGCTCAGCCAGAGAGGAGCTGAGCCCTGTGGAGCAGAACGGGAACCACT
GCAGAGGTCCCCAGACCCAAAGCAGGACGGGAGACAACCTGCTTGGAGGAGCGAAGAGCCCTGGCATTATCTCT
GGGTTTGAGAGCCCTAGAGTCAAAGGGAAAGCCTCCAGCCCTCAGGGCTTCTCTGTGTGTCTTGGTTGCTGCTC
TGGCCAGGGAGGCAGCCCCACTCCAGCAAGCAGAAGTGATCCTCGAGGGTCTGCCCCCTGTTGGCCATATCTTT
CCACCGACGGACTTGAGTGTTCATTTGTTTTGTGGGCATTTCCACACGAAGCCTACTCACACCCTCACTGGAGA
AGTCAGGGTAGAAATTGAGCCTTCAGAGCCCAACTCAAGGCTTCTACATCCTGGGGTGCAGCTGCAAAAGGCCAG
ACGTGGAAAGGCCTGTATCCTGCCAGTGTCCCTCCGTCCCAGGGGGCTGTGCTGGCACAGACCTGAGAATGGGGA
CACAGGTCAATCAGAGCTCCAGGCCTGGAAGCAGTGCTCTTGGTGCAACAAGAACTTCTCCCTCACCCCTCC
TTTACCCTCAGATTTGGAGATGGTAACCAAAGGAAGCAGCTGGGACAGGTGGAGAAGGAAGTAGGAATGAGTGCA
CGGCGACCCCGTGCTCCTCAGGGCCCTCCCCTGCTCTGGGTGGCACTGCTTTTTATAGGGTGGGGCAAAATTAG
CAAAAAACAAAACCAATGACAACCAAACTGAAACCGAAACGAAAAATCAACAAACACTCTGTCTCTATCCCTC
CAAAGAATGAAAATCAGAAAAAGCCCCCTGCCCTAGCTCACATTTCTATAAACAGAGGCCCCCATGATGAGGAGGTG
AAGATTTAGGTTGCAGAATCGACTCCAATGCCTTTCAGGAAAGGACTCGGCACTTCTCTGACTGCGGAGGCCCTG
ACCCTGCCAGCTGGCTCCGAGGGCAACACAGGGGCCCTGGCCTCTAGAGGGCTGGTGATTGAGGGGCCGGGCTGG
CGGCAAAAGAGGGGTTTGGTCTCGGGGCTTAAATGGCACCAAGACTCTTGCTTTTGGCCATCTGGAGACTGCAGGCT

2706/6881
FIGURE 2488B

CCCTTCCTTACCCTCAGAGAGTGCTTATGGTGGGTGTTTTTGCGGGGCTGCAATAGGGGCCAAAAGTCAGGGAAA
GGGGCACTGACCTGTAGTGAAAGGCCACAGGACACAGCCTTATTACTGCTGGGTGGGATAAGGGGAAGGAGAAG
AGGGAGAATGGAGCAGGAGGAAAAGCAGAGTTGGTCTAGAGAGGAGGAGGGCGGGGCTGGAGGAATGTGGGGGAT
TGAAACTAGCTCCCAGCCCCCATGGGGCAGCAGCTGGGCCACAATTGCCCTTTCCGTTTTCTAACCCCGACTCA
GATTTACCAACCCACACTCTTTTTAGGTGTAAAAGATGGAGTCCACGGAGGAGGGCAGAGCCAGGAGGCAGTG
GGGCTGTGGGCTCAGAGCTCAGGAGTCGCCTTACCTGAGAGAGATGTTCTAGCTGAGAGGGCCTGGCCCTGGGGT
GGGCTCCAGGAAAACGCTGGTTAGGCCTGGGATTGAGCTAACCTGAAACAAAGGTAGTAGGCAGGACCTAATGAC
CAGAGGTTAAATCCTCATCAAGAGAGACCAGGCGGCTGGAGGACAAGCGGCTCTAACCTGGGGGCGGCCATGTT
GTCCAGGCCCAGGCCCCCTCCAGGACTGTGGCTGCCTCCCCCTCCACGGCCTCCAGGGCGGCTGGCTGGAAAGCCAC
GCGTATGCTGCCCTCTACAGGCTGCTCGGCCTCCCTGCAGCTCAGCGCAGCCCAGGGCTCCAAGTGAGGCCCCAGA
AGCCCATGGGCAGGGCTGGGGGGACGAAGGGGGAACCCGGAGCACCTCCACTTCTAGGGAAGATGGACAGCGTGG
GGGCACACCTGGGCCTCCCGGAAGCTGTGGACGAAAGGGAGAGCGGGTCTCCAGGGCAAGGGGAACGGGAAATA
GGTCTCCTAGGTGCCTGAAGCGCTGAGCAACCTGGGTACCTGGTGGGGATGCAGGGAAGGCCGGGGCAGAGAAA
GCGAAGGTGACCCAGGGCTGTAGGAAGCCATAGGAGAGTGACCACGGGATTCCCTGAGAAACAGGGCCGGCCCC
CCAACCTCAGGGACCCACCGCCCATTCCTCCGAGAGCTGTGCGGAACCAGATGCAACCCGGCAGCCAGAGAACTCT
CCTGGGAGGCTGTGGGTGAGCCAGGCCAACATTGGTGTCCCTGTCCCCAGAGGGAGGAGCAGGCAGGAGAGAGAG
GGGAAGGAGGTATGAATCCCAGTCCCCAGGAACCTAGCTCTTTAACTCTGGGGAGTCGGATTACAGGAAACACCC
CCAGGAGGCCAAGCCTGAAAACAGAGGGGAGGGAGGAAGGAAGGAGTCCCAGCAGGAGCACAGCCCTGGTTTCCT
GTCACTCAGAGCTGATTCACAGGAGGAGGGGAGGTTGGGGGGCGGGAGACAAAACACACCTCTTTTTATATAA
GGTTTCATATTTAATTTGGTCATGGATTCATAAATACATAAGTATTTGTAC

2707/6881
FIGURE 2489

MDSDMDYERPNVETIKCVVVGDNVAGKTRLICARACNATLTQYQLLATHVPTVWVIDQYRVCQEVLEERSRDVVDD
VSVSLRLWDTFGDHHKDRRFAYGRSDVVVLCFSIANPNSLHHVKTMMWYPEIKHFCPRAPVILVGCQLDLRYADLE
AVNRARRPLARPIKPNEILPPEKGREVAKELGIPYYETSVVAQFGIKDVFDNAIRAALISRRHLQFWKSHLRNVQ
RPLLQAPFLPPKPPPIIIVVPDPPSSSEECPAHLLDPLCADVILVLQERVRIFAHKIYLSTSSSKFYDLFLMDL
SEGELGGPSEPGGTHPEDHQGHSDQHSHHHHHHHHGRDFLLRAASFDVCEVDEAGGSGPAGLRASTSDGILRGNG
TGYPGRGRVLSSWSRAFVSIQEEMAEDPLTYKSRLMVVKMDSSIQPGPFRAVLKYLYTGELDENERDLMHIAH
IAELLEVFDLRMMVANILNNEAFMNQEITKAFHVRRTNRVKECLAKGTFSDVTFILDDGTISAHKPLLISSCDWM
AAMFGGPFVESSTREVVFPYTSKSCMRVLEYLYTGMFTSSPDLDMDKLIILANRLCLPHLVALTEQYTVTGLME
ATQMMVDIDGDVLVFLLELAQFHCAYQLADWCLHHICTNYYNNVCRKFPRDMKAMSPENQEYFEKHRWPPVWYLKEE
DHYQRARKEREKEDYLHLKRQPKRRWLFWNSSPSSSAASSSSPSSSSAVV

2708/6881
FIGURE 2490A

GGTCTCAGCTGAGTCTGCTCTGATCACCCAACAAGACCTAGCTCCCCAGCAGAGAGCGGCCCCACAACAAAAGAG
GTCCAGCCCCCTCAGAGGGATTGTGTCCACCTGGACACCATATCTCAGAAGACGGTAGAGATTGCATCTCCTGCAA
ATATGGACAGGACTATAGCACTCACTGGAATGACCTCCTTTTCTGCTTGCCTGCACCAGGTGTGATTGAGGTGA
AGTGAGCTAAGTCCCTGCACCACGACCAGAAACACAGTGTGTGCTGCGAAGAAGGCACCTTCCGGGAAGAAGA
TTCTCCTGAGATGTGCCGGAAGTGCCGCACAGGGTGTCCAGAGGGGATGGTCAAGGTCGGTGATTGTACACCCTG
GAGTGACATCGAATGTGTCCACAAAGAATCAGGTACAAAGCACAGTGGGGAAGCCCCAGCTGTGGAGGAGACGGT
GACCTCCAGCCCAGGGACTCCTGCCTCTCCCTGTTCTCTCTCAGGCATCATCATAGGAGTACAGTTGCAGCCGT
AGTCTTGATTGTGGCTGTGTTTGTGCAAGTCTTTACTGTGGAAGAAAGTCCCTTACCTGAAAGGCATCTG
CTCAGGTGGTGGTGGGGACCTGAGCGTGTGGACAGAAGCTCACAAACGACCTGGGGCTGAGGACAATGTCTCTCAA
TGAGATCGTGAGTATCTTGCAGCCCACCCAGGTCCCTGAGCAGGAAATGGAAGTCCAGGAGCCAGCAGAGCCAAC
AGGTGTCAACATGTTGTCCCCCGGGGAGTCAGAGCATCTGCTGGAACCGGCAGAAGCTGAAAGGTCTCAGAGGAG
GAGGCTGCTGGTTCCAGCAAATGAAGGTGATCCCACTGAGACTCTGAGACAGTGTTCGATGACTTTGCAGACTT
GGTGCCCTTTGACTCCTGGGAGCCGCTCATGAGGAAGTTGGGCCTCATGGACAATGAGATAAAGGTGGCTAAAGC
TGAGGCAGCGGGCCACAGGGACACCTTGTACACGATGCTGATAAAGTGGGTCAACAAAACCGGGCGAGATGCCTC
TGTCCACACCCTGCTGGATGCCTTGGAGACGCTGGGAGAGAGACTTGCCAAGCAGAAGATTGAGGACCACTTGT
GAGCTCTGGAAGTTTATGTATCTAGAAGGTAATGCAGACTCTGCCATGTCCTAAGTGTGATTCTCTTCAGGAAG
TCAGACCTTCCCTGGTTTACCTTTTTTCTGGA AAAAGCCCAACTGGACTCCAGTCAGTAGGAAAGTGCCACAATT
GTCACATGACCGGTACTGGAAGAACTCTCCCATCCAACATCACCCAGTGGATGGAACATCCTGTAACTTTTCAC
TGCATTGGCATTATTTTTATAAGCTGAATGTGATAATAAGGACACTATGGAAATGTCTGGATCATTCCGTTTGT
GCGTACTTTGAGATTTGGTTTGGGATGTCATTGTTTTTACAGCACTTTTTTATCCTAATGTAAATGCTTTATTTA
TTTATTTGGGCTACATTGTAAGATCCATCTACACAGTCGTTGTCCGACTTCACTTGATACTATATGATATGAACC
TTTTTTGGGTGGGGGTGCGGGGCAGTTCACTCTGTCTCCAGGCTGGAGTGCAATGGTGCAATCTTGGCTCACT
ATAGCCTTGACCTCTCAGGCTCAAGCGATTCTCCACCTCAGCCATCCAAATAGCTGGGACCACAGGTGTGCACC
ACCACGCCCCGCTAATTTTTTGTATTTTGTCTAGATATAGGGGCTCTCTATGTTGCTCAGGGTGGTCTCGAATTC
CTGGACTCAAGCAGTCTGCCACCTCAGACTCCCAAAGCGGTGGAATTAGAGGCGTGAGCCCCCATGCTTGGCCT
TACCTTTCTACTTTTATAATTCTGTATGTTATTATTTTATGAACATGAAGAACTTTAGTAAATGTACTTGTTTA
CATAGTTATGTGAATAGATTAGATAAACATAAAAGGAGGAGACATACAATGGGGGAAGAAGAAGAGTCCCTGT
AAGATGTCACTGTCTGGGTTCAGCCCTCCCTCAGATGTACTTTGGCTTCAATGATTGGCAACTTCTACAGGGGC
CAGTCTTTTGAACCTGGACAACCTTACAAGTATATGAGTATTATTTATAGGTAGTTGTTTACATATGAGTCGGGAC
CAAAGAGAAGCTGGATCCACGTGAAGTCCTGTGTGTGGCTGGTCCCTACCTGGGCAGTCTCATTTGCACCCATAGC
CCCCATCTATGGACAGGCTGGGACAGAGGCAGATGGGTAGATCACACATAACAATAGGGTCTATGTATATCCC
AAGTGAACCTTGAGCCCTGTTTGGGCTCAGGAGATAGAAGACAAAATCTGTCTCCACGTCTGCCATGGCATCAAG
GGGGAAGAGTAGATGGTGCTTGAGAATGGTGTGAAATGGTTGCCATCTCAGGAGTAGATGGCCCGGCTCACTTCT
GGTTATCTGTACCCCTGAGCCCATGAGCTGCCTTTTAGGGTACAGATTGCCTACTTGAGGACCTTGGCCGCTCTG
TAAGCATCTGACTCATCTCAGAAATGTCAATTCTTAAACACTGTGGCAACAGGACCTAGAATGGCTGACGCATTA
AGGTTTTCTTCTTGTGTCTGTTCTATTATTGTTTTAAGACCTCAGTAACCATTTTACGCTCTTTCCAGCAAACC
CTTCTCCATAGTATTTTCAGTCATGGAAGGATCATTTATGCAGGTAGTCATTCCAGGAGTTTTTGGTCTTTTCTGT
CTCAAGGCATTGTGTGTTTTGTTCCGGGACTGGTTTGGGTGGGACAAAGTTAGAATTGCCTGAAGATCACACATT
CAGACTGTTGTGTCTGTGGAGTTTTAGGAGTGGGGGTGACCTTTCTGGTCTTTGCACTTCCATCCTCTCCCACT
TCCATCTGGCATCCACGCGTTGTCCCCTGCACTTCTGGAAGGCACAGGGTGTGCTGCTGCCTCCTGGTCTTTGCC
TTGCTGGGCCTTCTGTGCAGGACGCTCAGCCTCAGGGCTCAGAAGGTGCCAGTCCGGTCCCAGGTCCCTTGTCCC
TTCCACAGAGGCCTTCTAGAAAGATGCATCTAGAGTGTGAGCCTTATCAGTGTTTAAGATTTTTCTTTTATTTTT
AATTTTTTTGAGACAGAATCTCACTCTCTCGCCAGGCTGGAGTGCAACGGTACGATCTTGGCTCAGTGCAACCT
CCGCTCCTGGGTTCAAGCGATTCTCGTGCTCAGCCTCCGGAGTAGCTGGGATTGCAGGCACCCGCCACCACGC
CTGGCTAATTTTTTGTATTTTTAGTAGAGACGGGGTTTTACCATGTTGGTCAGGCTGGTCTCGAACTCCTGACCTC
AGGTGATCCACCTTGGCCTCCGAAAGTGCTGGGATTACAGGCGTGAGCCACCAGCCAGGCCAAGCTATTCTTTTA
AAGTAAGCTTCTTGACGACATGAAATAATTGGGGGTTTTGTTGTTTAGTTACATTAGGCTTTGCTATATCCCCAG
GCCAAATAGCATGTGACACAGGACAGCCATAGTATAGTGTGCTCACTCGTGGTTGGTGTCTTTTATGCTTCTGCC

2709/6881
FIGURE 2490B

CTGTCAAAGGTCCTATTTGAAATGTGTTATAATACAAACAAGGAAGCACATTGTGTACAAAATACTTATGTATT
TATGAATCCATGACCAAATTAAATATGAAACCTTATAT

2710/6881
FIGURE 2491

CGGACGCGTGGGCAGGCAGCAGCCGGGCAGGGATGCTCCTGCGCTCCCGGGCGGCCTCGGGCCCAGCCACCTGCT
CGCCGGGGAAGAGGACACGCAGAGGAGCAGCTGGCTTGCCCGGAGTCCTCCACCTTGACCCAAGCATGCAGGGC
CCACCCCGCAGCCTCCGCGCTGGGCTCAGCCTGGACGACTTCATCCCTGGCCACCTCCAGTCCCACATAGGGTCT
TCCTCCCGGGGGACACGGGTGCCCCGTGATCCGGAATGGTGGCTCCAACACCCTTAATTTCCAGTTCCACGACCCC
GCGCCCAGGACTGTGTGCAATGGGGGCTACACACCAAGACGAGATGCTTCCCAGCACCCGGACCCCTGCGTGGTAT
CAGACCTGGCCAGGCCCTGGGAGCAAGCCCTCTGCAAGCACAAAGATCCCTGCCTCCCAGCACACCCAGAACTGG
TCAGCCACGTGGACCAAGGACAGCAAGCGTCGGGACAAGCGCTGGGTCAAGTACGAGGGAATCGGGCCCCGTGGAC
GAGAGCGGCATGCCCATGCCCCCGATCCAGCGTTGACAGACCCAGAGACTGGTACCGGAGAATGTTCCAGCAG
ATTACCCGGAAAATGCCAGACTTGCAGCTGGACTGGACCTTCGAGGAGCCACCCAGAGACCCAGGCATCTAGGA
GCCCAGCAAAAGACCTGCCACAGGCCCGGGCCCGGCAACATCTTCCAGTGGAAGAAGCTGGGACCCTCTGAAGAG
TTACCTAGAAACACCTTCAACTACAGACCTGGAGCATTTCTCCACTGTGCTGCAGCCCTCAAATCAGGTGCTCAGA
CGCCGGGAAAAAGTAGACAATGTCTGGACGGAAGAGTCCTGGAACCAAGTTTCTGCAGGAAGTAGAGACTGGGCAG
AGGCCCAAGAAAACCGCTGGTGGACGACCCTGGTGAGAAGCCCTCCCAGCCATTGAGGTGCTGCTGGAGAGAGAG
CTGGCCGAGCTGAGCGCCGAGCTGGACAAGGACCTGCGGGCAATTGAGACCCGACTGCCGTCCCCCAAGAGCTCG
CCGGCGCCCCGACGGGCCCGGAGCAGCGGCCCGGGCCGGCCCGGCCTCAGCCTGGAGCTCCAGCTACCCACAT
GCACCTTACCTGGGTTCGCCCCGGTCCCTGAGTCCCCACAAAATGGCTGATGGAGGAAGCCCCCTTCCTAGGTGCG
AGGGACTTTGTCTACCTTCCCTCAACCCGAGACCCTAGTGCTCTAACGGAGGGGGCAGCCAGCCAGGAGGGAA
GAGAAGAAGAGAAAAGGCCGCCAGGCTCAAGTTTGACTTCCAGGCGCAGTCCCCAAGGAGCTGACTCTGCAGAAG
GGTGACATTGTCTACATCCACAAGGAGGTGGACAAGAAGCTGGCTGGAGGGAGAGCACCACGGCCGCTGGGCATC
TTCCCTGCTAATTATGTGGAGGTGCTGCCCCGAGATGAGATCCCTAAGCCCATCAAGCCCCGACCTACCAGGTG
CTGGAGTATGGAGAGGCTGTGGCCCAGTACACCTTCAAGGGGGACCTGGAGGTGGAGCTGTCTTCCGCAAGGGA
GAGCACATCTGCCTGATCCGCAAGGTGAACGAGAAGCTGGTACGAGGGACGCATCACGGGCACGGGGCGCCAAGGC
ATATTCCCTGCCAGCTACGTGCAGGTGTCTCGTGAACCCCGGCTCCGGCTCTGTGACGACGGCCCCAGCTCCCC
ACGTCTCCCCGCTGACCGCTGCCGCCCGCTCAGCCCGCTACCCCGAGCTCCCCCTCAGCCCTGCGCAGCCAGCT
GACCCACCCGACTTGGGGGGACAGACCTCCCCCGCTCGCACTGGCTTCTCCTTCCCCACCCAGGAGCCTAGACCC
CAGACCCAGAATCTTGGCACCCCTGGTCCAGCTCTGTCCCACTCTCGAGGTCCCAGCCATCCCCTGGACCTGGGG
ACCTCCTCTCCTAACACCTCTCAGATACACTGGACCCCGTACCGGGCGATGTACCAGTACAGGCCCCAGAACGAA
GACGAGCTGGAGCTGCGCGAGGGGGACAGGGTGGATGTCATGCAGCAGTGTGACGATGGCTGGTTTGTGGGTGTC
TCCCGGAGGACCCAGAAAATTGGAACGTTCCCTGGAATACGTTGCCCGGTGTGAGTGGTCTCCATGGCAACT
TGGAGCCAGCCAGGATGGGGTGGGGAGCGGTGGCACTCGTGGGAGGGAGAGGACCCCGCCACATCCTCCTTCC
CCAGGACCTGAGCTCCCAGCATCTGCAGACGACCCCGCAGCATTTCCCTCGGACCCCCCTCGAAGCCCCCTGGA
CTGATTCCCACCCACGACTCACAGGCATTCCCTCCACAGCCCTTTCATTTCTTCCCCACCCCACTCCCCAAATAC
AGAGGTCTGCTTTGAAGCGGAGACCATTTCAGGCCTTATTGAGACCAGACCCCAAGTCCCCACCCCATCCTG
CTCCAGCGTTTCCCTCTAACAGGGACCAGCTCTCCGCTTTGCCCCACGGGGTTCTCTAACAGAACAGCTTCC
TAGCCTCGTAGAGACCAAGGCCGCCCCCGCTGCTGGGGTTCTTCCAGCACCCAGCTTGCTGGCTGCCCTCT
TTGCCTTCTGGCCTCCAGCTGGGTGTGGGGGGGCGAGCAAGGCGGGGGACAGACGCAGCACCTTCTTAGCGATC
TAGGCCTGGCAAGAGCTCTGGCCCCAAGGCCTCTCTTCCCAGGGGCTGCCAAGTCTTGGCCCTGGCCCTGGCAT
ATCACCCCGCACTGTGGGGCCAGGCACCACTAGCCTGGCTCAAATATTCCCAGGGAGACTGCTGTGTGCTGCCC
GCCTGCCTGCTGGCTCTCCCCAGCCCCACATCCCCTCTGGAAGAGAATGTAAATAAACCTGGACACAAGGGCC
TTCGTGGCCTCGA

2711/6881
FIGURE 2492

MQGPPRSLRAGLSLDDFIPGHLQSHIGSSSRGTRVPVIRNGGSNTLNFQFHDPAPRTVCNGGYTFRRDASQHPDP
AWYQTWPGPGSKPSASTKIPASQHTQNWSATWTKDSKRRDKRWVKYEGIGPVDESGMPIAPRSSVDRPRDWYRRM
FQQIHRKMPDLQLDWTFEPPRPRLGAQQRPAHRPGPATSSSGRSWDHSEELPRSTFNYPGAFSTVLQPSNQ
VLRREKVDNVWTEESWNQFLQELETGQRPKKPLVDDPGEKPSQPIEVLLERELAELSAELDKDLRAIETRLPSP
KSSPAPRRAPFQRPFPAGPASAWSSSYPHAPYLGSARSLSPHKMADGGSPFLGRRDFVYPSSTRDPSASNGGGSPA
RREEKKRKAARLKFDFAQSPKELTLQKGDIVYIHKEVDKNWLEGEHHGRLGIFPANYVEVLPADEIPKPIKPPT
YQVLEYGEAVAQYTFKGDLEVELSFRKGEHICLIRKVNENWYEGRITGTGRQGIFPASYVQVSREPRRLRLCDDGP
QLPTSPRLTAAARSARHPSSPSALRSPADPTDLGGQTSRRTGFSFPTQEPRPQTQNLGTPGPALSHSRGFSHPL
DLGTSSPNTSQIHWTPYRAMYQYRPQNEDELELREGDRVDVMQQCDDGWFVGVSRRTQKFGTFPGNYVAPV

2712/6881
FIGURE 2493

ACTTCCGCCCCGGCGCGGAGACCGAAGGCTGGCGGCTGGTCGCGTTGCAGGCAACATGTCGGAAGGAAACGCCGCC
GGCGAGCCCAGCACGCCGGGAGGGCCCCGACCTCTCCTGACTGGGGCCCCGGGGGCTCATCGGGCGGCGGCCGGCG
CCTCCCCTCACCCCCGGCCGCTTCCCTCCATCCGTTCCAGGGACCTCACCCCTCGGGGGAGTCAAGAAGAAAACC
TTCACCCCAAATATCATCAGTCGGAAGATCAAGGAAGAGCCCAAGGAAGAAGTAACTGTCAAGAAGGAGAAGCGT
GAAAGGGACAGAGACCGACAACGAGAGGGGCATGGACGAGGGCGAGGCCGTCCAGAAGTGATCCAGTCTCACTCC
ATCTTTGAGCAGGGCCCAGCTGAAATGATGAAGAAAAAAGGGAACTGGGATAAGACAGTGATGTGTCAGACATG
GGACCTTCTCATATCATCAACATCAAAAAAGAGAAGAGAGAGACAGACGAAGAACTAAACAGATCTTGCGTATG
CTGGAGAAGGACGATTTCCCTCGATGACCCCGGCCTGAGGAACGACACTCGAAATATGCCTGTGCAGCTGCCGCTG
GCTCACTCAGGATGGCTTTTTTAAGGAAGAAAATGACGAACCAGATGTTAAACCTTGGCTGGCTGGCCCCAAGGAA
GAGGACATGGAGGTGGACATACCTGCTGTGAAAGTGAAAGAGGAGCCACGAGATGAGGAGGAAGAGGCCAAGATG
AAGGCTCCTCCCAAAGCAGCCAGGAAGACTCCAGGCCTCCCGAAGGATGTATCTGTGGCAGAGCTGCTGAGGGAG
CTGAGCCTCACCAAGGAAGAGGAAGTGTGTTTTCTGCAGCTGCCAGACACCCTCCCTGGCCAGCCACCCACCCAG
GACATCAAGCCTATCAAGACAGAGGTGCAGGGCGAGGACGGACAGGTGGTGTCTCATCAAGCAGGAGAAAGACCGA
GAAGCCAAATTGGCAGAGAATGCTTGTACCCTGGCTGACCTGACAGAGGGTCAGGTTGGCAAGCTACTCATCCGC
AAGTCTGGAAGGGTGCAACTCCTCTTGGGCAAGGTGACTCTGGACGTGACCATGGGAAGTGCCTGCTCCTTCCTG
CAGGAGCTGGTGTCCGTGGGCCCTTGAGACAGTAGGACAGGGGAGATGACAGTCTGGGACACGTGAAGCACAAA
CTTGTATGTTCCCTGATTTTGAATCCCTCTTGATCACAAACACCGGTAAAATGAGCAGGTGGAGGAGGACGGC
GCCTGTGCCCACGGCTGCTGCCTGCTCCAGACATTTTGTTCCTGAATCTGTGAGACCCAGAAGGGGCCCCACTGAG
CCCACTCACTCCAGCCTTTGGCAACCATTGTTCCAGGTCCCCCAGGGCTTCCTCCACAGCAGCTGTGAATGGCA
CAGTGACCTTCCTGCAGCGTGAGATGGCACATCCTTGCTGCTGGGGACTTGGCCCTGCTATTTATTTTTGTATT
TATGTCTTAATCTCTTCCACTGATGCATCCTCCAAGGGTAGATGGGGAGGGTCTGTGTGAAGGGGCCGGCTTCTC
TTGGTGCTGCTGGGTTGCAGGGGCAGGAAGCGTGTGGACTGCAGCTTCTGCTGGTGCTCCCCCGTCCTCCTGG
AGGCAGTATAGGAGAGAGAGCAAGGATTGAGTCTGAGACTTAAGCACTCGGTCCCAGCTTGCCAGTTCTGGTTC
TGTGTCCTTGACAAACTACCTAACCTTTCTGAGCCTCCTATACCTCATCCGACACAAATGGGGATGATACCTAC
CTCCAGGGTTGGCGTGAGGATTCATGGGCTATTATAGATGAAAAGTGCACAAGGCCAGAACCAGCAGGCACTCAA
TAAACGTTTCATGTCCTTTTTCTCT

2713/6881
FIGURE 2494

MSEGNAAGEPSTPGGPRPLLTGARGLIGRRPAPPLTPGRLPSIRSRDLTLGGVKKKTFTPNIISRKIKEEPKEEV
TVKKEKRERDRDRQREGHGRRGRPEVIQSHSIFEQGP AEMMKKGNWDKTVDVSDMGPSHIINIKKEKRETDEE
TKQILRMLEKDDFLDDPGLRNDTRNMPVQLPLAHSGWLFKEENDEPDVKPWLAGPKEEDMEVDIPAVKVKEEPRD
EEEEAKMKAPPKAARKTPGLPKDVSVAELLRELSLTKEEELLFLQLPDTLPGQPPTQDIKPIKTEVQGEDGQVVL
IKQEKDREAKLAENACTLADLTEGQVGKLLIRKSGRVQLLLGKVTLDTVMTGACSFLOELVSVGLGDSRTGEMTV
LGHVKKHLVCSPDFESLLDHKHR

2714/6881
FIGURE 2495

GCCGCTTCCCTCGCCGCCGCCCGCCAGCATGCCCGGCGTGGCCCGCCTGCCGCTGCTGCTCGGGCTGCTGCTGC
TCCCGCGTCCCGGCCGGCCGCTGGACTTGGCCGACTACACCTATGACCTGGCGGAGGAGGACGACTCGGAGCCCC
TCAACTACAAAGACCCCTGCAAGGCGGCTGCCTTTCTTGGGGACATTGCCCTGGACGAAGAGGACCTGAGGGCCT
TCCAGGTACAGCAGGCTGTGGATCTCAGACGGCACACAGCTCGTAAGTCCTCCATCAAAGCTGCAGTTCCAGGAA
ACACTTCTACCCCCAGCTGCCAGAGCACCAACGGGCAGCCTCAGAGGGGAGCCTGTGGGAGATGGAGAGGTTAGAT
CCCGTAGCCGGCGGGCGGCGACGTCCCGACCAGAGCGTGTGTGGCCCGATGGGGTCATCCCCTTTGTTCATTGGGG
GAAACTTCACTGGTAGCCAGAGGGCAGTCTTCCGGCAGGCCATGAGGCACTGGGAGAAGCACACCTGTGTACCT
TCCTGGAGCGCACTGACGAGGACAGCTATATTGTGTTACCTATCGACCTTGCGGGTGCTGCTCCTACGTGGGTC
GCCGCGGGGGGGGGCCCCAGGCCATCTCCATCGGCAAGAACTGTGACAAGTTCGGCATTGTGGTCCACGAGCTGG
GCCACGTGCTCGGCTTCTGGCACGAACACACTCGGCCAGACCGGGACCGCCACGTTTCCATCGTTTCGTGAGAACA
TCCAGCCAGGGCAGGAGTATAACTTCTGAAAGATGGAGCCTCAGGAGGTGGAGTCCCTGGGGGAGACCTATGACT
TCGACAGCATCATGCATTACGCTCGGAACACATTCTCCAGGGGCATCTTCTGGATAACATTGTCCCCAAGTATG
AGGTGAACGGGGTGAAACCTCCCATTGGCCAAAGGACACGGCTCAGCAAGGGGGACATTGCCCAAGCCCGCAAGC
TTTACAAGTGCCAGCCTGTGGAGAGACCCTGCAAGACAGCACAGGCAACTTCTCCTCCCCTGAATACCCCAATG
GCTACTCTGCTCACATGCACTGCGTGTGGCGCATCTCTGTACACCCGGGGAGAAGATCATCCTGAACCTCACGT
CCCTGGACCTGTACCGCAGCCGCCTGTGCTGGTACGACTATGTGGAGGTCCGAGATGGCTTCTGGAGGAAGGCGC
CCCICCGAGGCCGCTTCTGCGGGTCCAACTCCCTGAGCCTATCGTCTCCACTGACAGCCGCCTCTGGGTGAAT
TCCGCAGCAGCAGCAATTGGGTGGAAAGGGCTTCTTTGAGTCTACGAAGCCATCTGCGGGGGTGATGTGAAAA
AGGACTATGGCCACATTCAATCGCCCAACTACCCAGACGATTACCGGCCAGCAAAGTCTGCATCTGGCGGATCC
AGGTGTCTGAGGGCTTCCACGTGGGCCTCACATTCCAGTCTTTGAGATTGAGCGCCACGACAGCTGTGCCTACG
ACTATCTGGAGGTGCGCGACGGGCACAGTGAGAGCAGCACCCCTCATCGGGCGCTACTGTGGCTATGAGAAGCCTG
ATGACATCAAGAGCACGTCCAGCCGCCTCTGGCTCAAGTTCTGTCTCTGACGGGTCCATTAACAAAGCGGGCTTTG
CCGTCAACTTTTTCAAAGAGGTGGACGAGTGTCTCTCGGCCCAACCGCGGGGGCTGTGAGCAGCGGTGCCTCAACA
CCCTGGGCAGCTACAAGTGCAGCTGTGACCCCGGTACGAGCTGGCCCCAGACAAGCGCCGCTGTGAGGCTGCTT
GTGGCGGATTCTCACCAAGCTCAACGGCTCCATCACCAGCCCGGGCTGGCCCAAGGAGTACCCCCCAACAAGA
ACTGCATCTGGCAGCTGGTGGCCCCCACCAGTACCGCATCTCCCTGCAGTTTGACTTCTTTGAGACAGAGGGCA
ATGATGTGTGCAAGTACGACTTCGTGGAGGTGCGCAGTGGACTCACAGCTGACTCCAAGCTGCATGGCAAGTTCT
GTGGTTCTGAGAAGCCCGAGGTATCACCTCCAGTACAACAACATGCGCGTGGAGTTCAAGTCCGACAACACCG
TGTCAAAAAGGGCTTCAAGGCCCACTTCTTCTCAGAAAAGAGGCCAGCTCTGCAGCCCCCTCGGGGACGCCCCC
ACCAGCTCAAATTCCGAGTGCAGAAAAGAAACCGGACCCCCAGTAGAGGCTGCCAGGCCTCCCGGACCCCTTGT
TACTCAGGAACCTCACCTTGGACGGAATGGGATGGGGGCTTCGGTGCCCAACCCCCACCTCCACTCTGCCA
TTCCGGCCACCTCCCTCTGGCCGGACAGAACTGGTGCTCTCTTCTCCCACTGTGCCGTCCGCGGACCGGGGA
CCTTCCCCGTGCCCTACCCCTCCCATTTTGATGGTGTCTGTGACATTCCTGTTGTGAAGTAAAGAGGGACC
CCTGCGTCCTGC

2715/6881
FIGURE 2496

MPGVARLP LLLGL LLLLP RPGRPLDLADYTYDLAEEDDSEPLNYKDPCKAAAF LGDIALDEEDLRAFQVQQAVDLR
RHTARKSS IKA AVPGNTSTPSCQSTNGQPQRGACGRWRGRSRSRRAATSRPERVWPDGVIPFVIGGNETGSQRAV
FRQAMRHWEKHTCVTFLE RTDEDSYIVFTYRPGCCSYVGRRGGGPQAISIGKNCDKFGIVVHELGHVVGFWHEH
TRPDRDRHVSIVRENIQPGQEYNFLKMEPQEVESSLGETYDFDSIMHYARNTFSRGIFLDTIVPKYEVNGVKPPIG
QRTLSKGDIAQARKLYKCPACGETLQDSTGNFSSPEYPNGYSAHMHCVWRISVTPGEKIILNFTSLDLYRSRLC
WYDYVEVRDGFWRKAPLRGRFCGSKLPEPIVSTDSRLWVEFRSSSNWVGKFFAVYE AICGGDVKKDYGHIQSPN
YPDDYRPSKVCIWRIQVSEGFHVGLTFQSFEIERHDS CAYDYLEVRDGHSESSTLIGRYCGYEKPDDIKSTSSRL
WLKFVSDGSINKAGFAVNFFKEVDECSRPNRGGCEQRCLNTLGSYKCSCDPGYELAPDKRRCEAACGGFLTKLNG
SITSPGWPKEYPPNKNCIWQLVAPTQYRISLQFDFFETEGNDVCKYDFVEVRSGLTADSKLHGKFCGSEKPEVIT
SQYNNMRVEFKSDNTVSKKGFKAHFFSEKRPALQPPRGRPHQLKFRVQKRNRTPQ

2716/6881
FIGURE 2497

GCCGCTTCCCTCGCCGCCGCCGCCGCCAGCATGCCCGCGGTGGCCCGCCTGCCGCTGCTGCTCGGGCTGCTGCTGC
TCCCGCGTCCCGGCCGCCCGCTGGACTTGGCCGACTACACCTATGACCTGGCGGAGGAGGACGACTCGGAGCCCC
TCAACTACAAAGACCCCTGCAAGGCGGCTGCCTTTCTTGGGGACATTGCCCTGGACGAAGAGGACCTGAGGGCCT
TCCAGGTACAGCAGGCTGTGGATCTCAGACGGCACACAGCTCGTAAGTCCTCCATCAAAGCTGCAGTTCCAGGAA
ACACTTCTACCCCCAGCTGCCAGAGCACCAACGGGCAGCCTCAGAGGGGAGCCTGTGGGAGATGGAGAGGTAGAT
CCCGTAGCCGGCGGGCGGCGACGTCCCGACCAGAGCGTGTGTGGCCCGATGGGGTCATCCCCTTTGTCAATTGGGG
GAAACTTCACTGGTAGCCAGAGGGCAGTCTTCCGGCAGGCCATGAGGCACTGGGAGAAGCACACCTGTGTACCT
TCCTGGAGCGCACTGACGAGGACAGCTATATTGTGTTACCTATCGACCTTGCGGGTGCTGCTCCTACGTGGGTC
GCCGCGGGGGGGCCCCAGGCCATCTCCATCGGCAAGAACTGTGACAAGTTCGGCATTGTGGTCCACGAGCTGG
GCCACGTGCTCGGCTTCTGGCACGAACACACTCGGCCAGACCGGGACCGCCACGTTTCCATCGTTTCGTGAGAACA
TCCAGCCAGGGCAGGAGTATAACTTCTGAAGATGGAGCCTCAGGAGGTGGAGTCCCTGGGGGAGACCTATGACT
TCGACAGCATCATGCATTACGCTCGGAACACATTCTCCAGGGGCATCTTCTGGATAACATTGTCCCCAAGTATG
AGGTGAACGGGGTGAAACCTCCCATTGGCCAAAGGACACGGCTCAGCAAGGGGGACATTGCCCAAGCCCGCAAGC
TTTACAAGTGCCAGCCTGTGGAGAGACCCTGCAAGACAGCACAGGCAACTTCTCCTCCCCTGAATACCCCAATG
GCTACTCTGCTCACATGCCTGCGTGTGGCGCATCTCTGTACACCCGGGGAGAAGATCATCCTGAACCTTACGT
CCCTGGACCTGTACCGCAGCCGCCTGTGCTGGTACGACTATGTGGAGGTCCGAGATGGCTTCTGGAGGAAGGCGC
CCCTCCGAGGCCGCTTCTGCGGGTCCAACTCCCTGAGCCTATCGTCTCCACTGACAGCCGCCTCTGGGTTGAAT
TCCGCAGCAGCAGCAATTGGGTTGGAAAGGGCTTCTTTGAGTCTACGAAGCCATCTGCGGGGTGATGTGAAAA
AGGACTATGGCCACATTCAATCGCCCACTACCCAGACGATTACCGGCCAGCAAAGTCTGCATCTGGCGGATCC
AGGTGTCTGAGGGCTTCCACGTGGGCCTCACATTCCAGTCTTTGAGATTGAGCGCCACGACAGCTGTGCCTACG
ACTATCTGGAGGTGCGCGACGGGCACAGTGAGAGCAGCACCCCTCATCGGGCGCTACTGTGGCTATGAGAAGCCTG
ATGACATCAAGAGCACGTCCAGCCGCCTCTGGCTCAAGTTCTGTCTCTGACGGGTCCATTAACAAAGCGGGCTTTG
CCGTCAACTTTTTCAAAGAGGTGGACGAGTGTCTCTCGGCCAACCGCGGGGGCTGTGAGCAGCGGTGCCTCAACA
CCCTGGGCAGCTACAAGTGCAGCTGTGACCCCGGTACGAGCTGGCCCCAGACAAGCGCCGCTGTGAGGCTGCTT
GTGGCGGATTCTCACCAAGCTCAACGGCTCCATCACCAGCCCGGGCTGGCCCAAGGAGTACCCCCCAACAAGA
ACTGCATCTGGCAGCTGGTGGCCCCCACCAGTACCGCATCTCCCTGCAGTTTGACTTCTTTGAGACAGAGGGCA
ATGATGTGTGCAAGTACGACTTCGTGGAGGTGCGCAGTGGACTCACAGCTGACTCCAAGCTGCATGGCAAGTTCT
GTGGTTCTGAGAAGCCCGAGGTATCACCTCCCAGTACAACAACATGCGCGTGGAGTTCAAGTCCGACAACACCG
TGTCAAAAAGGGCTTCAAGGCCCACTTCTTCTCAGTCTTGGAGGGGGCAGGGGACCGACACTCACATCTATCAG
GCCTGGAGTTACTGCTCTGCCCCATGCCCTGGTTCGACACTGTGCCCCCCCCACCCTCAGCCCTGCACGGAGACA
CACACGCCCACACGCACACACATGTGCACACACATTGCCCATCGCACAAAGAACTGCAGAGGACCCCCACTGG
GGCATCGAGGCTCAGCCCTCAGGGCCCGGGCATCTGACTCTGGCCCCCAGGAGGGGAGCTATTTGGACTTTT
GGGACACCCACCGAGGAGACCCTAAGCCAAGAAGGAGAAGAAAGAGCCTGAAGACCTTCAGTCTGACCCCTGCCA
CCTTCCGGGGCATTGTTGGGCACTGTAGGAAAAAGAGGCCAGCTCTGCAGCCCCCTCGGGGACGCCCCACCAGCTCA
AATTCGAGTGCAGAAAAGAAACCGGACCCCCAGTGAGGCCTGCCAGGCCTCCCGGACCCCTTGTTACTCAGGA
ACCTCACCTTGGACGGAATGGGATGGGGCTTCGGTGCCACCAACCCCCACCTCCACTCTGCCATTCCGGCCC
ACCTCCCTCTGGCCGGACAGAACTGGTGCTCTTCTCTCCCACTGTGCCCCGTCCGCGGACCGGGGACCCCTTCCCC
GTGCCCTACCCCTCCCATTTTGATGGTGTCTGTGACATTTCTGTTGTGAAGTAAAAGAGGGACCCCTGCGTCC
TGC

2717/6881
FIGURE 2498

MPGVARLP LLLGLLLLPRPGRPLDLADYTYDLAEEDDSEPLNYKDPCKAAAF LGDIALDEEDLRAFQVQQAVDLR
RHTARKSSIKAAVPGNTSTPSCQSTNGQPQORGACGRWRGRSRSRRAATSRPERVWPDGVIPFVIGGNFTGSQRAV
FRQAMRHWEKHTCVTFLERTDEDSYIVFTYRPGCCSYVGRRGGGPQAISIGKNCDKFGIIVVHELGHVVGFWHEH
TRPDRDRHVSIVRENIQPGQEYNFLKMEPQEVESSLGETYDFDSIMHYARNTFSRGIFLDTIVPKYEVNGVKPPIG
QRTLSKGDIAQARKLYKCPACGETLQDSTGNFSSPEYPNGYSAHMHCVWRISVTPGEKIILNFTSLDLYRSRLC
WYDYVEVRDGFWRKÄPLRGRFCGSKLPEPIVSTDSRLWVEFRSSSNWVGKGGFAVYEACGGDVKKDYGHIQSPN
YPDDYRPSKVCIWRIQVSEGFHVGLTFQSFEIERHDSAYDYLEV RDGHSESSTLIGRYCGYEKPDDIKSTSSRL
WLKFVSDGSINKAGFAVNFFKEVDECSRPNRGGCEQRCLNTLGSYKCSCDPGYELAPDKRRCEAACGGFLTKLNG
SITSPGWPKEYPPNKNCIWQLVAPTQYRISLQDFFETEGNDVCKYDFVEVRSGLTADSKLHGKFCGSEKPEVIT
SQYNNMRVEFKSDNTVSKKGFKAHFFSVLEGAGDRHSHLSGLELLLCPHALVDTVPAPPSALHGDTHAHTHTHVH
THCPIAQETCRGPPLGASRLSPQGPGLTLAPQEGSYLDFWDTHRGDPKPRRRRKSLKTFSLTPATFRGIWAL

FIGURE 2499

TGGCTCCAGCTCACTAGGCCGATCTCTGCTGTGCCCCCGAGCTGCTCCCTTTTCTGACCTCCCAGGACCGCCCTT
CCCTGAACTGCTTTCCCTGAGTCCCTTATTCCCGCTCACTCCCTCTTGAGGACCTTGGCCTGTTTATTGTCAGA
GAAGATAGAAATGGCCACACTTATGACCCCTTAGCTCCCCCACTCCTCCCTACAGGCCACCCCTGAGGACACCC
AGGCCACCCTGCCTCCTCCCGTCCGCCCCAGAGGGACCAGACACAGGTCCCTGAGCCTTGGGGAGTCCACAGGCT
CCCCATCTTCTCCTTACTGCATCTCAGCCACATCTCAGCCCTTCCCCATGGCAGGGGCTCCCCGCAGACGATGC
CACCTTCTTGTCCCCGCAGCTGCTTGTGGCGGATTCTCACCAGCTCAACGGCTCCATCACCAGCCCGGGCTG
GCCCAAGGAGTACCCCCCAACAAGAACTGCATCTGGCAGCTGGTGGCCCCCACCAGTACCGCATCTCCCTGCA
GTTTGACTTCTTTGAGACAGAGGGCAATGATGTGTGCAAGTACGACTTCGTGGAGGTGCGCAGTGGACTCACAGC
TGACTCCAAGCTGCATGGCAAGTTCTGTGGTTCTGAGAAAGCCCGAGGTATCACCCTCCAGTACAACAACATGCG
CGTGGAGTTCAAGTCCGACAACACCGTGTCCAAAAAGGGCTTCAAGGCCACTTCTTCTCAGAAAAGAGGCCAGC
TCTGCAGCCCCCTCGGGGACGCCCCACCAGCTCAAAATCCGAGTGCAGAAAAGAAACCGGACCCCCCAG

2719/6881
FIGURE 2500

MPGVARLP LLLGLLLLPRPGRPLDLADYTYDLAEEDDSEPLNYKDPCKAAAF LGDIALDEEDLRAFQVQQAVDLR
RHTARKSSIKAAVPGNTSTPSCQSTNGQPQRGACGRWRGRSRSRRAATSRPERVWPDGVIPFVIGGNFTGSQRAV
FRQAMRHWEKHTCVTFLERTDEDSYIVFTYRPGCCSYVGRRGGGPQAISIGKNCDKFGIVVHELGHVVGFWHEH
TRPDRDRHVSIVRENIQPGQEYNFLKMEPQEVEESLGETYDFDSIMHYARNTFSRGIFLDTIVPKYEVNGVKPPIG
QRTLSKGDIAQARKLYKCPACGETLQDSTGNFSSPEYPNGYSAHMHCVWRISVTPGEKIILNFTSLDLYRSRLC
WYDYVEVRDGFWRKAPLRGRFCGSKLPEPIVSTDSRLWVEFRSSSNWVGKGGFAVYEAI CGGDVKKDYGHIQSPN
YPDDYRPSKVCIWRIQVSEGFHVGLTFQSFEIERHDS CAYDYLEVRDGHSESSTLIGRYCGYEKPDDIKSTSSRL
WLKFVSDGSINKAGFAVNFFKEVDECSRPNRGGCEQRCLNTLGSYKCSCDPGYELAPDKRRCEGCYDLQVGKPLL
WDRHCFRLSTHGPEMLGTALRG

2720/6881
FIGURE 2501

GCCAGC**ATG**CCCCGGCGTGGCCCCGCTGCCGCTGCTGCTCGGGCTGCTGCTGCTCCCCGCGTCCCGGCCGGCCGCTG
GACTTGGCCGACTACACCTATGACCTGGCGGAGGAGGACGACTCGGAGCCCCCTCAACTACAAAGACCCCTGCAAG
GCGGCTGCCTTTCTTGGGGACATTGCCCTGGACGAAGAGGACCTGAGGGCCTTCCAGGTACAGCAGGCTGTGGAT
CTCAGACGGCACACAGCTCGTAAGTCCTCCATCAAAGCTGCAGTTCCAGGAAACACTTCTACCCCCAGCTGCCAG
AGCACCAACGGGCAGCCTCAGAGGGGAGCCTGTGGGAGATGGAGAGGTAGATCCCGTAGCCGGCGGGCGGGCGACG
TCCCGACCAGAGCGTGTGTGGCCCCGATGGGGTCATCCCCTTTGTTCATTGGGGGAAACTTCACTGGTAGCCAGAGG
GCAGTCTTCCGGCAGGCCATGAGGCACTGGGAGAAGCACACCTGTGTACCTTCCTGGAGCGCACTGACGAGGAC
AGCTATATTGTGTTACCTATCGACCTTGGCGGTGCTGCTCCTACGTGGGTCGCCGCGGGCGGGGGCCCCCAGGCC
ATCTCCATCGGCAAGAACTGTGACAAAGTTCGGCATTGTGGTCCACGAGCTGGGCCACGTCGTCGGCTTCTGGCAC
GAACACACTCGGCCAGACCGGGACCGCCACGTTTCCATCGTTTCGTGAGAACATCCAGCCAGGCGTTCTCCACTCT
TCACTGCTCCTTCTCAGCTGTGGCTCTAGAAATGGTGCTTCCCTCCCATGTTCCCTTGAGTCCTCCACTCACCAG
GCCCTCTGCTGGACAGGACTCTTCCCTCAGACCCTCCCCATTCCCCAGGCTCCCCTTGGCTGCTCCCGGACCCCTC
AGGGCAGGAGTAT**TAA**CTTCTCTGAAGATGGAGCCTCAGGAGGTGGAGTCCCTGGGGGAGACCTATGACTTCGACAG
CATCATGCATTACGCTCGGAACACATTCTCCAGGGGCATCTTCCCTGGATACCATTTGTCCCCAAGTATGAGGTGAA
CGGGGTGAAACCTCCCATTGGCCAAAGGACACGGCTCAGCAAGGGGGACATTGCCCAAGCCCGCAAGCTTTACAA
GTGCCCAGCCTGTGGAGAGACCCTGCAAGACAGCACAGGCAACTTCTCCTCCCCTGAATACCCCAATGGCTACTC
TGCTCACATGCACTGCGTGTGGCGCATCTCTGTACACCCGGGGAGAAGATCATCCTGAACCTTACGTCCCTGGA
CCTGTACCGCAGCCGCCTGTGCTGGTACGACTATGTGGAGGTCCGAGATGGCTTCTGGAGGAAGGCGCCCCCTCCG
AGGGCCCAACACTGGCCAGGGATGACAACCTGGTATGGGAGCCAGGAGTCCCTGGCATCATTAGTCCCAGATAGCT
GCATTACTCACTTGCTGCGAGACTTCAGGCCGCTTCTGCGGGTCCAACTCCCTGAGCCTATCGTCTCCACTGAC
AGCCGCCTCTGGGTGGAATTCCGCAGCAGCAGCAATTGGGTTGGAAAGGGCTTCTTTGCAGTCTACGAAGCCATC
TGCGGGGGTGATGTGAAAAAGGACTATGGCCACATTCAATCGCCCAACTACCCAGACGATTACCGGCCAGCAAA
GTCTGCATCTGGCGGATCCAGGTGTCTGAGGGCTTCCACGTGGGCCTCACATTCCAGTCCTTTGAGATTGAGCGC
CACGACAGCTGTGCCTACGACTATCTGGAGGTGCGCGACGGGCACAGTGAGAGCAGCACCCCTCATCGGGCGCTAC
TGTGGCTATGAGAAGCCTGATGACATCAAGAGCACGTCCAGCCGCCTCTGGCTCAAGTTCGTCTCTGACGGGTCC
ATTAACAAAGCGGGCTTTGCCGTCAACTTTTTCAAAGAGGTGGACGAGTGCTCTCGGCCCAACCGCGGGGGCTGT
GAGCAGCGGTGCCTCAACACCCTGGGCAGCTACAAGTGCAGCTGTGACCCCGGGTACGAGCTGGCCCCAGACAAG
CGCCGCTGTGAGGCTGCTTGTGGCGGATTCTCACCAGCTCAACGGCTCCATCACCAGCCCGGGCTGGCCCAAG
GAGTACCCCCCAACAAGAACTGCATCTGGCAGCTGGTGGCCCCCACCAGTACCGCATCTCCCTGCAGTTTGAC
TTCTTTGAGACAGAGGGCAATGATGTGTGCAAGTACGACTTCGTGGAGGTGCGCAGTGGAATCACAGCTGACTCC
AAGCTGCATGGCAAGTTCTGTGGTTCTGAGAAGCCCGAGGTATCACCTCCCAGTACAACAACATGCGCGTGGAG
TTCAAGTCCGACAACACCGTGTCCAAAAAGGGCTTCAAGGCCCACTTCTTCTCAGAAAAGAGGCCAGCTCTGCAG
CCCCCTCGGGGACGCCCCACCAGCTCAAATTCCGAGTGCAGAAAAGAAACCGGACCCCCCAG

2721/6881
FIGURE 2502

MPGVARLP LLLGL LLLPRPGRPLDLADYTYDLAEEDDSEPLNYKDPCKAAAF LGDIALDEEDLRAFQVQQAVDLR
RHTARKSSIKAAVPGNTSTPSCQSTNGQPORGACGRWRGRSRSRRAATSRPERVWPDGVIPFVIGGNFTGSQRAV
FRQAMRHWEKHTCVTFLE RTDEDSYIVFTYRPCGCCSYVGRRG GGPQAISIGKNCDKFGIVVHELGHVVGFWHEH
TRPD RDRHVSIVRENIQPGVLHSS LLLSCGSRNGASFPCSLESSTHQALCWTGLFLRPSFPRLPLAAPRTLRA
GV

2722/6881
FIGURE 2503

GCAAGCCGGAGCCCTGGGGTTGGGCAGCACTCGGTTCCGTGCAACTTTCAAGTGAGTTGCGAACTCCGCCCTGTA
GGCCGGTGCTGGTGGCCCGGCGCGCTGGAACCGCGGCGACCCGCTCCAGCGCGGGACCAGCAGCAAGGGCCGAGC
GCCAGGTTCTCCGCGGCAGAAAGGGCGGGTGGGAGCTGTAACTGCCCCGGCCGCGGGGCGCGCCCGCTCCCAAGT
CGGCTTCCTCCCCGCCGGGGCCGCTTTGCCTCGGGTCTCCCCATTCTCCAGGTCCCCTGAACTGCACAGTCGGAG
GCCGTGGGCGGCGGGCTCTGCCTCCGCCGAGGGACAGCCGGATCGCCCCCTCTGCTTCCCGCAACTGCCCTGATCA
CCCCCGTCCCAGCCCTTGAGTGAACGTCCTTCTGAGCGGCTTCCTGGGGTCTCCCCACGTCCCAAAGGCCGGC
AAGATGGTGTCTCTGGATGATCTGTTCGCTGGTGGTGTGGTGTGGGATGCTGTGTCCAGCTTATGCTTCCTAT
AAGGCTGTGAAGACCAAGAACATTCTGTAATATGTGCGGTGGATGATGTACTGGATTGTTTTTGCACTCTTCATG
GCAGCAGAGATCGTTACAGACATTTTTATCTCTCTGGTTCCCTTTCTACTATGAGATCAAGATGGCCTTCGTGCTG
TGGCTGCTCTCACCTACACCAAGGGCGCCAGCCTGCTTTACCGCAAGTTTGTCCACCCGTCCCTGTCCCGCCAT
GAGAAGGAGATCGACGCGTACATCGTGCAGGCCAAGGAGCGCAGCTACGAGACCGTGCTCAGCTTCGGGAAGCGG
GGCCTCAACATTGCCGCTCCGCTGCTGTGCAGGCTGCCACCAAGAGTCAGGGGGCGCTGGCCGGCAGGCTGCGG
AGCTTCTCCATGCAGGACCTGCGCTCCATCTCTGACGCACCTGCCCCTGCTTACCATGACCCCTCTACCTGGAG
GACCAGGTGTCCACCGGAGGCCACCCATTGGGTACCGGGCCGGGGCCCTGCAGGACAGCGACACCGAGGATGAG
TGTTGGTCAGATACTGAGGCAGTCCCCCGGGCGCCAGCCCGCCCCGAGAGAAGCCCCTAATCCGCAGCCAGAGC
CTGCGTGTGGTCAAGAGGAAGCCACCGGTGCGGGAGGGCACCTCGCGCTCCCTGAAGGTTTCGGACGAGGAAAAAG
ACTGTGCCCTCAGACGTGGACAGCTAGGGTCTGCTGCATCTGCCCCCTTCTTACCTCGTGCCTTCAGGGCTCCA
GGGCTATTTGGAGGGACCTTGGGCTGCACATCTGGCCTGCCTGCACCAGCTGCCTGGGCCCCACCTCCTGACTC
CTGCTGATGGTTAAGGGCCGGGAGCAGATGCTGCCAAGGCCACATGCAGGGATGCACCCACAATGTACCAAAGCA
GGCTGGGCCCAGGGTTCTATTTATTGCCTTGCTCTGCCCTCTCCCTTCCCCGGTTGTGGGACAAGAGCCCTCCCT
GAACCCCTGCAACCCCTCCCTGAACCCCTGCAAATGAAACCAAACGTCCACCTGGGTGTGTTTATTCCTTCCTGTC
CTTCAAAGTACTTGATAGCCTTTTATAAGGCCTGGCACATGTGTCCTGGTTGTGTGTGTGTGTGTGTTGGTGAGTGA
GGTCAGGTTTGCAGTGTTTTGATAAATAAATACATAAAGGGGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAA

2723/6881
FIGURE 2504

MVSWMICRLVVLVFGMLCPAYASYKAVKTKNIREYVRWMMYWIVFALFMAAEIVTDIFISWFFFYIEIKMAFVLW
LLSPYTKGASLLYRK FVHP SLRHEKEIDAYIVQAKERSYETVLSFGKRGLNIAASA AVQAATKSQ GALAGRLRS
FSMQDLRSISDAPAPAYHDPLYLEDQVSHRRPPIGYRAGGLQDSDTEDECWSDTEAVPRAPARPREKPLIRSQSL
RVVKKRKPPVREGTSRSLKVRTRKKTVP SDVDS

2724/6881
FIGURE 2505

GACTGCAATGTGCCGATCTTAGCTGCTGCCTGAGAGGATGTCTGGGGTGTCCGAGCCCCTGAGTCGAGTAAAGTT
GGGCACGTTACGCCGGCCTGAAGGCCCTGCAGAGCCCATGGTGGTGGTACCAGTAGATGTGGAAAAGGAGGACGT
GCGTATCCTCAAGGTCTGCTTCTATAGCAACAGCTTCAATCCTGGGAAAACTTCAAACCTGGTCAAATGCACTGT
CCAGACGGAGATCCGGGAGATCATCACCTCCATCCTGCTGAGCGGGCGGATCGGGCCCCAACATCCGGTTGGCTGA
GTGCTATGGGCTGAGGCTGAAGCACATGAAGTCCGATGAGATCCACTGGCTGCACCCACAGATGACGGTGGGTGA
GGTGCAGGACAAGTATGAGTGTCTGCACGTGGAAGCCGAGTGGAGGTATGACCTTCAAATCCGCTACTTGCCAGA
AGACTTCATGGAGAGCCTGAAGGAGGACAGGACCACGCTGCTCTATTTTTTACCAACAGCTCCGGAACGACTACAT
GCAGCGCTACGCCAGCAAGGTCAGCGAGGGCATGGCCCTGCAGCTGGGCTGCCTGGAGCTCAGGCGGTTCTTCAA
GGATATGCCCCACAATGCACTTGACAAGAAGTCCAACTTCGAGCTCCTAGAAAAGGAAGTGGGGCTGGACTTGTT
TTTCCCAAAGCAGATGCAGGAGAACTTAAAGCCCAAACAGTTCCGGAAGATGATCCAGCAGACCTTCCAGCAGTA
CGCCTCGCTCAGGGAGGAGGAGTGCCTCATGAAGTTCTTCAACACTCTCGCCGGCTTCGCCAACATCGACCAGGA
GACCTACCGCTGTGAACTCATTCAAGGATGGAACATTACTGTGGACCTGGTCATTGGCCCTAAAGGGATCCGCCA
GCTGACTAGTCAGGACGCAAAGCCCACCTGCCTGGCCGAGTTCAAGCAGATCAGGTCCATCAGGTGCCTCCCGCT
GGAGGAGGGCCAGGCAGTACTTCAGCTGGGCATTGAAGGTGCCCCCAGGCCTTGTCCATCAAACCTCATCCCT
AGCAGAGGCTGAGAACATGGCTGACCTCATAGACGGCTACTGCCGGCTGCAGGGTGAGCACCAGGCTCTCTCAT
CATCCATCCTAGGAAAGATGGTGAGAAGCGGAACAGCCTGCCCCAGATCCCATGCTAAACCTGGAGGCCCCGGCG
GTCCACCTCTCAGAGAGCTGCAGCATAGAGTCAGACATCTACGCAGAGATTCCCGACGAAACCCTGCGAAGGCC
CGGAGGTCCACAGTATGGCATTGCCCGTGAAGATGTGGTCTCTGAATCGTATTCTTGGGGAAGGCTTTTTTGGGGA
GGTCTATGAAGGTGTCTACACAAATCACAAAGGGGAGAAAATCAATGTAGCTGTCAAGACCTGCAAGAAAGACTG
CACTCTGGACAACAAGGAGAAGTTCATGAGCGAGGCAGTGATCATGAAGAACCTCGACCACCCGCACATCGTGAA
GCTGATCGGCATCATTGAAGAGGAGCCACCTGGATCATCATGGAATTGTATCCCTATGGGGAGCTGGGCCACTA
CCTGGAGCGGAACAAGAACTCCCTGAAGGTGCTCACCTCGTGCTGTACTCACTGCAGATATGCAAAGCCATGGC
CTACCTGGAGAGCATCAACTGCGTGCACAGGGACATTGCTGTCCGGAACATCCTGGTGGCCTCCCCTGAGTGTGT
GAAGCTGGGGGACTTTGGTCTTTCCCGGTACATTGAGGACGAGGACTATTACAAAGCCTCTGTGACTCGTCTCCC
CATCAAATGGATGTCCCCAGAGTCCATTAACCTCCGACGCTTCACGACAGCCAGTGACGTCTGGATGTTCCCGCT
GTGCATGTGGGAGATCCTGAGCTTTGGGAAGCAGCCCTTCTTCTGGCTGGAGAACAAGGATGTCATCGGGGTGCT
GGAGAAAGGAGACCGGCTGCCCCAAGCCTGATCTCTGTCCACCGGTCTTTATACCCTCATGACCCGCTGCTGGGA
CTACGACCCCACTGACCGGCCCGCTTCACCGAGCTGGTGTGCAGCCTCAGTGACGTTTATCAGATGGAGAAGGA
CATTGCCATGGAGCAAGAGAGGAATGCTCGCTACCGAACCCCCAAAAATCTTGGAGCCCACAGCCTTCCAGGAACC
CCCACCCAAGCCCAGCCGACCTAAGTACAGACCCCTCCGCAAACCAACCTCCTGGCTCCAAAGCTGCAGTTCCA
GGTTCCTGAGGGTCTGTGTGCCAGCTCTCCTACGCTCACCAGCCCTATGGAGTATCCATCTCCCGTTAACTCACT
GCACACCCACCTCTCCACCGGCACAATGTCTTCAAACGCCACAGCATGCGGGAGGAGGACTTCATCCAACCCAG
CAGCCGAGAAGAGGCCACAGCAGCTGTGGGAGGCTGAAAAGGTCAAAATGCGGCAAATCCTGGACAACAGCAGAA
GCAGATGGTGGAGGACTACCAGTGGCTCAGGCAGGAGGAGAAGTCCCTGGACCCCATGGTTTTATATGAATGATAA
GTCCCCATTGACGCCAGAGAAGGAGGTGCGCTACCTGGAGTTCACAGGGCCCCACAGAAGCCCCCGAGGCTGGG
CGCACAGTCCATCCAGCCCACAGCTAACCTGGACCGGACTGATGACCTGGTGTACCTCAATGTCATGGAGCTGGT
GCGGGCCGTGCTGGAGCTCAAGAATGAGCTCTGTGAGCTGCCCCCGAGGGCTACGTGGTGGTGAAGAATGT
GGGGCTGACCCTGCGGAAGCTCATCGGGAGCGTGGATGATCTCCTGCCTTCCTTGCCGTATCTTCACGGACAGA
GATCGAGGGCACCCAGAACTGCTCAACAAAGACCTGGCAGAGCTCATCAACAAGATGCGGCTGGCACAGCAGAA
CGCCGTGACCTCCCTAAGTGAGGAGTGCAAGAGGCAGATGCTGACGGCTTCACACACCTGGCTGTGGACGCCAA
GAACCTGCTCGACGCTGTGGACCAGGCCAAGGTTCTGGCCAATCTGGCCCCACCCACCTGCAGAGTGACGGAGGGT
GGGGGCCACCTGCCTGCGTCTTCCGCCCTGCCTGCCATGTACCTCCCCTGCCTTGCTGTTGGTTCATGTGGGTCT
TCCAGGGGGAAGGCCAAGGGGAGTCACCTTCCCTTGCCACTTTGCACGACGCCCTCTCCCCACCCCTACCCCTGG
CTGTACTGCTCAGGCTGCAGCTGGACAGAGGGGACTCTGGGCTATGGACACAGGGTGACGGTGACAAAGATGGCT
CAGAGGGGGACTGCTGCTGCCTGGCCACTGCTCCCTAAGCCAGCCT

2725/6881
FIGURE 2506

GAATTCCGCCGCTGACCGAGGCGTGCAAAGACTCCAGAATTGGAGGCATGATGAAGACTCTGCTGCTGTTTGTGG
GGCTGCTGCTGACCTGGGAGAGTGGGCAGGTCTTGGGGACCAGACGGTCTCAGACAATGAGCTCCAGGAAATGT
CCAATCAGGGAAAGTAAGTACGTCAATAAGGAAATCAAAATGCTGTCAACGGGGTGAAACAGATAAAGACTCTCA
TAGAAAAAACAAACGAAGAGCGCAAGACACTGCTCAGCAACCTAGAAGAAGCCAAGAAGAAGAAAGAGGATGCCC
TAAATGAGACCAGGGAATCAGAGACAAAGCTGAAGGAGCTCCCAGGAGTGTGCAATGAGACCATGATGGCCCTCT
GGGAAGAGTGTAAGCCCTGCCTGAAACAGACCTGCATGAAGTTCTACGCACGCGTCTGCAGAAGTGCTCAGGCC
TGTTTGGCCGCCAGCTTGAGGAGTTCTTGAACCAGAGCTCGCCCTTCTACTTCTGGATGAATGGTGACCGCATCG
ACTCCCTGCTGGAGAACGACCGGCAGCAGACGCACATGCTGGATGTCATGCAGGACCACTTCAGCCGCGCGTCCA
GCATCATAGACGAGCTCTTCCAGGACAGGTTCTTCAACCGGGAGCCCCAGGATACCTACCACTACCTGCCCTTCA
GCCTGCCCCACCGGAGGCCTCACTTCTTCTTTCCCAAGTCCCGCATCGTCCGCAGCTTGATGCCCTTCTCTCCGT
ACGAGCCCCTGAACTTCCACGCCATGTTCCAGCCCTTCTTGAGATGATACACGAGGCTCAGCAGGCCATGGACA
TCCACTTCCACAGCCCCGGCCTTCCAGCACCCGCCAACAGAATTCATACGAGAAGGCGACGATGACCGGACTGTGT
GCCGGGAGATCCGCCACAACCTCCACGGGTGCCTGCGGATGAAGGACCAGTGTGACAAGTGCCGGGAGATCTTGT
CTGTGGAAGTGTTCACCAACAACCCCTCCCAGGCTAAGCTGCGGCGGGAGCTCGACGAATCCCTCCAGGTGCTG
AGAGGTTGACCAGGAAATACAACGAGCTGCTAAAGTCCTACCAGTGGAAGATGCTCAACACCTCCTCCTTGCTGG
AGCAGCTGAACGAGCAGTTTAACTGGGTGTCCCGGCTGGCAAACCTCACGCAAGGCGAAGACCAGTACTATCTGC
GGGTACACACGGTGCTTCCCACACTTCTGACTCGGACGTTCTTCCGGTGTCACTGAGGTGGTCTGTGAAGCTCT
TTGACTCTGATCCCATCACTGTGACGGTCCCTGTAGAAGTCTCCAGGAAGAACCCTAAATTTATGGAGACCGTGG
CGGAGAAAGCGCTGCAGGAATACCGCAAAAAGCACCGGGAGGAGTGAATGTGGATGTTGCTTTTGACCTTACG
GGGGCATCTTGAGTCCAGCTCCCCCAAGATGAGCTGCAGCCCCCAGAGAGAGCTCTGCACGTACCAAGTAAC
CAGGCCCCAGCCTCCAGGCCCCCAACTCCGCCCAGCCTCTCCCCGCTCTGGATCCTGCACTCTAACACTCGACTC
TGCTGCTCATGGGAAGAACAGAATTGCTCCTGCATGCAACTAATTCAATAAACTGTCTTGTGAGCTGAAAAAA
AAAAAAAAAAAAAAAAAAGGAATTC

2726/6881
FIGURE 2507

MMKTLLLFVGLLLTWESGQVLGDQTVSDNELQEMSNQGSKYVNKEIQNAVNGVKQIKTLIEKTNEERKTLLSNLE
EAKKKKEDALNETRESETKLKELPGVCNETMMALWEECKPCLKQTCMKFYARVCRSGSLVGRQLEEFNLNQSSPF
YFWMNGDRIDSLENDRQQTHMLDVMQDHFSRASSIIDELFQDRFFTREPQDTYHYLPFSLPHRRPHFFFPKSRI
VRSLMPFSPYEPLNFHAMFQPFLEMIHEAQQAMD IHFHSPAFOHPPTFEFIREGDDDRTVCREIRHNSTGCLRMKD
QCDKCREILSVDCSTNNPSQAKLRRELDDESLOVAERLTRKYNELLKSYQWKMLNTSSLLEQLNEQFNWVSRLANL
TQGEDQYYLRVTTVASHTSDSDVPSGVTEVVVKLFDSDPITVTVPVEVSRKNPKFMETVAEKALQEYRKKHREE